Minimal Sampling Criteria and Method for Nonmanifold Surface Reconstruction from Unorganized Points

Dissertation

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Leonid Tcherniavski

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Prof. Dr.-Ing. Hans-Siegfried Stiehl Dr. Peer Stelldinger Prof. Dr. Jianwei Zhang

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To Natalya, Paulina and Alyosha Für Natalja, Paulina und Alöscha Наталье, Паулине и Алёше

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Abstract

Surface reconstruction traditionally deals with the problem to reconstruct the outer boundary of a real world object from a set of boundary sampling points. The interior of the object is not relevant. In case of topology preserving surface reconstruction, the topological equivalence between the outcome of the method and the original object is guaranteed. The framework on topology preserving surface reconstruction answers three questions: First, what are the requirements on the shape of the real world object and how does it have to be sampled? Second, if these requirements are fulfilled, how to define an algorithm to reconstruct the surface. Third, can it be proved that the outcome of the reconstruction is topologically equivalent to the original?

Our research question extends the topology preserving surface reconstruction problem by assumption that several objects of the real world are given, i.e. the interior of the real world objects can consist of several regions with common boundary, and the sampling conditions of each object and its interior regions may vary. We generalize the surface reconstruction problem to a reconstruction of non-manifold boundary of multiple regions with guaranteed preservation of topological properties.

Recently a method called " (α, β) -shape reconstruction" was presented which — given a set of unorganized sample points — results in a topologically correct mesh representation of the original boundary. However the approach requires globally uniform sampling density for each point of the boundary and both the sampling density parameters and the maximum sample point deviation have to be known during the reconstruction process.

In our work we first theoretically and experimentally evaluate " (α, β) -shape reconstruction" and compare the method with related work.

Our main contribution is a framework for non-manifold boundary reconstruction of multi-regional real world scene with locally variable sampling conditions which provably preserves original topological properties. Founded on our new shape descriptor we define for each point of the original boundary a locally variable feature size which is nonzero even in the non-manifold and non-smooth points. Using the new feature size we define locally variable sampling conditions. The can be seen as an extension of the reconstruction method "Geomagic WRAP[©]". We prove that our reconstruction method results in a refinement of the original boundary which can provably be reduced to a topologically correct reconstruction.

The evaluation of our new framework consists of theoretical proofs, generalizations of sampling criteria to compare the results with related work, extensive discussion and experimental results on laser range scanner and computer tomography data. Based on our new shape descriptor we propose a method to estimate the original feature size on sampling points and use this as a criterion for data set decimation. The resulting data set is a very sparse, adaptively sampled set of points which is guaranteed to be correctly reconstructed by our algorithm, while the other related reconstruction methods fail.

Zusammenfassung

Oberflächenrekonstruktion beschäftigt sich traditionellerweise mit der Rekonstruktion der äußeren Hülle eines realen Objektes. Das Innere des Objektes ist irrelevant. Im Falle der topologieerhaltenden Oberflächenrekonstruktion wird die topologische Äquivalenz zwischen dem Resultat des Algorithmus und dem Original garantiert. Es sind drei Fragen im Rahmen der topologieerhaltenden Oberflächenrekonstruktion zu beantworten. Erstens: Welche Anforderungen an die Form des realen Objektes müssen erfüllt sein, und wie soll sie abgetastet werden? Zweitens: Wenn diese Anforderungen erfüllt sind, wie definiert man einen Rekonstruktionsalgorithmus? Drittens: Kann man beweisen, dass das Resultat der Rekonstruktion topologisch äquivalent zu dem Original ist?

Wir erweitern die Fragestellung der topologieerhaltenden Oberflächenrekonstruktion durch die Annahme, dass auch das Innere des Objektes relevant ist, und, dass es aus mehreren aneinandergrenzenden Regionen bestehen kann. Weiterhin nehmen wir an, dass die Abtastbedingungen lokal variieren können.

Der Hauptbeitrag unserer Arbeit ist die Definition und Evaluation eines Rekonstruktionsverfahrens und der Abtastbedingungen, unter denen das Ergebnis des Algorithmus nicht-mannigfaltige Oberflächen von multiplen Regionen rekonstruiert und garantiert, dass ursprüngliche topologische Eigenschaften in der Rekonstruktion erhalten bleiben.

Unsere neue lokal adaptive Abtastbedingung basiert auf einer Untermenge der medialen Achse, die wir "Homotopie Achse" nennen. Das Rekonstruktionsverfahren kann als eine Erweiterung des bekannten "Geomagic WRAP[©]" angesehen werden. Wir beweisen, dass das Resultat unseres Rekonstruktionsverfahrens eine Verfeinerung der ursprünglichen Oberfläche ist.

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Chapter 1

Introduction

Dot-to-Dot The game "Dot-to-Dot" is known to us since our childhood. The task is to connect the numbered dots. The solution is of course to connect each dot with a dot labelled with the subsequent number. The more challenging question is how to connect the dots if no numbers are given.

The aim of the game is to recognize some underlying shape by *drawing* its contour. That means that we assume an *object of the real world* whose shape is *similar* to the outline we draw. In geometric terms, "drawing" or "connecting dots" corresponds to *approximation* of a contour and "similarity" implies correspondence of properties. From the geometric point of view such correspondence is given if the approximated contour does not *deviate* much from the original. So, e.g. the solid circle is similar to the broken circle, if the interruptions in the drawing line are small enough. The similarity in topology stipulates equivalent *connectivity* of contours. That means that the solid outline of a triangle is *topologically equivalent* e.g. to the solid outline of a circle.

In our general case the dots are distributed in space. In geometry the notation for a dot with coordinates is *point*. No adjacency relation between points is given. In other words they are *unorganized*. But we assume some kind of distribution which allows us to connect the correct points and achieve the expected similarity. Consequently, we assume the distribution of the points to represent the original object. In other words the points contain certain information of the original shape. This information is hidden since only points are given. Our task is to *reconstruct* this information from a set of points.

The question remains open how to place the points to make it obvious which points to connect. Since it is the contour we want to draw and recognize or, as we call it now, reconstruct, the points have to be placed somewhere on or near the contour of the original shape. Obviously, the denser the points and the less their deviation from the original contour the more accurate is the reconstruction. So, we need to investigate what minimal density of points is necessary and what maximal deviation from the original is tolerable to reconstruct the original properties.

Contour Reconstruction In digital geometry *contour reconstruction* is a well studied subject. The proposed methods provide good results depending on the density of points and their deviation from the boundary. But the research question on how to *guarantee* to preserve the properties of the original object in the points is still open.

The solutions to the problem on how to preserve topological properties of the original object restrict the original contour to *manifolds*. A manifold is a contour which does not touch or cut itself. Furthermore the connectivity of the contour is often only guaranteed to be preserved if the original contour is *smooth* ie. does not contain corners. The topology is only reconstructible under the necessary condition of very high point density and very small deviation from the original contour.

Further theoretical and computational difficulties occur when the points are scattered in three dimensional space. The task here is to reconstruct a surface.

Surface Reconstruction In general the surfaces considered in surface reconstruction are assumed to be *two-manifolds*. Simply speaking the surface does not cut or touch itself. In more mathematical terms, the neighborhood of each point on the original surface has to be *continuously deformable* to a disc.

The closed two-manifold surface separates the space into foreground and background. The foreground is the interior of the three dimensional object and the background is the space around it. We speak of *binary partition of the space*. Such a restriction ignores the inner structure of the object. For example, the reconstruction of a human body delivers the geometrical properties on the skin but gives no information of the interior, e.g. bones. The reconstruction of the human body is then hollow.

Boundary Reconstruction If the interior of the three dimensional object is of interest then it is assumed that the interior of the object is subdivided into more than one cavity or, in terms of geometry, *region*. Since the infinite environment around the considered object can also be seen as an infinite region, we understand the world as a partition of the space into regions. The task now is to reconstruct the boundaries between the regions or, more generally, to reconstruct the *boundary of the space partition*.

In the human body example the boundary reconstruction is thus no longer hollow but additionally contains the inner structures like representations of skeletal, organ or vascular systems.

Sampling Points In our framework a set of points is the initial state of the reconstruction task. Why is it justified?

Obviously, our interest is to use a computer to process and analyze objects of the real world. So, the question is how to transform a physical object into digital data. This is done by some capturing device which collects *sensory data*. This process involves *sampling* of the object and *quantizing* the continuous measurement values e.g. intensities. The result is a finite set of *sampling points* with discrete intensity values representing some physical property.

The sensor for a three dimensional sampling can be of arbitrary type, e.g. the points could be acquired directly by a 3D laser range scanner, a time-of-flight camera, or a low-cost 3D scanning device like "Microsoft Kinect", but it could also be extracted from multiple 2D images using shape from stereo and wide baseline matching (see e.g. bundler in [Snavely et al., 2006]), or the points could be extracted from CT or MRT by using algorithms like the 3D canny edge detector in [Bähnisch et al., 2009].

1.1 Motivation

Depending on the kind of data acquisition different methods have been proposed to digitize the object properties. We distinguish between *surface based* and *volume base* digitization methods.

Surface based digitization methods are used if only the outer surface of the object is of interest. The corresponding techniques are based on the principle of 3D scene projection onto the image plane of a camera. Consequently, the data can only be acquired from points where the projection line meets the scene, or, simply speaking, which can be "seen" by the camera. Since not every point in 3D space can be sampled the data are said to be *two-and-a-half-dimensional* (2.5D). The typical sensor technologies are laser range scanners, structural light scanners and time-of-flight camera systems. But also the data acquired by multiple 2D images deliver a 2.5D data of the scene. Shape from shading, shape from stereo or wide-baseline matching are the typical examples of these techniques.

In contrast to surface-based methods, the volume-based methods are able to "see" through the object and so to sample the scene at any point in space. The 3D interval containing the object of interest is sampled, for example, with a regular grid. The typical examples are X-ray computed tomography (CT) and magnetic resonance imaging (MRI). The interior of the object can be subdivided into two and more regions which can have common boundaries. If three or more regions meet in one point then

1.2. RESEARCH QUESTION

the boundary of at least one of the regions will necessarily have a sharp corner on this point. The reconstruction methods which are used to find a correct representation of such multiregional objects must be able to handle non-smooth and non-manifold boundaries.

Digital representations of real world objects become increasingly important in a growing range of applications like medical science (computer-assisted-surgery), structural biology (protein folding simulation), robotics (navigation planning), engineering (reverse engineering), finite-element-simulation (fiber segmentation from fiber networks) or human-machine-interfaces (gaming).

The representation, visualization and analysis of the digitized objects is based upon constructing surfaces from the acquired data. The methods to process the sensory data differ according to the acquisition methods. Surface-based methods result in surface approximations which separate the interior of an object from its background. Volume-based methods classify each point of the space as interior or exterior of the object. In the first case, the reconstruction encloses the interior of the object and, in the second case, the reconstructed interior is bounded by the object boundary. So, we can infer the properties of the one from the properties of the other. Therefore, we speak of the *duality* between the two reconstruction approaches.

Surface reconstruction approaches from finite point sets have been designed to process scan data delivering depth information in the form of 3D coordinates. Depth information can also be extracted from other sensory data like multiple imaging. Because of the duality between the surface-based and volume-based approaches, surface reconstruction methods can be used to construct an object representation from volume data.

Early approaches constructed a surface without giving guarantees on correctness of the reconstruction. The goal of later research was reconstruction methods which under certain conditions guarantee the result to preserve certain topological properties of original object.

The *topological correctness* is crucial e.g. in medical applications where the automated or semiautomated diagnostic system depends on the digital model of the patient, and the further treatment obviously depends on the quality of diagnosis. For example, a surgeon analyzing the structure of blood vessels in order to find mechanical damage must rely on the correctness of the model. Another example is in using finite element methods to simulate surface tension. Topologically incorrect reconstruction may result e.g in a surface with holes or add non-manifold branches which is fatal for further simulation of surface tension.

Topological guarantees of early methods could only be given for very densely sampled smooth manifold surfaces. The approaches allowed either no or a very small amount of deviation of the sample points from the original boundary. We call this deviation *noise*. The smoothness condition implies that non-smooth parts of the surface like corners (e.g apex of a pyramid) and edges (e.g intersection of two faces of a cube) must theoretically be sampled with an infinite number of points which is obviously not practicable.

Consideration of the real world scene as shape subdivided into multiple regions with non-manifold boundary or highly noise-corrupted data remained an open problem for a long time. Only recent work on non-manifold boundary reconstruction (see [Stelldinger, 2008b]) solved the problem. But the topological correctness of the result can only be proven if the lowest sampling density is bounded by a known constant value and this value is equal on each point of the surface.

To our knowledge no reconstruction method has been proposed to result under guarantee in a topologically correct non-manifold surface if the sampling densities vary on the surface.

1.2 Research Question

In our research, we extend the surface reconstruction problem to *boundary reconstruction* (see above for terminology). In such a way we expand the range of considerable shapes to *non-manifold boundaries* of space partitions. To make our statements provable we define sampling conditions depending on an appropriate feature size. A feature is a distinct property and a feature size is a function mapping every point on the original boundary to the measurement of this property at this point . Finally we define a

reconstruction method and prove that the result of this method preserves the topological properties if the given point set fulfills certain sampling conditions.

Problem Statement

The problem of surface reconstruction is not new and was tackled in numerous related works (i.e. in [Hoppe et al., 1992]). In our framework we focus on the following research question:

Let the original scene be the whole space and let the space be partitioned into a finite set of open sets called regions. Let the boundary of the set of regions be a - not necessarily manifold - 2D surface. Let the boundary be sampled by a finite set of points on or near the boundary. Under which conditions and with which method the boundary of the computed reconstruction of the original regions preserves the topological properties?

What is the *topologically correct* reconstruction? Let us consider a cross like the letter X. The topologically equivalent reconstruction would be again a cross like letter χ . But to guarantee such a reconstruction without prior knowledge of the shape we need to ensure a sample point exactly in the crossing point. This requirement is not possible to guarantee in any practical digitization method. So, we define:

Topological Correctness Consider again the space to be partitioned into a finite set of open sets called regions. Another space partition is *topologically correct* to the original if and only if its set of open sets is topologically equivalent to the original regions and the boundary of the second space partition is homotopy-equivalent to the original.

The definition weakens the condition on boundaries. In such a way the letter H is a topologically correct reconstruction of X, and B is a topology correct reconstruction of Φ . The space partitioned by the shape of the letters is in both cases topologically equivalent. But the letters H and B consist of "Y intersections" only, and X and Φ consist of "X-intersections", which makes the shapes not topology but homotopy-equivalent.

Related work on topology preserving surface reconstruction pursues the goal of topological correctness. But under weaker sampling conditions, like very sparse point density or large amount of noise, the outcome of the reconstruction methods is not predictable. Our interest is to investigate the outcome depending on sampling conditions and to give provable guarantees even if the result is not topologically correct. So, we have a weaker requirement on reconstruction. Hence we investigate the reconstruction result which is under guarantee *reducible* to a topologically correct object representation.

Reducible Refinement A second space partition is a *reducible refinement* of the original space partition if and only if there is a subset of the boundary of the second space partition such that the complement of the subset is a topologically correct space partition to the original.

An example is the space partition of the letter B. B is the boundary of two smaller regions and the infinite background. B is a reducible refinement of P. We can remove the bottom loop of B to obtain an equivalent to P.

Novelty The novelty of our research is the parameter-free reconstruction of non-smooth and even nonmanifold boundaries under the most weak sampling conditions, without any restrictions on the shape. Additionally, we propose the definition of the simplest representation of topological properties and its approximation.

1.3 Computational Geometry

The digitization process including the reconstruction step requires deep mathematical and technical understanding. Since a full coverage of details, e.g. as in a text book, would be beyond the scope of this

1.3. COMPUTATIONAL GEOMETRY

work, we attempt to be as self-contained as necessary.

The mathematical preliminaries required for following our framework can be divided into geometry as science of shape properties concerning the position in space, and topology as a science which is concerned with how things are connected. Further we differentiate between the original real world object assuming its surface and boundaries between its interior regions to be continuous, and the result of switching on the data acquisition device which we assume to acquire a set of points represented only by positions in space. As a consequence we have to separate the mathematics required for our work into four issues.

Topology

In Section 2.1 we begin with the topology basics. Here we are interested in the definition of connectivity and neighborhood in and between sets. Topology investigates which shape properties are invariant under continuous deformation. A continuous deformation can be understood as stretching, bending or even knotting without tearing apart or sticking together the shape boundary.

Two shapes are topologically equivalent if there is such a deformation function which transforms the one shape into the other. In our framework we give guarantees on topological preservation. The results of our statements imply that there exists such a deformation function.

Geometry

Geometry is concerned with the shape of things. The main question here is which shape properties are invariant under rotation or translation. Since the interior of an object is of interest to us as well as multiple interconnected objects we can see the boundaries between them as the boundary between a number of regions including the background as an infinite region. So, the boundary *partitions the space* into regions.

The continuous boundary and the Euclidean distance induces a function which maps every point in space to its smallest distance to the boundary. This function is called *distance transform*. A distance transform is not smooth everywhere. So, the common differential methods fail to define the gradient and with it the steepest ascent on the distance transform. We use an extended version of the gradient definition first introduced in [Lieutier, 2004].

The gradient definition is crucial for the definition of critical points and the steepest ascend on the distance transform, which we need to establish a correspondence between the real world and the reconstructed digital world.

We define sampling conditions for every point on the boundary. Here we are interested in two aspects. First is the sampling density: according to this point on the boundary how close have to be two closest sampling points? Second is the sampling point deviation: according to this point on the boundary what is the greatest tolerable distance to the farthest sampling point? These two values are defined by a function which maps every point on the boundary to a scalar value which describes the properties of the shape at this point. This value is called *feature size*.

Digital Geometry

In our work we expect a set of data points coming from a data acquisition device or some postprocessing step e.g. an edge detector. So, the real world object or - as we see it - the original space partition is represented by this set of data points which we call *sampling points* or just *sampling*.

Again the set of points and the Euclidean distance induces the distance function which maps each point in space to its distance to the nearest point in the data set. Since the distance transform is defined on a finite set of points we call it *discrete distance transform*.

In Section 2.3 we generalize the definition of the gradient to define the set of critical points and the steepest ascend on the discrete distance transform. The question now is how do we establish the correspondence between the critical points on the continuous distance transform and the critical points on the discrete distance transform and prove the equivalent connectivity.

Digital Topology

We defined the critical points on the continuous distance transform in Section 2.2 and found the

well defined way to connect them, the steepest path. In Section 2.4 we defined the critical points in the discrete distance transform and here too found the way to connect them.

Our goal is not only to prove the preservation of topological properties but also to construct a method - an algorithm which computes the result in appropriate time on an appropriate machine.

In Section 2.4 we introduce the combinatorial structure *Delaunay triangulation* which is preliminary for our framework to prove the correspondence between the critical points on the continuous distance transform and the critical points on the discrete distance transform. The Delaunay triangulation consists of a finite number of elements containing the connectivity information between the points and, if the sampling conditions are fulfilled, between the corresponding critical points on the discrete and continuous distance transforms.

Delaunay triangulation connects two nearest points to an edge, three nearest points to a triangle and four nearest points to a tetrahedron. The condition in 3D is thatbthe circumsphere of each tetrahedron has to be empty of points.

Specifying the elements of the Delaunay triangulation, the so-called *simplices*, we also introduce an analogy to the discrete distance transform, a special ordering between the simplices called *flow relation*. Using the flow relation we simulate the distance values on the steepest paths on the discrete distance transform and so saving us the computation of distance values for each point in space.

The distance value can be understood as a metric for comparing points. A critical point with greater distance value is greater than the critical point with the lesser distance value. We use the analogy for simplices. The greater simplex is the one with the greater maximum distance value. Obviously, the flow relation simulation of the steepest path on the discrete distance transform also creates the ordering in the size of the simplices. But the new size definition is needed for simplices which do not belong to the same flow relation or - in analogy - which are not on the same steepest path.

1.4 Related Work

The methods for solving the surface reconstruction problem can be classified by their approach. We categorize the geometry processing methods resulting in some polygonal approximation under the name *computational geometry*. Many three-dimensional approaches may also be applied to the two-dimensional case: conversely, three-dimensional generalizations or extensions of methods may be proposed from 2D curve reconstruction approaches. Here we dwell on three dimensional surface reconstruction methods.

Computational Geometry

Reconstructions referable to computational geometry establish neighborhood relations between sample points and connects them by polygons. The easiest and most common way to do so is to connect three points to a triangle. In these cases the polygonal approximation of the original surface is some triangulated surface. The data structure suitable for these reconstruction methods consists of representations of *edges* (convex hull of two points), *triangles* (convex hull of three points) and *tetrahedrons* (convex hull of four points).

Early methods only delivered a reconstructed surface without any guarantee of topological correctness.

Algorithm	Citation
Alpha Shapes	[Edelsbrunner and Mücke, 1994]
Ball Pivoting	[Bernardini et al., 1999b]
Geomagic WRAP	[Edelsbrunner, 2003]
One Triangle at a Time	[Freedman, 2004]

One data structure for triangulated surface reconstruction is the *Delaunay triangulation*. Delaunay triangulation restricts the construction of tetrahedrons in the three-dimensional case to *empty ball* condition: the circumscribing ball of all tetrahedrons must not contain any other point. Under the assumption of the *general position* condition, where no four points on a plane are allowed, the Delaunay triangulation is unique.

1.4. RELATED WORK

A Voronoi diagram subdivides the space in convex cells such that each cell is associated with exactly one sample point. The samples associated with neighboring cells are at the same distance from their common boundary. There is a *duality* relation between Voronoi diagram and Delaunay triangulation. Each element in Delaunay triangulation is the convex hull of two or more points. The dual to this element is the intersection of the Voronoi cells of these points.

Even though the construction complexity is $O(n^2)$, where n is the number of points, the Delaunay triangulation is often used as the basis for reconstruction. In many approaches, its mathematical properties provide the origin for the theoretical framework and the basis for proofs.

Algorithm	Citation
r-Regular Shapes, Normalized Mesh	[Attali, 1997]
Crust	[Amenta et al., 1998]
Cocone	[Amenta et al., 2000a]
Lower Dimensional Localized Delaunay Triangulation	[Gopiy et al., 2000]
New Technique using Umbrella and Gabriel complex	[Adamy et al., 2000]
Power Crust	[Amenta et al., 2000b],[Amenta et al., 2001]
Tight Cocone	[Dey and Goswami, 2003]
Lipschitz Surfaces	[Boissonnat and Oudot, 2006]
Guarantees with Alpha Shapes	[Ramos and Sadri, 2007]
r-Stable Reconstruction	[Stelldinger, 2008b]

The reconstruction method in [Giesen and John, 2003] does not base its proof on Delaunay triangulation. The guarantee is given that the resulting "Flow Shape" preserves the topological properties if the original manifold surface is sampled sufficiently dense. In [Dey et al., 2003] it is proven that "Flow Shape" and "Alpha-Shapes" are homotopy equivalent.

In the theoretical results of [Niyogi et al., 2004] (or newer [Niyogi et al., 2009]) new sampling conditions are defined. The proof is given that under these very sparse sampling conditions the topological properties are preserved in the point set.

Surface Fitting Another surface-based approach towards surface reconstruction is to algebraically define a parameterized surface representation approximating the point set in some way. The next step is to deform the surface by changing the parameters until some termination criterion is achieved.

Algorithm	Citation
Adaptive Meshes	[Terzopoulos and Vasilescu, 1991]
Balloon Fitting	[Chen and Medioni, 1995]
Surface Inferencing	[Guy and Medioni, 1997], [Tang and Medioni, 1998]
Moving Least Squares, Mesh Independent	[McLain, 1974],[Levin, 2003]

Distance Functions The volumetric methods to reconstruct a surface from sample points compute for each point of the space the distance to the nearest sample point. If the surface orientation is given on each sample point the distance value can be signed. The task in this case is then the reconstruction of a surface where for each point on the surface the distance value is zero. In cases where no surface orientation is given the surface normals are either computed from the data set or statistically estimated.

Algorithm	Citation
Marching Cubes	[Lorensen and Cline, 1987], [Stelldinger et al., 2007]
Surfaces from Unorganized Points	[Hoppe et al., 1992]
Radial Basis Functions	[Carr et al., 2001]
Level Sets	[Zhao et al., 2001], [Zhao and Osher, 2002]
FFT-Based Reconstruction	[Kazhdan, 2005]
Watertight 3D Models	[Hornung and Kobbelt, 2006]

Discussion Our collection of reconstruction algorithms is only a small selection which, in our opinion, best represents the basic approaches from the great variety of methods. The methods based on surface fitting and distance functions make strong assumptions about the original shape and the data set.

In [Stelldinger et al., 2007] the proof is given that Marching Cubes results in a topologically correct reconstruction of an r-regular surface. To our knowledge all further methods which give guarantees of topology preservation are based on computational geometry approaches.

In Chapter 3 we focus our attention to related works on reconstruction with topological guarantees based on computational geometry approaches which are strongly related to our method.

1.5 Evaluation of "Thinned- (α, β) -Shape-Reconstruction"

Our work on non-manifold boundary reconstruction has achieved fundamental results and made contributions to conferences. In Chapter 4 we evaluate the new reconstruction algorithm called "thinned- (α, β) -shape-reconstruction" [Stelldinger, 2008b].

In [Stelldinger, 2008b] a boundary reconstruction algorithm is presented to reconstruct a non-manifold boundary of a space partition if the sampling density p and the greatest deviation q of points from the original boundary do not exceed a certain value. The space partition is assumed to be r-stable, which ensures that the boundary can be dilated by r without changing its homotopy type. The values p and q depend in a certain way from r and must be known by the algorithm before reconstruction.

There are two disadvantages of "thinned- (α, β) -shape-reconstruction". First, the sampling conditions are defined for the whole shape. In the worst case a shape with a very tight waist needs to be very densely sampled according to this tightness value. Second, the method is only guaranteed to result in a topologically correct reconstruction if p and q values are known.

The major contribution of this algorithm is its ability to reconstruct non-manifold boundaries and to handle highly noisy data sets.

Our work originated from the evaluation of the "thinned- (α, β) -shape-reconstruction". The experimental part of the evaluation required a robust implementation. So, on the basis of "Computational Geometry Algorithms Library" (CGAL) a system has been developed to evaluate the algorithm.

The experimental comparison of related surface reconstruction algorithms would require an implementation with uniform data structure. But the choice of the appropriate data structure for an algorithm is decisive for memory and processing time management. Therefore, the methods are compared theoretically. The criteria for a qualitative comparison are the sampling criteria. We computed the p, q values of sampling conditions required by the methods and visualized the sampling density by the number of required sample points to reconstruct a unit sphere surface. The sampling conditions are subdivided according to three criteria: global or locally adaptive definition of the sampling conditions on the surface, sampling density and allowed deviation from the original surface.

1.6 Locally Adaptive Approach

The great disadvantage of the "thinned- (α, β) -shape-reconstruction" is its dependence on known parameters and the requirement of globally defined sampling conditions. So, the next logical step is to develop a *parameter-free* non-manifold boundary reconstruction method the result of which preserves the topology of the original space partition.

Refinement Reconstruction

In Chapter 5 we introduce and evaluate an algorithm which can be seen as an extension of Geomagic Wrap[©] [Edelsbrunner, 2003]. The new method, called *elementary thinning*, reconstructs non-manifold boundaries resulting in a *refinement* of the original space partition.

Refinement associates the local maxima of the distance transform defined on original space partition with the maxima of the distance transform defined on the sample points. The computed space partition is a *refinement* of the original if and only if the discrete maxima are located in the same region as their associates. Refinement is a special case of an *oversegmentation* with the requirement of the correct separation of the local maxima.

1.6. LOCALLY ADAPTIVE APPROACH

The next step is to reduce the refinement in such a way that the result is still a refinement. This is done by *undersampled merge* which merges two computed regions into one if they are separated by a boundary component which is too large compared with the distance value of the local maxima of the computed regions.

The new method is parameter-free and handles locally adaptive samplings of non-manifold boundaries. The conditions on the sampling are based on a new locally adaptive feature size called *local region size* (Irs). Local region size on a boundary point is the minimal distance value of all local maxima of the distance transform *reachable by steepest ascent*. The sampling is *stable* if and only if the point density and deviation from the boundary are locally bound by Irs.

Our refinement reconstruction method results under guarantee in a refinement of the original space partition if and only if the sampling is stable. But a refinement does not guarantee for all shapes to contain a topologically correct reconstruction. In other words, it is not guaranteed that further refinement reduction by removing reconstructed boundary components would result in a topologically correct reconstruction for any shape.

Homotopy Axis The insufficiency of the sampling conditions and with it the proof of correctness require extended results on sampling criteria. Refinement does not necessarily contain a topologically correct boundary reconstruction. The goal now is to investigate under which sampling conditions a refinement can under guarantee be reduced to a correct reconstruction.

Refinement on stable samplings only ensures correct separation of local maxima. But a topologically correct reconstruction separates all critical points correctly. To define new sampling conditions taking into account the critical points we define a new subset of the *medial axis*.

The medial axis is the set of centers of *maximal inscribing balls* into the shape. Intuitively, medial axis is the skeleton of a region bounded by a shape. In [Lieutier, 2004] it is shown that the medial axis is homotopy equivalent to its open set.

We consider only a subset of the medial axis. As introduced in Section 2.2.4, the *homotopy axis* is the minimal connected homotopy equivalent subset of the medial axis containing all criticals. The algebraic construction starts with the set of criticals and then collects all points of the medial axis which are reachable by a *steepest path* starting on any already contained element of the homotopy axis. The steepest path is the set of points reachable by a *gradient ascent*.

The medial axis transform is a mapping of points on medial axis to their distance values. The definition of the steepest path on the medial axis transform depends on the gradient. But since the distance transform is not everywhere smooth the original gradient definition cannot be applied here. The algebraic framework in [Lieutier, 2004] extends the definition of the gradient. The direction of the gradient maximizes the growth of the distance transform.

The new locally adaptive feature size called *local homotopical feature size* (lhfs) (see Section 2.2.5) is the minimum between the minimal distance to the homotopy axis and the minimal local maximum reachable from the boundary point by steepest ascent.

The sampling is said to be *local homotopy stable* (see Section 5.10) if the sampling density and deviation from the boundary are bounded by lhfs. In [Tcherniavski et al., 2010a] we prove that under the condition that the sampling is *local homotopy stable* the result of the refinement reduction is reducible to a topologically correct reconstruction of the boundary. Note that in [Tcherniavski et al., 2010a] the sampling conditions are called *locally stable* and the parameters are restricted. In Section 5.11 we firstly prove the equivalent result for a general definition of sampling conditions.

Comparison to Other Approaches

The difficulty of comparing theoretical results on sampling conditions is that the sampling definitions presume different parameters and limits. In our work the theoretical evaluation consists of two parts.

In Section 5.13.1 we show that the globally set sampling conditions for thinned- (α, β) -shape - reconstruction in Chapter 4 are a special case of our generally defined locally adaptive sampling conditions. Using the result we prove for the first time that the equivalent results as produced by thinned- (α, β) shape-reconstruction can be achieved with our new locally adaptive refinement reconstruction method.

CHAPTER 1. INTRODUCTION

The comparison of approaches based on locally adaptive sampling conditions in Section 5.13.2 involves the unified representation of sampling conditions. Using our new definition we can compute the appropriate parameters of the related definitions and so compare the conditions. Obviously, the weaker the sampling conditions the greater is the class of shapes and the broader are the limits on the sampling.

Stability of Criticals Our intention is of course to develop a parameter-free method for topologically correct reconstruction of non-manifold boundaries. In [Tcherniavski et al., 2012] we also recognized the problem of the local homotopy stable sampling. The condition is not sufficient to distinguish between two shapes of different topology (see discussion in Section 5.15). The new question then is: How to restrict the conditions on the sampling to ensure the correct reconstruction?

To answer this question we investigate in Section 6.2 the stability of criticals according to perturbations on the surface, and the influence of noise on reconstruction.

In [Tcherniavski et al., 2012] we have already introduced the differentiation between criticals. We distinguish the criticals which can vanish, newly occur or are stable for each sampling in the reconstruction.

Point Set Decimation The results of our work contain investigations of sampling conditions based on certain volume-based feature sizes. Preserving the conditions in the point set ensures also the corresponding guarantees on reconstruction.

The corresponding feature size restricts the lower bound of the sampling density. So, denser sampling preserves the topological properties. Consequently, using this bound we can reduce the sampling density under guarantee to preserve the topological properties. The results of the so-called *point set decimation* are presented in Chapter 6.

The difficulty here is to estimate the feature size. The feature size is measured by distance values on certain points on the medial axis. So, a *robust* medial axis approximation is crucial for feature size estimation. Consequently, we have to investigate how the approximation of the medial axis can ensure the estimation error to be bounded by some certain value.

1.7 Structure and Content of Thesis

In Chapter 2 we introduce geometrical as well as topological concepts which are required for our work on boundary reconstruction with guaranteed preservation of topological properties. The theoretical concepts among others include:

- Introduction of space partition, distance transform, different axes to describe the homotopy of the shape and feature sizes.
- Definition of extended gradient and continuous flow on piecewise non-smooth distance transform.
- Introduction of simplicial complex, Delaunay triangulation and Voronoi diagram.
- Definition of alpha-shapes as sub-complex of the Delaunay triangulation.
- Flow relation defined on Delaunay simplices to imitate the continuous flow and the constructive retraction algorithm known as "WRAP" applied on Delaunay triangulation without inclusion of infinite simplices, such that the convex hull consists of simple simplices.
- Discussion on how to compare the simplices and introduction of a new size defined by the greatest distance value in the simplex.

There have been proposed numerous reconstruction methods on topology preserving surface reconstruction proposed previously. In Chapter 3 we introduce only the computational geometry-based approaches relevant for our work. The methods are presented in a clearly arranged synopsis for simple

1.7. STRUCTURE AND CONTENT OF THESIS

comparison of requirements on shape and sampling and the guarantees given by the method along with a short introduction to the method and a brief note on possible extensions.

For the purpose of a better overview and a comparison of reconstruction methods we also introduced the thinned (α, β) -shape reconstruction and the refinement reconstruction in Chapter 3.

Since the first step in our research was the theoretical and practical evaluation of the thinned- (α, β) -shape reconstruction, in Chapter 4 we introduce in detail the theoretical concepts of the approach including:

- Concept of *r*-stability to classify the shapes.
- Definition of the (p, q)-sampling and the conditions required by the algorithm.
- Differentiation between relevant and not relevant reconstructed regions.
- Detailed description of the proof of the topological correctness of the approach.
- Illustration of the reconstruction results on several examples including the determination of the algorithm parameters by parameters of the sampling.

The evaluation of the thinned- (α, β) -shape reconstruction has been:

- Comparison to other approaches by unification of the sampling conditions and requirements on the shape. For better understanding of the sampling conditions we computed the lower bound of points needed for correct reconstruction of the surface of the unit ball.
- Detailed discussion of the problems of the approach resulting from non-smooth shape assumption and excessive noise amount.
- Experiments done on well known data sets from the "Stanford 3D Scanning Repository" as well as on artificially generated data sets for better demonstration of the method's advantages.

Since our new reconstruction algorithm results in a refinement of a space partition which preserves topological properties, the correct separation of critical points is of particular interest. So, our framework in Chapter 5 consists of:

- Introduction of unique mapping called *association* between the original and the discrete local maxima. A *refinement* correctly separates the associated local maxima. A *stable refinement* correctly separates the connected components of the smallest superset the *homotopical axis* of the original medial axis containing all critical points. A *reducible refinement* can be reduced to a stable refinement by the removal of boundary components.
- Definition of locally adaptive (ψ, ρ) -sampling conditions, where ψ is a parameter to control the sampling density and ρ is the parameter which influences the sampling density and the maximal sample point deviation from the boundary. In this way the sampling density depends on noise. The factors ψ and ρ are used to scale a locally variable feature size. The sampling conditions defined by local region size preserve the correct separation of local maxima. The refinement reconstruction on sampling conditions defined by the local homotopical feature size results in a reducible refinement.
- Introduction of a *minimal refinement* with a boundary consisting of Delaunay simplices being minimal in the flow relation.
- The proof that application of the constructive retraction (WRAP) [Edelsbrunner, 2003] on all Delaunay tetrahedrons containing their own circumcenters results in a minimal refinement. We call this processing step *elementary thinning*

- The proof that the boundary simplices of a minimal refinement can be measured according to the largest circumradius of a Delaunay simplex contained in a reconstructed region. The boundary simplices exceeding a certain measurement may be deleted from the reconstruction preserving the minimal refinement conditions. Since the reconstructed regions are merged when boundary simplices are removed, we call the processing step *refinement reduction*.
- A demonstration of performance of the algorithm on three examples: almost noise-free and very sparse sampling, very noisy but dense sampling, and a sampling which does not fulfill our conditions.

The evaluation of our results is done both theoretically and experimentally:

- To compare the sampling conditions we unified the requirements for previous reconstruction methods and proved that they can be expressed by (ψ, ρ) -sampling conditions.
- We proved that given the sampling parameters for thinned- (α, β) -shape-reconstruction, the refinement reconstruction has an equivalent result.
- The experiments have been done on well-known laser range scan data from the "Stanford 3D Scanning Repository": almost noise-free, blurred and corrupted by salt-and-pepper noise. Further experiments have been done on volume-based samplings resulting from 3D-Canny edge detection on computer tomography data sets [Bähnisch et al., 2009].
- The discussion concerns also problems due to insufficiency of the sampling conditions two shapes with different topology can have equal sampling sets. We also argue that the problems of the theoretical framework defining refinement are not problems of our reconstruction method.

The evaluation of the refinement reconstruction in Chapter 5 lacks experiments with locally nonuniform sampling fulfilling our conditions but being too sparse to be handled by previous reconstruction methods. To our knowledge no data set provably fulfilling the requirements exist. In Chapter 6 we propose an algorithm and theoretical framework for data set decimation which results in a non-uniform locally stable (ψ, ρ) sampling. The refinement reduction on locally stable (ψ, ρ) sampling results in a reducible refinement while the result of decimation is too sparse to be handled by previous reconstruction methods.

For derivation of the data set decimation constraints we included in Chapter 6 the following:

- Definition of stable critical points in discrete distance transform defined for low-quality data sets and proof of correct separation by refinement reconstruction.
- Method for discrete homotopical axis computation and local homotopical feature size estimation.
- Usage of the estimated local homotopical feature size for proposed data set decimation algorithm.
- Experiments on decimation of dense laser range scan data and reconstruction.
- Discussion on provability of the results.

The framework introduced in Chapter 6 promises to be a sound basis for future work on homotopy equivalence of the reconstructed space partition.

1.8 Related Publications

The work contained in this dissertation is partly based on the contribution in [Stelldinger, 2008b] and has led to several publications. In the following we summarize the correspondences between parts of this thesis and the publications as well as clarify of the author's contributions.

1.8. RELATED PUBLICATIONS

[Tcherniavski and Stelldinger, 2008]: This work consists of the evaluation results of the 3D "Thinned- (α, β) -Shape-Reconstruction" framework introduced in [Stelldinger, 2008b]. Section 3 (Comparison to other Approaches) and section 6 (Conclusions and Future Work) were developed in collaboration with the second author, Peer Stelldinger. Section 4 (Implementation and timings) and section 5 (Experimental Evaluation) together with the computation and visualization of Figure 1,2,3 and 4 as well as the presentation of the experimental results are own contribution and can also be found in Section 4.9 and Section 4.10. Following an invitation the publication [Stelldinger, 2008b] was published in the journal "Pattern Recognition". So, the experimental results are also part of [Stelldinger and Tcherniavski, 2009c].

The content of the following publications is the basis for Chapter 5. However we generalize the constant sampling factor $(\frac{1}{2})$ introduced in the published results by variable parameters (ψ, ρ) .

[Stelldinger and Tcherniavski, 2009a] and [Stelldinger and Tcherniavski, 2009b]: The personal contribution of the second author, Leonid Tcherniavski, is the first draft of the paper and the significant contribution to the algorithm development, Lemma 4.1, Definition 4.2, collaboration on Definition 4.4, Observation 4.5, Definition 4.6, Observation 4.7, strong contribution to and first draft of Lemma 4.8, of Definition 5.2, 5.3 and of Theorem 5.4. These results are also parts of Section 5.2, Section 5.4, Section 5.5, Section 5.6, Section 5.7 and Section 5.8

[Tcherniavski et al., 2010a], [Tcherniavski et al., 2010b]: The personal contributions of the second and third authors are proofreading of the writing and verification of the mathematical correctness. In these publications we introduced a new stability criterion and sampling conditions which mainly contributed to Section 2.2.4, Section 5.11, Section 5.10 and Section 5.11.

[Tcherniavski et al., 2012]: The paper [Tcherniavski et al., 2010a] was published as an extended version in "Special Issue of Pattern Recognition Letters" [Tcherniavski et al., 2012]. The extension of the paper contains considerations on stability of criticals which can also be found in Section 6.2. A new volume-based point set decimation algorithm was proposed which has been used to provide artificial data for experimental evaluation of the refinement reduction algorithm on locally stable samplings. The framework of the point set decimation algorithm is also part of Section 6.4 and 6.5. The work [Tcherniavski et al., 2012] also contains a discussion on the insufficiency of the newly defined sampling conditions which can also be found in Section 5.15.

Chapter 2

Theoretical Concepts

2.1 Topology

While geometry investigates the real world to describe "how the things look like". Topology is the science which is concerned with "how things are connected". To provide an understanding on topological properties we start with examples firstly introduced in "Topology for computing" by Afra Zomorodian [Zomorodian, 2005].

Example Loops and Strings First let us consider a string and a loop (which is a string while the two ends are stuck together) as they are shown in Figure 2.1 (the curves with scissors). Both consist of one connected component. To find out the difference in the connectivity we cut the string and the loop. By cutting a string we change its connectivity since we get two string pieces but we get just one piece if we cut a loop. The results are different, consequently the original connectivity has been different.



Fig. 2.1: If you cut a string you get two pieces. Cutting a loop results in one piece.

Example Spheres and Donuts Consider now a sphere (i.e. a hollow ball) and the surface of a donut (i.e. a hollow torus) in Figure 2.2. Now we look at their connectivity. No matter how we cut the surface of a sphere along a simple closed curve on its surface, we get two pieces. But we can cut the donut in such a way, that we get one piece only. Somehow the donut imitates the loop.



Fig. 2.2: (a) No matter how the sphere is cut, we get two pieces. (b) A donut can be cut in such a way that we still get only one piece.

Consider any point on the loop of our first example. Each point has two neighborhood components. The same is valid for almost every point on the string but the two end points which have only one neighbor.

Cutting changes the connectivity of the points. In other words the neighborhood components of the points can change. Cutting through the neighborhood of two points divides them leaving two points with one neighborhood component only.

Topology investigates the global connectivity of an object by considering local connectivity of the object. Topology studies properties that do not change under continuous and continuously invertible transformations. The neighborhood of a point on the loop consists of two components no matter how we stretch or deform the loop.

On the other hand topology is concerned with how the object is placed in space. Consider for example a string again. But before we stick the ends, we put a knot in the string and then stick its ends. No matter how we stretch and pull on the string we cannot unknot the knot without tearing the string.

2.1.1 Homeomorphism

Topology is concerned with connectivity in continuous spaces and thus with *neighborhoods* of objects. In the Euclidean world we know the neighborhood of a point as

Definition 2.1 (Euclidean Neighborhood). Let $x \in \mathbb{R}$ be a point in Euclidean space \mathbb{R} . A neighborhood of x is the set which is defined as $\{y \in \mathbb{R} \mid \exists \epsilon > 0 : ||x - y|| < \epsilon\}$

We can give the definition on neighborhoods in Euclidean space since we know the distance metric between points. Using the definition of a neighborhood we can define an *open set*. A subset $U \subset \mathbb{R}$ is *open* if every point in U has a neighborhood contained in U. But what if no metric is given?

Topology can be defined in several definitions. We use the definition by open sets.

Definition 2.2 (Topology). A topology on a set X is a subset $T \subseteq 2^X$ such that:

- 1. If $S_1, S_2 \in T$, then $S_1 \cap S_2 \in T$
- 2. If $\{S_J \mid j \in J\} \subseteq T$, then $\cup_{j \in J} S_j \in T$
- 3. $\emptyset, T \in T$.

Definition 2.3 (Open,Closed). Let X be a set and T be a topology on X. Then every $S \in T$ is called an open set. The complement $X \setminus S$ of an open set S is closed.

Definition 2.2 implicitly states that only finite intersections and infinite unions of open sets are open. A *topological space* is a combination of a set with its topology.

Definition 2.4 (Topological Space). The pair (X,T) of a set X and a topology T on X is a topological space X.



Fig. 2.3: (a) A set A consisting of four squares and a dot. (b) The closure \overline{A} of the set A. (c) The interior \mathring{A} of the set A. (d) The boundary ∂A of the set A.

Definition 2.5 (Closure, Interior, Boundary). Let $A \subseteq \mathbb{X}$, the closure \overline{A} of A is the intersection of all closed sets containing A. The interior \mathring{A} of A is the union of all open sets contained in A. The boundary ∂A of A is $\partial A = \overline{A} \setminus \mathring{A}$.

In Figure 2.3, we see a set A consisting of four squares differently related to each other. In (b) we see its closure, in (c) its interior and in (d) its boundary. Notice, the interior of the set are four disconnected open squares whereas three of squares are connected in (a) either by a line segment or by a point. The dot does not have any interior.

The boundary of the set may also be defined as the set of points whose neighborhoods intersect the set and its complement. The closure of a set A may be seen as minimum closed set which contains the set A.

Using the open sets we can define following notations:

Definition 2.6 (Neighborhood). Let $\mathbb{X} = (X,T)$ be a topological space. A neighborhood of $x \in X$ is any $A \subseteq T$ such that $x \in A$.

Definition 2.7 (Continuous Function). A function $f : \mathbb{X} \to \mathbb{Y}$ is continuous if for every open set $A \in \mathbb{Y}$, $f^{-1}(A)$ is open in \mathbb{X}

Definition 2.8 (Homeomorphism). A homeomorphism $f : \mathbb{X} \to \mathbb{Y}$ is a bijective continuous function with continuous inverse. The inverse of a homeomorphism is again a homeomorphism. Two sets \mathbb{X} and \mathbb{Y} are homeomorphic or topologically equivalent if there is a homeomorphism between them.

2.1.2 Homotopy

We often observe two shapes to be topologically "similar" even if the shapes are not topologically equivalent. Consider for example Figure 2.4. The letter A drawn with a thick line is also recognizable as A if it is drawn with a thin line. The shapes are similar. Both enclose one region. In fact we can imagine different thickness of the line and still have the letter A. *Homotopy* describes this similarity.

Consider again our example in Figure 2.4. How do we compare the shapes? Starting with the thick line drawn A we reduce the thickness until it is one point thick. In other words we continuously shrink the shape into its subset. In the extreme left illustration we denote the direction of this "shrinking" by arrows towards the thin A. In our case such a shrinking line can be found for every point on the contour of the thick A such that the lines are not crossing each other and if they intersect they stay intersected.



Fig. 2.4: Deformation retraction of an A shape.

Let us think of the shrinking process as a continuous deformation over time. Let the starting point on the shrinking line on the contour be the starting time and the ending point on the thin A be the ending time. We normalize the time line in such a way that the starting time is zero and ending time is 1. So, for every time point in interval between 0 and 1 we observe a thinner version of A as it is shown in Figure 2.4. At time 1 the shrinking is complete and the deformation process results in thin A. Actually we can go even further and define such a shrinking on the "legs" of the thin A resulting in a triangular loop.

The following definitions we adopted from [Hatcher, 2002]:

Definition 2.9 (Deformation Retraction). A deformation retraction of space X onto a subspace A is a continuous family of maps $f_t : X \to X, t \in [0,1]$ such that f_0 is the identity map, $f_1(X) = A$, and $f_t|A$ is the identity map, for all t. The family is continuous in the sense that the associated map $X \times [0,1] \to X, (x,y) \mapsto f_t(x)$ is continuous.

A deformation retraction is a special case of a *homotopy*. Homotopy relaxes the requirement of the final space being a subspace.

Definition 2.10 (Homotopy). A homotopy is a family of maps $f_t : \mathbb{X} \to \mathbb{X}, t \in [0,1]$ such that the associated map $F : \mathbb{X} \times [0,1] \to \mathbb{Y}$ given by $F(x,t) = f_t(x)$ is continuous. Then $f_0, f_1 : \mathbb{X} \to \mathbb{Y}$ are homotopic via the homotopy f_t .

Definition 2.11 (Homotopy equivalence). A map $f : \mathbb{X} \to \mathbb{Y}$ is called a homotopy equivalence if there is a map $g : \mathbb{Y} \to \mathbb{X}$, such that $g \circ f$ is homotopic to the identity map of \mathbb{X} and $f \circ g$ is homotopic to the identity map of \mathbb{Y} .

If two spaces X and Y are homeomorphic, then they are homotopy equivalent.

Theorem 2.12. Let two spaces X and Y be topologically equivalent. Then X is homotopy equivalent to Y.

We can rephrase Theorem 2.12 by: *if two spaces are not homotopy equivalent, they are not homeomorphic.* In general, the converse to Theorem 2.12 is not true. We illustrate this statement by examples adopted from [Hatcher, 2002].



Fig. 2.5: Deformation retraction of a shape resulting in final subspaces of different topology.

Consider a shape with two holes as in Figure 2.5. The arrows demonstrate possible retraction trajectories into subsets which are drawn with thick lines. Since there is a deformation retraction the final thin shapes are homotopy equivalent to the starting set and homotopy equivalent to each other. But the sets are not homeomorphic. The two circles in the left illustration do not have common boundary as is the case in the right. In the middle example there is a point with four componnets in its neighborhood.

However, homotopy equivalence (compare Definition 2.11) between topological spaces implies a one-to-one correspondence between connected components, cycles, holes, tunnels, cavities, or higher-dimensional topological features.

Definition 2.13 (Contractible). A space with homotopy type of a point is called contractible.

In Figure 2.5 the starting set is not contractible.

2.1.3 Isotopy

A homeomorphism is a one-to-one function which maps one topological space onto another. A topological space is a description of a connectivity in a set. So, a homeomorphism maps one-to-one all connectivity information. If there is a homeomorphism between two topological spaces then the corresponding sets are equivalently connected - they are topologically equivalent.



Fig. 2.6: Topologically equivalent shapes are not necessarily isotopic .

Homotopy is a family of continuous functions on sets which is itself continuous. We can visualize this family by time variable as deformation. Obviously, there is a homeomorphism between the thicker A in Figure 2.4 and the thinner A. But there is no homeomorphism between the thicker A and the final thin A where the line is one point thick. The neighborhood of an interior point in thicker A is an open 2-dimensional disk whereas in the thin A no interior points exist. Still there is a continuous deformation between them which is done in certain time. Each function between a thicker A and a thinner A is a homeomorphism and corresponds to a point in the time. The time variable is continuous. Only in the limit the last function which maps the A with infinitesimal thickness to the thin A is not a homeomorphism but is continuous.

The homotopy which restricts every function in the family to be a homeomorphism is called *Isotopy*.

Definition 2.14 (Isotopy). Let two continuous functions $f, g : \mathbb{X} \to \mathbb{Y}$ be homeomorphisms. f is isotopic to g if there is a homotopy H between f and g such that for every $t \in [0, 1]$ H(., t) is a homeomorphism.

For example a torus and a trefoil knot as represented in 2D example in Figure 2.6 are homeomorphic but not isotopic. We cannot deform one to each other without tearing or self-intersection. However *homotopy* allows shrinking to a single point, which makes a trefoil homotopy equivalent to the torus. To see that consider the trefoil knot, where the "trefoil part" is contained in a small region of the knot. Putting the two ends of it tight shrinks the knotted part to a single point, resulting in a circle which is homotopy equivalent to the torus.

2.2 Geometry

While topology is concerned with the properties of shapes which are invariant under continuous functions, geometry is interested in invariants under rotation or translation in space. Following the well known comparison, the topologist does not see the difference between a cup and a donut because he is only looking into local environment of points - the geometer does see the difference since the cup cannot be transformed into a donut neither by rotation nor by translation.

Here we introduce geometrical concepts concerning our work and present a framework which is suitable to derive the correspondence between the shape descriptors and topological properties. This framework is then used in the following chapters for reconstruction methods with topological guarantees.

2.2.1 Space Partition

Let us examine the illustration in Figure 2.7. We can recognize a shape of a fish consisting of a fish-eye, two fins and fish-corpus. Mathematically speaking we see a 2D-space divided or partitioned into five open regions by a non-manifold boundary. One region corresponds to the infinite background. One region relates to the fish-eye, two regions which we recognize as fins and an open region with a hole - the corpus.

In our example the neighboring regions share at least one piece of one dimensional contour. If we consider a space partition which results by two crossing lines we observe that the resulting diagonally-placed regions share a boundary which consists of one point only. If there are more than two line crossing in this point, more than two regions would be sharing this point as common boundary. So in 2D we differentiate the direct neighbors which share a contour piece and so are the only possible regions adjacent to the common boundary and the neighbors sharing a lower dimensional boundary.



Fig. 2.7: Space partition consisting of 5 open regions. Thick line is the boundary.

Definition 2.15 (Space Partition [Stelldinger and Tcherniavski, 2009b]). A space partition \mathcal{R} is a finite set of pairwise disjoint regions $\mathcal{R} = \{R_i \subset \mathbb{R}^n\}$ such that each region $R_i \in \mathcal{R}$ is a connected open set and the union of the closures of the regions covers the whole space, i.e. $\bigcup_i \overline{R_i} = \mathbb{R}^3$. The boundary of the partition is $\partial \mathcal{R} := \bigcup_i \partial R_i$. Two regions R_i, R_j are called m-neighbors if the intersection $\overline{R_i} \cap \overline{R_j}$ contains an m-dimensional manifold, but no (m + 1)-dimensional manifold. Two (n - 1)-neighbors are also called direct neighbors.

The simplest case of a space partition is a *binary partition*, where the regions can be classified into foreground (e.g. a contractible solid object) and background (the rest).
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2.2.2 Distance Transform

A space partition together with its boundary covers the whole space. For each point in the space we can compute the Euclidean distance to the nearest point on the boundary. The function which maps each point in space to this distance value is called *distance transform*.

In Figure 2.8 (a) we illustrate the distance transform on the space partition in Figure 2.7 by gray values. The more distant to the boundary is a point in space the brighter is the gray value. The gray values are normalized in such a way that the maximum distance value has the gray value 255.

In 2D the distance transform is a function which maps a 2D coordinate to its distance value. In Figure 2.8 (b) the distance values are additionally represented as height levels.



Fig. 2.8: Distance Transform

Definition 2.16 (Distance Transform). The distance transform d of a set $B \subset \mathbb{R}^3$ is defined as $d(x) = \min_{y \in B} ||x - y||$. The distance transform is called continuous if B is infinite, and discrete otherwise. The reversed distance transform is defined as $rd(x) = \{y \in \partial \mathcal{R} \mid ||x - y|| = d(x)\}$. x is a local maximum of the distance transform iff $\exists \epsilon > 0 \forall x' : (||x' - x|| < \epsilon) \to (d(x') < d(x))$.

Gradient

The "mountains" in Figure 2.8 (b) motivate the question, how do we climb up? Obviously the steeper we chose our way to the tip of the mountain the harder it is to climb. The ways leading into the mountains are usually serpentine to reduce the ascent per step. So, the actual question is, what is the steepest ascent starting on some point in space?

Standing on this starting point in space the direction of our further way defines the slope. The slope is negative if we climb down, and positive if we climb up. We may represent the direction and the hardness to climb the slope as vectors.

The slope is computed on a 1D curve by the first derivative. The second derivative results in the amount of change of the slope. In 2D we compute the slope by the first derivative in the two basic directions. The vector consisting of the two directed slopes in the basic directions is called *gradient*. So, the function on which the gradient is to be computed must be derivable on each point in the domain. We call derivable functions *smooth*.

As we may observe in our example in Figure 2.8 (b) the distance function is not everywhere smooth. So, the computation of a gradient by derivation cannot be applied in our framework. We use the extended definition of the gradient firstly introduced in [Lieutier, 2004].

Definition 2.17 (Gradient and Criticals [Lieutier, 2004]). Let $\Theta(x)$ be the center of the smallest closed ball enclosing rd(x). Then the gradient on x is defined as

$$abla(x) = rac{x - \Theta(x)}{\mathrm{d}(x)}$$



and the set of critical points of ∇ is given by $\mathbf{F}(\mathcal{R}) = \{x \in \mathcal{R} \mid \|\nabla(x)\| = 0\}$. More generally, $\mathbf{F}_{\beta}(\mathcal{R}) =$

Fig. 2.9: (a) Distance value and the center of the smallest closing ball of the closest boundary points. (b) Critical points on the distance transform.

Consider our 2D example of a space partition in Figure 2.9 (a). We want to define the gradient in point x. The distance value in x is d(x) and is the radius of the maximum inscribing ball centered in x. This ball touches the boundary in two points. The smallest ball enclosing the two points is centered in a point denoted by $\Theta(x)$. The direction of the gradient as it is defined in Definition 2.17 is given by the difference vector between x and $\Theta(x)$ and the length of the gradient normalizes the difference by the distance value. Since the distance between x and $\Theta(x)$ is less than d(x) the magnitude of the gradient on the point x is less than 1. In fact, since the maximum inscribing ball is always greater than or equal to the minimal enclosing ball of the touching points the gradient value never exceeds 1.

Let us consider now the gradient on point x' in Figure 2.9 (a). The maximum inscribing ball touches the boundary in one point only. We follow that the minimum enclosing ball of this point has the zero radius and is centered on the touching point. This touching point is also the nearest neighbor for point x'. So, the difference $(x' - \Theta(x'))$ between the point and the center of the minimum enclosing ball of the touching point is equal to the distance value on the point x'. Consequently the gradient value is 1.

We observe that the extended version of the gradient has the magnitude 1 on every point where the maximum inscribing ball touches the boundary in one point which are the derivable pieces of the distance transform - the linear ascends in Figure 2.8 (b). We also notice sharp edges on the "mountains". These are the points where the maximum inscribing ball touches the boundary in more than one point.

In Figure 2.9 (b) we specified the points where the center of the minimum enclosing ball of the touching points overlay the point itself. The gradient has the magnitude zero. The centers of the balls are the critical points on the distance transform.

The thin circles denote the maximum inscribing balls which touch the boundary in exactly two points. The thick circles correspond to the maximum inscribing balls touching the boundary in more than two points. We will see in the following that the centers of thin circles correlate with the saddles and the centers of the thick circles are the maximum on the distance transform.

The general definition of the β -critical point in the infinitesimal β -environment of a point tends to the desirable set of critical points: $\lim_{\beta\to 0} (\mathbf{F}_{\beta}(\mathcal{R})) = \mathbf{F}_0(\mathcal{R}) = \mathbf{F}(\mathcal{R})$ and $\beta \leq \beta' \Rightarrow \mathbf{F}_{\beta}(\mathcal{R}) \subset \mathbf{F}_{\beta'}(\mathcal{R})$.

Flow

The gradient ∇ gives the direction of the *steepest ascent*. In other words the direction which maximizes the growth of the distance transform. But as we may observe in Figure 2.8 (b) the mountains have sharp ridges. For example in the "eye" the mountain is a cone. The slope being 1 on the sides of the cone jump to zero on the critical point. The gradient is not continuous. But the path to the tip of the mountain is continuous.

 $\{x \in \mathcal{R} \mid \|\nabla(x)\| \le \beta\}.$

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In [Lieutier, 2004] the authors prove using the vector field ∇ that Euler schemes converge uniformly when the integration step decreases. Then integrating the gradient results in a continuous flow which describes the *path* to the critical.

Definition 2.18 (Flow [Lieutier, 2004]).

$$\mathfrak{C}: \mathbb{R}^+ \times \mathcal{R} \mapsto \mathcal{R} \quad \text{with} \quad \mathfrak{C}(t, x) = x + \int_0^t \nabla\left(\mathfrak{C}(\tau, x)\right) d\tau$$

Notice, that the t variable in Definition 2.18 is no longer the time in the interval [0,1] as it is considered for example in the definition of homotopy in Definition 2.10. t is the continuous integration step such that a critical is reached for $\lim_{t\to\infty}$. Once the critical is reached the gradient becomes zero. Consequently, for any integration step the additive parameter is zero and the flow stays in the critical point.

Simple Path The flow is a path with steepest ascent toward a critical point where the gradient magnitude is zero. So, a flow is a continuous set of points an interval mapped to space. Since the flow is strictly increasing it is not crossing itself.

Throughout our research, we follow certain paths and investigate the distance values along these paths. So, we characterize a path - or, as we call it, a *simple path* to emphasize that it is not crossing itself - by means of the values of the distance transform along the path:

Definition 2.19 (Simple Path). A continuous map $\pi : [0, 1] \to \mathbb{R}^3$ is also called a simple path. Further, π is an increasing (strictly increasing, decreasing, strictly decreasing) path on the distance transform if and only if $d \circ \pi$ is increasing (strictly increasing, decreasing, strictly decreasing) on [0, 1] respectively. π with $\pi(0) = x$ is a steepest path (starting at x) iff $\forall t \in [0, 1] \exists t' \in \mathbb{R}^+ : \pi(t) = \mathfrak{C}(t', x)$.

2.2.3 Medial Axis

In this section we take a closer look at the ridges of the mountains in Figure 2.8 (b). On these ridges the regular derivation method fails to define the original gradient. These are the places where the maximum inscribing balls touch the boundary at least twice and where the magnitude of the extended gradient is less then 1.

The union of the ridges is called the *medial axis* and is defined as the union of the centers of maximum inscribing balls which touch the boundary in at least two points.

Definition 2.20 (Medial Axis [Blum, 1967]). The medial axis of a set $B \subset \mathbb{R}^3$ is defined as

$$\mathsf{MA} = \{ x \in \mathbb{R}^3, \, |\mathrm{rd}(x)| > 1 \}$$

Let $\Omega(x, \epsilon)$ be the intersection of an open ball placed on x with radius ϵ and MA. x is a local maximum on MA iff $\exists \epsilon > 0 \forall x' \in \Omega(x, \epsilon) : d(x') > d(x)$.

In Figure 2.10 we illustrate the construction and the definition of the medial axis leaving out the maximal inscribing balls outside the fish shape. Notice the absence of small circles touching the smooth pieces of the boundary. The smallest maximum inscribing ball overlays the smooth piece of the boundary completely. Which means that the smoothness can be measured by the radius of the smallest maximum inscribing ball.

In cases of sharp edges the maximum inscribing balls tend to disappear, becoming very small. The maximum inscribing ball in the corner has the radius zero.

Medial axis is also known as a complete shape descriptor since it is homotopy equivalent to its open set as it is proven in [Lieutier, 2004].

Theorem 2.21 (Homotopy Equivalence of Medial Axis [Lieutier, 2004]). Let \mathcal{O} be a bounded open subset of \mathbb{R}^n and MA be its medial axis, then \mathcal{O} is homotopy equivalent to MA.



Fig. 2.10: (a) Construction of medial axis by centers of maximum inscribing balls. (b) The medial axis (thin line), local maxima (\oplus) , saddles (\otimes) .

The maxima on the medial axis - consider for example Figure 2.10 (b) - are considered as points with maximal distance value in certain environment on the medial axis. The environment of a minimum on the medial axis is in 2D always one-dimensional. In 3D it can be one-dimensional, then we call it a 2-saddle, and it can be two-dimensional - homeomorph to a disc - then we call such a minimum a 1-saddle.

In the following, we will see that the maxima on the medial axis are congruent with the maxima of the distance transform. We will use this fact to show in Theorem 5.19 the relation between *stable* and *unstable* results of our reconstruction algorithm when applied on samplings taken with different conditions.

Observation 2.22 (Local Maxima on Distance Transform and MA:). x is a local maximum on MAT if and only if x is local maximum on the distance transform (d).

Proof: I. Let x be a local maximum on the distance transform. Then there is an $\epsilon > 0$ such that x is the maximum of all x' in the open ball $\mathcal{B}_o x \epsilon$ centered on x with radius ϵ . d(x) is the distance to the nearest boundary point b, so the maximal closed ball $B_{mc}x$ centered on x has the radius r = d(x) and touches the boundary at point b. Let us assume that there is only one boundary point on the boundary of $B_{mc}x$. So r can be increased to r' such that a closed ball on x' touches another boundary point. Since d(x') = r' and r' > r, there must be an increasing path between x and x', which is a contradiction to x being a maximum in $\mathcal{B}_o x \epsilon$. Thus the boundary of $B_{mc}x$ must touch another boundary point and so $x \in MA$. Let $\Omega(x, \epsilon)$ be an intersection of any surface with $\mathcal{B}_o x \epsilon$. Since x is maximal for all $x' \in \mathcal{B}_o x \epsilon$, x is maximal for all $x'' \in \Omega(x, \epsilon)$. Thus x is a local maximum on MA.

II. Let x be a local maximum on MAT. Let us assume the opposite: x is not a local maximum on d. Then there exists an increasing path π_m on d between x and a local maximum on d. Since x is maximum on MAT and π_m is increasing, there is a t' > 0 and a subpath $\pi \subset \pi_m$ with $\pi(0) = x$ and $\pi(1) = \pi_m(t')$, such that $\forall t \in (0,1] : \pi(t) \notin MA$. Let $t \in (0,1]$ be a π -coordinate, then the maximal closed ball $B_{mc}\pi(t)$ touches the boundary in only one point b. The center points of all growing balls touching b construct an increasing path π_t with $\pi_t(0) = \pi(t)$. The greatest ball on π_t touches the boundary in b and an additional point b', so $\pi_t(1) \in MA$.

Let $f_{\pi} : \pi([0,1]) \times [0,1] \to \mathsf{MA}$ be a function where for all $t \in [0,1]$ the path $f_{\pi}(\pi(t), \cdot)$ is increasing with $f_{\pi}(\pi(t), 0) = \pi(t)$ and $f_{\pi}(\pi(t), 1) \in \mathsf{MA}$. Since the distance transform has a locally Libschitz continuous gradient on $\mathcal{R} \setminus \mathsf{MA}$ (see for proof [Wolter, 1992]), f_{π} is continuous. So $f_{\pi}(\pi(t), 1)$ with $t \in [0, 1]$ is an increasing path in MA, which is a contradiction to the assumption $\pi(0)$ is a local maximum on MA. Thus, x is a local maximum on d.

In [Chazal and Lieutier, 2005a] a subset of the medial axis is introduced which remains stable for certain perturbations on the boundary:

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Definition 2.23. (λ -Medial Axis [Chazal and Lieutier, 2005a]) Let $\mathcal{F}(x)$ be the radius of the smallest closed ball enclosing rd(x). The λ -medial axis is defined as

$$\mathsf{MA}_{\lambda} = \{ x \in \mathcal{O}, \ \mathcal{F}(x) \le \lambda \}$$

The radius \mathcal{F} of the smallest closed ball enclosing the touching points on the boundary is zero for all points not on the medial axis. The maximum inscribing ball outside the medial axis touches the boundary in one point only, following \mathcal{F} is zero. We imply that the points on the λ -medial axis are also points on the medial axis.

Consider the set of critical points. The Hausdorff distance between the boundary and the set of critical points is the smallest distance value on critical points. This value is globally defined for the open set. We introduce the concept in Definition 2.31. In [Chazal and Lieutier, 2005a] the proof is given that the λ -medial axis is homotopy equivalent to its open set if λ is smaller than the Hausdorff distance between the boundary and the set of critical points. Setting λ less than that value we observe that λ -medial axis is constructed by cutting the ends of the medial axis where the maximal enclosing balls have the radius greater than λ . Equivalently, we observe that λ -medial axis is the subset of the medial axis which does not intersect the bou λ -dilation of the boundary. The λ -dilation results by placing a λ -ball on each point of the boundary.

2.2.4 Homotopical Axis

We introduce an even smaller subset of the medial axis which is homotopy equivalent to the open set. The drawback of the λ -medial axis is that the Hausdorff distance between the boundary and the set of critical points has to be known. The definition of our *homotopical axis* does not depend on any parameter settings and is a direct property of the medial axis. It is the smallest set of steepest ascents on the medial axis containing the critical points.



Fig. 2.11: The dotted line is the medial axis and the dashed line is the homotopical axis

The thick line in Figure 2.11 is the homotopical axis of our fish shape. Notice, even if the smallest subset of the medial axis which is homotopy equivalent to the corpus is the loop around the eye, the homotopy axis still contains the extension to the maximum in the fish tail leading though a saddle (\otimes). The homotopy axis of the eye is the local maximum only (\oplus).

The gradient in the critical points is zero. So, no ascend can start in a critical point. The β -parameter denotes the infinitesimal environment around a saddle where the gradient magnitude is greater than zero. So, the definition of the homotopical axis is given by general definition of the gradient

Definition 2.24 (Homotopical Axis). The homotopical axis(HA) is defined as:

$$\mathsf{HA} = \lim_{\beta \to 0^+} \mathbf{G}_{\beta}(\mathcal{R}) \quad \text{where}$$
$$\mathbf{G}_{\beta}(\mathcal{R}) = \{ x \in \mathcal{R} | \exists t \in \mathbb{R}^+ \exists y \in \mathbf{F}_{\beta}(\mathcal{R}) : x = \mathfrak{C}(t, y) \}.$$

 $\mathbf{G}_{\beta}(\mathcal{R})$ is the smallest superset of the set of critical points \mathbf{F}_{β} . $\mathbf{G}_{\beta}(\mathcal{R})$ contains all points reachable via the flow \mathfrak{C} ; this concept and notation has been introduced in [Chazal and Lieutier, 2005a] where the proof is given that $\mathbf{G}_{\beta}((O))$ is homotopy equivalent to the open set:

Lemma 2.25 (Homotopy Type of \mathbf{G}_{β} [Chazal and Lieutier, 2005a]). Let \mathcal{O} be a bounded open set. Then for any $\beta > 0$, $\mathbf{G}_{\beta}(\mathcal{O})$ has the same homotopy type as \mathcal{O} .

Lemma 2.25 states the homotopy equivalence between an open set and the β -superset of the critical points $\mathbf{G}_{\beta}(\mathcal{O})$ which consists of exactly one connected component. The homotopical axis is the subset of $\mathbf{G}_{\beta}(\mathcal{R})$ if β tends to zero. So, to derive the homotopical equivalence of our axis we first imply that the homotopy equivalence remains if β tends to zero. Then we infer that the result Lemma 2.25 is also applicable to the set of open sets - the space partition, and finally proceed with the result again for β tending to zero.

Corollary 2.26 (Homotopy Type of HA on \mathcal{O}). Let $HA_{\mathcal{O}}$ be the homotopical axis of a bounded open set \mathcal{O} . Then, since $HA_{\mathcal{O}}$ is defined with $\beta > 0$, $HA_{\mathcal{O}}$ has the same homotopy type as \mathcal{O} .

Corollary 2.27 (Homotopy Type of $\mathbf{G}_{\beta}(\mathcal{R})$). Since \mathcal{R} is the union of pairwise disjoint bounded open sets, then for any $\beta > 0$, $\mathbf{G}_{\beta}(\mathcal{R})$ has the same homotopy type as \mathcal{R}

Corollary 2.28 (Homotopy Type of HA). Since HA is defined with $\beta > 0$ and $\mathbf{G}_{\beta}(\mathcal{R})$ has the same homotopy type as \mathcal{R} (Corollary 2.27), HA has the same homotopy type as \mathcal{R} .

The medial axis is also called a *complete shape descriptor* because it is homotopy equivalent to its open set. In the last two sections we learned of two further homotopy equivalent subsets of the medial axis. In fact every deformation step converting the starting shape into its axis has the same result. There is an infinite class of shapes of equal homotopy type having the same axis.

In the following we use the homotopy equivalent axis to define a function which maps each point of the boundary to a certain value.

2.2.5 Feature Sizes

The goal of our work is to define sampling conditions and a reconstruction method which preserves topological properties. We approach this by defining a function which maps each point of the boundary to a value. This value then serves as a sampling density and maximal sampling point deviation factor.

Local Feature Size

The function called *local feature size* directly relates to the medial axis and describes for each point on the boundary the curvature. The local feature size of a boundary point is simply its shortest distance to the medial axis. The local feature size satisfies the Lipschitz property [Amenta and Bern, 1999].

Definition 2.29 (Local Feature Size). Let $b \in \partial \mathcal{R}$ be a boundary point of a space partition \mathcal{R} and let MA be the medial axis of \mathcal{R} . Then the local feature size (lfs) of a boundary point b is defined as:

$$\mathsf{lfs}(b) = \min_{y \in \mathsf{MA}} \|b - y\|$$

Since the local feature size is zero at non-smooth boundary points (e.g. corners), all reconstruction algorithms which require a sampling density based on the local feature size can only be applied to smooth boundaries. Such methods require an infinite number of points to sample a corner.

Local feature size on a boundary point can also be seen as the radius of the maximal inscribing ball touching the boundary in this point. The class of shapes for which the minimal local feature size is greater than a certain value r is called *r*-regular. The equivalent definition given in [Attali, 1997] states that a 2D shape is *r*-regular if an open ball of radius r > 0 can be inscribed on both sides of the boundary.

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Definition 2.30 (*r*-Regular Shape [Attali, 1997]). Let $\partial \mathcal{R}$ be *r*-regular shape if it is morphologically open and closed with respect to a ball of radius r > 0.

In [Attali, 1997] 2D reconstruction method is given and it is proven that it results in a topologically equivalent contour for r-regular shapes if the sampling points lie on the original boundary and the sampling density is less than 0.5r.

Weak Feature Size

A weaker condition on sampling density has been proposed to recover topological properties of a bounded set [Chazal and Lieutier, 2005b]. The so-called *weak feature size* is defined as the distance between the boundary and the set of criticals. Even though this feature size is suitable for non-smooth boundaries, the definition is global for the whole boundary.

Definition 2.31 (Weak Feature Size [Chazal and Lieutier, 2005b]). Let $\mathbf{F}(\mathcal{R})$ be the set of critical points of the space partition \mathcal{R} , the weak feature size (wfs) of a boundary point b is defined as follows:

$$\mathsf{wfs}(b) = \min_{y \in \mathbf{F}(\mathcal{R})} (\mathrm{d}_{\mathcal{R}}(y))$$

For λwfs , the weak feature size can also be seen as the value of the maximal dilation which does not change the homotopy type of the original boundary. This interpretation is verified by the following theorem.

Theorem 2.32 (Homotopy Equivalence of λ -Medial Axis [Chazal and Lieutier, 2005a]). Let \mathcal{O} be a bounded open subset of \mathbb{R}^n and MA_{λ} be its λ -medial axis with $\forall bin \partial \mathcal{O} \lambda < \mathsf{wfs}(b)$, then \mathcal{O} is homotopy equivalent to MA_{λ} .

In Chapter 4 we discuss a related concept of r-stable sets, where the r-value corresponds to wfs. A shape is then called r-stable if its r-dilation is of the same homotopy type. The reconstruction method and the proof of its *topological correctness* (see Definition 2.46) based on this globally-set parameter is given in [Stelldinger and Tcherniavski, 2009c].

Strongly related to the wfs is the *homological feature size* introduced in [Cohen-Steiner et al., 2007]. Its definition uses homological critical values instead of classical critical values, and in general the homological feature size is greater than or equal to the weak feature size. Nevertheless, in our case of a Euclidean distance transform in \mathbb{R}^3 , both types of critical values are identical.

The weak feature size is always greater than or equal to the smallest value of the lfs, which is often called *reach* [Federer, 1959]. The reach of the boundary of a set strongly relates to the definition of *r*-regular sets [Attali, 1997],[Stelldinger, 2008c].

Reachable Critical Points

Following the steepest path we expect to arrive on the tip of a mountain. In fact the case is more complex. First, there is no gradient definition for the boundary of the open set. So, how can we ascend the mountain of the distance transform starting on the boundary? The answer is we follow the steepest path which starts in the infinitesimal environment of our starting point. Here we face the following problem: there are two sides of the boundary. Consequently, we can ascend two different paths leading to at least two different tips of different mountains separated by our boundary.

Even if we decide to follow the path on one side only, we face the next problem: arriving at a saddle the gradient becomes zero. We have to use the general definition of the β -critical points and look for the steepest ascend if β tends to zero. Again we face the forking problem. So, we can *reach* more than one tip of a mountain following steepest ascends even if we decide to choose one side of the boundary.

In fact on the way to the tip of the mountain we can *reach* more than one saddle. So, the steepest ascend to a maximum may consist of numerous critical points. In order to be able to escape critical points (where the gradient vanishes) and include maxima that can only be reached by passing other criticals, we use the following recursive definition, starting in the ϵ environment of an arbitrary point $x \in \mathbb{R}^3$:

Definition 2.33 (Reachable Critical Points). Let $x \in \mathcal{R} \cup \partial \mathcal{R}$ be a certain point in space. Let

$$\mathbf{F}^{0}_{\beta}(\mathcal{R}, x) = \left\{ y \in \mathbf{F}_{0}(\mathcal{R}) \mid \forall \epsilon \in \mathbb{R}^{+} \exists y' \in \mathbb{R}^{3} : \|y' - x\| < \epsilon \land y = \lim_{t \to \infty} \mathfrak{C}(t, y') \right\}$$
$$\mathbf{F}^{i}_{\beta}(\mathcal{R}, x) = \left\{ y \in \mathbf{F}_{0}(\mathcal{R}) \mid \exists y' \in \mathbf{F}^{i-1}_{\beta}(\mathcal{R}, x) \exists y'' \in \mathbf{F}_{\beta}(y') : y = \lim_{t \to \infty} \mathfrak{C}(t, y'') \right\}$$

The set of all criticals reachable by steepest paths starting on an arbitrary point $x \in \mathbb{R}^3$ is given by $\mathbf{F}^{\infty}(\mathcal{R}, x) = \lim_{\beta \to 0^+} \mathbf{F}^{\infty}_{\beta}(\mathcal{R}, x).$

Notice in Definition 2.33 the set $\mathbf{F}^{0}_{\beta}(\mathcal{R}, x)$ is the first set of reachable critical points in the recursive definition. The starting points for the steepest paths are in the infinitesimal ϵ -environment of x. This is needed for the case if x is in the boundary of the space partition. Some of criticals in $\mathbf{F}^{0}_{\beta}(\mathcal{R}, x)$ may already be local maxima.

If there are saddles in $\mathbf{F}^{0}_{\beta}(\mathcal{R}, x)$ then a following set of reachable criticals has to be defined starting in that saddle. Here we need the β -environment. Notice that β is the parameter in the general definition of a gradient and denotes the gradient magnitude.

Using the set of all reachable critical points we can select only the local maxima and define the set of *reachable maxima*:

Definition 2.34 (Reachable Maxima). Let $\mathbf{F}^{\infty}(\mathcal{R}, x)$ be the set of reachable critical points for $x \in \mathcal{R} \cup \partial \mathcal{R}$, then the set for f is: $\mathbf{H}(\mathcal{R}, x) \subseteq \mathbf{F}^{\infty}(\mathcal{R}, x)$ and is called the set of reachable maxima if it contains all local maxima of $\mathbf{F}^{\infty}(\mathcal{R}, x)$.

The set of reachable local maxima is the basis for the following new feature size which measures the minimal size of a neighboring region.

Local Region Size

The new feature size is only "quasi"-local. It measures the minimal size of the neighboring region. The size of a region is defined by the greatest radius of the maximal inscribing balls. In other words the size of a region is the greatest distance value of the local maxima on the distance transform defined by the boundary of this region.

The *local region size* gives the evidence on the minimal neighboring region for a boundary point. The function was developed for multiregional space partitions to describe the minimal density of points to enclose a region in such a way that the distance function defined on the sampling points develops a local maximum inside the region. The goal here is to establish a correspondence between local maxima on the distance function defined on the continuous boundary and the local maxima defined on the set of sampling points.



Fig. 2.12: (a)Medial axis (dotted line), steepest paths (thick arrows), Irs: distance value of minimal reachable maximum (radius of dashed circle). (b) Homotopical axis (dotted line), distance to nearest point on homotopical axis (radius of dashed circles)

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Definition 2.35 (Local Region Size [Stelldinger and Tcherniavski, 2009b]). Let $b \in \partial \mathcal{R}$ be a boundary point of \mathcal{R} . Let $\mathbf{H}(\mathcal{R}, b) \subseteq \mathbf{F}^{\infty}(\mathcal{R}, b)$ contain all local maxima of $\mathbf{F}^{\infty}(\mathcal{R}, b)$. Then the local region size (lrs) of a boundary point b is defined as:

$$\mathsf{lrs}(b) = \min_{y \in \mathbf{H}(\mathcal{R}, b)} \mathbf{d}(y)$$

The advantage of the local region size is that it is never zero since no zero maximum exists. The disadvantage can be observed in Figure 2.12 (a). The thick lined arrows denote the steepest paths to the minimal reachable local maximum. The minimum maxima for the boundary points on the tail of the fish is the smaller maximum of the region. So, the local region size does not measure here the absolute region size.

Obviously, for any boundary point, the local region size is greater than or equal to the local feature size, since at least one steepest path passes through the nearest point of the medial axis. The weak feature size never exceeds the local region size, since the smallest value of the local region size relates to the smallest local maximum of the distance transform, which is greater than or equal to the smallest distance value of a critical point.

Local region size is strongly related to the watershed transform (see e.g. [Roerdink and Meijster, 2000]). Taking the positions of the local maxima as seeds, the combined boundary of the resulting regions covers the boundary of the space partition, and the locally adjacent region with smallest corresponding maximum defines the local region size in a boundary point. Simply speaking, the space is then partitioned into regions containing exactly one maximum of the distance transform each. The size of the regions is defined by the distance value of the corresponding maximum, and the local region size of a boundary point is defined as the size of the smallest adjacent region.

Local Homotopical Feature Size

The local region size introduced before has one disadvantage. It loses the volumetric information between the local maxima of one and the same region. Consider our fish example. The local region size on the boundary of the tail would be the same even if we separate the tail from the corpus. So, the local region size is not suitable for regions with saddles. The appropriate shape class for the local region size is called *star-like shapes* containing exactly one local maximum in each region.

Here we introduce a locally variable feature size based on the homotopical axis. The homotopical axis contains all critical points. The feature size based on the homotopical axis has the advantage of enabling measurements using the connection between the local maxima of a region. In particular, we take the smallest distance value of the *reachable* local maxima which - as we learned before - is the local region size and the distance to the homotopical axis into account:

Definition 2.36 (Local Homotopical Feature Size). Let $b \in \partial \mathcal{R}$ be a boundary point of \mathcal{R} . Then the local homotopical feature size of a boundary point b is defined as

$$\mathsf{lhfs}(b) = \min\left(\min_{x \in \mathsf{HA}}(\|b - x\|), \min_{y \in \mathbf{H}(\mathcal{R}, b)}(\mathbf{d}(y))\right)$$

The smaller value between the local region size and the distance to the homotopical axis defines the local homotopical feature size. Consider the illustration in Figure 2.12. The dashed circles in (a) denote the minimal reachable local maxima. The thick drawn arrows are the steepest paths to the corresponding minimal reachable maximum. Comparing the results to the figure in (b) where the dashed circles denote the distance to the homotopical axis, we observe that for the points near the eye the distance to the homotopical axis is much less than the distance value of the minimal reachable maximum. This is not the case for the points in the boundary of the fish tail and the fins.

Comparing the Results

In Figure 2.13 we present the distribution of the different feature sizes introduced previously. For a better illustration we choose the following procedure. Assume that the pen drawing the boundary has the thickness of the corresponding feature size. Since the local region size is the greatest, and since



Fig. 2.13: (a) 0.9lfs-distribution. (b) 0.9wfs-distribution. (c) 0.5lrs-distribution. (d) 0.8lhfs-distribution.

taking the pen size as the whole value would oversize the illustration, we uniformly scaled the local region size by the factor 0.5.

Notice that while the local feature size in (a) and the weak feature size in (b) are continuous, the local region size and the local homotopical feature size are not. The consequence is, in (c) and (d) the pen size jumps from thin to thick as for example in the boundary changing from the fins to the corpus.

As discussed before the weak feature size is always greater than or equal to the minimal local feature size.

$$\forall b \in \partial \mathcal{R} : \mathsf{wfs}(b) \ge \min_{b' \in \partial \mathcal{R}} \mathsf{lfs}(b')$$

Since the homotopical axis is a subset of the medial axis, and the local homotopical axis is always at least the distance to the homotopical axis, the local homotopical feature size is always greater than or equal to the local feature size. Since the criticals are in the homotopical axis, the equivalent statement can be made: the local homotopical feature size is always greater than or equal to the weak feature size. To sum up, we get the following hierarchy:

$$\forall b \in \partial \mathcal{R} : \mathsf{lfs}(b), \mathsf{wfs}(b) \leq \mathsf{lhfs}(b) \leq \mathsf{lrs}(b)$$

2.2.6 μ -Critical Point Theory

In [Chazal et al., 2009] the definition of a critical point is extended to μ -critical point which is a point of a compact set with gradient norm less than or equal to μ . From the gradient definition in Definition 2.17 we recall that the norm of the gradient does not exceed 1.0 and approximates 1.0 outside the medial

axis. On the medial axis the gradient norm is smoothed and is equal to zero at critical points. In "small" environments of the critical points the gradient values approximate 0.

The *critical function* maps a distance value to the infimum of the gradient norm on points at this distance. We can visualize the critical function as the boundary of a boundary dilation: the value of the dilation is the distance value, and the gradient values on the boundary of the dilation determine the value of the critical function. Again, according to Definition 2.17 the critical function has greater values if the boundary of the dilation does not intersect the medial axis, and lower values if it does. The critical function is zero if the boundary of the dilation intersects a critical point.

Definition 2.37 (Critical Function [Chazal et al., 2009]). Given a compact set $\partial \mathcal{R}$, its critical function $\chi_{\partial \mathcal{R}} : (0, +\infty) \to \mathbb{R}^+$ is the real function defined by:

$$\chi_{\partial \mathcal{R}}(d) = \inf_{\mathbf{d}_{\partial \mathcal{R}}^{-1}(d)} \|\nabla_{\partial \mathcal{R}}\|$$

The function $d_{\partial \mathcal{R}}^{-1}(d)$ is the inverse to the distance function and returns the set of points with distance value d. $\nabla_{\partial \mathcal{R}}$ is the gradient function defined on the distance function of $\partial \mathcal{R}$ and $\|\nabla_{\partial \mathcal{R}}\|$ is its norm.

The μ -reach is the infimum of all distances at which the critical function is less than μ .

Definition 2.38 (μ -Reach [Chazal et al., 2009]). The μ -reach $r_{\mu}(\partial \mathcal{R})$ of a compact set $\partial \mathcal{R}$ is defined by:

$$r_{\mu}(\partial \mathcal{R}) =) \inf \{d \mid \chi_{\partial \mathcal{R}}(d) < \mu\}$$

Setting $\mu = 0$ the μ -reach becomes the *weak feature size* (see Definition 2.31.). Weak feature size, as we recall, is the minimal distance value of critical points. So, the μ -reach is some kind of weak feature size but it investigates the distance values on points around the critical points.

2.3 Digital Geometry

In our framework we assume that there is a process which converts a scene in the real world into a computer file. The scene in the real world is a space partition. The converting or as we call it digitization process performs a data acquisition device. The data acquisition device samples the boundary of the real space partition.

2.3.1 Boundary Sampling Points

The point set resulting from sampling the original boundary may be seen as the starting point for the reconstruction method. Our investigation starts earlier. As described previously, we can use shape descriptors like medial axis to determine the homotopy type of the shape. Using the shape descriptor we can define a function mapping each point on the boundary to a unique value called feature size. According to the assumed feature size we determine the sampling density and the maximal sample point deviation from the boundary. Using these limits we can state that the guarantees on the reconstruction can be given if the sampling conditions do not exceed these limits.

Definition 2.39 (Boundary Sampling Points). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} . Let $f, g: \partial \mathcal{R} \to \mathbb{R}$ be well-defined functions. The set of points S is called boundary sampling points if

$$\begin{array}{lll} \forall b \in \partial \mathcal{R} \, \exists s \in \mathsf{S} : & ||b - s|| & \leq & f(b) \quad \text{and} \\ \forall s \in \mathsf{S} \, \exists b \in \partial \mathcal{R} : & ||b - s|| & \leq & g(b) \end{array}$$

In our work we investigate the poorest sampling conditions under which the topological guarantees can be given. Consider our 2D fish example in Figure 2.15. The points illustrate the result of a very turbulent sampling. We observe that the sampling points deviate from the boundary, building not very dense clouds of points, some of which build shape-like groups, some of which quite uniformly distributed. However, we also observe that the points densify the closer they are to the boundary. The relative closure between the boundary and the points is measured and limited by the f-function in Definition 2.39. Phrasing the formula we say, the distance between each boundary point and its closest sampling is at most f(b). So, f(b) measures the *density* of sampling points relative to boundary point b.

The maximal deviation from the boundary is measured by g(b). Phrasing the formula, we say, the distance between each sampling point and its closest boundary point is at most g(b). In our framework we do not differentiate between the case of sampling point deviation from the boundary and the sampling points which do not correspond to any point on the boundary. The latter points are known as *outliers*. We generalize the two concepts and call the input set as *noisy* or *noise-corrupted* if not all sampling points are on the boundary. So, g measures the maximal *amount* of noise which a reconstruction method can handle.



Fig. 2.14: Left: for all sampling points the maximal distance to the closest boundary point is zero. Right: the maximal distance between any boundary point and its closest sampling point tends to zero.

In Figure 2.14 we illustrate the difference between the measurements f and g. In the left figure the maximal distance between any sampling point and its closest boundary point is zero. All sampling points are on the boundary. So, $\forall s \in S \exists b \in \partial \mathcal{R} : ||b - s|| = g(b) = 0$. But there are no points around the boundary point b. The closest sampling point for b is s. This distance is ignored by the function g which measures the sampling points deviation from the boundary.

The right illustration in Figure 2.14 demonstrates a very dense sampling. For each boundary point there is a sampling point a some close distance: $\forall b \in \partial \mathcal{R} \exists s \in S : ||b-s|| = f(b) \rightarrow r$. Here the function f ignores the fact that there is an outlier s at great distance from the boundary.

2.3.2 Discrete Distance Transform

In Section 2.2.2 we learned the function which maps any point in space to the distance to its closest boundary point - the *distance transform*. The distance transform measures the Hausdorff distance between two sets, the set consisting of the current space point only and the continuous set of boundary points.

The concept of the distance transform is generalized to Hausdorff distance between a point in space and any set of points. According to the definition in Definition 2.16 we define the *discrete distance transform* as:

Definition 2.40 (Discrete Distance Transform). Let $\partial \mathcal{R}$ be a boundary of a space partition \mathcal{R} and let S be a finite set of boundary sampling points. The discrete distance transform d_{S} of a set $\mathsf{S} \subset \mathbb{R}^3$ is defined as $d_{\mathsf{S}}(x) = \min_{y \in \mathsf{S}} ||x - y||$. The reversed discrete distance transform is defined as $\mathrm{rd}_{\mathsf{S}}(x) = \{y \in \mathsf{S} \mid ||x - y|| = d_{\mathsf{S}}(x)\}$.

Consider the very noisy set of sampling points in Figure 2.15 (a). The points are very dense on some parts of the boundary and strongly deviate from the boundary at others. Illustration of the discrete distance transform is given in Figure 2.15 (b). The greater the distance value the brighter is the gray value. Mapping each coordinate to its gray value we also illustrate in Figure 2.15 (d) the discrete distance transform as gray value mountains, which corresponds to the illustration of the continuous distance transform in Figure 2.8 (b).



Fig. 2.15: Boundary sampling points distributed around the original boundary.

Gradient

The gradient notation in Definition 2.17 introduced in [Lieutier, 2004] is based on the center of the smallest closed ball enclosing the nearest boundary points. In discrete case it is the center of the smallest ball enclosing the nearest points in the sampling which are given by $rd_{s}(x)$ for any point x in space

Let $\Theta(x)$ be the center of the smallest closed ball enclosing $rd_{\mathsf{S}}(x)$. Then gradient on x on the discrete distance transform is defined in the same way as in Definition 2.17, where the set of critical points is straightforwardly defined by replacing the continuous set of boundary points \mathcal{R} by the finite set of sampling points S : set of critical points of ∇ is given by $\mathbf{F}(\mathsf{S}) = \{x \mid \|\nabla(x)\| = 0\}$ for each point x in space but not in S . The general definition is then: $\mathbf{F}_{\beta}(\mathsf{S}) = \{x \mid \|\nabla(x)\| \le \beta\}$.

The discrete distance transform is not everywhere smooth. So ∇ is not continuous, which can be seen by sharp "ridges" on the gray value "mountains" in Figure 2.15 (d). These sharp ridges are the points on the distance transform where the gradient value is less than 1. Everywhere else but on the sampling points the gradient value is 1.

Using the gradient we again know how to "climb the mountains" (compare Section 2.2.2). Gradient maximized the growth of the distance transform. The flow induced by the gradient is also defined here, as in [Lieutier, 2004] where the authors prove that using the vector field ∇ Euler schemes converge uniformly when the integration step decreases. In 3D the definition is then as follows:

$$\mathfrak{C}: \mathbb{R}^+ \times \mathbb{R}^3 \setminus \mathsf{S} \mapsto \mathbb{R}^3 \setminus \mathsf{S}$$
 with $\mathfrak{C}(t, x) = x + \int_0^t \nabla \left(\mathfrak{C}(\tau, x)\right) d\tau$

Starting in any point in space we reach for $\lim_{t\to\infty}$ a critical point on the distance transform. The

resulting *flow line* is the *steepest increasing path* on the discrete distance transform. In Section 2.4.8 we will use the flow lines to specify elements of a combinatorial structure and in Section 2.4.9 to imitate the flow using a relation between these elements.

2.3.3 Discrete Medial Axis

Here we introduce for the first time the relation between the distance transform and the combinatorial structures which will be used for reconstruction in our framework. Consider the construction of the medial axis for a continuous shape in Section 2.2.3. As introduced in [Blum, 1967] we used the centers of maximal inscribed balls to define the medial axis. The points on the medial axis are exactly the points where the gradient value is not 1. In the 2D example in Figure 2.8 the medial axis is the sharp "ridges on the mountains".

The radius of the maximum inscribed ball is the distance value of the distance transform on the center of this ball. So, we obviously can build the medial axis on our set of sample points. If the maximum inscribed ball touches at least two points we define its center as a point of the *discrete medial axis*. So, for a finite set of sample points S the *discrete medial axis* is defined as

$$\mathsf{MA}_{\mathsf{S}} = \{ x \in \mathbb{R}^3 | \mathrm{rd}_{\mathsf{S}}(x) | > 1 \}$$

The result for our 2D example is illustrated in Figure 2.15 (c). We observe that the lines of the discrete medial axis correspond to the sharp ridges of the discrete transform mountain in Figure 2.15 (d).

Each point in Figure 2.15 (c) is enclosed by the lines of the discrete medial axis. The seemingly open cells separate the corresponding points from the others by infinite lines. Such *cells* are also called "Voronoi cells" and the union lines of the discrete medial axis is called "Voronoi diagram". We introduce this concept in Section 2.4.6.

2.4 Digital Topology

Topological spaces can hardly be used on computers. So, combinatorial structures based on a finite set of points are used for the representation. Here we introduce the geometric elements that make up the combinatorial structures. Furthermore we introduce certain special structures *Voronoi diagram* and *Delaunay triangulation* used in our framework.

2.4.1 General Position

Throughout our work we assume that the points of the finite set S are in *general position*. We mean by general position that no 3 points lie on a common line, no 4 points lie on a common plane, no 5 points lie on a common sphere.

The assumption simplifies the coming definitions, considerations and algorithms and relieves us from dealing with special cases. This is justified since the points can be brought into the general position by infinitesimal perturbation of the points. The corresponding programming technique to simulate the perturbation is known as "SoS" and was introduced in [Edelsbrunner and Mücke, 1990].

2.4.2 Simplicial Complex

Before we come to the definition let us undertake some steps to get an intuition. Consider four nonplanar points in space. A convex hull of the points is a filled tetrahedron. The sides of the tetrahedron are triangles. Or convex hulls of three nonlinear points. The sides of a triangle are edges which again are convex hulls of two points. So, a convex hull of a specified number of points which does not contain any other point is called a *simplex*. The convex hulls of any subset of points of any simplex is called a face of the simplex. A complex is a set which collects simplices together with their faces.

Definition 2.41. Let $S \subset \mathbb{R}^3$ be a finite set of points. Then the convex hull of $n \in \{1, 2, 3, 4\}$ points $s_1, ..., s_n \in S$ is called an (n - 1)-simplex with n - 1 being its dimension. Any simplex σ_1 based on the convex hull of a subset of the points defining a second simplex σ_2 , is called a face of σ_2 , and σ_2 is called a coface of σ_1 . A face and a coface are called proper if their dimensions differ by exactly 1. The 3-simplices are called tetrahedra, the 2-simplices are triangles, the 1-simplices are edges, and the 0-simplices are the points of S. Now a (simplicial) complex \mathcal{K} is a set of simplices in \mathcal{K} is also a simplex in \mathcal{K} , and the intersection of any two simplices in \mathcal{K} is also a simplex in \mathcal{K} . A simplicial complex \mathcal{K} is called complete, if the union of the simplices $|\mathcal{K}| := \bigcup \sigma \in \mathcal{K}$ equals the convex hull of S. A subcomplex of a complex is a subset, which itself is also a complex. Let σ be an (n-1)-simplex with corner points $s_1, ..., s_n \subset S$ for a finite point set $S \in \mathbb{R}^3$. Then the smallest sphere containing all corner points $s_1, ..., s_n$ is called the circumsphere of the simplex. The interior, the center and the radius of the sphere are called the circumspliel , the circumcenter and the circumradius of the simplex.

2.4.3 Delaunay triangulation

The basis for our framework builds on a special simplicial complex called *Delaunay triangulation*. A triangulation is a notation taken from a 2D framework and is used to describe some connectivity of 2D points in space. Usually, the crucial criterion to build a triangulation is to connect any three points in such a way that the resulting triangle does not cut any already existing.

A Delaunay triangulation restricts the triangles by *empty ball* condition: the circumcircle of any triangle is not to contain further points. We visualise the empty ball condition in Figure 2.16. The illustrations in (a) and (b) are both triangulation: the build triangles do not cut each other. But in (a) a circumcircle of the thicker triangle does contain a point whereas in (b) all circumcircles are empty.

The notation *triangulation* is often carried into the 3D framework and in fact stands for tetrahedralization. The definition of a 3D Delaunay triangulation does not allow the circumsphere of any tetrahedron to contain further points. Notice, the rule is valid for tetrahedrons only not for triangles.



Fig. 2.16: (a) Triangulation not fulfilling the empty ball condition. The circumcircle of the thick triangle contains a point. (b) Delauany triangulation: the circumcircles of all triangles are empty.

Definition 2.42 (Delaunay triangulation [Delaunay, 1934]). Let P be a subset of S, with |P| = 4 and let σ_P be the convex hull of P. σ_P is a Delaunay cell if and only if the circumsphere of P does not contain any other point of S. Delaunay triangulation or Delaunay complex of a point set S is the simplicial complex D where all 3-cells are Delaunay cells.

2.4.4 Elementary Collapse

A simplicial complex contains the information on connectivity between the points. Obviously, deleting any simplex changes the neighborhood relation of the corresponding points and so their connectivity. Here we want to remove simplices from the complex without changing the neighborhood relations between the connected components of its complement.

In our framework the original scene object is represented by a set of points. In our approach we carve the Delaunay triangulation to retrieve an equivalent of the original object.

Here we introduce a technique to reduce the given complex to its homotopical equivalent. In other words we map the existing complex to its homotopy equivalent subset. The goal is to produce a most simple object representation.

Definition 2.43 (Elementary Collapse). Elementary collapse (denoted by \searrow) removes a pair of simplices (σ, τ) from a simplicial complex provided σ is simple and τ is its proper coface. A simplex σ is simple if and only if there is exactly one simplex τ in the simplicial complex such that σ is a face of τ .

Fact 2.44 (Homotopy Equivalence of the Elementary Collapse). Let D be a simplicial complex and D' be the result of elementary collapse on D, then D is homotopy equivalent to D'.

Consult [Edelsbrunner, 2003] 7 for the proof of Fact 2.44 and the construction of the deformation retraction.



In Figure 2.17 we see an example of elementary collapse first on the simple triangle $\{ABC\}$ and its proper coface the tetrahedron $\{ABCD\}$ (in (b) notated by shrunk tetrahedron). The result of the first collapse is in (c). The edges, the three triangles and the vertices of the original tetrahedron remain constant. Notice, in (a) all triangles of the tetrahedron are simple. The choice of the triangle $\{ABC\}$ is arbitrary.

The first collapse results in three simple edges: $\{AB\}$, $\{AC\}$ and $\{BC\}$. The next collapses remove the edges (result in (d)) and their adjacent triangles. The result of the collapses is in (e). Here the

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vertices $\{A\}, \{B\}$ and $\{C\}$ became simple. The last collapses remove the vertices and the adjacent edges from the complex. So, the original complex is reduced by a series of collapses to the vertex $\{D\}$. Notice, that the choice of another simple triangle would lead to another result. But the final result on this complex without any simple simplices is always one vertex.

As an exercise consider a simplicial complex of a filled donut. All faces on the surface are simple. What remains if we reduce the filled donut by a sequence of elementary collapses as long as simple simplices can be found? The answer is, a loop, topologically a circle. Or consider the surface of a donut: no tetrahedron is in the complex. Is there any simple simplex? The answer is no. Consequently, the surface of the donut is irreducible by elementary collapsing.

2.4.5 Reconstruction

Now, our task is to reconstruct the spatial and topological information from a given set of sampling points lying on or near the boundary of the original partition. In many applications the given set of points is considered as the reconstruction. Consider for example the 3D images engraved into a crystal cube. The spatial and topological similarity is then expected to be done by the observer.

Further, any set of connections can be considered as the reconstruction as long as the user sees any sense in the result. In our case we develop a method starting with the construction of the Delaunay triangulation on the set of points. The resulting connections between the points is a result of the convex hull reconstruction. Further steps intend to carve the Delaunay block into the correct reproduction of the original scene. Obviously, the carving in our case is a matter of well-defined and reproductive mathematical procedures. However, the convex hull block is already some reproduction and can be considered as a result. Then the resulting space partition consists of two regions, the outer infinite space or background, and the block with the convex boundary between the regions.

Obviously, the result is not guaranteed to generally be spatially very similar to the original. We think for example of concave shapes. Since in our case the original scene is mostly divided into more than two regions, and furthermore assuming a non-manifold boundary, the topological correctness is at this step irrelevant. But any step does retrieve relevant information - i.e. the nearest neighbor connections between the points - and can be considered as a result.

The carving steps label the Delaunay simplices, resulting in a set of simplices representing the boundary - the remaining simplices - and the set of simplices representing the interiors of the regions - the removed simplices. The result of the boundary reconstruction is the underlying space of the set of simplices representing the boundary. Any reconstruction step removes more simplices from the remaining set, reducing the complexity and - as is our target - enhancing the spatial and topological correctness of the reconstruction. Now the result of a reconstruction can be defined in the following way:

Definition 2.45 (Reconstruction). Let \mathcal{K} be a simplicial complex based on a set of points $S \subset \mathbb{R}^3$. Then a simplicial complex partition \mathcal{D} is a set of disjoint subsets D_i of \mathcal{K} , such that the regions $|D|_i$ covered by the sets D_i define a space partition $|\mathcal{D}| := \{|D|_i\}$. In the case of \mathcal{K} being a Delaunay triangulation, the subcomplex $\partial \mathcal{D} \subset D$, $\partial \mathcal{D} := \mathcal{K} \setminus \bigcup_i D_i$ is called the result of a reconstruction. Then, $|\partial \mathcal{D}|$ is called the reconstructed boundary, and the pairwise disjoint components D_i interiors of reconstructed regions. For each D_i , the underlying space $|D|_i = |D_i|$ is the reconstructed region. A simplex σ is called a boundary simplex if at least two of its cofaces lie in different interiors of reconstructed regions.

Given the size of the greatest simplices τ_i, τ_j in the regions $|D|_i$ and $|D|_j$ we write $|D|_i < |D|_j$ if and only if the size of τ_i is less than the size of τ_j .

In Definition 2.45 the notation *size* defines a function which uniquely maps a simplex to a scalar value. The definition of the size induces an order in the simplices. According to this order the simplices can be sorted and compared during the reconstruction procedure. This order establishes the relevance of a simplex or the probability of its belonging to the reconstructed boundary. So, different definitions of size differently sort the simplices and therefore the reconstructed regions which results in different reconstructed boundaries. We imply that the choice of the *size* definition is crucial for our method. In Section 2.4.11 we discuss this issue more closely.

Correctness. In our context we deal with discrete representations of the continuous world. The simplicial complex is abstract and is represented by a data structure holding the topological information. We often reference the *reconstruction* to the simplicial complex, but speaking mathematically correctly, the underlying space of the simplicial complex is the result of reconstruction.

The topological guarantees given by the reconstruction method may differ depending on the approach and the initial setting in the scene and data. The setting of nonmanifold boundaries makes it impossible to achieve the boundary of the reconstruction to be topologically equivalent. We make this clear in the following example.

Consider the letter 'X'. The topologically correct reconstruction must have a point which has four neighboring points in its infinitesimal environment. To achieve that, the sampling must guarantee to contain the topological information about the occurrence of such a point. The sampling conditions based on Hausdorff distance between the original boundary and the points in the sampling set cannot uniquely be defined to preserve the topological properties for such a point unless it is guaranteed that a sampling point meets this nonmanifold boundary point. But this restriction requires the sampling to be infinitely dense in the infinitesimal environment of the nonmanifold points, which is not practicable for any data acquisition device.

The consequence is, defining the sampling conditions based on Hausdorff distance between the original boundary and the points in the sampling set, the reconstruction methods cannot result in a topologically equivalent boundary. The result is then homotopically equivalent only. In the 'X' example the reconstruction can only guarantee to result in 'H' or in 'X'.

So, in our context we have to adapt the concept of guaranteed preservation of topological properties. We say the reconstruction is *topologically correct* if the reconstructed space partition - the union of interiors of the reconstructed regions - is topologically equivalent to the original and the boundary of the reconstructed space partition is homotopically equivalent to the original.

Definition 2.46 (Topological Correctness). Let \mathcal{D} be a simplicial complex partition and $|\partial \mathcal{D}|$ be the reconstructed boundary of the boundary $\partial \mathcal{R}$ of a space partition \mathcal{R} . $|\partial \mathcal{D}|$ is said to be topolocially correct reconstruction of $\partial \mathcal{R}$ if and only if $|\mathcal{D}| \setminus |\partial \mathcal{D}|$ is topologically equivalent to \mathcal{R} and $|\partial \mathcal{D}|$ is homotopically equivalent to $\partial \mathcal{R}$.

Minimal Reconstruction

Given the reconstructed region and the set of points in its boundary, there may be numerous different boundaries which enclose the region in a topologically correct way. Consider for example a 2D example illustrated in Figure 2.18. The first example in (a) is a reconstruction of a three-regions boundary including the infinite background. Let us assume this reconstruction to be topologically correct. So, the original space partition also consists of three regions topologically equivalent to the reconstructed regions and the boundary is homotopy equivalent. Here the boundary is thick - it contains triangles. A thin boundary consists of edges only.

The example in Figure 2.18 (b) is also a topologically correct reconstruction. The boundary in (b) is thin. The thinning process removed the greater edge collapsing on the adjacent triangle. The reconstruction method uses the length of an edge and results in a topologically correct reconstruction with a thin boundary consisting of edges of minimal length. In Figure 2.18 (c) the topologically correct reconstruction results in a thin boundary with minimal sum of lengths of boundary edges.

The thin reconstructions in (b) and (c) are topologically correct but differ spatially. However, we observe some spatial similarity between the results in (a), (b) and (c). In this example the reconstructed regions in (a) are subsets of reconstructed regions in (b) and (c). The thinning step compares two sets of boundary simplices and chooses which simplex is going to be removed next. Obviously, if the two reconstructed boundaries enclose topologically different regions, the comparison becomes senseless. So, we speak of topological and spatial similarity between the reconstructed regions if their sets of boundary simplices are to be compared. We call this similarity the *compatibility between space partitions*. The comparison criterion such as length of the edge orders the sets of boundary simplices such that one set becomes *minimal*. So, for our context we can define:



Fig. 2.18: (a) Some boundary reconstruction. The union of thick edges and gray triangles is the boundary of the reconstructed space partition (the union of white triangles and dashed edges). (b) Topologically correct reconstruction with boundary thinned according to minimal length of each edge. (c) Topologically correct reconstruction with boundary thinned according to minimal length of all edges.

Definition 2.47 (Minimal Reconstruction). Two reconstructed space partitions are called compatible, if there exists a one-to-one mapping between their reconstructed regions, such that every reconstructed region is mapped onto a topologically equivalent reconstructed region.

For compatible reconstructions let less (<) be a well-defined ordering relation, then a reconstruction is called minimal, if there exists no compatible lesser compatible reconstruction.

The ordering relation as it is assumed in Definition 2.47 is defined by edge length in (b) and number of edges in (c). So, the thinning step in (b) orders the simplices according to their length and removes the greatest. Consider for example two thinning results if from the thickness in the reconstruction in (a) two different edges are removed. The boundary set of simplices where the greater edge is removed is the smaller boundary. In example (c) two boundary simplex sets are compared which enclose the supersets of reconstructed regions from (a). The boundary set with the lesser number of simplices is the smaller reconstruction.

In Section 4.7.3 we introduce a minimal reconstruction as a result of "thinned- (α, β) -shape-reconstruction" where the ordering relation is defined by the circumradius of a simplex. Two α, β -regions are defined to be compatible if both contain the erosion of the same original region.

In Section 5.6 the minimal reconstruction is defined by the minimum distance value in a simplex. There is compatibility if two regions contain the same local maxima of a distance transform.

Reducible Reconstruction

Starting with the Delaunay triangulation as a "block" we assume the topologically correct boundary to be somewhere inside this block. So, with each "carving" step we have to prove that its result contains a topologically correct boundary. Since each carving step can be seen as a reconstruction we say the result of any reconstruction step is *reducible* if it contains a topologically correct boundary.

In our context any reconstruction step is in fact the removal of certain Delaunay simplices. Then, simply speaking, our goal after each step is to still have a set of simplices where further simplices can be removed to obtain a topologically correct result.

A counter example in 3D is a reconstruction of a ball from a highly noise-corrupted sampling. Consider a greater accumulation of sample points at one side. Consider further that a reconstruction step results in two regions - the background is ignored. One of the regions expands over almost all original interior of the ball. The other has a form of a handle on the greater region. We illustrate the example in a detailed discussion on results of a reconstruction in Section 5.15.1. Obviously, this boundary can be reduced to a topologically correct reconstruction by removing the handle region. But by forcing through the boundary in such a way that the interior of the handle merges with the greater region on both sides, the resulting interior region becomes topologically a donut. The boundary of a donut cannot be reduced to a boundary of a ball. We call such boundary to be *irreducible*.

2.4.6 Voronoi Diagram

We approach the solution of the reconstruction problem from two points of view: the differential geometry using the distance transform, and the combinatorial structures built on point sets. The Delaunay triangulation is a combinatorial structure which can be built on a finite set of points without undertaking any steps from differential geometry.



Fig. 2.19: Building Vornoi with two (left) and three (right) starting points.

Here we see a combinatorial structure which combines both points of view. Let us begin with intuitive construction which we know from school geometry. How do we draw a line between two points which evenly separates them? In other words all points on the line are equidistant to the two given points. We need compasses for it. Adjusting the compasses to have a greater radius than the distance between the points (compare Figure 2.19 left), we draw a half circle centered on the first point and without changing the radius of the compasses draw a second half circle centered on the second point. The half circles intersect in two points. The line through these two intersecting points is our required line.

Consider an edge between the two starting points. The length of this edge is the smallest diameter for our compasses and its center is the nearest point with the same distance between the two starting points. Our newly drawn line also goes through the center of this edge.

The constructed line is the *Voronoi diagram* (the continuous line in Figure 2.19) for the two starting points. The Voronoi diagram combines all points which are equidistant to any two points in the starting set.

To construct a Voronoi diagram for three points (Figure 2.19 right) we need to draw three lines one between each pair of starting points. The three lines intersect in one point. Now we just remove the half lines which start in this meeting point and do not intersect the center of the edge between the two corresponding points of the pair. Notice, somehow this half line corresponds with the edge between the points of the starting pair. But, we will come to this later.

The Voronoi drawing for greater point sets is a bit trickier. Following the iterative procedure we consider there is already a drawn Voronoi diagram (the continuous line segments in Figure 2.20) for the same point set except one last (m) we want to add. First we find the nearest neighbor k to m. In fact this is the one which is not separated by a line segment from m. Next, we draw a line, as we introduced in the case of two points, between k and m starting and ending on the intersecting point with the line segment which separates k from the others. By doing that we find the neighbor l of k, on which we proceed in the same manner. The drawing is completed when m is separated from all existing points which is equivalent to stopping if k is reached again.

As we have seen the intention is to separate each given point from the others by a line segment in such a way that each point on this line segment is equidistant to the point we want to separate and its neighbor. The result is a set of line segments and the polygons enclosed by these line segments. The union of the line segments is the Voronoi diagram. The set containing the line segments, their



Fig. 2.20: (a) Voronoi diagram construction by adding a new point m to the point set. (b) Duality between Voronoi (dashed lines) and Delaunay (continuous lines)

intersection points and the polygons enclosed by them is again a simplicial complex. Notice, that the line segments can be seen as intersections of the closures of the polygons.

The 3D Voronoi diagram is the extension of the previous considerations, but the points are elements of 3D space and planes are needed to separate them.

Definition 2.48 (Voronoi diagram [Voronoi, 1907, Voronoi, 1908]). For a point $p \in S$, define V(p), the Voronoi cell, as $V(p) = \{x \in \mathbb{R}^3 | \forall p' \in S : ||x - p|| \le ||x - p'||\}$. A Voronoi cell is also called 3-cell. The intersection of two Voronoi cells is a 2-cell or Voronoi polygon. The intersection of three Voronoi cells is called 1-cell or Voronoi edge. The Voronoi vertex is the nonempty intersection of four 3-cells.

A Voronoi diagram of S denoted as V is defined as the collection of the Voronoi cells for each point of S

If the points are in general position two Voronoi cells are either disjoint or the intersection is a twodimensional polygon; three Voronoi cells are either disjoint or the intersection is a line segment or half line. Four Voronoi cells meet either in one or in no point. The nonempty intersection of Voronoi cells is also called *face*.

Voronoi cells are convex polyhedrons and since the intersection of convex sets is a convex set, their intersections or *faces* are also convex. Voronoi cells have disjoint interiors and the collection of all Voronoi cells covers \mathbb{R}^3 .

Duality between Delaunay and Voronoi Let us consider again our 2D example construction. We build the Voronoi diagram in such a way that pairs of neighboring points are considered to draw a line which is an affine expansion of the corresponding Voronoi edge. The linear connection between these two points is an edge in the Delaunay triangulation. We imply that at least for each Voronoi edge there is a corresponding Delaunay edge. Vice versa, each Delaunay edge is the connection of two closest points. Exactly the points which are needed to construct a Voronoi line. In fact the construction of Delaunay is equivalent to the construction of the Voronoi diagram. The correspondence between Voronoi and Delaunay is a one-to-one mapping.

Let V and D be the Voronoi diagram and Delaunay triangulation on S and P be a subset of S, with d = |P| and $0 \le d \le 3$ and let V(P) be defined as $V(P) = \bigcap_{p \in P} V(p)$ then

 σ_P is a d-simplex of D iff V(P) is a (3-d)-cell of V

The Voronoi cell V(P) is called the *dual* cell to the Delaunay cell σ_P and vice versa.

Critical Points The duality between Delaunay and Voronoi establishes the connection between the

combinatorial structures and the differential geometry. As it is stated in [Giesen and John, 2003] the intersection between a Voronoi cell and its dual Voronoi simplex is the critical point on the distance transform defined on the data points. Note that this notation of critical point is the same as the one considered in the setting of nonsmooth analysis [Clarke, 1990] and Riemannian geometry [Cheeger, 1991, Grove, 1993]

2.4.7 Alpha-Shapes

In our framework we use the term *shape* to denote the underlying space of a combinatorial structure. So, a Delaunay 3-cell is an element of 3D Delaunay triangulation while its underlying space is the tetrahedron.



Fig. 2.21: (a) Point set. The circles denote the α -ball. (b) The union of gray triangles and thick line segments is the α -shape which is extended by dashed edges to Delaunay triangulation. (c) The union of α -balls is homotopy equivalent to α -shape.

The concept of α -shapes generalizes the convex hull of a point set. In [Edelsbrunner and Mücke, 1994] the authors give an illustration of α -shapes by considering the space to be filled with styrofoam and the points to be rocks. Then a spherical eraser (the circles in Figure 2.21 (a)) carves out the styrofoam at all positions where the rocks allow it. So, the eraser does not pass through the space between two rocks if their distance is less than 2α or if the maximal inscribed empty ball between more than two points has the radius less than α . Obviously, the remaining styrofoam is circular between the points where the eraser did not pass through. The generalized convex hull fills the remaining styrofoam in such a way that the connection between the rocks where the eraser did not pass is linear (planar in 3D). The resulting object is the so called α -hull. The α -shape (union of thicker line segments and gray triangles in Figure 2.21 (b)) is the underlying space of the α -hull.

 α -shapes may be disconnected or concave, may have holes or linear segments. In 3D, α -shapes may have cavities or tunnels, may consist of two-dimensional surface patches. α -shapes can even contain single points. I.e. the set of points is an α -shape for a too small α . The α -shape with α equal to the smallest distance between points adds to the shape only one edge. The increasing α adds further edges, triangles or tetrahedrons to the shape. The convex hull of the point set is the α -shape for too large α .

For our context we use the definition introduced in [Edelsbrunner and Mücke, 1994] which is based on the definition of the Delaunay complex. The α -shape is the underlying space of α -complex which is the subcomplex of Delaunay complex (the thick continuous line segments extended by the dashed lines to Delaunay triangulation in Figure 2.21 (b)).

Definition 2.49 (α -Shape [Edelsbrunner and Mücke, 1994]). Let D be a Delaunay complex of a finite set of points S. The α -complex D_{α} is the subset of D for which is valid: σ is a simplex in D, the open circumball of σ is free of points and the circumradius of σ is less than or equal to α then σ is in D_{α} The polytope $|D_{\alpha}|$, i.e. the underlying space $|D_{\alpha}|$ of D_{α} , is called α -shape and is denoted by \mathscr{S}_{α} . The closed ball with circumradius α is called α -ball.

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To establish an intuitive correspondence to Delaunay complex let us consider closed balls centered on points. All balls have the same radius which is continuously increasing up to α -value. Starting with zero and increasing the radius of balls, one connects two points to an edge, three points to a triangle, and four points to a tetrahedron if the balls overlap without containing any other point of the point set. The points connected by this construction are equivalently considered by construction of Voronoi diagram. So, the construction by increasing ball radii is a subset of Delaunay triangulation and of α -shape.

Notice the difference. In our 2D-example with an eraser and styrofoam the eraser is not allowed to contain any point. In contrast to that the balls are centered on the points in the other example.

The correspondence between the above construction and the resulting α -shape (see Figure 2.21 (c) for illustration) is stated by Theorem 2.50 which is proven in [Edelsbrunner, 1995].

Theorem 2.50 (Union of Balls [Edelsbrunner, 1995]). The union of closed α -balls centered at the points $p \in S$ covers the α -shape of S, and the two sets are homotopy equivalent.

Notice here again the correspondence between our combinatorial construction and the differential geometry: the α -shape changes its topology if the increasing α -value and with it the α -ball achieves a distance value of a critical on the distance transform.

2.4.8 Specifying the Simplices

In previous sections we learned about *simplices* - the elements of a Delaunay complex as well as their dual Voronoi cells. We also learned than the intersections of Delaunay simplices and its duals are the critical points on distance transform defined on the sampling points. So, using the combinatorial structures we made implications about local differential properties of a continuous function. The critical points are the combining link between a continuous function and the combinatorial structure defined on the points.

Here we start with the continuous function and proceed towards the concept of critical points to make specifications about intersections of Delaunay simplices and their duals and, following, about the properties of certain simplices.

A gradient of a function defines a first-order differential equation. A solution is a curve whose tangent vectors agree with the gradient of the function. For each non-critical point x there is a unique solution, the *flow curve* that contains x. In our context the flow curve is piecewise linear which justifies the notation *flow line*.

Every flow line starts in a critical point and ends in a critical point or in the infinite. We adopt the notation from [Edelsbrunner, 2003] of the infinite as a critical point with infinitely large distance value. We call it the *infinite maximum*.

The distance function on a point set S measures the distance to the nearest point. The flow line follows the steepest increasing path for every point in space. How do we introduce some intuition towards the trajectory of a flow line? The distance values increase linearly with the distance to the nearest point. So, the nearest point or nearest points push the point is space away. The direction of the gradient is then the vector starting on the nearest point and ending in the point in space - our measuring point. If more than one point is equidistant to our measuring point then the sum of vectors is the direction of the gradient.

Let us consider a two-dimensional example as illustrated in Figure 2.22. Let us consider further a closed ball with steadily increasing radius. If the closed ball centered on a point x_4 (compare Figure 2.22 (a)) in space touches a sample point A but does not contain any other points of $S = \{A, B, C\}$ then the sample point A pushes x_4 at most and the flow is directed from the sample point through x_4 (dashed arrow).

If the closed ball centered on x_4 contains two sample points (A and C) there is to decide which sample point is nearer. The nearest pushes the most until the distance to both sample points is equal (the end of the arrow through x_4 in Figure 2.22 (a)). The sum of the pushing vectors results in the new direction of the flow line (the short arrow starting on the end of the arrow though x_4 and ending in O).

If the pushing vectors are of the same length (the distance to the nearest is equal as for example in the center of AB) and are in opposite directions then the sum is zero and the flow line stays in the



Fig. 2.22: Flow lines on distance transform defined on points *ABC* which build (a) an acute (b) an obtuse triangle.

meeting point. This meeting point is a critical point of the distance function. This is the case for all flow lines starting on edges opposite to an acute angle. Otherwise the flow then makes a kink (compare the flow line through x_4) and follows the line perpendicular to the line connecting the sample points the dual Voronoi edge. This is the case for all measuring points in space not on the edge connecting the points.

Increasing the radius of the ball centered on x_4 until it contains a third sample point, and connecting the three sample points with edges, we construct a Delaunay triangle (ABC). The flow line from our previous construction with two sample points in the ball only follows the line perpendicular to the edge connecting the sample points until the circumcenter of the triangle is reached. If the triangle is acute (Figure 2.22 (a)) then the circumcenter is contained in the triangle's interior and the flow cannot leave. The circumcenter is equally pushed by points and in the case of an acute triangle the sum of pushing vectors is zero. In the case of an obtuse triangle (Figure 2.22 (b)) the flow does not end in the circumcenter. The sum of pushing vectors results in a vector in the direction perpendicular to the edge (AC) opposite to the obtuse angle away from the sample points.

In Figure 2.22 (b) x_3 is a point on the edge AC. But there is a sphere centered on x_3 containing further sample point B. This sample point B pushes x_3 the most and so the flow line on x_4 breaks addiff towards the circumcenter of the triangle and so the point which is equidistant to AC. The flow does not end in the center but the distance values increase along the dual Voronoi line to AC away from the sample points.

The simplices which contain the endpoint of the flow line are called *centered* and the simplices which do not contain its flow are *equivocal*. In 2D equivocal edges are opposite obtuse angles. The opposite sample point is too close to the sample points such that it pushes the flow away from the edge. This is the case if the circumsphere of the edge contains another sample point.

Let us extend our example to 3D. The radius of the ball centered on x is increased until it contains the fourth sample point. The convex hull of the four sample points is a Delaunay tetrahedron. If the circumsphere of three sample points of the tetrahedron does not contain any further sample point, or as we call it now - the vertex of the tetrahedron, then there are two cases to consider. The triangle built of these three sample points is acute - then it again is called *centered*. If the triangle is obtuse, then the flow is contained in the affine hull of the triangle but not the triangle itself. In such a case the triangle is called *confident*.

If the circumsphere of the triangle does contain the further vertex of the tetrahedron then we again have the case where the vertex pushes the flow away from the simplex. Such a triangle is *equivocal*.

In [Edelsbrunner, 2003] the specifications are summed up under the following properties:

Fact 2.51 (Centered Simplex [Edelsbrunner, 2003]). A Delaunay simplex σ with its dual Voronoi cell ν is centered if and only if the intersection of σ and ν is not empty. The intersection is a critical point of f_{ϵ} and its index is the dimension of σ .

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In our 2D example in Figure 2.22 (a) the triangle and its edges are centered. The triangle contains its own circumcenter which is its dual Voronoi 0-cell. The half-lines starting in the circumcenter and going through the centers of the edges are the dual Voronoi 1-cells of the edges. Since the intersection is not empty, the edges are centered.

Fact 2.52 (Equivocal Simplex [Edelsbrunner, 2003]). A Delaunay simplex σ with its dual Voronoi cell ν is equivocal if and only if the intersection of ν and the affine hull of σ is empty.

The 2D example in Figure 2.22 (b) illustrates the triangle with one equivocal edge AC. Its dual starts in the circumcenter O of the triangle and extends perpendicularly away from the center of the edge AB. The intersection is empty even if we expand the edge to a line.

The flow starting inside a Delaunay simplex necessarily crosses the circumcenter of its greatest dimensional coface. The flow starting inside a tetrahedron of a 3D Delaunay complex ends or crosses the circumcenter of the tetrahedron. The affine expansion of a triangle divides the space into the half-space containing the tetrahedron and the half-space not containing any point of the tetrahedron. Equivalent consideration is valid in 2D. Since the flow is pushed through the equivocal triangle and necessarily intersects the circumcenter of the tetrahedron we conclude that the circumcenter is on the other side of the plane containing the triangle:

Corollary 2.53 (Equivocal Separates the Simplex from its Circumcenter). Let σ be a n-1-dimenional equivocal proper face of τ in n-D Delaunay complex. Then the affine expansion of σ divides the n-dimensional space into a half-space containing the τ and a half-space containing the circumcenter of τ .

We use the result of Corollary 2.53 as intuition in the following 3D examples. For example in Figure 2.23 (a,b) the triangle ABD is equivocal.

Fact 2.54 (Confident Simplex [Edelsbrunner, 2003]). A Delaunay simplex σ with its dual Voronoi cell ν is confident if and only if the intersection of σ and ν is empty and the intersection of ν and the affine hull of σ is not empty.

The greatest-dimensional Delaunay simplex is never equivocal since its affine expansion covers the whole space and, so, its dual Voronoi. The triangle in Figure 2.22 (b) is not centered since it does not contain its own circumcenter: consequently, the triangle is confident. The lower-dimensional 2D Delaunay simplices cannot be confident. This property occurs first in higher dimensions.

In the following we are going to investigate the possible constellations and relations of different Delaunay simplices. In Figure 2.23 (a) for example we observe a lower-dimensional 2-simplex (the triangle ABC in 3D Delaunay triangulation) whose affine expansion, denoted by the gray circumcircle, contains its circumcenter, denoted by a small opaque ball. Notice, the dual of the triangle is the half-line starting in the circumcenter of the tetrahedron (the small opaque ball in the center of the wired ball) and going through the circumcenter of the triangle. The dual Voronoi half-line does not intersect the triangle: consequently, the triangle is confident.

The dual Voronoi half-lines are included into Figure 2.23 (b). The bottom triangle is acute but neither the triangle nor its affine expansion intersects its dual. We conclude that the bottom triangle is equivocal.

Observation 2.55 (In a Cell with One Equivocal All Triangles can be Acute). Let τ be a Delaunay triangle and σ be its only proper equivocal face. All proper faces of τ may be acute triangles.

Not-Gabriel Simplices

In the context of Delaunay triangulation the concept of *Gabriel graph* originally introduced in [Gabriel and Sokal, 1969] plays an important role and is the basis for our further investigations.

Definition 2.56. Let D be a nD Delaunay complex and $\sigma \in D$ be a m < n dimensional simplex. Let σ be the convex hull of $\{p_1, \ldots, p_m\} \subset D$ points. σ is called Gabriel or is said to have the Gabriel - property if its circumball does not contain any further points D but $\{p_1, \ldots, p_m\}$ otherwise σ is called not-Gabriel



Fig. 2.23: (a) *ABD* is the only proper equivocal face of the cell. ABC is confident. BC is equivocal but not a face of ABD. (b) Equivocal *ABD* is the only face of tetrahedron *ABCS*. All proper faces of *ABCD* are acute triangles.

The edge AC in Figure 2.22 (b) does contain the point B. We observe that the point B is the one point which pushes the flow on the points on the edge away from the triangle. In fact, we may observe that if a circumball of a simplex contains a further point, this point will be nearer to the circumcenter than the vertices of the simplex and consequently will push the flow away from the circumcenter before it can reach it. It wollows that the simplex can neither be centered nor confident. In Theorem 2.57 we prove that the not-Gabriel property is given if and only if the simplex is equivocal.

Theorem 2.57 (Equivocal is equivalent to Not-Gabriel). Let τ be a Delaunay simplex. σ is its proper equivocal face if and only if the circumsphere of σ contains a further vertex of τ (not-Gabriel).

Proof: I τ is a 3-simplex (tetrahedron) and σ is a 2-simplex (triangle).

If equivocal then not-Gabriel: The dual Voronoi ν to σ is an edge between the circumcenter of τ and the circumcenter of the neighboring proper coface of σ . The affine hull of σ divides the space into a half-space containing τ and a half-space not containing any point of τ . If ν does not intersect the affine hull of σ , then the circumcenter of τ is separated by the affine hull of σ from τ . It follows τ does not contain its own circumcenter.

The intersection of the affine hull of σ and the circumsphere of τ is the circumcircle of σ . Let the distance between the circumcenter c_{σ} of σ and the circumcenter c_{τ} of τ be p and the circumradius of τ be r. Let α be the angle between c_{σ} , c_{τ} and one of the vertices of σ . Since the edge between c_{σ} , c_{τ} is orthogonal to the circumcircle of σ , $\alpha = \frac{p}{c}$.

orthogonal to the circumcircle of σ , $\alpha = \frac{p}{r}$. Let the vertex opposite to σ be v and let the angle between v, c_{τ} and c_{σ} be α' . Since the affine hull of σ separates τ from c_{τ} : $0 \le \alpha' < \alpha$. Then the squared distance between v and c_{σ} is $r^2 - 2rp \cos \alpha + p^2$ which is maximized by $\alpha' \to \alpha$, and since $\lim_{\alpha' \to \alpha} (r^2 - 2rp \cos \alpha + p^2) = r^2 - p^2$ which is the circumradius of σ , σ contains τ .

If not-Gabriel then equivocal: The circumsphere of σ contains the vertex v opposite to σ . The distance d between the circumcenter c_{σ} of σ and v is less than the circumradius r_{σ} of σ . Since $r_{\sigma} \leq r_{\tau}$, it follows $d < r_{\tau}$. Since the convex hull of σ separates the space into a half-space completely containing τ and the half-space not containing any point in τ and $d < r_{\tau}$, it follows that c_{τ} is not in the same half-space as τ and the dual to σ cannot intersect the affine hull of σ .

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2.4.9 Flow Relation

The Voronoi diagram is computed by using a distance function. The distance function induces a flow with steepest increasing paths. The Delaunay triangulation is dual to Voronoi diagram. We conclude that the Delaunay simplices can be ordered according to the behavior of the distance function defined on points.

The distance function is not everywhere smooth and, so, does not qualify as a Morse function, and so no gradient field can be defined. In the [Edelsbrunner, 2003] a function f_{ϵ} is used to imitate the distance function. f_{ϵ} smoothes the distance values on edges - the intersections of Delaunay tetrahedrons. So, the notions of a gradient, critical point and flow line can be defined. The *limit curves* approximate for each point in space the flow lines for sufficiently small environment tending to zero. We claim that the flow defined in [Lieutier, 2004] is the union of the limit curves. So, instead of using the notation *limit curve* as it is done in [Edelsbrunner, 2003] we use in following our established notation *flow curve*. By a flow curve we understand the steepest increasing path induced by the gradient introduced in [Lieutier, 2004] (see Definition 2.17).

The paths along the flow curves are strictly increasing and pass uniquely through the Delaunay simplices. So, starting on some point in the interior of a Delaunay simplex and following the flow curve we at some point leave the simplex and enter its adjacent neighbor. Since the distance values increase along the flow curves the sequence of visited simplices is acyclic. This fact is proven in [Edelsbrunner, 2003] Claim 9.

According to the infinite critical point which was introduced in Section 2.4.8, we also adopt the notion of an infinite Delaunay tetrahedron which represents the complement of the convex hull of the sample points. The sequences of simplices which are visited by following the flow curves construct the flow relation, $\prec \subseteq D \times D$, (compare [Edelsbrunner, 2003]) to "mimic" the behavior of flow curves. I.e. $\tau \prec \sigma \prec \tau'$ if σ is a proper coface of τ and τ' and the flow curve starting in the interior of τ passes through σ to interior of τ' . The set of all visited simplices before the flow curve passes through a simplex σ is called *descendents* and the set of all visited simplices visited by a flow curve after passing though σ is called *ancestors*. So, τ' is an element of ancestors of σ and is also called the *successor* of σ , and τ is the *predecessor* of σ .

Inconsistent Cell A triangle can only have one obtuse angle, so, only one edge can be opposite the obtuse triangle. Consider the line segment connecting two points of a circle and crossing its center. The triangle which results by connecting the two endpoints of the edge and any further point on the circle is perpendicular. So, pushing the point on the perpendicular angle inside the circle increases the angle, becoming obtuse, and pulling the point away results in an acute angle. We imply that the edge is not-Gabriel or contains a further point in its circumball if and only if it is opposite an obtuse angle. Consequently, a triangle may have at most one equivocal edge.

In 3D, the case is more complicated. Any tetrahedron has triangles and edges as faces which can be equivocal.

A not centered tetrahedron, as for example illustrated in Figure 2.24 (a), consists of two equivocal faces ACB and ADB. The dual Voronoi line segments end in the circumcenter of the tetrahedron (the most left small ball) and do not cut the affine extensions of the triangles. We denote the affine extensions of the equivocal triangles by their circumcircles. The triangles do not contain their circumcenters. The circumsphere of each equivocal face contains the fourth vertex of the tetrahedron. The flow lines pass through both equivocal faces. Whereas in 2D there is only one possible direction for the flow to go and so, starting with the obtuse triangle, the set of following ancestors in the flow relation is unique, in 3D we observe the flow relation forking. Starting with such a tetrahedron we have two different sets of ancestors.

A 2D projection of the tetrahedron along the AB edge is in Figure 2.24 (b) with two directions of the flow. The edge AB - the intersection of the equivocal faces - is also equivocal. Consequently the flow is passing through the edge too. In our framework as well as in [Edelsbrunner, 2003] these Delaunay cells are called *inconsistent cells*.

We call the equivocal faces of an inconsistent cell τ containing τ in its circumsphere the *inconsistent*



Fig. 2.24: (a) Inconsistent cell: a tetrahedron with two equivocal faces (ABC and ABD). (b) A 2D projection of (a) along the AB edge. The arrows illustrate the two flow directions.

faces.

Fact 2.58 (Only two Inconsistent Triangles). A Delaunay cell has at most two inconsistent proper faces.

In Figure 2.24 (b) the dashed lines denote the affine expansions of the simplices ABC and ABD (triangles projected along the edge AB). Notice again, the affine expansions of the triangles ABC and ABD, which are illustrated now as edges both separate the tetrahedron from its circumcenter. This is the hint to construction of the inconsistent cell. O is always in the empty "quarter-ball" which is the intersection of half-balls resulting from cutting the circumball of the tetrahedron with affine extensions of the equivocal triangles.

We constructed our example by leaning one obtuse triangle on another obtuse triangle in such a way that the planes containing them both separate the tetrahedron from its circumcenter. In the construction, the obtuse triangles share the edge which in both triangles is opposite to the obtuse angle. In the following we prove that this observation is generally valid.

Claim 2.59 (Two Obtuse Triangles sharing an Equivocal Edge are Equivocal). Let τ be a Delaunay triangle and σ and σ' be its proper obtuse faces. Let ρ be their proper common face opposite the obtuse angle in σ and σ' . Then σ and σ' are equivocal.

Proof: Since σ is obtuse the circumsphere of ρ contains σ and respectively σ' . Since the circumsphere of ρ contains σ , σ cannot be centered. If σ is confident then the dual of σ intersects the affine hull of σ . The affine hull of σ divides the circumsphere of ρ into two half-spheres. One half-sphere contains the vertex of σ' opposite to ρ . Since the distance between the circumcenter of ρ and the vertex of σ' opposite to ρ is less than the circumradius of ρ , the circumcenter of τ cannot be in the same half-sphere. It follows, that σ is equivocal. The equivalent construction is valid for σ' .

Obviously, in the construction as it is valid for Claim 2.59, the common edge of the two equivocal triangles is also equivocal for both triangles. So, the circumball of the edge contains the third vertex of both triangles. In other words, the circumball of the edge contains both further vertices of the tetrahedron. It follows, that the circumball of the edge contains the tetrahedron.

Claim 2.60 (Circumsphere of an Equivocal Edge contains Inconsistent Cell). Let ρ be an edge of a tetrahedron τ . If the circumsphere of ρ contains τ , then τ is inconsistent.

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Fig. 2.25: (a) Inconsistent cell: a tetrahedron with two equivocal faces (ABC and ABD). ABD is acute. (b) (a) ABC and ABD are obtuse equivocal faces but BD the opposite the obtuse angle in ABD and AB is opposite obtuse angle in ABC. ABC and ABD do not share an equivocal edge.

Proof: The circumsphere of ρ contains τ , then it also contains its proper cofaces σ and σ' . It follows that σ and σ' are obtuse and ρ is their common equivocal edge. Then by Claim 2.59 σ and σ' are equivocal and consequently τ is inconsistent.

The construction of an inconsistent cell by joining two obtuse triangles on their equivocal edge is not the general case. As can be seen in Figure 2.25 (b) the equivocal edge of one of the inconsistent obtuse triangles may not be an equivocal of the other.

Observation 2.61 (Obtuse Equivocal Triangles May Not Share an Equivocal Edge). Let τ be a Delaunay triangle and σ and σ' be its proper obtuse equivocal faces. Let ρ be their proper common face. Then ρ is not necessarily equivocal.

In our previous example in Figure 2.23 (a) we observe an equivalent result for two obtuse triangles one of which is confident. The tetrahedron is not inconsistent. Observe, though faces ABC and DBC are obtuse the affine expansion of triangle ABC denoted by its circumcircle does not separate the tetrahedron from its circumcenter.

Observation 2.62 (Equivocal and Confident May not Share an Equivocal Edge). Let τ be a Delaunay tetrahedron and $\sigma \neq \sigma'$ be its faces. Let σ be equivocal and σ' be confident. Let ρ be the equivocal edge of σ' , then ρ is not necessarily a face of σ .

In Figure 2.25 (a) we see further that the inconsistent faces need not be obtuse. The triangles ABD and ABC are equivocal but the triangle ABD contains its own circumcenter and consequently is acute.

Observation 2.63 (Inconsistent Cells can have an Acute Equivocal). Let τ be inconsistent and σ and σ' be its proper equivocal faces which share an edge ρ . The circumsphere of ρ does not necessarily contain τ . It follows that one of equivocal faces can be acute.

2.4.10 Wrapping Surface

The existence of inconsistent cells troubles the analogy between the ancestor sets and stable manifolds. The stable manifolds which are unions of flow lines ending in the same critical point are pairwise disjoint. In contrast to stable manifolds the ancestor sets may overlap in inconsistent cells. So, the ancestor sets are too large to represent stable manifolds.

Conservative ancestor sets introduced in [Edelsbrunner, 2003] contain only the simplices whose cofaces have descendent sets contained in ancestor set. The inconsistent cell has descendents which are not necessarily in the ancestor set. Consequently, the conservative ancestor set would not contain any inconsistent cell.

The boundary \mathcal{W} of the smallest subcomplex Ω containing the conservative ancestor set of the infinite cell is the *wrapping surface*. The complement $\mathcal{X} = \mathsf{D} \setminus \Omega$ is the union of closures of ancestor sets of all finite centered cells.

Constructed Retraction (WRAP) The construction of \mathcal{X} is done by collapsing on a pair of simplices which admit the following conditions:

Definition 2.64 (Collapsible Pair [Edelsbrunner, 2003]). An *l*-simplex $\sigma \in D_{\mathcal{X}} \subset D$ is free if there is a k > l and a k-simplex $\tau \in D_{\mathcal{X}}$ such that all cofaces of σ in $D_{\mathcal{X}}$ are faces of τ .

A pair σ, τ is collapsible if:

1. σ is free, σ is equivocal and

2. $\tau \prec \sigma, \tau$ is the highest-dimensional coface of σ in $\mathsf{D}_{\mathcal{X}}, \sigma$ is the lowest-dimensional successor of τ .

The deletion of the collapsible pair from the subcomplex is an extension of elementary collapse. It collapses on equivocal simplices only. The notion *simple* is extended to *free* such that the collapsible higher-dimensional coface does not have to be a proper coface. So, a collapse on an edge is possible if it is on the boundary and its adjacent tetrahedron is the only tetrahedron left in the subcomplex. The same is possible on a vertex if there is only one adjacent tetrahedron left in the subcomplex. Notice, the collapses on inconsistent cells are also possible if all descendents are in the same conservative ancestor set of the infinitive cell.

The WRAP or *constructive retraction algorithm* starts with Delaunay triangulation D which is constructed without including infinite simplices and ends if no collapsible pair can be found in the subcomplex $D_{\mathcal{X}}$. So, the convex hull is the boundary of the D. The triangles of the convex hull are free and can be considered as candidates for a collapse.

At some step of the constructive retraction algorithm there might be more than one collapsible pair. But in [Edelsbrunner, 2003] proof is given that the result of the algorithm is independent of the order of collapses.

Theorem 2.65 (Constructed Retraction Correctness [Edelsbrunner, 2003]). $D_{\mathcal{X}} = \mathcal{X}$ for every constructed retraction.

2.4.11 Comparing Simplices by Distance Values

The flow relation as it is introduced in Section 2.4.9 orders the Delaunay simplices using the flow curves. A simplex σ' is said to be the successor of σ if there is a flow line staring in σ and ending in σ' . Since the distance values on the flow lines continuously increase we may say that the successor contains points with greater distance values. But how do we compare simplices which are not in the same ancesstor set?

Why not Circumradius?

In 2D the greatest distance value of a triangle (Delaunay 2-cell) is in its circumcenter. If the triangle is acute than it contains its own circumcenter and, so, the point with the greatest distance value. Acute triangles may be compared by their circumradius. Obtuse triangles do not contain their circumcenter. The flow lines starting in the triangles are pushed away through the equivocal edge towards the circumcenter of the triangle. We conclude that the point with the greatest distance value of an obtuse triangle is somewhere on the equivocal edge. So, we may say, the equivocal edge is greater than its obtuse triangle and consequently the both other edges.



Fig. 2.26: $\triangle ABC$ is equivocal. The circumsphere of ABC contains *D*. The circumsphere of $\triangle ABD$ is greater than circumsphere of $\triangle ABC$

However the circumradius of the equivocal edge is not the value to compare equivocal edges. Consider for example an obtuse triangle. The circumcircle of the equivocal edge contains the third vertex of the triangle. Leaving the edge length constant but moving the third vertex closer towards the center of the edge, the distance value in the edge's center decreases.

In 3D the assumption that the equivocal face is greater than non equivocal faces of the same tetrahedron (Delaunay 3-cell) is no longer valid. In Figure 2.26 we demonstrate the counter example. The left wired ball is the circumball of the confident face whereas the smaller right wired ball is the circumball of the equivocal face (in this example the base triangle of the tetrahedron). The circumball of the confident face has a greater circumradius. But the equivocal face is the successor of the tetrahedron and so contains points with greater distance values where the flow lines are passing through. We conclude, that the simplex comparison by their circumradius is not adequate to the flow relation.

Observation 2.66 (Circumradius of an Equivocal is Not necessarily Greater). Let τ be a Delanay tetrahedron and $\sigma \neq \sigma'$ be its faces. Let σ be equivocal and σ' be not equivocal. If the $\sigma' > \sigma$ then it is obtuse.

Why not α -Value?

The "filtration" in α -shape construction in [Edelsbrunner and Mücke, 1994] sorts the Delaunay simplices by their α -value. So, the simplices are compared by the α -value. The α -value is the radius of a maximal ball which can be inscribed into the simplex without containing its vertices.

Consider an obtuse triangle. The circumball of the edge opposite to the obtuse angle contains the third point of the triangle. To make the ball free of points we need to move the center of the ball away from the third point of the triangle. The radius of the ball increases until it overlaps the circumball of the triangle. The center of the ball moves towards the circumcenter of the triangle, continuously increasing its radius. So, the maximal inscribing ball into the edge is the circumball of the triangle. The closer the third point is to the edge the greater is the circumball of the triangle and the greater the α -value of our equivocal edge. But the closer the third point is to the edge the smaller are the distance values on the edge.

The equivalent consideration is valid for 3D. Consider now the inconsistent cell. How do we compare its equivocal faces? Using the filtration the greater triangle has the greater α -value but according to our previous considerations lesser distance values. If we are looking for flow lines with minimal distance values the filtration method would not suit the condition. The α -shape would remove the triangle with greater α -value but leave the triangle with greater distance values.

Furthermore consider an equivocal and a centered triangle with the same α -value. Obviously, the greatest distance value of the centered triangle is in its circumcenter. The circumcenter of the maximal empty ball inscribed into the equivocal triangle is not in the triangle. It follows that two triangles with the same α -value may have different maximal distance values.

Obviously, considering an equivocal triangle with its corresponding empty maximal inscribing α -ball, we may move the fourth vertex of the tetrahedron on the surface of the ball and so vary the closeness of the point to the triangle. We imply, that equal triangles with equal α -values may have different maximal distance values.

Nevertheless the property of the α -ball inscribed into the simplex to be maximal and empty implies that only the points on the ball's surface influence the distance values inside it and consequently on the simplex itself. Since the inscribing α -ball of an equivocal triangle is the same as the circumball of its proper coface the tetrahedron, and under assumption of general position and since the circumball of Delaunay tetrahedron is empty, we imply that the α -ball is touched only by the vertices of the tetrahedron. However to compute the maximal distance value on a simplex we need all points which are closer to the simplex than its vertices. In other words we compute which further points of the data set are in the circumball of the simplex. The equivalent question is, which are the intersecting points of the Voronoi diagram and our particular simplex?

Maximal Distance Value

The maximal distance value in a simplex is a well-defined value which allow us to compare and sort Delaunay simplices. Furthermore this criterion corresponds to the criterion in the flow relation which orders simplices according to the trajectory of the flow lines which are increasing paths on discrete distance transform. Using the maximal distance value we are able to compare the simplices in different ancestor sets which is the case for inconsistent

As discussed earlier the computation of the maximal distance value in a simplex is realized by similar procedure to finding the intersections between the simplex and the complete Voronoi diagram. Obviously, this approach is very resource-consuming. In the following we investigate which triangles have greater distance values and how to compute them without the complicated computations.

Obviously, centered triangles contain their own circumcenter and the distance values on such triangles are not troubled since the circumsphere of centered triangles does not contain any further points. So, we compare the centered triangles by their circumradius.

Fact 2.67 (Maximum Distance Value on Centered). The greatest distance value of a centered Delaunay triangle is its circumradius.

The circumsphere of a confident triangle does not contain any further points and so the distance values on the triangle are computed by considering the vertices of the triangle only. Since the confident triangle is the unique predecessor of the equivocal edge, and consequently for every point in the triangle, there is a flow line starting on this point which intersects the equivocal edge. It follows that for every point in the confident triangle there is a point in the equivocal edge with a greater distance value than on the starting point. Thus, we compute the *size* of a confident triangle by the distance values on the equivocal edge by using the following statement:

Fact 2.68 (Maximum Distance Value on Confident). The greatest distance value of a confident triangle is the greatest distance value of its equivocal edge.

Why not α -Ball?

The "filtration" in α -shape construction in [Edelsbrunner and Mücke, 1994] maps to each simplex in the Delaunay triangulation the radius of the maximal empty ball containing the vertices of the simplex in its boundary. The circumradius of an equivocal simplex is less than its α -value. So, to compare the simplices a proposition can be made to use the α -ball.



Fig. 2.27: The greatest distance value on AC is not its circumcenter.

Consider for example Figure 2.27. The edge AC is equivocal. The α -ball of AC is the circumball of the triangle ABC which is the proper coface of AB. The value to compare the simplices is then the point on AC which has the greatest distance to the boundary of the α -ball. In our example it is the circumcenter ($_{\times}$) of AC.

The distance between the point B and the circumcenter of AC is less than the radius of AC. Consequently, the point with greatest distance values moves to the right such that the distance between new point (\blacksquare) is equidistant to B and C.

Consider now a further point D. D fulfils the Delaunay condition and is closer to the new point than B or C. So, the greatest distance value on AC is again reduced and the corresponding point moved to the intersection of the Voronoi edge dual to BD. The distance value on the simplex AC depends on the points with dual Voronoi cells intersecting the simplex.

Computing Distance Value

According to previous considerations we propose to compare the simplices by the greatest distance value. The distance values in the simplex are influenced by other points of the Delaunay triangulation. The Voronoi cells dual to the influencing points intersect the simplex. The intersection between a Voronoi cell and a Delaunay simplex is a planar polygon.

Let us first assume that the set of intersections between Voronoi diagram and the Delanay simplex is given. Obviously, since the Voronoi cells are disjoint a point in the Delaunay triangle can only be within one Voronoi cell or in its faces. The distance function is piecewise linear and increases monotonously on linear paths towards the faces of the Voronoi cell. Since intersection between a Voronoi cell and a Delaunay triangle is a planar polygon, it follows that the distance values increase monotone within the intersection polygon. Consequently, the greatest value is measurable in the corners of the intersection polygon. Notice that the corners of the polygon are not necessarily on the faces of the Voronoi cell but may be linear pieces of Delaunay edges. So, the greatest value on the vertices of the intersections is the resulting maximum of the triangle.

We propose the following algorithm to compute the maximal distance value by a given set of influencing points and the intersections of their dual Voronoi cells with the given simplex.

Algorithm 2.69 (Greatest Distance by Given Intersections). Let σ be a triangle in a 3D Delaunay triangulation D on a point set S. Let V be the Voronoi complex dual to D, then:

- 1. Compute the set of intersections E between the 2-simplices of V and σ .
- 2. Let x be any point in σ . Until E is not empty:
 - (a) Let e be the top element of E. Pop E.

- (b) If e is a point and $d_{\mathsf{S}}(\mathsf{e}) > d_{\mathsf{S}}(x)$ then $x = \mathsf{e}$
- (c) Else if e is a line segment with end points p_1 and p_2 . Let $p = p_1$ if $d_{\mathsf{S}}(p_1) > d_{\mathsf{S}}(p_2)$ else $p = p_2$. Then if $d_{\mathsf{S}}(p) > d_{\mathsf{S}}(x)$ then x = p.
- (d) Continue with 2.

3. Return $d_{\mathsf{S}}(x)$.

Simply speaking, Algorithm 2.69 checks, for all the intersection polygons, the distance value in their corners and saves the maximum value which is then returned if all polygons have been considered. The more challenging task is to determine the points whose dual Voronoi cells intersect the given simplex. In the worst case, all points of the Delaunay triangulation can be considered as candidates for influencing the distance points. The task then is to select the Voronoi cells which intersect the simplex. But the intersection between the complete Voronoi diagram and the one given simplex is very resource-intensive.

Increasing Efficiency

The centered simplices intersect their dual. The intersection is the point with the greatest distance value. The confident simplices do not intersect their dual and the maximal distance value is on their equivocal face. In the latter case we would need to find the intersections on the equivocal face and not on the simplex itself. Even though the equivocal triangles in 3D Delaunay triangulation have a unique successor - the neighboring tetrahedron, the equivocal edges may have arbitrary number of successors. In both cases there might be arbitrary number of Voronoi cells which intersect the simplices.

The simplex vertices are separated by their dual Voronoi cells. So, their dual Voronoi cells cut the simplex. Consider an equivocal edge. The edge vertices are equidistant to the center of the edge. If the edge were not equivocal the both vertices would be the closest to the center and be the only two points which influence the distance values on the edge. But the circumsphere of the equivocal edge contains the third vertex of the corresponding triangle. So, this third vertex is closer to certain points on the edge than the edge vertices and consequently influences the distance values more than the edge vertices. We conclude that the influencing points have to be closer to the points in the edge than its vertices. Following this, the influencing points have to be contained in the circumsphere of the edge.

Consider now a triangle. The influencing points for the edges are in their circumspheres. Since only one edge in a triangle can be equivocal and none is confident, two circumspheres are empty. In 3D, the influencing points for a Delaunay triangle can be in the circumsphere of the triangle and in the circumsphere of its edges.

In the worst case we would need to check for all points in the Delaunay triangulation if a point is contained in a sphere. Using the connectivity information of the Delaunay triangulation we can minimize the number of candidates.

Claim 2.70 (Influencing Neighboring Point is Opposite to an Equivocal). Let τ be a Delaunay cell and σ be its proper equivocal face. Let v be a vertex of σ and τ' be a neighboring Delaunay cell opposite to v. Let v' be a vertex of τ' opposite to the common proper face σ' between τ and τ' . If the Voronoi cell ν' dual to v' intersects σ then the circumsphere of σ' contains v'.

Proof: The affine hull of σ' separates τ' from τ and σ . If τ' contains its own circumcenter c', the affine hull of σ' separates ν' from τ . Which is a contradiction to the assumption. σ' cannot be confident, because otherwise the circumcenter of τ' and τ are on the same side of affine hull of σ' which implies that ν' does not intersect the affine hull of σ' and consequently σ . It follows that c' is separated from τ' by the affine hull of σ' and so, the circumsphere of σ' contains ν' .

According to Claim 2.70 a Voronoi cell can intersect the triangle only if the dual point is opposite to an equivocal. So, to find influencing points for an equivocal Delaunay triangle we inspect the corresponding Delaunay tetrahedron first. The tetrahedron has to be contained in the circumsphere of the triangle. If there are no other equivocal triangles in the tetrahedron, the fourth vertex in the tetrahedron is the single point influencing the distance values in the triangle. If the tetrahedron contains further equivocal triangles the forth point of the neighbor is a candidate.

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The affine expansion of the equivocal triangle divides the space into two half-spaces. The influencing points are in the same half-space as the corresponding confident tetrahedron. So, we directly imply the vice-versa statement:

Corollary 2.71. Let τ be a Delaunay cell and σ be its proper equivocal face. Let v be a vertex of σ and τ' be a neighboring Delaunay cell opposite to v. Let v' be a vertex of τ' opposite to the common proper face σ' between τ and τ' . If the Voronoi cell ν' dual to v' intersects σ then the circumsphere of σ does not contain v.

Proof: According to Claim 2.70 σ' is equivocal and contains v'. But according to empty sphere condition of Delaunay triangulation the circumsphere of a triangle cannot contain both adjacent tetrahedrons.

The result in Corollary 2.71 is in so far relevant that a statement can be made about a cell with two equivocal faces containing the same confident tetrahedron - the inconsistent cell.

Corollary 2.72 (The Equivocals of an Inconsistent Cell are Not Influenced by Neighbors sharing Inconsistent Faces). Let τ be an inconsistent Delaunay cell and σ and σ' be its proper equivocal faces. Let v be a vertex opposite to σ' and τ' be a neighboring Delaunay cell opposite to v. Let v' be a vertex of τ' opposite to the common proper face σ' between τ and τ' . Then the Voronoi cell ν' dual to v' does not intersect σ .

Proof: Since the circumsphere of σ' does contain v, so, according to Corollary 2.71 ν' cannot intersect σ .

According to Corollary 2.72 we know that in inconsistent cells the in-sphere test does not need to be performed on neighboring cells sharing the second inconsistent face.

Assume again an equivocal triangle σ . Its affine expansion divides the space into a half-space consisting of the confident tetrahedron τ - the coface of our triangle - and the second half-space contains the circumcenter of the tetrahedron τ .

Let us assume further some point v' which is not a vertex of τ and let ν' be its dual Voronoi cell. The duality between Delaunay and Voronoi states that the faces of the Voronoi cell ν' are dual to Delaunay simplices with a vertex v'. The Voronoi vertices of the Voronoi cell ν' are the circumcenters of the Delaunay tetrahedrons sharing v'.

If the Voronoi cell ν' intersects our initial equivocal Delaunay triangle σ , then there has to be a Voronoi face of ν' which intersects σ such that the Voronoi vertices of this intersecting Voronoi face are in different half-spaces of the affine expansion of σ . It follows that there has to be a Voronoi vertex of ν' which is separated from ν' and τ by affine expansion of σ . This separated Voronoi vertex is the circumcenter of some of Delaunay tetrahedron. We summarize:

Corollary 2.73 (The Circumcenter of the Cell and of an Influencing Neighboring Cell are on the Same Side). If a Voronoi cell ν' dual to ν' intersects a Delaunay triangle σ , ν' has a vertex separated from ν' by the affine expansion \mathcal{A}_{σ} of σ .

Equivalently: if a Voronoi cell ν' dual to ν' intersects a Delaunay triangle σ , then there is a Delaunay tetrahedron with vertex ν' separated from its circumcenter by \mathcal{A}_{σ} .

So, searching for candidates for the intersection between Voronoi diagram and a Delaunay simplex can be reduced to the traversing through the Delaunay triangulation starting in the confident cell (tetrahedron) with the given equivocal simplex (triangle) crossing equivocal faces and testing if the circumcenter of the visited Delaunay cell is on the other side of the affine extension of the given triangle.

Algorithm 2.74 (Computing the Candidates). Let τ be a confident Delaunay tetrahedron and σ be its equivocal triangle and let \mathcal{A}_{σ} be the affine extension of σ . Let $C = \emptyset$ be a set of Delaunay tetrahedrons and $F = \{\sigma\}$ be a set of Delaunay triangles. Let τ' be τ

1. For all equivocal proper faces σ' of τ' not in F let τ' be the neighbor of τ' adjacent to σ' .

- 2. Push σ' into F.
- 3. If the circumcenter of τ' is on the same side of \mathcal{A}_{σ} as the circumcenter of τ then push (τ', v') into C.
- 4. Continue with 1.

Return C;

Notice, the candidates found in Algorithm 2.74 are dual to Voronoi cells intersecting the affine extension of the given Delaunay triangle but nor necessarily the triangle itself.

Computing Intersection

Let τ be a confident Delaunay triangle with an equivocal triangle σ . Let v be the vertex of τ opposite to σ . Since σ is equivocal and v is a vertex of τ the Voronoi cell dual to v intersects σ . The Voronoi cells dual to vertices of σ necessarily intersect σ .

The Voronoi edge dual to a certain proper face σ' (triangle) of τ joins two Voronoi vertices dual to the circumcenters of τ and its neighbor adjacent to σ' . According to previous considerations, if the neighbor's circumcenter is on the other same side as the circumcenter of τ then the Voronoi edge dual to σ' cuts the affine extension (\mathcal{A}_{σ}) of σ .

According to previous consideration the found candidates are vertices of tetrahedrons with circumcenters on the other side of the affine extension of σ . So, our task to find the intersections is to start with the candidates and traverse to their neighbors with circumcenters not on the other side of affine extension of σ . The Voronoi faces dual to Delaunay faces of the candidate tetrahedron and adjacent to its non-candidate neighbor intersect the \mathcal{A}_{σ} . So, the next step is to compute the intersection and determine if the intersection is in σ .

Algorithm 2.75 (Computing the Intersections). Let τ be a confident Delaunay tetrahedron and σ be its equivocal triangle and let A_{σ} be the affine extension of σ . Compute the set of candidates C. Let E be a set of Delaunay edges. Let $I = \emptyset$ be a set of intersections.

- 1. While C is not empty:
 - (a) Let τ' be the first candidate in C.
 - (b) For all edges σ' of τ' not in E and adjacent to Delaunay tetrahedrons not in C: push σ' into E and compute the dual Voronoi polygon μ . Push the intersection between μ and σ into I.
 - (c) Remove the first candidate from C.
 - (d) Continue with 1.
- 2. Return I.

The distance values on points in the triangle are always influenced by certain input points of the triangulation. The influencing points push the flow line starting in a Delaunay cell through the triangle. This is the property of an equivocal simplex. Since all points on the flow line are pushed by one and the same input point of the triangulation, all Delaunay simplices passed by the flow curve are equivocal. This agrees with our Claim 2.70. The predecessors of equivocal simplices are unique. We conclude, if we follow the equivocal simplices of neighboring cells starting on our triangle σ we find all influencing points.

Claim 2.76. Algorithm 2.75 results in all intersections between the input Delaunay triangle and the Voronoi diagram.

Proof: The limit curves ending on the equivocal triangle start on input points of the triangulation. The flow relation imitates the behavior of the limit curves. Since the points in the intersection of the Voronoi cell ν and the triangle are in ν the limit curve connecting the triangulation point dual to ν and the

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point in the intersection is a line segment. It follows that all simplices intersected by the limit curve are equivocal. The equivocal simplices have unique predecessors. The claim follows since by construction of the algorithm all equivocals and its predecessors are processed.

Notice, we do not claim Algorithm 2.75 to be the most efficient. In fact the computation of an intersection between a Voronoi polygon and a Delaunay triangle may have an empty result because the Voronoi polygon which intersects the affine extension of a triangle does not necessarily intersect the triangle itself.

We use an abstract definition of an intersection in the set returned in Algorithm 2.75. The set of intersections may be differently defined. An intersection may be the intersection between a Voronoi cell and the triangle. In such a case, the union of intersections would result in the given triangle. The set of intersections defined in such a way is expected in Algorithm 2.69. But Algorithm 2.75 may also return the corners of the intersection saving us the steps done in Algorithm 2.74 and allowing us the direct computation of maximal distance values.

2.5 Summary: From Geometry to Topology and Back Again

Geometry describes how objects are placed and shaped in space and what is invariant under rotation and translation. Topology is concerned with how the objects are connected. Our task is, without knowledge of the placement, or shape, or topological properties of the object, to give guarantees that these geometrical and topological properties are preserved during the digitization process. But what we require is that certain conditions on geometry are fulfilled. The more general these conditions are the more general is the class of shapes we can reconstruct under guarantee.

There are two points of view. In our framework we derive the conditions on the shape and define the reconstruction method. To do so, we start with an object in the real world. We consider the interior of the object to be of relevance and generalize the scene by partition \mathcal{R} of the whole space into regions. These regions are interconnected in certain ways which we intend to preserve in our result.

We have conditions on the space partition. To investigate if the conditions are fulfilled, we make geometrical measurements on the shape. We measure the feature size (i.e. lhfs) on the continuous boundary between the regions. According to the feature size the limits are given on sampling density and deviation from the boundary. These measurements are made by terms of differential geometry in continuous space.

The second step in the digitization process is the result of a sampling of the continuous boundary: a data set S. The point set and the Euclidean distance induce the discrete distance transform d_S . We expect certain association between the critical points on the continuous distance transform and the discrete distance transform.

Using the feature size measured previously we can state if the sampling conditions are fulfilled. The set of sampling points is finite. All knowledge on original scene which we can use for reconstruction is now contained in the point set.

Given the points, we generalize the connectivity information contained in the point set by building a combinatorial structure named Delaunay triangulation D. So, the topological properties are contained in an abstract structure consisting of abstract elements like simplices. The discrete distance transform $d_{\mathcal{R}}$ is then imitated by the flow relation $\prec \subseteq D \times D$. Which is then used to carve the regions from the convex hull of the Delaunay triangulation.

The reconstruction method carves regions from the convex hull of the Delaunay triangulation resulting in a simplicial complex corresponding to the boundary D_R and the complementary set of simplices corresponding to the set of interiors of the regions. The boundary D_R of the reconstructed regions contains the connectivity information of the regions and so corresponds to topology.

The underlying space of the set of reconstructed regions is a subset of real space and again a space partition. The continuous boundary of the space partition - a polytop - is the underlying space of the simplicial complex corresponding to the boundary of the reconstructed regions. Summarizing the reconstruction procedure, we obtain the following activity diagram: continuous boundary \rightarrow sampling points \rightarrow vertices \rightarrow Delaunay subcomplex \rightarrow shape of the subcomplex. Where the vertices are the sample points representation in the combinatorial structure, the Delaunay complex represents the boundary of the set of reconstructed regions and the shape of the subcomplex is the continuous boundary of the reconstructed space partition.

Continuous	Topology	Discrete
distance transform $d_{\mathcal{R}}$	Simplex specification	distance transform d_S
Flow on $d_{\mathcal{R}}$	Flow relation	Flow on d _S
Continuous boundary $\partial \mathcal{R}$	Boundary of the set of reconstructed regions D_R	Underlying space of $ D_R $
Space Partition \mathcal{R}	Set of reconstructed regions $D \setminus D_R$	Underlying space of $ D \setminus D_R $

Chapter 3

Previous Reconstruction Algorithms

3.1 Introduction

The previous work on surface reconstruction can be classified into at least three approaches. Computational geometry based approaches connect the points in the underlying set by polygons. The surface fitting approach defines a parameterized algebraic surface model. Iteratively adjusting the surface parameters the resulting surface approximates the point set. The volume based approach using computes for each point in space the distance to the dearest data point. The task here is to find a surface where for each point on the surface the distance value is zero.

Our framework is based on computational geometry approach and is based on Delaunay triangulation. So, here we present a selection of well-known reconstruction methods with guarantees on topological preservation which are based on Delaunay triangulation. The computation of 3D-Delaunay triangulation is of worst case complexity $O(n^2)$ where n is the number of sample points. So, the complexity of postprocessing steps in the presented algorithms as well as in our reconstruction method is dominated by the complexity of the Delaunay triangulation.

For better comparison the approaches are presented in a synopsis. First we extract which conditions on the shape and the sampling are required to obtain the promised results. The prerequisites on the original shape limit the reconstruction on the most algorithms to smooth manifold surfaces of contractible objects. The reconstruction has in all cases the guaranteed result if certain sampling conditions are fulfilled. We classify the approaches into two classes according to the requirements on the sampling: the methods which handle locally adaptive sampling densities and the algorithms which require the sampling with a globally uniform density. Further we indicate if the reconstruction method requires some known parameters.

Second we retrieve which guarantees are given by the reconstruction method and under which parameter setting the guaranteed result is achieved. We give our comments to the approach to outline the characteristics of the framework. Third we outline the idea, i.e. we give a summary of the approach to explain why and how the reconstruction works. The algorithm steps are given in note form to indicate the main reconstruction steps. In the final point we report if and which extensions on the method are proposed.

Our research results which we present in this work consist of evaluation of the theoretical framework originally introduced in 3D domain in [Stelldinger, 2008b] and the introduction of a new framework and reconstruction method called "Refinement Reconstruction". We include the synopses to both methods in this chapter to enable the reader to simply compare the results.

3.2 Locally Adaptive Sampling Conditions

3.2.1 Crust

[Amenta et al., 1998]



Fig. 3.1: (a) Two dimensional point set and its Voronoi diagram. The sample points are notated as dots and the voronoi vertices are squares (b) "Crust": heavier edges connect sample points. (c) In three dimensions the voronoi vertices may lie near the boundary - the squared vertex in the center. The figures are redrawn according to Figure 5 and 6 in [Amenta et al., 1998]

Prerequisites:

- Shape: twice differentiable orientable manifold surface embedded in \mathbb{R}^n
- Parameter: parameter free
- Sampling: locally adaptive, no noise, r-sampling with $r \leq 0.06$

Definition 3.1 (*r*-Sampling). Let $\partial \mathcal{R}$ be the boundary of a space partial \mathcal{R} and $S \subset \partial \mathcal{R}$ be a finite set of points. Then S is said to be an *r*-sampling of $\partial \mathcal{R}$, if

 $\forall b \in \partial \mathcal{R} : \exists s \in S : ||b - s|| \le r \mathsf{lfs}(b)$

Guaranties: Given an *r*-sampling of a smooth surface, with $r \leq 0.06$, then the *crust* of the sample contains a set of triangles forming a mesh topologically equivalent to the original surface.

Comments: The result of the algorithm is not necessarily the topologically equivalent reconstruction. It only contains the correct mesh.

In case of manifold surface an additional step is required to remove simplices. This is done by elementary collapse (see Definition 2.43)T

Idea: The sampling conditions are defined in such a way that the distance between adjacent sample points is much smaller than the distance to the medial axis. In such a way the circumcircle of the edge connecting the adjacent points does not cut the medial axis and does not contain any other point of the sampling set. The goal of the method is to construct a set of such edges. The 2D method first computes the Voronoi Diagram on the sampling points (see Figure 3.1 (a)) and then computes the Delaunay triangulation on both the sample points and vertices of the Voronoi diagram. The *crust* is the set of Delaunay edges which connect the sample points (see Figure 3.1 (b)).

In 2D all Voronoi vertices are near the medial axis. This property is no longer true in 3D. Independently on sampling density Voronoi vertices can appear near the boundary (see Figure 3.1 (c)). But

3.2. LOCALLY ADAPTIVE SAMPLING CONDITIONS

since the sampling is very dense compared with the distance to the medial axis the Voronoi cell which correspond to the sampling points are very long and thin. The idea is to mark two vertices of the Voronoi cell which approximate the medial axis on different sides of the boundary. The first marked is the farthest vertex of the Voronoi cell from the sample point. The second marked is the farthest vertex on the other side of the boundary. The two marked vertices are called *poles*. The further procedure is then like in 2D.

Algorithm: Please notice, we use our notations for point set (S), poles (P) and the Delaunay D.

- 1. Compute the voronoi diagram on the set of sample points S.
- 2. Compute the *poles* P of the Voronoi diagram.
- 3. Compute Delaunay D on $S \cup P$.
- 4. Keep only the triangles of D with all vertices in S.

Extensions: Using the fact that the line connecting the poles of a sample point is nearly orthogonal to the original surface further simpleces can be deleted. In [Amenta and Bern, 1999] the proof is given that the remaining set of simpleces still contains the topologically correct surface reconstruction

3.2.2 Power Crust

[Amenta et al., 2000b, Amenta et al., 2001]

Prerequisites:

- Shape: twice differentiable manifold surface
- Parameter: parameter free
- Sampling: locally-adaptive, no noise, r-sampling (Definition 3.1) with $r \leq 0.1$

Guaranties: Given an r-sampling with $r \leq 0.1$ of a smooth manofild surface the method approximates the surface with a topologically correct mesh.

Comments: The regular triangulation faces connecting the interior poles approximate the medial axis.

Idea: The algorithm is an extension of the previously introduced *crust*-method. The idea here is based on the assumption of a sufficiently dense sampling which for each sample point guarantees long and thin Voronoi cells nearly perpendicular to the original surface. By using this fact first pole can be found as the farthest Voronoi vertex from the sample point. The pole builds together with the sample point a vector nearly collinear with the surface normal. The second pole is the farthest Voronoi vertex which together with the sample point builds a negatively directed vector to the other pole vector.

The second idea used in this approach is that the ball centered on the poles with pole-sample distance as the radius (*polar balls*) are either almost contained in the interior of the original surface or entirely in the exterior. Then the interior and exterior polar balls intersect only "shallowly" (see section 4 in [Amenta et al., 2001]). Figure 3.2 demonstrates the labeled power balls. The algorithm labels the poles either as interior or as interior by traversing the cells which share a two-dimensional face.

The polar balls approximate the maximal inscribing balls in the interior and exterior of the surface. So, the radii of the polar balls are used to define the weights of the poles and with it the *power distance* to the poles. The *power diagram* of the poles approximates then the inverse medial axis transform. The set of two-dimensional polygonal faces of the power diagram dividing the power diagram into the interior and the exterior is called the *power crust*. The *power shape* is the connection of interior poles according



Fig. 3.2: Labeled polar balls on the poles. The grey balls are labeled as interior. White balls denote exterior poles. Notice, the intersection between interior and exterior polar balls is only "shallowly".

to the connectivity given by the power diagram. The power shape is the approximation of the interior medial axis.

Algorithm:

- 1. Compute the Voronoi diagram on the set of sample points.
- 2. Compute the poles of the Voronoi Diagram.
- 3. Construct the power diagram on the power balls of the poles.
- 4. Label the poles either as interior or exterior.
- 5. Output the faces of the power diagram separating the power cells of differently labeled poles as power crust.

Extensions:

- The labeling algorithm is proposed to be extended to handle data sets which do not meet the sampling conditions. The implementation uses values of "certainty" and processes the poles in a priority queue. The uncertain poles are processed by the algorithm as late as possible. The algorithm then labels the poles with the highest priority i.e. the most certain as interior or exterior. The new label is then used to recompute the priorities of the unprocessed poles.
- A processing step with variable value of "skinnyness" (see section 6.1 in [Amenta et al., 2001]) is proposed to hande noisy data. The output is no longer guaranteed to be topologically correct reconstruction but the authors claim to get watertight models. The "skinnyness" test can also indicate the presence of sharp corners.
- The large holes in the model which do not need to be filled can be detected by test of intersection of the polar balls.
- Increasing the radius of the polar balls by small value and using the medial axis transform approximation results in a watertight offset surface of the original.
- The medial axis simplification is done by assumption that the each sample point is perturbed from the surface by at most some constant value.

3.2.3 Modified Power Crust

[Mederos et al., 2005]

Prerequisites:

- Shape: twice differentiable manifold surface
- Parameter: smallest local feature size of the surface.
- Sampling locally-adaptive, noisy r-sampling (see Definition 3.3) with $r \leq 0.1$

Definition 3.2 (Point Set Projection). Let $S \subset \mathbb{R}^3$ be a point set, then projection S' of S onto $\partial \mathcal{R} \subset \mathbb{R}^3$ is defined as $S' = \{s' \in \partial \mathcal{R} | \exists s \in S : ||s - s'|| = d_{\partial \mathcal{R}}(s)\}.$

Definition 3.3 (Noisy ϵ -Sampling). Let the projection S' of S onto $\partial \mathcal{R}$ be an ϵ -sampling and let k be a constant. $S \subset \mathbb{R}^3$ is the noisy ϵ -sampling of $\partial \mathcal{R}$ iff

$$\forall s \in \mathsf{S} \, \exists s' \in \mathsf{S}' : \|s - s'\| \le kr \mathsf{lfs}(s')$$

Guaranties: Let $|\mathsf{lfs}_{\min}|$ be the minimal $|\mathsf{lfs}|$ for all points on the boundary and $|\mathsf{lfs}_{\max}|$ be the maximal. Given a noisy *r*-sampling with $r \leq 0.1 \wedge r \leq |\mathsf{lfs}_{\min}/|\mathsf{lfs}_{\max}|$ of a smooth manifold surface the method approximates the surface topologically correct.

Comments: This method is an extension of *power crust* [Amenta et al., 2000b]. The algorithm requires a known parameter for the minimal local feature size. since no such parameter can be given in general case, the estimation is done by trial and error.

Idea: The "skinnyness" test on Voronoi cells (compare section 6.1 in [Amenta et al., 2000b]) is no longer in this context since the sample points are not necessarily on the boundary. But the idea is based on the fact that some polar balls contain points of medial axis. The corresponding poles build a vector with the sampling point which is nearly collinear to the surface normal. Assuming the sufficiently dense sampling the radius of such polar balls exceed some value. The polar balls not containing the points of medial axis must not be considered in the power diagram and the corresponding pole is to be deleted.

The key to the algorithm is this minimal polar ball size, which is some fraction of minimal local feature size and must be known before processing the data.

Algorithm:

- 1. Compute the Voronoi diagram on the set of sample points.
- 2. Compute the poles of the Voronoi Diagram.
- 3. Delete poles with the radius of the corresponding polar ball is less than $\frac{1}{c}$ lfs_{min} for some constant c > 1.
- 4. Construct the power diagram on the power balls of the poles.
- 5. Label the poles either as interior or exterior.
- 6. Output the faces of the power diagram separating the power cells of differently labeled poles as power crust.

Extensions: No extensions are given in [Mederos et al., 2005].



Fig. 3.3: If the angle between the estimated surface normal \vec{n} and the vector \vec{v} from the sample point (apex of cones) to a Delaunay vertex intersects the intevall $[\pi/2 - \theta, \pi/2 + \theta]$ the edge is marked. If all Delaunay edges of a triangle are marked the algorithm marks the triangle as a candidate for the reconstruction.

3.2.4 Cocone

[Amenta et al., 2000a]

Prerequisites:

- Shape: smooth manifold surface
- Parameter: parameter free
- Sampling: locally-adaptive, no noise ϵ -sampling (see Definition 3.4) with $\epsilon \leq 0.06$

Definition 3.4 (ϵ -Sampling). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} and $S \subset \mathbb{R}^3$ be a finite set of points. Then S is said to be an ϵ -sampling of $\partial \mathcal{R}$, if

$$\forall b \in \partial \mathcal{R} : \exists s \in \mathsf{S} : ||b - s|| \le \epsilon \mathsf{lfs}(b)$$

Guaranties: Given an ϵ -sampling of a smooth manifold surface with $\epsilon \leq 0.06$ then the method results in a piecewise-linear 2-manifold homeomorphic to the original surface.

Comments: The *co-cone* algorithm was developed by Amenta et al. [Amenta et al., 2000a] as successor of the *crust* [Amenta et al., 1998] method. Co-cone improves crust by computational power and simplicity of development.

Idea: The sampling conditions depend on the local feature size and so on the curvature of the original surface. The sample points are assumed to lie on the surface and the distance to the nearest sample depends on some factor less than one of local feature size. So, the vector to the nearest sample point

3.2. LOCALLY ADAPTIVE SAMPLING CONDITIONS

is approximately orthogonal to the surface normal and its length is much less than the distance to the medial axis. So, the idea is to use these facts for the algorithm.

Correspondingly to crust algorithm [Amenta et al., 1998], the surface normal is estimated by pole computation. The vector from sample point to its pole approximates the direction of the surface normal. See \vec{n} in Figure 3.3 for illustration. The rotating opening angle around the normal shapes a cone. The negatively directed normal and the rotating opening angle shapes another cone with apex on the same sample point. The complement of this double cone is the *co-cone* as it is demonstrated in Figure 3.3.

In [Amenta et al., 2000a] is is stated that the Delaunay triangle is the candidate for the reconstruction if its dual Voronoi edge intersects the co-cone. The intersection test can be done on Delaunay edges checking if the angle between the the edge and the estimated surface normal on edges vertices is in co-cone. A Delaunay triangle is the candidate if all its edges pass the cocone test.

The resulting set of Delaunay triangles is not necessarily homeomorphic to the original surface but contains under guarantee the one. So, a cleaning step removes triangles on edges with only one adjacent triangle.

Algorithm:

- 1. Compute the Delaunay triangulation D and V on the the point set.
- 2. Compute poles for every sample point.
- 3. Mark all Delaunay edges if angle the estimated surface normal (vector from vertex to pole) and the vector to the another vertex is in range $[\pi/2 \theta, \pi/2 + \theta]$.
- 4. For all Delaunay triangles: if all edges are marked, mark the triangle as a candidate.
- 5. Remove all edges with only one adjacent triangle.
- 6. Remove all edges with no adjacent triangles.

Extensions: In [Dey and Giesen, 2001] the authors propose a method to detect undersampled 2D-regions on the surface. This extension leaves holes in the surface in the environment of sparse sampling. The detection is done by two tests which checks the "skinniness" of Voronoi cells and the normal condition. The Voronoi cells in the undersampled environment are no longer long and thin. The estimated normal differs greatly from the neighbor normals.

3.2.5 Tight Cocone

[Dey and Goswami, 2003]

Prerequisites:

- Shape: robust results on smooth manifold surface
- Parameter: parameter free
- Sampling: locally-adaptive almost noise-free, not necessarily ϵ -sampling but mostly on surface

Guaranties: No guarantees.

Comments: The method relies on the fact that the points in the undersampled areas are still dense enough. To great undersampled areas or to sparse sampling lead to an empty result. The output is a "2-complex embedded in \mathbb{R}^3 whose underlying surface is same as the boundary of the closure of a 3-manifold in \mathbb{R}^3 ." (Definition of *water-tight surface* in [Dey and Goswami, 2003]). **Idea:** It is assumed that the surface is mostly well sampled but may contain areas on the surface which are sparsely sampled. This areas are detected using the result of *co-cone* extension proposed in [Dey and Giesen, 2001]. The method uses *in* and *out* labeling to mark the appropriate Delaunay tertrahedra. The estimated normals on points in densely sampled surface areas approximate the original surface normal. If the sampling conditions defined for *co-cone* are met, the normal estimation is accurate. The points with accurate normal estimation are called *good*. The set of surface triangles on *good* points is called *umbrella*.

So, the task of the first step is to traverse trough the Delaunay triangulation without crossing the *umbrella* on good points and to mark the tetrahedra. The consequence is, because of undersampling not all tetrahedra which should be marked are marked. Not all points are good.

The second step is to "peel" out all marked tertraedra and detect the *out* tetraehdra which have not been marked leaving the *in* tetrahedra whose boundary is the *water-tight* surface. The *peeling* is based on the observation that in undersampled surface areas the Delaunay tetrahedra are *small*. This observation is based on the assumption, that all points of such tetraedra are contained in the same undersampled surface area. The *small* tetrahedra can be seen as thick triangles of the umbrella. So, to erroneously delete any of *in* tetrahedra the *peeling* must pass through *small* tetrahedron which can be detected.

Algorithm:

- 1. Compute the Delaunay triangulation D on the the point set.
- 2. Mark tetrahedra in D beginning with infinite tetraedra as *out*. Mark the nonmarked tetrahedra as *in*.
- 3. On all triangles $\sigma \in \mathsf{D}$:
 - (a) if the adjacent tetrahedron τ is marked in push σ into output set
 - (b) else if τ is marked *out* or all vertices of τ are not *good* and σ is not the smallest in τ , peel τ and push the triangles of τ but not σ into output set.

Extensions: The *marking* and *peeling* steps can be modified to reconstruct the boundary of internal voids. The method can be iteratively applied in the interior of the object marking a tetrahedron adjacent to the reconstructed boundary as *out*.

3.2.6 Robust Cocone

[Dey and Goswami, 2004]

Prerequisites:

- Shape: compact smooth surface without boundary
- **Parameter:** k is taken in range [3, 5], θ measures the deepness of ball intersection and is set to be $\theta = 15^{\circ}$, ratio between the Delaunay ball the k-nearest neighbor.
- Sampling locally adaptive density and noise deviation. " ϵ , k-sampling" see Definition 3.5. The orthogonal projection of the sample points is assumed to be an ϵ -sampling. The minimal distance between a sample point and its nearest sample point is locally adaptive but limited by a positive factor.



Fig. 3.4: Robust Co-cone: Polar balls on noisy sampling. Assuming sufficient sampling density and small sampling point deviation there is a definite difference between the minimal radius of the interior (light gray) or exterior (white) balls and the maximal radius of balls in the dilation of the boundary (dark gray).

Definition 3.5 (Noisy ϵ , k-sampling). Let $f : \mathbb{R}^3 \to \partial \mathcal{R}$ map any point in \mathbb{R}^3 to its nearest point in $\partial \mathcal{R}$. Let $S \subset \mathbb{R}^3$ be a point set and $S' \subset \partial \mathcal{R} = \{f(p) | p \in S\}$ be an ϵ -sampling of $\partial \mathcal{R}$. Let $n_k : S \to S$ map a point in S to its k-nearest neighbor in S. S is a noisy (ϵ, k) -sample of $\partial \mathcal{R}$ for two positive constants k_1 and k_2 iff:

$$\begin{aligned} \mathsf{S}' \text{ is an } \epsilon\text{-sampling of }\partial\mathcal{R} \\ \forall s \in \mathsf{S} : \|s - f(s)\| \leq k_1 \epsilon \mathsf{lfs}(f(s)) \\ \forall s \in \mathsf{S} : \|s - n_k(s)\| \geq k_2 \epsilon \mathsf{lfs}(f(s)) \end{aligned}$$

Guaranties: Assuming the sampling conditions to be fulfilled, the result of the method is homeomorphic to the original surface.

Comments: The method is not an extension of the original *co-cone* [Amenta et al., 2000a] method.

The name in Definition 3.5 is modified: κ is replaced by k because of unambiguity with the name in Definition 3.6

In the work [Dey and Goswami, 2004] the authors derive up to nine new ϵ -parameters for the proof and requires four k parameters for the sampling condition and further proof steps. The final sampling conditions depend on at least two further k parameters and the algorithm expects at least three parameters k, one of the k's and a crucial angle parameter θ . On θ depends the separating between inner and outer Delaunay balls.

The sampling is required to be "sufficiently dense", i.e. the guarantee holds if ϵ is assumed to be "sufficiently small" and the distance to the k-nearest neighbor is "sufficiently large".

Idea: The method is based on the idea of *power crust* [Amenta et al., 2000b]. In *power crust* it is assumed that the inner and outer Delaunay balls intersect only shallowly. In presence of noise however the assumption does not hold. But, there are still relatively big Delaunay balls in the interior and exterior of the original surface.

Here the method first detects the big Delaunay balls (white and light gray balls in Figure 3.4) from small ones (dark gray balls in Figure 3.4) contained in the thin but locally adaptive surface dilation containing all sample points. This is done by ratio between the radius of the Delaunay ball and the distance to k-nearest neighbor on the vertices.

The second step is to separate the balls into *inner* and outer. This is initiated on infinite balls. The further procedure marks the balls which deeply intersect. The intersection is measured by an angle θ ,

which is assumed to be small.

The boundary of the *outer* balls and the boundary of the *inner* Delaunay balls is respectively proven to be the homotopy correct reconstruction.

Algorithm:

- 1. Compute the Delaunay triangulation D on the the point set.
- 2. Mark tetrahedra in D as *big* if the circumradius of corresponding Delaunay ball is greater than *k*-times the distance to the *k*-nearest neighbr.
- 3. Beginning with infinite tetraedra mark the *big* Delaunay tertrahedra as *out* if the corresponding Delaunay ball intersects the neighboring marked ball by an angle less than θ .
- 4. Mark the not marked *big* Delaunay tetrahedra as *in*.
- 5. Output the restricted Delaunay triangulation on points touched by *outer* Delaunay balls.
- 6. Output the restricted Delaunay triangulation on points touched by inner Delaunay balls.

Extensions: No extensions introduced.

3.2.7 Reconstruction from Noisy and Non-Uniform Sampling

[Chazal and Lieutier, 2006, Chazal and Lieutier, 2008]

Prerequisites:

- Shape: smooth manifold surface
- **Parameter:** $0 < \epsilon < 0.1$, κ and wfs
- Sampling locally adaptive density and noise deviation, noisy non-uniform ϵ, κ -sampling, see Definition 3.6

Definition 3.6 (Noisy, non-uniform ϵ, κ -sampling). Let S' be an ϵ -sampling of $\partial \mathcal{R}$. Given $\kappa > 0$, $S \subset \mathbb{R}^3$ is the noisy non-uniform ϵ, κ -sampling of $\partial \mathcal{R}$ iff

 $\begin{array}{l} \mathsf{S}' \text{ is an } \epsilon\text{-sampling of } \partial \mathcal{R} \\ \forall b \in \partial \mathcal{R} \; \exists s \in \mathsf{S} : \|b - s\| < \epsilon \mathsf{lfs}(b) \\ \forall s \in \mathsf{S} \; \exists s' \in \mathsf{S}' : \|s - s'\| \le \kappa \epsilon \mathsf{lfs}(s') \end{array}$

Guaranties:

- 1. **Global:** The boundary of the union of balls is two connected components each isotopic to the original surface.
- 2. Locally adaptive: The original surface is a deformation retract of the union of balls.

Comments: No algorithm for surface reconstruction is given. The sampling conditions extend the bounds assumed for *co-cone* method [Amenta et al., 2000a].

Notice, in [Chazal and Lieutier, 2006, Chazal and Lieutier, 2008] the authors use the term "approximation" for "sampling".

Idea: The implication of the results in [Chazal and Lieutier, 2005a] is that the dilation of a compact



Fig. 3.5: (a) Uniform sampling, thick gray line is the ϵ -dilation of the boundary and medial axis. The critical points (contained in Voronoi) are in the ϵ -dilation. (b) Union of balls (dark gray) is homotopy equivalent to the surface ϵ -dilation. (c) Non-uniform sampling and the union of balls. (d) Light gray levelset intervalls contain the boundary of the union of balls

manifold surface is homotopy equivalent to the surface if the dilation value is less than *weak feature* $size \; (wfs)$ of the surface. Simply speaking, wfs is radius of the greatest ball inscribed into the tightest narrowing or neck of the region bounded by the surface.

Global sampling conditions: The idea here is to use this result for definition of new sampling conditions and for guarantees. Here the authors first define uniform sampling conditions which bound the sampling density and maximal sample point deviation from the boundary for all points on the surface by a fraction of the wfs. The consequence is that all sample points are in the dilation of the surface which is homotopy equivalent to the surface.

The key then is the guarantee that the criticals of the distance transform d_S on the sample points S are either very close to the surface or very close to the medial axis. In Figure 3.5 (a) the thick light gray line is the dilated surface and the medial axis. The critical points are the intersections between the Delaunay and Voronoi (gray lines).

The consequence is that d_5 is strictly increasing along the surface normals outside the dilation (The white space in Figure 3.5) of the surface and the dilation of the medial axis. Using this fact the authors define a homotopy to prove that the boundary of the union of balls centered on sample points of a certain radius is two connected components each of which is isotopic to the surface. The radius of balls depends on the sampling density (in particular the parameter ϵ) and the weak feature size. The consequence is the union of balls (see Figure 3.5 (b)) is homotopy equivalent to the ϵ -dilation of the boundary.

Locally adaptive sampling conditions: Assuming the sampling conditions to be non-uniform, the homotopy equivalent surface dilation does no longer contain all sample points. and so the homotopy definition using the boundary of the dilation is no longer valid. The goal is to define a homotopy between a union of non-uniform balls and the surface. The solution is done by usage of *level sets* defined as inverse of a function which maps points in space to the ratio between the distance value on these points and the local feature size of point projection onto the surface.

The first key step of the proof is to show that the level set of a certain value is isotopic to the boundary of the homotopy equivalent dilation of the surface with a uniform value. The second key argument is that the distance values along the surface normals starting on the boundary of the union of balls (dark gray in Figure 3.5 (c)) and ending on a level set of a certain value (b') are strictly increasing. The fact that the boundary of the union of balls is enclosed between two sublevel sets (light gray 2-intervalls between levelsets in Figure 3.5 (d)) uniquely determines the value b' for the level set. The third key step to complete the well-formed definition of a homotopy is that the surface normals cut the boundary of the union of balls in a unique point.

Algorithm: According to homotopy equivalence between the union of balls and its dual α -shape in [Edelsbrunner, 1993], the appropriate algorithm for globally set conditions is α -shape.

Extensions: The work also presents proofs on topology guaranteeing approximations of the medial axis for noisy uniform sampling conditions.

3.3 Globally Uniform Sampling Conditions

3.3.1 Sampling Conditions for Nonsmooth Manifolds by Critical Points Theory

[Chazal et al., 2009]

Prerequisites:

- Shape: nonsmooth manifold surface
- **Parameter:** κ and μ -reach of the boundary: the distance of μ -critical points to the boundary. The norm of the gradient on μ -critical points is μ .
- Sampling globally uniform, noisy, κ , μ -sampling where the Hausdorff distance between the sample points and the boundary is less than κ times the μ -reach (see Section 2.2.6) of the boundary. For the definition if μ -reach consult

Definition 3.7 (Noisy, uniform κ, μ -sampling). Given $\kappa \ge 0, \mu \ge 0, S \subset \mathbb{R}^3$ is the κ, μ -sampling of $\partial \mathcal{R}$ iff the Hausdorff distance between $\partial \mathcal{R}$ and S does not exceed κ times the μ -reach of $\partial \mathcal{R}$.

Guaranties: Let the union of balls be the union of α -balls with $\frac{1}{\mu}4d_H \leq \alpha < r_{\mu} - 3d_H$, where d_H is the Hausdorff distance between the point set and the boundary and r_{μ} is the μ -reach (compare Definition 2.38). Then, given κ and μ such that the critical point stability holds, the complement and respectively the of the union of balls is homotopy equivalent to the sufficiently small dilation of the boundary and respectively its complement.

Comments: The paper states the homotopy equivalence between the dilation of the sample points by the certain parameter and the dilation of the boundary by certain values computed by κ and μ . Our interpretation of the guarantee follows from the homotopy equivalence between the dilation and the boundary [Chazal and Lieutier, 2005b] and the homotopy equivalence between the α -shape and its dual shape [Edelsbrunner, 1993].

Idea: The main idea here is based on the *critical point stability* theorem which states that the critical points of the one compact set is not more than a certain value distant from the critical point of the other compact set if the Hausdorff distance between the two surfaces of the compact sets are not greater than another certain value. The two surfaces may be for instance the original and the approximated one. So, having the critical points of the one we can know the interval where the critical points of the other are to find.

Using the result of the theorem, perturbations on the surface may be assumed which do not change the intervals where the new critical points are. The deviation of sample points from the boundary can

3.3. GLOBALLY UNIFORM SAMPLING CONDITIONS

be seen as perturbation of the approximated surface from the original. The trick here is to bound the maximal perturbation in such a way that the critical point stability holds.

This is done first by bounding the maximum perturbation uniformly for each point on the surface. Second, to ensure the Hausdorff distance between the surfaces not to exceed a certain fraction of the weak feature size of the original compact set.

Algorithm: α -shape.

Extensions: The authors propose a method to estimate the input parameter by analyzing the critical function. The critical function maps a certain distance from the boundary to the infimum of the gradient norm on points at this distance.

3.3.2 Reconstructing r-Regular Manifold Contours with α -Shapes

[Bernardini and Bajaj, 1997]



Fig. 3.6: Sampling construction and conditions for 1-manifold (a) The sampling density does not allow the disc to "fall" through the contour. (b) The disc radius is chosen in such a way that the intersection between the disc and the contour is either empty or one point or one connected component the counterexample in (c)

Prerequisites:

- Shape: 2D only. smooth, r-regular manifold
- Parameter: r
- Sampling: globally uniform, noise-free

Guaranties: The contour approximation homeomorphic to the original boundary.

Comments: The construction of the proof assumes a disc such that the intersection of the disc and the boundary is exactly one connected component. The condition on both sides of the contour is equivalent to the definition of the r-regularity. Notice, disc radius is less than r.

The authors state a conjecture with equivalent conditions for 3D reconstruction of a 2-manifold. But as it is shown in [Stelldinger, 2008c] this conjecture is not true. The counter example can be constructed by placing four nearly coplanar points on the surface in a concavity such that they build almost a square. By construction the all points lie on the surface of the α -ball and the reconstruction method leaves the tetrahedron in the surface. Consequently, the surface is not everywhere thin and cannot be homeomorphic to the original.

Idea: Here the proof is based on the idea to construct a set of points such that the α -shape is

homeomorphic to the original. To do that one can think of a disc (2D reconstruction) of certain radius. First point can be placed arbitrary on the contour. The second one is place onto the contour in such a way that the disc touches the both but does not "fall" through the contour. So, the center of the disc must always be on the same of the contour, while the distance between the points is less than the diameter of the disc. The successive placement of sample points onto the boundary is illustrated in Figure 3.6 (a).

Second, the intersection between the disc and the contour must be either empty or one connected component (see Figure 3.6 (b) and the counterexample in Figure 3.6 (c)). Third the placing the next point and the disc between the points the disc is not allowed to cover any other point.

The proof the authors show that for each intersection of the disc with the boundary there is a hoeomorphic component in the α -shape.

Algorithm: α -shape

Extensions: Finding an optimal α -value in [Bernardini et al., 1999a]

3.3.3 α -Shapes, Normalized Mesh and Ball Pivoting

[Stelldinger, 2008c]



Fig. 3.7: (a) Four nearly coplanar points on the surface with circumradius less than α . (b) noise-free α -sampling. (c) "Normalized mesh" in [Attali, 1997]. (d) and (e) outer and inner boundary of the α -shape.

Prerequisites:

- Shape: smooth *r*-regular manifold
- Sampling: global, no noise, α-sampling: the greatest distance between a boundary point and the nearest sample points is less α
- Parameter: α

Guaranties: If $2\alpha < r$ then the the reconstructed polytope is homotopy equivalent to the original boundary, the outer and the inner boundary of the polytope are homeomorphic to the original surface.

Comments: The authors present a counterexample to prove that the conjecture for 3D reconstruction in [Bernardini and Bajaj, 1997] is not true.

With permission of the author, the illustrations in Figure 3.7 are taken from [Stelldinger, 2008a].

Idea: The author describes a correspondence and guaranteed topological expectations on algorithm result between the "normalized mesh" in [Attali, 1997], the "ball pivoting" in [Bernardini et al., 1999b] and the " α -shape" in [Edelsbrunner and Mücke, 1994] on noise free α -samplings.

The normalized mesh consists of Delaunay simplices whose dual Voronoi simplices intersect the original boundary. Since any simplex of the normalized mesh has an empty circumball less than α , the normalized mesh is a subset of the α -shape on α -samplings. In Figure 3.7 the insufficiency of the normalized mesh in 3D is demonstrated. The normalized mesh in (c) on α -sampling results in a hole in the boundary.

The correspondence between the α -shape and the "ball pivoting" method is given by two proven properties. First, for a *r*-regular set (see Definition 2.30) and an α -sampling on it, the α -shape triangle normals build with the surface normals on surface points in the projection of the triangle onto the surface an angle not greater than $\pi/6$. Second the α -shape edges have at least two adjacent triangles. These two properties are use by ball pivoting to build the mesh.

Since the α -balls cannot break through the boundary without touching a sample point of an α -sampling the pivoting ball always stays on the same side of the α -shaoe and, consequently, reconstructs the outer boundary of the α -shape.

The next trick to prove the correctness o the algorithm results is to show that the outer and the inner boundary of the α -shape on an α -sampling of an *r*-regular shape with $2\alpha < 2$ is homeomorphic to the original boundary.

Algorithm: α -shape and ball pivoting.

Extensions: The drawbacks of normalized mesh are holes in the reconstruction which develop in exactly the cases if four almost planar points lie on the surface of an α -ball. The α -shape closes such holes which can be used for detection of such cases.

3.3.4 Finding Homology

[Niyogi et al., 2008]

Prerequisites:

- Shape: smooth manifold, *r*-regular
- Sampling: noise-free (p, q)-sampling mit p < 0.48r and q = 0, noisy (p, q)-sampling mit p < 0.172rand q < 0.172r
- Parameter: p, q, r, α

Guaranties: For p < 0.48r, q = 0 the union of balls deformation retracts to the original smooth manifold. Therefore homology of the union of balls equals to the homology of the manifold.

For $p < (\sqrt{9} - \sqrt{8})r < 0.172r$ and $q < (\sqrt{9} - \sqrt{8})r < 0.172r$ the union of balls deformation retracts to the original smooth manifold. Therefore homology of the union of balls equals to the homology of the manifold.

Comments: Recommended reading on concept of *homology* can be found in [Hatcher, 2002] and [Munkres, 1984]. In [Dey et al., 1998], [Dumas et al., 2003] and in [Kaczyński et al., 2004] is the secondary literature on omputing homology from simplicial complexes.

The compact manifold in this work is a smooth manifold surface (limited maximal curvature). The conditional number τ defined for each manifold relates to the maximal curvature of the surface and corresponds to r-value in case of r-stability.

The authors give the lower bound for the number of sampling points. The guarantees are given first, for assumed sampling conditions and second, for the probability of fulfilled sampling conditions for rising number of sample points. Above, we mention only the guaranteed result for assumed sampling conditions.

Notice, we use the notations from our framework for simpler results comparison. The correspondence between our work notations and the notations in [Niyogi et al., 2008] are $\alpha \sim \epsilon$, $r \sim \tau$, $p \sim s$, $q \sim r$

Idea: Here is the intention to prove the homotopy equivalence between the union of balls placed on sample points of a certain radius and the manifold. The deformation retract of the union of balls is proven by *fibers*. Fiber connects any point of the surface with the boundary of the union of balls by a subset of the normal space on this point. The fibers correspond to the inverse distance transform for the boundary points on the union of balls and are defined as the intersection of union of balls with the normal space and a closed *r*-Ball on any boundary point. Under the assumption of the fulfilled sampling conditions the fibers do not intersect and contract uniquely to their boundary point.

In case of noise-free sampling, the union of balls is a simple expression of union of α -balls with $2p < \alpha < 0.96r$. In case of a noise sampling the union of balls is a simple expression of union of α -balls with $\alpha \in \left(\frac{1}{2}\left((q+r) - \sqrt{q^2 + r^2 - 6r}\right), \frac{1}{2}\left((q+r) + \sqrt{q^2 + r^2 - 6r}\right)\right)$. In limit: $\alpha \in \left((2 - \sqrt{2})r, (2 + \sqrt{2})r\right)$. Here the centers of the balls are not necessarily on the surface.

Algorithm: According to homotopy equivalence between the union of balls and its dual α -shape in [Edelsbrunner, 1993], the appropriate algorithm is α -shape

Extensions: The authors give probability statements in cases if the sampling conditions are not guaranteed. So, the authors compute the probability for the sampling to fulfill the conditions for a rising number of sample points.

In noise-free case the points are sampled from the uniform probability distribution on the surface. In case of noisy sampling Here the probability measure has to satisfy two regularity conditions. First, the probability is not zero only in the r-dilation of the manifold. Second, the probability for a sample point to occur in a q'-ball (0 < q' < r) around a boundary point depends on value q' only, not the boundary point. The second condition ensures the probability measure to be independent on curvature or manifold conditions like surface narrowing. The distance to the boundary determines the probability measure.

Given the sampling criteria for the guaranteed deformation retract of the union of balls and the confidence that the sampling criteria are met, the authors prove the homology equivalence between the union of balls and the manifold under the confidence that the sampling conditions are fulfilled. So, the proof is valid without the assumption on the sampling conditions but its probability.

3.3.5 Thinned- (α, β) -Shape-Reconstruction

[Stelldinger and Tcherniavski, 2009c], see also Chapter 4

Prerequisites:

• Shape: "r-stable" space partition with nonmanifold boundary (The thin line in Figure 3.8(a)). r is the greatest value by which the boundary can be dilated without to change the homotopy type. Each region contains a γ -ball.



Fig. 3.8: (a) r-stable space partition. (b) The union of thick edges, black and dark gray triangles is (α, β) -shape reconstruction. The thin line segments are Delaunay edges.

- Sampling: globally uniform density and noise. "(p,q)-sampling" with sampling density p less than 0.5 of the radius r and maximal deviation of sample points q less than r 2p.
- **Parameter:** The parameters α and β are computed depending on given r, γ, p, q .

Guaranties: If the p < 0.5r, q < r - p and the parameter α is chosen such that $p < \alpha \leq r - q$ and each region contains an open γ -ball with $\gamma \geq p + \alpha + 2q$ than the resulting reconstruction preserves connectivity and neighbourhood relations of reconstructed regions and defines a one-to-one mapping of reconstructed and original regions.

Comments: The maximal sampling deviation is the difference between the radius of the tightest narrowing in the shape and the sampling density. Consequently, the denser the sampling the greater can the points deviate from the boundary and the closer the points are to the boundary the sparser can be the sampling.

The reconstructed boundary may consist of chains of edges without any adjacent triangles.

Idea: The value r can equivalently be seen as the radius of the maximal inscribing ball into the tightest narrowing in the shape (the radius of the circle in Figure 3.8 (a)) or the *Hausdorf-distance* between the boundary and the set of critical points on the distance transform, or the smallest distance value on the critical points of the distance transform. It can also be seen as the value of the greatest dilation (gray thick line in Figure 3.8 (a)) of the boundary which does not change the original homotopy type.

The trick here is to know the tightest narrowing (the r-parameter) and the size of the smallest region (the γ -parameter) in the original shape as well as the sampling parameters p and q. Then the minimal sampling density p can be limited in such a way that connecting the points at distance greater than p somehow encloses the regions. Which is possible because the sampling conditions do not change on the boundary.

Of course if we connect the points at too great distance the regions will be completely covered. So, the other trick is to limit the maximal distance of connected sample points such that the regions are enclosed by edges or triangles but still recall the shape of the origonal region. This is done by limiting the maximal sample point deviation q to be less than r - p and setting the connecting parameter α less than or equal to r - q.

The union of connections between points consisting of triangles and edges leaves spaces which are not covered by any edge or triangle. These free spaces are called *holes*. The next trick here is to set up a parameter to distinguish between too great holes (union of white triangles in Figure 3.8 (b)) which correspond to original regions and the too small holes (union of gray triangles in Figure 3.8 (b)) which are result of noise. The limitation which guarantees this differentiation is beside r the of the size of minimal orignal region (the γ). If the minimal region is big enough the too small holes are less than the β -parameter.

The last step is intuitive. It is to remove the too small reconstructed regions. This is done by elementary collapse after filling the too small regions with Delaunay simplices.

Extensions: Under assumption that the edges of the resulting reconstructed boundary have at least two adjacent triangles the set of singular edges may be removed from the reconstruction.

Minimal extension of reconstructed boundary fills the chains of singular edges with Delaunay triangles less than β . The subsequent elementary collapsing on simple edges removes the topological distortion.

Extended β -Filling fills the boundary with Delaunay tetrahedrons such that non-orientable surface patches contain simple boundary triangles.

3.4 Refinement Reconstruction

[Stelldinger and Tcherniavski, 2009b], , see also Chapter 5



Fig. 3.9: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denotes the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b) The results of refinement reconstruction.

Prerequisites:

- Shape: Nonmanifold, non-smooth boundary of multi-regional objects.
- **Parameter:** Parameter free. The parameters can be set by upper bound of sampling conditions.
- Sampling: Region Stable (ψ, ρ) -Sampling Definition 5.4, Local Homotopy Stable (ψ, ρ) -Sampling Definition 5.17

Guaranties: The result of reconstruction on region stable (ψ, ρ) -sampling is a correct separation of local maxima. The result of reconstruction on local homotopy stable (ψ, ρ) -sampling is reducible to a correct separation of connected components of the homotopical axis and one-to-one mapping between original regions and the reconstruction.

Comments: Further knowledge and processing steps may be required to reduce the reconstructed boundary to a homotopy equivalent of the original.

3.4. REFINEMENT RECONSTRUCTION

Idea: The idea of refinement reconstruction is to define relevant parts of the object which has to be reconstructed and to ensure the sampling to be denser around these parts than in the interior of them. The homotopy of the relevant parts are here represented by the subset of the medial axis. So, we ensure by the sampling conditions that the steepest increasing paths on the discrete distance transform starting on the relevant parts of the medial axis not to leave the interior of the regions. The steepest increasing paths do not cross the original boundary.

Star-like shape have only one local maximum. The homotopy type is the same as of a ball. So, we only need to ensure the discrete distance value on the original local maximum to be greater than the discrete distance values on the original boundary. This is done by the locally adaptive sampling scaled by a fraction of the local region size.

The homotopy type of more complex shapes (i.e. Figure 3.9 (a)) with more than one local maximum is represented by homotopical axis (dashed line in Figure 3.9 (a) and (b)). The locally adaptive sampling conditions scaled by the local homotopical feature size ensure that the steepest increasing paths starting on the homotopical axis do not cross the original boundary. Observe the sample point density on the dashed line in Figure 3.9 (b) and the density on the thin line (corresponds to the heavier line in Figure 3.9 (a)).

Since the steepest increasing paths staring on the original local maxima stay in the original regions, we can uniquely associate the discrete local maxima reachable by steepest ascent on discrete distance transform with the original maxima. So separating the discrete local maxima we already correctly separate the original local maxima and so the corresponding original regions.

The first step of the reconstruction step is deletion of Delaunay tetrahedrons containing their own circumcenter. This is due to the fact that the reachable discrete local maxima correspond to Delaunay Delaunay tetrahedrons containing their own circumcenter. So, deleting them we hit each original region at least once.

Using the fact that the steepest increasing paths starting on local maxima stay in the local region we use the "flow relation" which imitates the continuous flow on the discrete distance transform. According to the flow relation between Delaunay simplices we descend on the discrete distance transform deleting the Delaunay simplices. The result is the set of reconstructed regions with one discrete maximum and the boundary consisting of smallest Delaunay simplices due to the flow relation.

Obviously, we most probably hit each regions a number of times. The result is there are several reconstructed regions which correspond to the same original region. We call this phenomenon a *re-finement*. The next reconstruction step bases again on the sampling conditions which ensure that the steepest increasing paths do not cross the original boundary. So, the steepest increasing paths starting in the reconstructed boundary have to be small enough to separate different regions. The ratio between the appropriate boundary simplex and the size of the region is given by the sampling parameters. So, the boundary simplices which exceed this ratio cannot separate different regions and correspondingly the adjacent regions correspond to the same original regions. The simplices exceeding the ratio are called *undersampled simplices*. On the other hand, the reconstruction step which deletes such boundary simplices is called *undersampled merge*.

Algorithm: According to Definition 5.10 a boundary simplex is ψ -undersampled if its size is greater than ψ times the smaller circumradius of the greatest cells in the adjacent regions.

- 1. Compute Delaunay triangulation.
- 2. Delete all Delaunay tetrahedrons which contain their own circumcenter.
- 3. Perform constructive retraction ("WRAP" see Section 2.4.10) on all Delaunay tetrahedrons which have been deleted in 2.
- 4. Merge regions on undersampled simplices lexicographically sorted in decreasing order according to their size. Collapse on all simple simplices.

Extensions: We propose to extend the sampling conditions and the definition of the homotopy axis to enable the sampling to be uniquely mapped to the shape. Consult dissolution problem in Section 5.15.1.

3.5 Conclusion

In this chapter we analyzed the properties and procedure of surface reconstruction methods based on computational geometry approach. The presented algorithms are a close selection of numerous previously proposed reconstruction methods. The description of the algorithms is given in form of a synopsis for better comparison of the requirements and results of the methods. The reconstruction algorithms are classified into two groups according to the sampling conditions: the reconstruction methods based on locally adaptive samplings and globally approaches assuming globally uniform sampling conditions.

We also added the synopsis of the thinned- (α, β) -shape-reconstruction and the refinement reconstruction. The thinned- (α, β) -shape-reconstruction is the initial point for our work and will be introduced and evaluated in the next chapter. Refinement reconstruction is the result of this theses and will be introduced and evaluated in Chapter 5.

As it can be seen in this chapter, the refinement reduction has the weakest requirements on the original shape and the sampling conditions.

Chapter 4

Thinned- (α, β) **-Shape-Reconstruction**

4.1 Introduction

Various applications motivate a globally uniform sampling setting for the whole shape. For instance, a laser scan projects equidistant lines onto the surface and samples these at nearly equidistant points. In computer tomography, the sampling is done in equidistant layers where each layer is a rigid lattice of sampling points.

The α -shape concept ([Edelsbrunner and Mücke, 1994]) introduced in Section 2.4.7 takes advantage of globally uniform sampling density. This algorithm uses the sampling density for establishing an internal parameter (α). Using this parameter, the method may be implemented by Delaunay complex where the Delaunay simplices are deleted from the complex if their empty circumball is of greater radius than α . The union of remaining simplices is the surface reconstruction. For the case in which the global sampling parameter is unknown, an approach for estimating the optimal α -value is presented in [Edelsbrunner and Mücke, 1994].

The surface reconstruction with α -shapes results in a polytope which approximates the original surface, but does not give guarantees on topology preservation. In [Bernardini and Bajaj, 1997] the authors prove the correctness of the α -shape-reconstruction for smooth shapes.

"Ball pivoting" [Bernardini et al., 1999b] is another well-known reconstruction algorithm which takes advantage of a globally uniform sampling parameter. The method builds a mesh if the "pivoting ball" of certain size meets the points at certain angle to the previous position. As proven in [Stelldinger, 2008c] the "ball pivoting" algorithm is related to α -shapes.

Research on global sampling parameters extends to deriving proofs for weaker sampling conditions under which well-established reconstruction methods are guaranteed to preserve the topological properties of the original surface. In [Chazal et al., 2009] the sampling conditions also cover *non-smooth* manifold surfaces. Comparing the sampling density by number of points required to reconstruct the surface of a unit ball, in [Stelldinger, 2008c] the global parameter is weakened to half of the radius. In [Niyogi et al., 2008] the authors approach an equivalent result and give weakened density for noisy sampling of smooth manifold surfaces.

The combination of noisy sampling and non-manifold, non-smooth surfaces was first tackled in [Stelldinger and Tcherniavski, 2009c], which gives appropriate sampling conditions and guarantees on preservation of topological properties. The idea is to repair the topology broken by α -shape reconstruction in a thinned- (α, β) -shape-reconstruction method. The algorithm contains a post-processing step which fills the holes in the α -shape, such that the resulting shape preserves the original connectivity of

the regions enclosed by the non-manifold surface.

The aim of this chapter is to evaluate the results in [Stelldinger and Tcherniavski, 2009c]. Stability is a widely used word which stands for numerous different concepts. In [Stelldinger and Tcherniavski, 2009c] shapes are divided into classes by a scalar value r. This value represents the thickness of the boundary dilation which preserves the homotopy type of the original. That means, the original surface homotopy remains stable under dilation by value r (Section 4.2).

This r-stability defines the limits for globally set sampling conditions which we introduce in Section 4.3. The homotopy equivalence between the α -shape and the union of α -balls [Edelsbrunner, 1993] is the key prerequisite for theoretical framework in [Stelldinger and Tcherniavski, 2009c]. These concepts are introduced in Section 4.4. As already mentioned the α -shape is not suitable for reconstruction of non-manifold non-smooth surfaces. The approximation consists of additional regions which are called *holes* in this framework. In Section 4.5 we define how to classify relevant or non-relevant holes.

Filling irrelevant holes in the reconstructed boundary already results in a reconstruction that under certain conditions preserves the original connectivity of the regions. In Section 4.6 we describe in depth the proof which can originally be found in [Stelldinger, 2008b]. The reconstruction by α value with postprocessing filling of irrelevant regions results in a surface reconstruction which contains tetrahedrons, so, is not thin. The last step in the thinned- (α, β) -shape-reconstruction is the topology-preserving thinning which we introduce in Section 4.7.

In Section 4.8 we visualize the reconstruction on three 2D examples: sparsely noise-free sampling, very noisy sampling and insufficient sampling.

The evaluation of the results of the thinned- (α, β) -shape-reconstruction is done in three ways. In Section 4.9 we compare the sampling conditions of well-known related methods with topological guarantees by computing the minimal number of required points to reconstruct the surface of a unit ball. Then Section 4.10 gives experimental results by applying the reconstruction methods on well-known datasets as well as on artificially constructed data sets. Section 4.11 discusses open problems of the thinned- (α, β) -shape-reconstruction method, the defined sampling conditions and for future work.

In summary, the algorithm presented in this chapter is a solid and fundamental result from both a theoretical as well as an experimental perspective. It has advantages over all related Delaunay triangulationbased methods known to us; it extends the limits of admissible shapes to non-manifolds and handles great amounts of noise. Remaining problems of the approach are based on too large sample point deviation from the boundary. In practice, we expect extra computation steps to be a solution.

4.2 *r*-Stability

Stability is a widely-used term and stands for a lot of roughly and subtly different concepts in mathematics, engineering, natural and social sciences, sports, medicine or even entertainment. We can find the following simple examples. In engineering we may hear: "The vehicle is stable", if this vehicle preserves its direction and road contact in cases of environmental disturbances like wind, curve radius or road surface. The stability of a chemical substance is its ability not to react across a variety of chemical systems. The ecological stability is the measure of probability of a population to return to its previous state or not to extinct. Numerical stability describes error propagation through the algorithm procedure. In discrete geometry we may refer to the instability of the medial axis against perturbations on the shape.

Here we introduce the concept of a stability of a shape which refers to its homotopy type. Simply speaking we want to replace an infinitely thin boundary with a strip such that the resulting shape is of the same homotopy type as the original. In particular we want to preserve the number and enclosure hierarchy of the resulting regions. The maximal thickness r of the strip is the value of the stability.

Consider Figure 4.2 (a). The space is divided or, as we say, partitioned by the black line into five regions. The black line is the boundary between the four inner regions and the infinite space. To find the maximal thickness value we inspect the shape for waists. The tightest waist determines our stability value r. In Figure 4.2 (a) we denoted the waist by a circle r. The radius of this circle is our desired value of the maximal thickness of the implied strip. We can also say the black line can be dilated up to value r without changing the original homotopy type. The r-stability is defined as follows:

4.3. SAMPLING CONDITIONS FOR R-STABLE SETS.

Definition 4.1 (r-Stable Space Partition[Stelldinger, 2008b]). A space partition \mathcal{R} is r-stable when its boundary $\partial \mathcal{R}$ can be dilated with a closed ball of radius s without changing its homotopy type for any $s \leq r$.

The center of the maximal inscribing ball in the tightest waist is a critical of the distance transform defined on the shape. So, our simple description "tightest waist" refers to the smallest distance value on the criticals, or, in other words, the "Hausdorff distance" between the shape and the set of critical points of the distance transform. The value r is also known as "weak feature size" (Definition 2.31 or [Chazal and Lieutier, 2005b]).

r-regular sets independently introduced in [Pavlidis, 1982] and [Serra, 1982] require for every point on the boundary a tangential ball with radius r. Consequently, a tangential r-ball can also be centered on any critical point. It follows that any r-regular shape is r-stable.



Fig. 4.1: Koch snowflake fractal (a) after two iterations (b) after three iterations (c) after four iterations.

In [Stelldinger, 2008a] a detailed study on sets generalized by the concept of r-stability is given. In particular, the generalization to r-sets allows consideration of nonsmooth and/or nonmanifold shapes.

In [Stelldinger, 2008a] it is stated that the fractal "Koch snowflake" Figure 4.1 with the side length 1 of the base triangle is r-stable for any $r < \frac{1}{\sqrt{3}}$. This can easily be seen, since the distance transform of the "Koch snowflake" consists of one critical point only. That is the local maximum and is located in the center of the base triangle.

The radius of the inscribing ball in any other triangle is smaller than the side length of the triangle. So, there is a strictly increasing simple path starting in the center of the maximal inscribing ball of any triangle and the center of the open side. The distance value in the center of the side with the recursively next triangle is only one-third of the original length and is less than the radius of the inscribing ball. It follows that there also is a strictly increasing path starting in the center of the triangle side where the fractal recursively grows and ending in the center of the inscribing ball. This is valid for all triangles but the base triangle since all its sides are closed - starts for further recursive fractal growth.

Back in our example in Figure 4.2 (a) we additionally see that r-stability generalizes shapes with crossings or junctions which are the necessary result if three or more regions meet in one boundary point.

The next question we are going to answer is, how to sample the boundary of an r-stable space partition to fulfill the preconditions for the thinned- (α, β) -shape-reconstruction method?

4.3 Sampling Conditions for *r*-Stable Sets.

The uniformly defined sampling conditions limit the minimal sampling density and the maximal sampling point deviation from the boundary by a globally set scalar parameter. The (p, q)-sampling uses two scalar parameters to control sampling density independently from the maximal sampling point deviation. The p parameter is a value which is defined for each boundary point. p is the maximal distance between each boundary point and the nearest sampling point. q defines the maximal sampling points deviation from the boundary and is defined for each sampling point. Each sampling point is at most at distance q from the boundary.



Fig. 4.2: (a) r-stable space partition. The boundary (black line) partitions the space into five regions: the environment region and four interior regions. The boundary is continuous: consists of one connected line component only. The boundary can be dilated (the gray strip around the black line) by the value r. The value r is also the radius of the smallest maximal inscribing ball (circle) into the regions. (b) Illustration of the sampling modeling. Every region (white space) contains a γ -ball (dashed circle). The circles in the center of the illustration and in the bottom left region represent the choice of the parameters to model the sampling conditions.

The p, q values ensure that all relevant sampling points are in the p-dilation and that all sampling points are in q-dilation.

Definition 4.2 (pq-Sampling). Let \mathcal{R} be a r-stable space partition and S be a point set, then S is a (p,q)-sampling if following is valid:

$$\begin{aligned} \forall b \in \partial \mathcal{R} \, \exists s \in \mathsf{S} : & ||b - s|| \leq p \\ \forall s \in \mathsf{S} \, \exists b \in \partial \mathcal{R} : & ||b - s|| \leq q \end{aligned}$$

Further it is required for thinned- (α, β) -shape-reconstruction that each original region contains a γ -ball. During the thinned- (α, β) -shape-reconstruction the parameters r, p, q and γ have to be known during the reconstruction process to compute the intervals for the choice of α and β -parameters which are also visualized in Figure 4.3

$$p < \alpha \leq r - q, \ \beta = \alpha + p + q, \ \gamma \geq \beta + q > 2(p + q)$$

The parameter r is measured on the original shape and represents the level of detail the reconstruction has to guarantee. In Figure 4.2 (a) the definition of an r-stable space partition is illustrated. The gray strip is the maximal boundary dilation which does not change the homotopy type of the space partition. r is the maximal value by which the boundary can be dilated. The center and the radius on the r-ball on the tightest narrowing illustrates the location of the critical point on the distance transform with the smallest distance value which is the radius of this maximal inscribing ball. On this critical point the dilation intersects if the dilation value is greater than r.

In Figure 4.2 (b) the r-ball is used to model the sampling conditions with very high noise corruption. The radius of the left and right q-balls represents the maximal sample point deviation from the boundary. Since the condition p < r - q has to be valid in the sampling, the inner ball with radius less than r - q models the p-value. The interval for the α value is illustrated by the dilated circle with p-ball as inner circle and the r - q-ball as outer circle.

In Figure 4.3 (a) the equivalent illustration is given. Here again the q-ball is chosen to model large amount of noise. In our sampling example the data acquisition device guarantees a dense sampling, so we model the p-value by a small p-ball. The algorithm sets the α -value in the interval (p, r-q] (the gray circle in Figure 4.3 (a)).

The α -value has a further dependency and, so, a further condition has to be taken into account. The regions must be "big" enough. Regions are the connected components enclosed by the boundary



Fig. 4.3: Sampling conditions for thinned- (α, β) -shape-reconstruction. (a) Dependency between r, p, q and the choice of α with p = 0.22r, q = 0.6r and $\alpha = 0.29$. The interval $p < \alpha \le r - q$ for the arbitrary choice of α is gray. (b) β and γ dependency from the choice of α . $\beta = p + \alpha + q$ and $\gamma \ge \beta + q$

of the space partition. In our example regions are the white spaces in Figure 4.2 (b). We choose the parameters in such a way that a great amount of noise can be modeled. The sampling condition restricts the smallest size of a region to γ . It means that every region encloses a ball with radius at least γ . Consequently, the sampling parameters p and q as well as the γ -value restrict the choice of α according to sampling condition 3: $\gamma \geq \beta + q = \alpha + p + 2q$ or $\alpha \leq \gamma - p - 2q$.

The γ -value as composition of p, q and α parameters is illustrated in the smallest region in Figure 4.2 (b). The equivalent illustration is also given in Figure 4.3 (b): $\gamma = p + \alpha + 2q$. The α -parameter is given again as interval. We see that here the interval is limited to $(p, \gamma - 2q]$, where the upper bound is less than r - q in Figure 4.3 (a). So, this condition determines the choice of the α -parameter and, consequently, the β -parameter.

Now, we summarize: in our example there is a shape or as we call it in our context the boundary $\partial \mathcal{R}$ of a space partition ($\partial \mathcal{R}$ is the thick line in Figure 4.2 (b)). The shape is *r*-stable and each region enclosed by the shape contains a γ -ball, with $\gamma = 1.42993r$ (see Figure 4.2 (b) for illustration). We want to digitize the shape with a data acquisition device which delivers very noisy data but still guarantees a sampling dense enough to the boundary $\partial \mathcal{R}$. We model the parameters of the data acquisition device with p = 0.16r and q = 0.53r and ensure that the sampling conditions are fulfilled. So, we choose the the α in the interval (0.16r, 0.20993r] with $\alpha = 0.20493r$.

4.4 Sampling Points, the Union of Balls and its Dual Shape.

In Figure 4.4 (a) we demonstrate the set of sampling points taken by our modeled acquisition device as well as the set of α -balls where an α -ball is a ball centered on a sample point with radius α . According to the sampling conditions for every boundary point there has to be a sample point at distance less than or equal to p. In the illustration we differentiate between the α -balls (gray) centered on such sample points and the α -balls (dark gray) centered the sample points which deviate from the boundary more than p but less than q. The union of gray balls completely cover the boundary $\partial \mathcal{R}$. We call the union of all α -balls simply union of balls. So, the union of balls completely cover the boundary $\partial \mathcal{R}$.

Since α is chosen such that $p < \alpha \leq r - q$, the $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ of the boundary is homotopy equivalent to the original boundary $\partial \mathcal{R}$. In Figure 4.4 (a) $\partial \mathcal{R}^{\oplus}$ is the light gray strip. The complement of the $\partial \mathcal{R}^{\oplus}$ (white space in Figure 4.4 (a)) is topology equivalent to the original space partition. So,



Fig. 4.4: (a) The $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ (light gray) of the space partition covers the union of α -balls \mathscr{U} (the union of gray and dark gray balls). \mathscr{U} covers $\partial \mathcal{R}$ (black curve), $\partial \mathcal{R}$ has the same number of components as \mathscr{U} (one connected component only in this case; but a circle is one connected component too). (b) \mathscr{U} (union of gray balls) is homotopy equivalent to the α -shape (union of black edges and dark gray triangles).

the question arises under which conditions the union of balls preserves the topological properties of the original boundary and how to reconstruct them?

Given the union of balls it is easy to construct its dual α -shape. To do so, we connect the centers of the intersecting balls. Two intersecting balls result in such a way in an edge. Three intersecting balls develop three edges and the triangle which is completely covered by the intersection balls. Consequently in 3D, four intersecting balls with nonplanar centers develop six edges, four triangles and one tetrahedron, all completely covered by these four intersection balls. The duality between the union of α -balls and the α -shape is stated by the following theorem and is proven in [Edelsbrunner, 1993].

Theorem 4.3 (Homotopy Equivalence of α -Shape and the Union of Balls [Edelsbrunner, 1993]). Let S be a set of points and \mathscr{S}_{α} be an α -shape constructed on S. The union of closed α -balls centered on points in S covers \mathscr{S}_{α} , and the two sets are homotopy equivalent.

We see the duality between the union of α -balls and the α -shape in our example in Figure 4.4 (b). The union of dark gray triangles and black edges is the α -shape and the union of gray filled circles is the union of α -balls. Notice, three intersecting balls correspond to three edges but, if there is no common intersection between those three balls, there will be no dual triangle.

In [Bernardini and Bajaj, 1997] the authors use the α -shapes with $\alpha < r$ to construct a homeomorphic 2D boundary approximation from a noise-free (q = 0) sampling of an *r*-regular shape and describe in [Bernardini and Bajaj, 1997] a practical method to select an optimal α -value to fit a piecewise smooth algebraic surface to the sample points which do not fulfill the sampling conditions.

r-regular shapes are shapes of everywhere smooth surfaces such that on both sides of the surface one can find a tangential ball with radius r. Consider the opposite case - a corner of a nonsmooth surface. If we place a tangential ball into the corner, the corner is not going to be completely filled. We will find some space behind the ball. So, we need a smaller ball to make the space behind the ball smaller. But the space remains. So, we take even smaller ball and so on. The consequence is, if we want to fill out the corner by a ball, we need take an always smaller ball, which then converges to a ball with zero radius.

In [Stelldinger, 2008c] the authors derived an analog result for 3D under equal conditions. The guaranteed homeomorphic surface approximation is the outer boundary of the α -shape. The outer boundary of an α -shape is then defined as the union of the triangles of the corresponding α -complex, which can be seen from the outside.

Why do the results in [Bernardini and Bajaj, 1997] and [Stelldinger, 2008c] work? The trick is to set the α -value small enough in reference to the *r*-value. Consider a sample point an *r*-circle. If we assume the nearest two different sample points on the circle near enough to the first, and connect them by edges

4.5. (α, β) -HOLE

then the angle between those edges is obtuse and the edge opposite to the first point is then very long, in comparison to the edges to the nearest points. In this way we ensure that only the relevant edges are small enough to be counted to the contour reconstruction.

The same trick does not work for nonsmooth boundaries because no r-value can be given and so no α -value can be set. Noisy sampling of a smooth boundary brings additional sample points which deviate from the boundary. So, the condition of an obtuse and, so, too long edge is destroyed.

If we consider again our noisy example of a nonmanifold contour in Figure 4.4 (b) and gaze at the α -shapes with slitted eyes we might think then the α -shape already does what we want. The reconstructed contour encloses in some way the same regions and corresponds in some way to the original contour. However, if we examine the α -shape we observe, that even if the α -shape does not connect different regions it does enclose smaller regions all of which are covered by the α , q-dilation (the thick gray strip) of the original boundary. We detect certain correspondence between the α -shape and the original boundary. In the following we examine, which further steps are needed to recover the homeomorphic approximation from the correspondence we recognized before.

In 2D this problem of small regions or holes in the α -shape has been solved in [Stelldinger et al., 2006] by filling the small holes. The method leads to a homeomorphic reconstruction if the sampling conditions are the same as for the actual method.

In the following section we will go into this step similarly crucial for actual 3D extension of the results introduced in [Stelldinger et al., 2006]. In 3D the problem extends to handling of artifacts on the reconstructed boundary which do not enclose any further small regions and, consequently, cannot be filled.

4.5 (α, β) -Hole

An α -shape (\mathscr{S}_{α}) is the underlying space of an α -complex D_{α} which is a subset of Delaunay complex (D). An α -shape consists of points in space. An α -complex is a set of Delaunay simplices. Now we introduce the complement ($\mathscr{H}_{\alpha} = \mathscr{S}_{\alpha}^{c}$) of the α -shape which is again a subset of space and, so, a set of points. \mathscr{H}_{α} is the union of connected components in \mathscr{S}_{α}^{c} .

We combine the connected components in \mathscr{S}^c_{α} in a set H_{α} and denote each element in H_{α} as an α -hole H_{α} . We may also say: "an α -hole is an element in the set of connected components H_{α} " which is equivalent to the statement: "an α -hole is one connected component in the complement ($\mathscr{K}_{\alpha} = \mathscr{S}^c_{\alpha}$) of the α -shape". The corresponding subset of the Delaunay complex is D_{α} . Notice that either for each simplex $\sigma \in D_{\alpha}$ there is another simplex $\sigma' \in D_{\alpha}$ which is adjacent to σ , or D_{α} consists of exactly one component. Consequently, we have the correspondence: the underlying space $|D_{\alpha}|$ of D_{α} is H_{α} .



Fig. 4.5: (a) black lines and polygons: α -shape (b) α -holes: light gray (α, β)-holes, gray not-(α, β)-holes

As mentioned before, under certain sampling conditions the 2D- α -shape is the topologically correct contour reconstruction [Bernardini and Bajaj, 1997]. In 3D the topologically correct reconstruction is the outer boundary of the 3D- α -shape [Stelldinger, 2008c]. However, the reconstruction methods in [Bernardini and Bajaj, 1997, Stelldinger, 2008c] require noise-free sampling of smooth manifolds. What happens, if the original boundary is not smooth or nonmanifold or the sampling is noise corrupted as in our example in Figure 4.4? The α -shape contains artifacts. The artifacts can be regarding the *r*-value small holes in the α -shape or in 3D small voids or regions as well as tails of linked edges or thickenings of α -contiguous simplices. In 3D a great amount of noise leads to topological and/or geometrical distortions of the α -shape boundary like tunnels, loops or knots which do not separate different regions.

In this section we deal with α -holes in the α -shape or holes consisting of contiguous Delaunay simplices with circumradius greater than α completely enclosed by simplices of the α -shape. Thus, deleting them from the Delaunay triangulation results in *holes* in the underlying space which we call α -holes. In Figure 4.5 (a) the α -holes are the white space, the whole space without the α -shape. We notice a great difference between the α -holes containing the β -ball and the remaining much smaller α -holes.

In the further context we distinguish between the α -holes containing a Delaunay simplex with circumradius greater than β and call such α -holes the (α, β) -holes and the remaining not- (α, β) -holes.

Definition 4.4 (Stelldinger). Let D_{α} be the α -complex and $\mathscr{S}_{\alpha} = |D_{\alpha}|$ be its α -shape. Then the α -holes of \mathscr{S}_{α} are the components of \mathscr{S}_{α}^{c} . The (α, β) -holes of \mathscr{S}_{α} are the set of α -holes H_{α} , where the largest radius of some n-cell in H is at least $\beta \geq \alpha$. The union of the α -shape $|D_{\alpha}|$ with all α -holes of D_{α} that are not α, β -holes is called the (α, β) -shape-reconstruction $(D_{\alpha,\beta}^{\oplus})$.

An α -hole in the Delaunay complex means that a connected group of simplices greater than α are enclosed by simplices less than or equal to α . The α , β -hole D_{α} contains a simplex which is even greater than β . So, we may have the intuition that there is a point x in D_{α} such that the distance to the nearest sample point is greater than β . In other words, the α , β -hole is thick enough to contain a β -ball free of sample points. In [Stelldinger, 2008c] this correspondence is proven to be an equivalence by:

Lemma 4.5 (Stelldinger). An α -hole H_{α} is an (α, β) -hole if and only if it contains a point whose distance to the nearest sampling point is at least β .

I, simplex \leftarrow point: if an α -hole contains a point x with distance to the nearest sample point greater than β then the α -hole is an (α, β) -hole. Consider first that the point x is outside the α -shape somewhere in the infinitive space. Then the claim follows immediately. Otherwise the α -hole is a union of simplices greater than α . It follows that the point x is in some simplex σ greater than α . The circumball of this simplex is free of sample points except for the vertices of σ . Consequently, the nearest sample point from x is one of the vertices of σ . Since by assumption the distance between x and its nearest sample point is greater than β we conclude that the distance between a point in σ and one of the vertices of σ is greater than β . Since the point x is in σ then its distance to the vertices is less than the circumradius of σ . It follows that the circumradius of σ is greater than β .

II, simplex \rightarrow point: if an α -hole is an (α, β) -hole then it contains a point whose distance to the nearest sample point is at least β . The proof of this implication in [Stelldinger, 2008c] does not use the fact that the adjacent simplex opposite to an obtuse angle has a greater circumradius. The face opposite the obtuse angle is called *not-Gabriel face* and has the property to include in its circumball the remaining vertex of the simplex. The same is valid in nD.

Considering a simplex σ in an α -hole whose circumradius is greater than β we do not know if this simplex contains its own center and, so, we do not know if there is any point whose distance to any vertex of σ is inside σ and so inside the (α, β) -hole. So, if σ contains its own circumcenter then the claim follows.

Otherwise σ has at least one not-Gabriel face and the neighboring simplex which shares this not-Gabriel face has a greater circumradius. Proceeding with this consideration moving to next greater neighboring simplex we reach a simplex containing its own circumcenter.

The sequence of simplices with monotone growing circumradii is part of the *flow relation* presented in [Edelsbrunner, 2003]. Without loss of generality let us assume the addition of an adjacent simplex to

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the sequence if the sharing not-Gabriel face is the greatest. Then the sequence of not-Gabriel faces we pass through is also monotone increasing.

By Definition 2.49 (compare [Edelsbrunner and Mücke, 1994]) the circumball of an α -face only contains the vertices of the face in its boundary and is empty elsewhere. So, an α -face cannot be not-Gabriel. It follows, that the sequence of growing simplices and not-Gabriel faces is part of the same α -hole and the last simplex containing its own circumcenter is in the same α -hole too.

Since the last simplex σ' is greater than σ the circumradius of σ' is greater than β , and since the circumcenter of σ' is in σ' and σ' is in the α -hole, the circumcenter of α' is in an α -hole and is the point whose distance to the nearest sample point is greater than β .

Our aim in a further section is to establish a correspondence between the union of α -holes and the original space partition. In fact Theorem 4.6 proves that the homotopy equivalent boundary reconstruction can be achieved by construction of the α -shape and by subsequent filling of the not- (α, β) -holes.

4.6 (α, β) -Shape-Reconstruction

In Section 4.3 we learned how to sample a boundary of a space partition to preserve the topological properties for the thinned- (α, β) -shape-reconstruction method. First step was to construct an α -shape, with $p < \alpha < r - q$. The (p, q)-values depend on the *r*-value of the space partition and the conditions of the data acquisition device.

In Section 4.4 we learned the homotopy equivalence between the union of α -balls and the α -shape and discussed why the α -shape is not a sufficient reconstruction in our weakened assumptions on original boundary and sampling conditions.

In Section 4.5 we learned one kind of distortion on the α -shape, the α -holes, and distinguished them by size.

In this section we discuss the results in [Stelldinger, 2008c] on sampling conditions and, so, value settings for building a superset of the α -shape such that the resulting thick boundary preserves connectivity and neighborhood relations and bijectively maps the original to the reconstructed regions. The superset of the α -shape is the (α, β) -shape-reconstruction, the union of the α -shape and the not- α -beta holes. The remaining (α, β) -holes correctly reconstruct the original regions.

Theorem 4.6 (Topology Preserving (α, β) -Shape-Reconstruction [Stelldinger and Tcherniavski, 2009c]). Let \mathcal{P} be an r-stable partition of the space \mathbb{R}^n , and S be a (p,q)-sampling of \mathcal{P} 's boundary B. Then the (α, β) -shape-reconstruction \mathcal{R} preserves connectivity and neighborhood relations and defines a one-to one-mapping of the (α, β) -holes of \mathcal{R} to the regions r_i of \mathcal{P} , if (1) $p < \alpha \leq r - q$, (2) $\beta = \alpha + p + q$ and (3) every region r_i contains an open γ -disc with $\gamma \geq \beta + q > 2(p+q)$.

I. Union of balls has as many connected components as the original boundary.

The first step in the proof is to show that the number of connected components of the union of α -balls \mathscr{U} is equal to the number of connected boundary components. In Figure 4.4 (a) the union of gray and dark gray balls illustrate \mathscr{U} . \mathscr{U} has holes but is one connected component in our example.

All sample points are at lesser distance to the boundary than q. It follows that the q-dilation of the boundary covers the points and $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ covers \mathscr{U} . Every connected component of the boundary dilation contains at least one connected component of the boundary and, consequently, at least one sample point and its α -ball. Therefore, the number of connected components of $\partial \mathcal{R}^{\oplus}$ is less than or equal to the number of connected component of \mathscr{U} .

Let # denote a function which maps a set to its number of connected components. Then the dilation has $\#\partial \mathcal{R}^{\oplus}$ connected components, the union of balls has $\#\mathscr{U}$ connected components and according to previous implication the following is valid: $\#\partial \mathcal{R}^{\oplus} \leq \#\mathscr{U}$. The union of balls completely covers the boundary, so, \mathscr{U} has less or equal connected components than $\partial \mathcal{R}$: $\#\mathscr{U} \leq \#\partial \mathcal{R}$ (See Section 4.11.1 for discussion).

Since $\partial \mathcal{R}^{\oplus}$ is homotopy equivalent to $\partial \mathcal{R}$, the number of connected components of $\partial \mathcal{R}^{\oplus}$ and $\partial \mathcal{R}$ is equal, $\#\partial \mathcal{R}^{\oplus} = \#\partial \mathcal{R}$. It follows, that the number of connected components of the union of balls is

equal to the number of connected components of the boundary: $\#\partial \mathcal{R}^{\oplus} \leq \#\mathscr{U} \leq \#\partial \mathcal{R} = \#\partial \mathcal{R}^{\oplus} \Rightarrow \#\mathscr{U} = \#\partial \mathcal{R}.$

According to Theorem 4.3 an α -shape is homotopy equivalent to the union of balls. It follows that the α -shape has the same number of connected components as the union of balls: $\#\mathscr{U} = \#\mathscr{I}_{\alpha}$. Consequently, α -shape and the boundary have the same number of connected components: $\#\mathscr{I}_{\alpha} = \#\partial \mathcal{R}$.

II. Each erosion of an original region is contained in a single α -hole

In Figure 4.4 (b) the union of balls \mathscr{U} is illustrated as the union of gray balls. The complement of \mathscr{U} is the space without \mathscr{U} and can also be considered as a set of connected components. The union of balls \mathscr{U} completely covers the α -shape. Consequently the connected components of the complement of the union of balls are completely contained in the connected components of the complement of the α -shape. The connected components of the complement of the α -shape are called α -holes. In Figure 4.4 (b) the α -holes are regions surrounded by black edges and/or dark gray triangles but not the unions of dark triangles.

The white spaces in Figure 4.4 (b) are the connected components of the complement of $\partial \mathcal{R}^{\oplus}$ and are called erosions of the regions. We denote them by R^{\ominus} . The boundary dilation by a value less than r does not change the homotopy type of the boundary and the topology type of the regions. So, the erosions of regions are topologically equivalent to the regions of the original space partition.

Since \mathscr{U} is completely contained in $\partial \mathcal{R}^{\oplus}$ (light gray strip in Figure 4.4 (b)) and the erosions of the regions do not intersect $\partial \mathcal{R}^{\oplus}$, each erosion of a region is contained in a single connected component of \mathscr{U} and, consequently in a single α -hole (darkened region on Figure 4.6 (b)).

III. α -hole containing erosion of an original region is an (α, β) -hole

 α -holes are the connected components of the complement of an α -shape. As we may see in Figure 4.4 (b), not all α -holes correspond to an original region (α -holes without any white spaces).

An α -hole is the underlying space of Delaunay simplices which have been deleted during the α shape construction. So, we can say an α -hole is an (α, β) -hole if the corresponding set of Delaunay simplices contains a simplex with circumradius greater than $\beta \geq \alpha$. According to Lemma 4.5 (compare [Stelldinger and Tcherniavski, 2009c]) we also can say that an α -hole is an (α, β) -hole if and only if it contains a point whose distance to the nearest sample point is at least β . Example (d) in Section 4.8 demonstrates the consequences of insufficient sampling if γ -ball is not contained in a region.



(a)

(b)

Fig. 4.6: (a) Light gray $q + \alpha$ -dilation. Gray q-dilation. Each region contains the γ -ball, with $\gamma = \beta + q$ and $\beta = p + q + \alpha$. The inner circle in the bottom region illustrates the distance $(\gamma - q - \alpha)$ between the center of the γ -ball and the boundary of the $\alpha + q$ -erosion R^{\ominus} (boundary of the white space). (b) α -hole (for example the right darkened region) containing the erosion of an original region contains a γ -ball. The greatest inscribing ball (dashed circle) contains the γ -ball as in (a). If the radius of the greatest inscribing ball is greater than γ and $\gamma \geq \beta + q$ then the α -hole is an (α, β) -hole.

4.6. (α, β) -SHAPE-RECONSTRUCTION

 (α, β) -shape-reconstruction requires that every original region contains an open γ -ball with $\gamma \geq \beta + q$ and $\beta = \alpha + p + q$. This means that the distance between the center of the γ -ball and its nearest boundary point is γ . Consider for example in Figure 4.6 (a) the region on the extreme right. It contains a γ -ball with $\gamma = \beta + q$.

Since the original region R completely contains its erosion R^{\ominus} (the white space in Figure 4.6 (a)), the distance between the center c_{γ} of the γ -ball and the boundary of R^{\ominus} is greater than $\gamma - \alpha - q$. The distance is illustrated as the radius of the inner circle in Figure 4.6 (a) in the bottom region.

Since an α -hole completely contains R^{\ominus} (illustrated by the darkened region in Figure 4.6 (b)) and all sample points have the distance to the boundary of R^{\ominus} greater than α , the distance between c_{γ} and its nearest sample point is $\gamma - q \ge \beta$. It follows that the α -hole containing R^{\ominus} is an (α, β) -hole.

IV. Every original region can be mapped to exactly one (α, β) -hole

II states that each erosion of an original region is completely contained in a single α -hole. It follows that each original region can be mapped to exactly one α -hole, and according to III α -hole containing an erosion of an original region is (α, β) -hole. Consequently, each original region can be mapped to exactly one (α, β) -hole.

V. An α -hole that does not intersect any erosion of an original region is completely contained in the α , q-dilation $\partial \mathcal{R}^{\oplus}$ and cannot be an (α, β) -hole.

Erosion of regions contains all points of space which are at greater distance to the boundary of the space partition than some value. In our case the value is $\alpha + q$. If an α -hole does not intersect any erosion of an original region, then there is no point in the α -hole with distance to the boundary greater than or equal to $\alpha + q$. In other words, all points of the α -hole are at lesser distance to the boundary than $\alpha + q$ and, consequently, the α -hole must be completely contained within the $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$.

All points in the $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ of the boundary are at lesser distance to the boundary than $\alpha + q$. The sampling conditions on the data set require for each point on the boundary the distance to the nearest sample point to be less than p. Consequently, the distance between any point in the dilation $\partial \mathcal{R}^{\oplus}$ and its nearest sample point is less than $\beta = \alpha + q + p$.

Now, first, we know that if an α -hole does not intersect any erosion of an original region then the α -hole must be completely contained within the $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$. Second, we know that the distance between any point in the dilation $\partial \mathcal{R}^{\oplus}$ and its nearest sample point is less than $\beta = \alpha + q + p$. Third, according to Lemma 4.5 an α -hole is an (α, β) -hole if and only if it contains a point whose distance from the nearest sampling point is at least β . It follows that if an α -hole does not intersect any erosion of an original region then the distance between any point in the α -hole and its nearest sample point is less than $\beta = \alpha + q + p$.

VI. The correspondence between (α, β) -holes and original regions is 1-to-1.

We have two kinds of α -holes: those which do not intersect erosions and are not (α, β) -holes (V) and those which do intersect erosions and necessarily are (α, β) -holes (III). According to IV each original region can be mapped to exactly one (α, β) -hole.

Can each (α, β) -hole be mapped to exactly one region? Let us consider the opposite. There is an α -hole which cannot be uniquely mapped to exactly one original region.

We consider only α -holes which intersect erosions of original regions and according to III are (α, β) -holes. So, using II the erosions are completely contained in (α, β) -holes, consequently one (α, β) -hole must either not contain any erosion which is a contradiction of III or contain more than one erosion.

Consider an α -hole that contains more than one erosion. The two corresponding original regions are separated by at least one boundary point. Consequently the erosions are separated by at least one open $\alpha + q$ -ball. Since both erosions are completely contained in the α -hole the boundary of the α -hole does not intersect the $\alpha + q$ -ball. It follows that the α -balls placed on the sample points in the $\alpha + q$ -ball do not intersect. This implies that there has to be a point in the $\alpha + q$ -ball which is not contained in the union of balls and thus has a distance to the nearest sample point greater than α

But according to the sampling conditions the distance between each boundary point and its nearest

sample point is at most $p < \alpha$. Since the original shape is assumed to be embedded into a continuous space two different regions cannot be separated by one point only. The boundary point which corresponds to the $\alpha + q$ -ball has a neighbor at infinitesimal distance. The sample points of the two boundary points are at distance p and, consequently, the α -balls placed on those sample points would intersect and this contradicts the assumption.

From the previous consideration we conclude that each (α, β) -hole can be mapped to exactly one region and together with IV we establish a 1-to-1 correspondence between (α, β) -holes and original regions. The boundary of the space partition and the (α, β) -shape-reconstruction (union of edges, gray and dark gray triangles in Figure 4.7 (a)) enclose the same number of regions.

VII The original boundary has the same number of connected components as the (α, β) -shape-reconstruction.



Fig. 4.7: (α, β) -shape-reconstruction is the α -shape (union of edges and dark gray triangles) with filled not- (α, β) -holes (union of thin edges and gray triangles). (α, β) -holes are α -holes with the greatest inscribing ball (circles in the illustration) greater than a β -ball (circle with the β -notation)

The (α, β) -shape-reconstruction is the union of the α -shape (union of thick edges and dark gray triangles in Figure 4.7) and the not- (α, β) -holes (union of thin edges and gray triangles in Figure 4.7).

According to V all not- (α, β) -holes are contained in the α, q -dilation $\partial \mathcal{R}^{\oplus}$ of the boundary. The union of not- (α, β) -holes is the difference between the (α, β) -shape-reconstruction and the α -shape. So, all differences between (α, β) -shape-reconstruction and the α -shape are confined within $\partial \mathcal{R}^{\oplus}$. This implies that the number of connected components $\partial \mathcal{R}^{\oplus}$ is less than or equal to the number of connected components in (α, β) -shape-reconstruction $(\mathsf{D}^{\oplus}_{\alpha,\beta})$ $(\#\partial \mathcal{R}^{\oplus} \leq \#\mathsf{D}^{\oplus}_{\alpha,\beta})$.

The α -holes are bounded by elements of the α -shape, so, a union of the α -shape and not- (α, β) -holes does not increase the number of connected components of the α -shape. It only fills the holes of the α -shape. This implies that (α, β) -shape-reconstruction $(\mathsf{D}^{\oplus}_{\alpha,\beta})$ has not more connected components than the α -shape (\mathscr{S}_{α}) $(\#\mathsf{D}^{\oplus}_{\alpha,\beta} \leq \#\mathscr{S}_{\alpha})$

the α -shape (\mathscr{S}_{α}) $(\#\mathsf{D}_{\alpha,\beta}^{\oplus} \leq \#\mathscr{S}_{\alpha})$ According to I, the α -shape has as many connected components as the boundary. Consequently, the same is valid for the α, q -dilation $(\partial \mathcal{R}^{\oplus})$ of the boundary: $\#\mathscr{S}_{\alpha} = \#\partial \mathcal{R} = \#\partial \mathcal{R}^{\oplus}$.

Hence, the original boundary and the (α, β) -shape-reconstruction have the same number of connected components: $\#\partial \mathcal{R}^{\oplus} \leq \# \mathcal{D}_{\alpha,\beta}^{\oplus} \leq \# \mathscr{S}_{\alpha} = \#\partial \mathcal{R} = \#\partial \mathcal{R}^{\oplus}$.

VIII The complement of any region has the same number of connected components as the complement of the corresponding (α, β) -hole.

Erosion R^{\ominus} of a region R is by definition contained in the region itself. According to II+III the erosion is also contained in a single (α, β) -hole $H_{\alpha,\beta}$ and according to VI the correspondence between $H_{\alpha,\beta}$ and R is 1-to-1.

Consider the components of the complement $(R^{\ominus})^c$ of an erosion of an original region R.



Fig. 4.8: (a) Noisy sampling of a contour. The complement of the light gray region consists of three connected components: two white circles and the surrounding region. (b) Light gray is the boundary $\alpha + q$ -dilation, white space is the complement of the erosion of the light region in (a). Dark gray is the (α, β) -shape-reconstruction. Gray region is the (α, β) -hole $(H_{\alpha,\beta})$ corresponding to the gray region in (a) The complement of $H_{\alpha,\beta}$ also consists of three connected components.

Notice that $(R^{\ominus})^c$ can have more connected components than one. Consider, for example, a space partition divided by a smaller ball which is inside a greater ball. We have a boundary of the space partition consisting of two connected components (the inner ball and the outer ball) and we have three regions (the background or the infinitive region, the region between the greater ball and the smaller ball and the inner region of the inner ball). So, the complement of the second region consists of the union of the boundary (the two balls), the outer region and the inner region, which results in two connected components. The complement of the inner region of a greater ball with two smaller balls side by side inside the greater one results in three connected components (see Figure 4.8 for illustration).

So, the complement of a region is everything else but the region itself. We want to show that the complement of an original region (white space in Figure 4.8 (a)) and the complement of the corresponding (α, β) -hole (union of white space, light gray space and the dark gray α -shape in Figure 4.8 (a)) have the same number of connected components (in our example three).

Consider two original regions whose boundaries are not connected and the two original regions are adjacent to R (the two white circles in Figure 4.8 (a)). The corresponding (α, β) -holes are then expected to be two unconnected components of $H^c_{\alpha,\beta}$ (in Figure 4.8 (a) each α -hole is the union of the white erosion and the light gray part of the boundary dilation).

Let us assume the opposite. The two implied different components of $H_{\alpha,\beta}^c$ are connected. Then there has to be a sequence of cells in the boundary of $H_{\alpha,\beta}^c$ which connects the boundaries of two different (α,β) -holes. The boundary of any (α,β) -hole is a subset of the (α,β) -shape-reconstruction $\mathsf{D}_{\alpha,\beta}^{\oplus}$ and, consequently, is completely contained in the α, q -dilation of the boundary. Consequently, the sequence of connecting cells is in the α, q -dilation. It follows that the α, q -boundary dilations of the two implied different regions are connected which is a contradiction to the *r*-stability of the original shape.

Is it possible for the boundary of an (α, β) -hole to be inappropriately disconnected? According to VI the correspondence between the (α, β) -holes and the regions of the space partition is 1-to-1, and, as we have seen before, the regions cannot be connected, consequently, the 1-to-1 mapping cannot result. The result is then the subdivision of one region and equivalently the merge of two neighboring regions.

The question is, can the 1-to-1 mapping between regions and (α, β) -holes be preserved but the topological properties of a region be destroyed during the reconstruction process? There are two cases to consider.

First, two different regions only touch, so, the intersection of their boundaries is not empty. The reconstructed boundaries of the corresponding (α, β) -holes must be connected too. The destroyed connection between the region boundaries does not increase or decrease the number of (α, β) -holes but changes the topology of the boundary and the (α, β) -hole containing the two regions. In this case, the

number of connected boundary components increases.

Consider for example two equal cones one opposite to the other touching at the end. The space partition consists of the two enclosed regions and the infinite background region. The boundary is only one connected component. Each cone encloses an open ball whose radius determines the value r. The boundary of corresponding (α, β) -holes is one connected component.

Let in our first example the boundaries of the (α, β) -holes not intersect. Recall that the boundary of an (α, β) -hole is the union of simplices adjacent to the (α, β) -hole. But the boundary can have artifacts which are adjacent to the boundary but not adjacent to the interior of the (α, β) -hole. Such cells are on the other "side" of the boundary. So, we consider a connection which is on the other side of both (α, β) -holes. Removing the connection between the boundaries preserves the 1-to-1 correspondence between regions and the (α, β) -holes but not the 1-to-1 correspondence between the connected boundary components.

Is it possible that such a connection is deleted during the reconstruction process? The union of α -balls completely covers the original boundary and is homotopy equivalent to the α -shape. It follows that there is a subset of the union of α -balls which completely covers the original boundary including the touching points of the implied regions. Then the corresponding subset of the α -shape consists of the boundaries of the two (α , β)-holes and the connection between them. Consequently, the connection could not have been removed in the α -shape construction.

The (α, β) -shape-reconstruction does not delete any simplices but fills not- (α, β) -holes with cells which are greater than α . Consequently, the connection is preserved in the (α, β) -shape-reconstruction.

The second case in which the 1-to-1 mapping between regions and (α, β) -holes is preserved but the topological properties of a region could be destroyed is if a region is touching itself. Here the boundary of the corresponding (α, β) -hole could have adjacent simplices which are not adjacent to the (α, β) -hole itself. In such a case we would have the same consideration as in the first case. Or the boundary could have simplices which have the same adjacent (α, β) -hole on both sides.

This can occur in 3D but not in 2D. Consider for example a donut but let the hole of the donut be closed by a membrane. This membrane is a boundary which has the same infinite region on both sides. Forcing through the membrane does not destroy the 1-to-1 mapping between regions and (α, β) -holes and does not change the number of connected boundary components but destroys the topology of the original infinite region. Forcing through the membrane in the α -shape would need a hole in the union of α -balls. But sampling conditions ensure the union of α -balls to cover the membrane, consequently, the membrane is also preserved in the (α, β) -shape-reconstruction.

4.7 Thinned- (α, β) -Shape-Reconstruction

The (α, β) -shape-reconstruction is a *thick* shape of a simplicial subcomplex of the Delaunay triangulation. Consider the (α, β) -shape-reconstruction of our 2D example in Figure 4.9. The corresponding (α, β) -complex - the union of α -shape (black in Figure 4.9) and the not- (α, β) -holes (gray in Figure 4.9) - contains triangles. The original contour is a thin line, i.e for all points of the boundary there is no $\delta \in \mathbb{R}_+$ such that the δ -neighborhood of the point is topologically equivalent to a 2D-ball (disc). The neighborhood of any inner point of a triangle in the 2D-reconstruction is topologically equivalent to the original contour. In 3D we consider the thin boundary between regions, consequently, for every point on the boundary there is no $\delta \in \mathbb{R}_+$ such that the δ -neighborhood of the point is topologically equivalent to a 3-ball.

To achieve our aim we need to thin out the shape by preserving its original homotopy type. The homotopy-type-preserving deformation retraction on simplicial complexes can be done by *elementary* collapse (see Definition 2.43, compare with [Dey et al., 1998]) on simple simplices, i.e. simplices which have only one coface of any higher dimension.


Fig. 4.9: (a) (α, β) -shape-reconstruction is the α -shape (union of edges and dark gray triangles) with filled not- (α, β) -holes (union of thin edges and gray triangles) (b) result of collapse on all simple edges of the (α, β) -shape-reconstruction. (c) thinned- (α, β) -shape-reconstruction ($\mathscr{S}_{\alpha,\beta}$) (d) original boundary $(\partial \mathcal{R})$

4.7.1 Thinning in 2D

Returning to our 2D example, the (α, β) -shape-reconstruction Figure 4.9 (a) is partially thick. It contains plane components (gray and dark gray polygons). Polygons are unions of Delaunay triangles. Some of such triangles are on the boundary of the shape. In our illustration these triangles have white space on at least one side. The edge between a gray triangle and the white space is simple. This edge has on one side a triangle of the (α, β) -shape-reconstruction and on the other side a triangle of an (α, β) -hole.

The (α, β) -shape-reconstruction contains *tails* as well. Tails are sequences of linked edges having at least one edge which is linked on one side only. We say one of its vertices is simple, i.e. the simple vertex has only one incident simplex (the edge in the tail).

The next step of the algorithm is to perform the elementary collapse until no simple simplex can be found. Notice that by deleting the pair consisting of the simple simplex and of its coface from the reconstructed complex the adjacent not deleted simplices may become simple.

Deleting an edge and its adjacent triangle leaves the two other edges of the triangle in the complex. If one of the remaining edges has been adjacent to two triangles of the (α, β) -shape-reconstruction then by deleting one of them the edge is simple. Otherwise if the remaining edge has had only the one triangle then by deleting it the edge becomes thin or as we call it *singular*. Singular edges may be parts of the reconstructed contour or parts of tails.

The result of *thinning* on simple edges in our 2D example is illustrated in Figure 4.9 (b). The gray plane parts are not completely enclosed by edges. The result of thinning on simple vertices is shown in

Figure 4.9 (c). We notice a great amount of free vertices not linked by the reconstructed contour. Such singular vertices are artifacts of the noise corruption of the sampling. The concurrent effect of noise is the distorted contour which seems to have lost its smooth pieces. But as Theorem 4.6 states and the deformation retraction of elementary collapse implies the contour in Figure 4.9 (c) is topologically equivalent to the original contour in Figure 4.9 (d).

4.7.2 Thinning in 3D

The (α, β) -shape-reconstruction in three-dimensional cases already correctly separates different regions from each other. The not- (α, β) -holes are filled and can be thinned out to result in a thin boundary. However the boundary (α, β) -shape-reconstruction in three-dimensional cases may consist of topological noise which does not contribute to separate different three-dimensional regions. These topological artifacts are also the result of noise corrupted sampling but cannot be completely deleted by thinning.



Fig. 4.10: α -shape of a unit surface. Marked are some irregularities of the α -shape: concavities (C), tunnels (T), bridges (B).

In Figure 4.10 we illustrate the topological distortions on the surface of a ball. For illustration the thinning on simple edges was not performed so we differentiate the tunnels (T) from bridges (B) and discover cavities (C) which are not completely enclosed by triangles. Considering for example a tunnel we observe simple edges, so the thinning step removes these simple edges and the adjacent triangle. The result is a sequence of linked edges. This sequence is connected on both ends to the boundary, such that no vertex is simple.

Under assumption that no such sequences of edges are in the reconstruction the algorithm can be extended to get rid of such distortions on the surface. The simple sequences of edges are then removed in the last step of the reconstruction algorithm.

4.7.3 Minimal Reconstruction

The new reconstructed regions which result from thinning the (α, β) -shape-reconstruction are (α, β) holes. In Section 2.4.5 we discussed how the boundary of the reconstructed regions may differ depending on the order in which the simple simplices are chosen in thinning steps. The illustrations in Figure 2.18 demonstrate the difference. Here we intend to derive a *minimal reconstruction* as the thinning result of the (α, β) -shape-reconstruction.

We propose to reconstruct the boundary with the smallest triangles possible. So, we compare the reconstructions by the size of Delaunay simplices which are needed for topologically correct reconstruction.

4.8. ALGORITHM

Definition 4.7 (Minimal reconstruction). Let $H_{\alpha,\beta}$ be an (α,β) -hole and let $\partial H_{\alpha,\beta}$ be its boundary. Let R^{\ominus} be the erosion of an original region completely contained in $H_{\alpha,\beta}$. An (α,β) -hole $H'_{\alpha,\beta}$ is said to be compatible to $H_{\alpha,\beta}$ if and only if R^{\ominus} is completely contained in $H'_{\alpha,\beta}$.

Let $H_{\alpha,\beta}$ and $H'_{\alpha,\beta}$ be compatible and let D and respectively D' be the corresponding subsets of Delaunay triangulation. We have the following correspondence $H_{\alpha,\beta} = |D|$ and $H'_{\alpha,\beta} = |D'|$ Let ∂D and $\partial D'$ be the boundaries of D and D' respectively. So, ∂D and $\partial D'$ are subsets of Delaunay complex. Let $T := (\sigma_0, \sigma_1, \ldots, \sigma_n)$ with $T' := (\sigma'_0, \sigma'_1, \ldots, \sigma'_m)$ be the lists of all simplices of ∂D and $\partial D'$ respectively ordered descending by their size. Then we say ∂D is smaller than $\partial D'$ ($\partial D < \partial D'$) if and only if T < T' regarding lexicographic order. The boundary ∂D is minimal, if there exists no compatible boundary $\partial D''$ such that $\partial D'' < \partial D$.

Notice, that we compare ordered sets of simplices of different length. The first occurrence of a different element in the tuple decides the order (compare lexicographic order in numbers: $\ldots \{1, 1, 2\} < \{1, 2\} < \{2\}$).

The implementation of the thinning step is done by a priority queue. A thinning step deletes the greatest simplex in the queue and its adjacent coface. The new simple simplices are then pushed into the queue. The thinning process proceeds until the queue is empty and no new simple simplices are in the boundary. Obviously, the thinning terminates since only a finite number of simplices is in the boundary.

Corollary 4.8 (Minimal (α, β) -shape-reconstruction). The result of thinning of (α, β) -shape-reconstruction is minimal if the thinning is performed in descending order regarding the circumradii of simple simplices.

Proof: Consider the opposite: there is a thin boundary reconstruction $\partial \mathcal{D}_{\mathcal{R}}$ which is smaller than the thinned- (α, β) -shape-reconstruction. Consider the list of simplices in the assumed lesser boundary reconstruction sorted in increasing order and consider the first simplex σ which is not in the boundary of the thinned- (α, β) -shape-reconstruction. This simplex must have been deleted in the thinning process before a greater simplex σ' became simple.

Consider the not- (α, β) -holes in the boundary of the (α, β) -shape-reconstruction containing σ . σ' is in the not- (α, β) -hole and is greater than σ . It follows that there is an increasing flow starting in σ into the interior of the not- (α, β) -hole. The not- (α, β) -hole must contain a local maximum. If there is no further neighboring not- (α, β) -holes then the boundary is already minimal according to flow relation in the interior of the not- (α, β) -hole and the assumption leads to a contradiction.

So, there have to be adjacent not- (α, β) -holes, and σ' and σ is in their boundary. Consider the boundary of all the neighboring not- (α, β) -holes. σ is the greatest in this boundary. All remaining simplices in the boundary are lesser than σ . So, all new simple simplices are either greater and are removed before the aforesaid remaining simplices or are lesser than the implied remaining simplices. It follows that σ' is either lesser or is removed before the smallest simplex in the said remaining simplices which is a contradiction to the assumption.

Consider a boundary as a result of thinning an (α, β) -shape-reconstruction with topological noise on the boundary. Let one of these topological distortions be a tunnel. The thinning process removes all simple simplices, so a chain of singular edges remains after thinning process. Comparing this boundary and the boundary without this chain, we notice that the compatible regions are equivalently separated from each other but the boundary with the chain is smaller.

In [Stelldinger, 2008c] it is assumed that the reconstructed boundary consists only of simplices which contribute to separate the regions. So, the chain of singular simplices - in 3D, edges - is removed in the extended step.

4.8 Algorithm

In this section we summarize the algorithm steps derived in the sections above. For illustration we choose three samplings of one and the same space partition. Two of them fulfil the required sampling

conditions and one does not. The example used in the above sections illustrates a very noisy but very dense sampling. With the second example we demonstrate the algorithm performance on very rough sampling but which does not permit great amounts of noise. The last example demonstrates the result of the algorithm on an insufficient sampling.

4.8.1 Sampling Parameters.

The first step in the reconstruction procedure is to determine the sampling parameters. The parameters r and γ are given by the original shape. We assume for all three examples the values in proportion to r. So, we may say r = 1 and $\gamma = 1.42993r$ or simply $\gamma = 1.42993$.

The reconstruction requires the following conditions to be fulfilled to result in correct shape.

$$1: p < \alpha \leq r - q \land 2: \beta = \alpha + p + q \land 3: \gamma \geq \beta + q > 2(p + q)$$

The next example illustrates a very sparse sampling with p = 0.16, q = 0.53. According to first condition $0.16 < \alpha \le 1 - 0.53 = 0.47$. According to the third condition $\alpha \le 0.20993$. So, we choose for the first example $\alpha = 0.20493$. The union of α -balls and the sampling is illustrated in Figure 4.11 (b).

At first we take our example from previous sections with p = 0.4512, q = 0.08939. According to first condition $0.4512 < \alpha \le 1 - 0.08939 = 0.91061$. According to the third condition $\alpha \le 0.79996$. In this example we set $\alpha = 0.5$. The sampling is demonstrated in Figure 4.11 (c).

Our last 2D-example demonstrates the consequences of an insufficient sampling. In this example the data acquisition device delivers only very noisy data with q = 0.54607 and is not able to ensure a dense boundary sampling. The only possible density is p = 0.3765. Here we badly choose $\alpha = 0.5684$ (see Figure 4.11 (d)). So, we break the first condition $0.3765 < \alpha \leq 1 - 0.54607 = 0.45393$. The third condition requires $\alpha \leq -0.0387$ and, consequently, is not possible to be met.

4.8.2 (α, β) -Shape-Reconstruction.

The first step of the algorithm is to compute the α -shape on the sample points. The α -shape is a subset of Delaunay triangulation and as we introduced in Section 4.4 the α -shape is dual to the union of α -balls shown in Figure 4.11 as union of gray balls.

An α -shape (thick black edges and dark gray triangles in Figure 4.12) is a subcomplex of the Delaunay triangulation (light gray edges). Once the Delaunay triangulation is computed the construction of the α -shape is done by selecting the Delaunay simplices which, first, are less than α and, second, the circumball does not contain any other vertex. The second condition is easily checked since only vertices on adjacent simplices have to be tested and the neighborhood relation is already given by Delaunay construction.

Building the (α, β) -shape-reconstruction is the second step of the algorithm. The greatest simplex in the not- (α, β) -hole is less than β . So, the construction can be done by sorting the simplices in decreasing order. Starting with the greatest simplex greater than β the first greatest simplex of the greatest (α, β) -hole is found. In 2D the greatest simplex is a triangle and in 3D it is a tetrahedron.

A simplex of the same dimension as the greatest one is in the same (α, β) -hole if the incident simplex of the same dimension is in the (α, β) -hole and the intersection of the two simplices is not in the α -shape. The intersections of simplices - the faces of simplices - are in the same (α, β) -hole if they are not α -shape.

In fact we described the traversal though the Delaunay triangulation starting in the greatest simplex greater than β and ending on the bounds of the α -shape. All simplices we pass through are in the same (α, β) -hole.

The (α, β) -shape-reconstruction is then the Delaunay triangulation without the (α, β) -holes. The (α, β) -holes are illustrated as white spaces in Figure 4.12 and the (α, β) -shape is then the union of gray polygons (not- (α, β) -holes) and dark gray polygons and thick black edges (α -shape).

If we compare the results of the (α, β) -shape-reconstruction we notice that the not- (α, β) -holes are the consequence of great amounts of noise or, more precisely, the great ratio between the noise q and the chosen α .

In the first example the ratio is 0.53/0.20493 which allows more α -holes to hide inside the q-dilation.



Fig. 4.11: (a)original space partition (b) The $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ (light gray) of the space partition covers the union of α -balls \mathscr{U} (the union of gray and dark gray balls). \mathscr{U} covers $\partial \mathcal{R}$ (black curve), $\partial \mathcal{R}$ has the same number of components as \mathscr{U} (one connected component only in this case; but a circle is one connected component too).

Whereas in the second example the q-dilation with q = 0.08939 is too thin to include α -holes with $\alpha = 0.5$.

The third example demonstrated consequences of two problems. First the α -value has been overestimated. The consequence is, too great alpha balls intersect more than allowed which results in more connections between vertices in the α -shape. In the center of the example in Figure 4.12, the narrowing of the middle region develops a connection which in our 2D example divides the (α, β) -hole in two. So, the one-to-one mapping between the (α, β) -holes and the original regions is no longer valid.

In 3D there are two different ways in which a narrowing can develop in the boundary. First is the "bottle neck". The result of insufficient sampling or overestimated α -value would close the narrowing with a surface membrane and divide the corresponding region in two.

The other kind of a narrowing in 3D develops if the circular surface of a disc is pressed together. Invalid reconstruction of such a narrowing results in a connection, a chain of singular simplices in such a narrowing which connects the upper surface with the bottom one and does not divide the inner region in two but destroys the topology of the inner region and the surface. The reconstructed surface is then a nonmanifold and the inner region is a donut.

The second problem in the third example is the too great amount of noise. According to the parameter values the γ -value has to be $\gamma = p + \alpha + q + q = 0.3765 + 0.5684 + 0.54607 + 0.54607 = 2.03703$ but the greatest inscribing ball in the bottom region has the radius 1.42993. Consequently, the computed β -value is too great and the bottom α -hole is computed to be a not- (α, β) -hole and is filled in the (α, β) -shape-reconstruction (greatest of gray polygons in Figure 4.12 (d)).



Fig. 4.12: (a)original space partition. (b,c,d) Gray thin edges: Delaunay triangulation. Dark gray polygons and thick edges: α -shape. Gray polygons: not- (α, β) -holes. Union of thick edges, gray and dark gray polygons: (α, β) -shape-reconstruction. (b) Small α , highly noise corrupted sampling (c) very sparse sampling density, almost no noise (d) Overestimated α , insufficient sampling density, highly noise corrupted sampling.

4.8.3 Topology Preserving Thinning

The original boundary is assumed to be infinitely thin. So, to achieve the topologically correct reconstruction the (α, β) -shape-reconstruction has to be thinned. Homotopy preserving thinning is done by elementary collapse (see Definition 2.43).

Elementary collapse removes a simple simplex and its proper coface from the reconstructed simplicial complex. The (α, β) -shape-reconstruction infills the not- (α, β) -holes. So, it adds the interiors to the holes until it touches the boundary. Consequently, the filling elements are bound by the α -shape and cannot be simple. It follows that the first simple candidates to be collapsed on are simplices of the α -complex. This fact can effectively be used in the implementation since only a subset of simplices needs to be checked for the property to be simple.

Thinning vs. Merging Consider a singular simplex which bounds a not- (α, β) -hole. After the filling this simplex becomes simple. The elementary collapse on the simplex deletes it and the first element of the interior of the hole, a Delaunay simplex greater than α . So, the new simplices which become simple are in the interior of the not (α, β) -hole.

The elementary collapse does not change the homotopy type. So, proceeding on simple simplices inside the not- (α, β) -hole is homotopy equivalent to any other collapsing order. The thinning on simplices in the not- (α, β) -hole completely contracts its interior leaving the boundary, and as we concluded before the boundary is in the α -complex.

4.8. ALGORITHM

We notice that the thinning on simple simplices inside the not- (α, β) -hole can be seen as the merging of two reconstructed regions on their boundary simplex. In this case one of the reconstructed regions is the not- (α, β) -hole. We use this observation to compare the (α, β) reconstruction algorithm with the algorithm in the following chapter. (See in Section 5.13.1, Theorem 5.25)

Thinning Order



Fig. 4.13: (a) original space partition. (b) (α, β) -shape-reconstruction thinned in increasing order - on a smaller simple simplex first.

If more than one simple simplex is to be deleted the order determines the geometrical properties of the outcome. The topological properties are preserved in any case.

The result of elementary collapse in increasing order is demonstrated in our first example in Figure 4.13 (b). The thinning on the same (α, β) -shape-reconstruction in decreasing order is presented in Figure 4.14 (b).

The choice of the thinning order may depend on the difference between the sampling density in closer environment of the boundary compared with the sampling density at farther distance. In cases of laser range scanners the sampling points are very close to the boundary. The sampling points at greater distances from the boundaries are outliers and are great deal less probable. In this case the decreasing thinning is preferable. The algorithm prefers to connect vertices near the boundary and by doing so to approximate the boundary geometrically more precisely. Since the number of simplices connecting the more distant points is minimized the reconstructed boundary is smoother.

The volume based digitization methods based for example on edge detection may deliver samplings where the density in the *p*-environment of the boundary does not differ from the sampling density in the *q*-environment of the boundary. In such case the difference between the greatest simplex and the smallest simplex is not sufficient. The result of thinning in decreasing order is then hardly distinguishable from the thinning in increasing order. Such consequence may be observed on the boundary reconstruction of top left region in Figure 4.13 (b) and in Figure 4.14 (b).

4.8.4 Thinned- (α, β) -Shape-Reconstruction Method.

Summarizing the previously derived and discussed reconstruction steps into one method we obtain the following algorithm:

- 1. Reconstruction Parameters: Given the set of sample points S and the sampling parameters r, γ, p and q, choose α such that $p < \alpha \leq r q \land \alpha \leq \gamma p 2q$
- 2. (α, β) -Shape-Reconstruction
 - Compute the Delaunay triangulation D and α -complex D_{α} on S



Fig. 4.14: (a)original space partition. (b,c,d) Thinned- (α, β) -shape-reconstruction. (b) Small α , highly noise corrupted sampling (c) very sparse sampling density, almost no noise (d) Overestimated α , insufficient sampling density, highly noise corrupted sampling.

- Compute the not- (α, β) -holes the connected components of $\mathsf{D}\backslash\mathsf{D}_{\alpha}$ with the greatest Delaunay simplex greater than β , with $\beta = p + \alpha + q$.
- The (α, β) -Shape-Reconstruction $\mathsf{D}_{\alpha,\beta}^{\oplus}$ is the union of D_{α} and the not- (α, β) -holes.
- 3. Homotopy Preserving Thinning. Put all simple simplices simplices in $\mathsf{D}_{\alpha,\beta}^{\oplus}$ with only one adjacent proper coface in $\mathsf{D}_{\alpha,\beta}^{\oplus}$ in priority queue Q in increasing order according to their circumradius. Until Q is not empty do:
 - (a) σ = Top element of Q.
 - (b) Pop Q.
 - (c) If σ is not simple, continue.
 - (d) Else remove σ and its proper coface τ from $\mathsf{D}_{\alpha,\beta}^{\oplus}$
 - (e) Add all simple simplices adjacent to τ to Q.

Extension: If it is assumed that the reconstructed boundary consists only of simplices which contribute to separate regions as it is in [Stelldinger, 2008c], then remove all singular edges from D_{α} .

Resulting Reconstruction. Let us observe now the result of the thinning. Notice that it is not the aim of the algorithm to connect all sample points. In very noise corrupted cases connecting all sample

4.9. COMPARISON TO OTHER APPROACHES

points would result in outrageously disturbed boundary reconstruction. In Figure 4.14 (b) we notice that our guaranteed topologically correct boundary reconstruction leaves nearly every second sample point not connected to the boundary approximation. The resulting reconstruction compresses the input data which makes the possible postprocessing steps less computationally consuming.

The built-in problems of the third example in Figure 4.14 (d) demonstrate the consequences on the resulting reconstruction. Since the (α, β) -shape-reconstruction is homotopy equivalent to the thinned result the consequence of additional connections remains. The connection in the narrowing in the middle region still divides the originally one region into two reconstructed regions. The completely filled reconstructed region contracts to a point and, so, one of the original regions disappears in the reconstruction. Even so in our case the one-to-one mapping between the reconstructed regions and the original ones can still be established accidentally.

4.9 Comparison to Other Approaches

In this section we compare the related work with the result of thinned- (α, β) -shape-reconstruction using the sampling requirements, conditions on the shape and the guaranteed preservation of topological properties. To illustrate the differences in the sampling density we compute the lower bound of needed sample points to correctly reconstruct the surface of a unit sphere.

4.9.1 Points on Sphere

The sampling requirements in related results on uniformly sampled boundary reconstruction vary depending on parameter settings and frameworks of the corresponding theorems. To compare the results we have to generalize the conditions for guaranteed reconstruction. To do that we choose the following aspects: the sampling density (p), the maximal deviation of sample points from the boundary q.

Using the sampling density we can compute a more intuitive measure: the number N of sampling points one needs in order to reach such a density in case of a unit sphere. To compute this number is commonly known as the *sphere covering problem* and there exist very tight lower bounds for estimating this minimal number of sampling points for a given p, e.g. following [Fejes, 1948] we get:

$$N \ge 2 + 2\pi / \left(6 \operatorname{arccot} \left(\frac{\sqrt{3}}{2} (2 - p^2) \right) - \pi \right).$$

We denote this computed number in Table 4.1 by # which means that the method and the guaranteed result require more than this number of points to correctly reconstruct the boundary of a unit sphere. The correctness also varies between the methods and is discussed below.

4.9.2 Sampling Conditions

In [Bernardini and Bajaj, 1997] a noise-free sampling is assumed to reconstruct a smooth 1-manifold - a contour. This contour may partition the plane into multiple regions but the boundaries of these regions may not intersect. The construction of the sampling described by the authors for the proof ensures a ball which intersects the boundary in no or one point, or the intersection is one connected component. This corresponds to the requirement for an empty tangential ball for each boundary point which is the definition of r-regular set (compare Definition 2.30). We imply the sampling density p to be less than r which corresponds to p < 1 and q = 0 parameters for the unit sphere sampling.

The 3D generalization of the result in [Bernardini and Bajaj, 1997] is not valid as proven by counterexample in [Stelldinger, 2008c]. Nevertheless, with p < 0.5r and q = 0 the α -shape on the sampling is proven in [Stelldinger, 2008c] to be homotopy equivalent to the original 2-manifold.

The authors in [Niyogi et al., 2008] present sampling conditions for noise-free and noisy cases. The sampling density in noise-free cases has to be less than 0.48τ . The conditional number τ controls the curvature of the manifold and corresponds to the value r for r-regular sets. So, we have for a noise-free

sampling of unit sphere p < 0.48 and q = 0. The noisy sampling is modeled by a probability distribution with support less than $(\sqrt{9} - \sqrt{8})\tau < 0.172\tau$. Since the density and noise are modeled by the support we have the sampling with p, q < 0.172 for the unit sphere.

The result on uniform noisy sampling in [Chazal and Lieutier, 2006] is guaranteed, if the Hausdorff distance between the sampling points and the original surface is less than 1/8 of the weak feature size of the manifold. For the unit sphere sampling we imply p, q < 0.125.

The reconstruction in [Chazal et al., 2009] preserves the topological properties of the original, if the point set taken from the original boundary - not neccessarily a smooth 2-manifold - is a κ , μ -sampling (in Definition 3.7) with

$$\kappa = \frac{\mu^2}{5\mu^2 + 12}$$

The sampling condition requires the maximal Hausdorff distance between the sampling and the original boundary of κ times the μ -reach of the surface. We recall that the results in [Chazal et al., 2009] are based on μ -critical point theory, where a μ -critical point is a point at which the gradient norm does not exceed μ . The μ -reach (compare Definition 2.38) is the infimum of all distance values at points with gradient norm less than μ .

Consider the gradient values for the surface of a sphere. The norm of the gradient is 1 at all points except on the boundary and the center of the sphere which is a critical point with zero gradient norm. We set $\mu = 1$. There is only one point with gradient norm less than 1 and this is the center of the sphere with gradient norm zero. Its distance value is 1, so, the μ -reach and the weak feature size are equal for the sphere.

We compute κ with $\mu = 1$ and obtain $\kappa = 1/17$. The sample points may deviate by 1/17 from the boundary. It follows that a unit sphere can be reconstructed by p = q < 1/17.

The thinned- (α, β) -shape-reconstruction in [Stelldinger and Tcherniavski, 2009c] requires p < 0.5rand q < r - p. The maximal deviation of sample points from the original boundary depends on the sampling density p. In fact we have even more conditions on the sampling depending on the space partition and the size of the regions (compare Section 4.3). In case of the unit sphere γ is equal 1. According to third condition, following is valid $\gamma \ge \beta + q > 2(p+q)$. So, if we choose to sample the unit sphere with $p \approx 0.5r$ the sampling conditions would not allow any noise.

In the noise-free case the number of required points to correctly reconstruct the surface of a unit sphere is 22. Allowing for example the same amount of noise as the sampling density we obtain $p, q \approx 0.25r$. In this case the lower bound of needed sample points is 78.

4.9.3 Comparing Results

We order the relevance of the requirements in following way. The condition to reconstruct a 2-manifold is weaker than the restriction to 1-manifold. Nonsmooth manifold generalizes the reconstruction of a smooth manifold. The extension of the shape to be nonmanifold has obviously the highest priority. We use these priorities to sort the related work in Table 4.1 in increasing order.

The methods we consider for the comparison differ in the definition of the correct reconstruction. The weakest equivalence between the reconstruction and the original boundary is the homotopy equivalence. Homotopy equivalence allows the reconstruction to be thick.

In [Stelldinger, 2008c] the reconstruction (α -shape) is homotopy equivalent to the original boundary. Union of balls in [Chazal et al., 2009] is homotopy equivalent to the sufficiently small dilation of the boundary. The Union of balls in [Niyogi et al., 2008] is homotopy equivalent to the manifold.

The 2D reconstruction in [Bernardini and Bajaj, 1997] is homeomorphic to the original contour. The homeomorphic reconstruction does not allow thickness. So, the homeomorphic reconstruction is infinitely thin if and only if the original contour is thin.

In [Chazal and Lieutier, 2006] the boundary of the union of balls is two connected components each of which is proven to be isotopic to the original surface. The isotopy is the strongest equivalence here. Simply speaking, two sets are isotopic if they can be deformed one into the other without tearing or self-intersection.

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4.10. EXPERIMENTS

method	р	q	#	comments	
Bernardini and Bajaj	1	0	4	2D smooth manifold contour	
[Bernardini and Bajaj, 1997]				4 points for circle, α -shape	
Niyogi at al.	0.48	0	22	smooth manifold	
[Niyogi et al., 2008]				homotopy by α -shape	
Stelldinger	0.5	0	22	smooth manifold	
[Stelldinger, 2008c]				homotopy by α -shape	
Chazal and Lieutier	0.1	0.1	484	smooth manifold, λ -medial axis	
[Chazal and Lieutier, 2006]				homotopy by α -shape	
Niyogi at al.	0.172	0.172	164	smooth manifold	
[Niyogi et al., 2008]				homotopy by α -shape	
Chazal and Lieutier	0.059	0.059	1390	nonsmooth manifold	
[Chazal et al., 2009]				homotopy by α -shape	
thinned- (α, β) -shape-reconstruction	0.5	1 - p	22	22 points for $q = 0$, 78 points for $p, q < 0.25$	
[Stelldinger and Tcherniavski, 2009c]				nonsmooth nonmanifolds	

Table 4.1: Comparison of different surface reconstruction algorithms. The values p, q and the number of sample points # refer to the correct reconstruction of a unit sphere. The p, q and # values are considered to be less than the given number.



Fig. 4.15: Surface of a unit sphere. The data set consists of 1001 nearly evenly distributed sample points with p, q < 0.45

The result of thinned- (α, β) -shape-reconstruction is a space partition which is proven to preserve connectivity and neighborhood relations and to define a one-to-one mapping of the reconstructed and original regions.

We notice that the related works do not always present an algorithm and the correct reconstruction is only a union of balls of a certain radius centered on sample points. Fact is that by [Edelsbrunner, 1993] the union of balls is homotopy equivalent to its dual α -shape. so, for any result on union of balls with equal radius (like [Chazal and Lieutier, 2006, Niyogi et al., 2008, Chazal et al., 2009]) the reconstruction with α -shape and α equal to the radius of the balls is homotopy equivalent to the original.

4.10 Experiments

In the previous sections we already used real sampling examples for illustrations and evaluated the algorithm on three 2D-examples in Section 4.8. The demonstrated 2D results can be directly generalized to 3D.

The homotopy-preserving thinning step has more to do in 3D. To illustrate the additional steps we use the surface of a unit sphere and expose the sampling of the surface to a great amount of noise. In Figure 4.15 (a) the original not disturbed sampling is shown as black surface mesh, while the disturbed triangulation demonstrates the result of noise corruption. The sphere surface is sampled by 1001 sample points. The maximal sample point deviation from the boundary is p, q < 0.45.



Fig. 4.16: (a)Surface reconstruction of a sufficiently sampled cube containing 8 regions. (b) (α, β) -shape-reconstruction of an undersampled cube. (c) result of thinning

Although the geometrical distortion is relatively high due to the linear dependence on the amount of noise, the reconstruction is topologically correct and it lies geometrically inside the dilation of radius q of the original surface (which is approximated in (b)). The (α, β) -shape-reconstruction is shown in (c).

As we discussed in Section 4.7.2 the surface of the (α, β) -shape-reconstruction may contain cavities, tunnels, knots or even "Klein bottles" on the reconstructed surface. Here we understand "Klein bottles" as non-manifold surfaces without boundary (simple edges) with the same regions adjacent to both sides of the surface. This understanding is in fact only a 3D projection of the 4D "Klein bottle" where the surface is manifold.

In our example we take advantage of knowing that the original shape did not contain touching regions or surfaces with one and the same region on both sides, and extend the homotopy-preserving thinning by deletion of singular simplices and "Klein bottles". The result of the extended reconstruction as demonstrated in (d). The reconstruction is very distorted but topologically correct surface.

Nonmanifold Example The novelty of the thinned- (α, β) -shape-reconstruction algorithm is the handling of non-manifold boundaries. Nonmanofold boundaries develop if the surface touches itself. The reconstruction of such boundary would contain edges with more than two adjacent triangles. Here we constructed an intuitive example of a multi-regional space partition with a non-manifold boundary. The interior of a cube is subdivided into four chambers. The topologically correct reconstruction of the example is demonstrated by the transparent approximated boundary in Figure 4.16.

Inadequate Parameter Values. The previous nonmanifold example also demonstrates the effect of undersampled boundary or underestimated α -value. The (α, β) -shape-reconstruction in Figure 4.16 (b) exposes a hole in the boundary. The thinning procedure detects the edges of this hole as simple edges and contracts the whole region as it is demonstrated in Figure 4.16 (c). The reconstruction of an originally 8-region cube consists of 7 regions only - the infinite space is not counted.

The built-in problems of the third example in Section 4.8 have equivalent effects in 3D. The overestimated α -value has two effects on the reconstruction result since there are two cases of a narrowing in 3D. A "waist" is a narrowing like in a dumbbell and corresponds to a 2-saddle on the distance transform. A "dell" or a two-sided dell is a narrowing like in a disc where the centers of the circular surfaces are pressed together. A dell corresponds to a 1-saddle on the distance transform. So, an overestimated α -value closes the narrowing in a waist and divides the original region in more than one reconstructed region. Whereas in a dell the pressed surfaces are connected by a chain of singular edges such that the interior of the original disc becomes a topological donut.

Real Data Sets from Laser Range Scanner The results of the thinned- (α, β) -shape-reconstruction algorithm on real data sets coming from laser range scanner are demonstrated in Figure 4.17. In Table 4.2

we show the breakup of the timings of the thinned- (α, β) -shape-reconstruction algorithm for the data sets on PC with 2000Mhz "Intel Centrino Duo" CPU and 2GB memory. The data sets "Skeleton hand" and "Dragon" are taken from "The Stanford 3D Scanning Repository"¹. The data set "Knots" is taken from data base "3D Model Retrieval".²

data set	points	α	q	α -shape (s)	reconstruction (s)
Skeleton hand noise-free	29176	0.045	0	33.83	18.86
Skeleton hand noise-corrupted		0.047	0.01	36.92	18.45
Knots noise-free	23232	0.013	0	25.14	10.97
Knots noise-corrupted		0.015	0.012	25.32	18.64
Dragon noise-free	28395	0.0026	0	32.26	13.39
Dragon noise-corrupted		0.0026	0.0011	25.58	20.30

Table 4.2: Parameter Settings and timings of the thinned- (α, β) -shape-reconstruction. α is the estimated absolute value. q is the absolute maximal sample point deviation estimated according to α . The first step of the algorithm is the computation of an α -shape. The second step of (α, β) -shape reconstruction and subsequent thinning is denoted by "reconstruction" in the right

column.

We subdivided the algorithm into two steps. The computational run-time of Delaunay triangulation and the α -filtration construction is presented in column " α -shape" in Table 4.2. The run-time of subsequent (α , β)-shape reconstruction step and topology preserving thinning is given in column "reconstruction" in Table 4.2.

Since the actual r-values for these data sets are unknown, the α -value had to be estimated. According to the estimated algorithm parameters we computed maximal sample point deviation and added noise to the data sets (right column) in Figure 4.17 and column q in Table 4.2.

The parameter estimation has been carried out empirically. To do so, we computed a *filtration* on the data sets. Filtration is a sorted list of α -values computed for every simplex in the Delaunay triangulation. Since the data set is finite, the Delaunay triangulation contains finite number of elements and, consequently, the list of α -values is finite. Consequently, the filtration arranges the Delaunay simplices according to their belonging to the actual α -shape.

So, we may just iterate on the list of α -values and see the changes of the α -shape for the current α . In this way we adjusted an α -value for each dataset.

As we can see in Figure 4.17 thinned- (α, β) -shape-reconstruction results in topologically equivalent components of the boundary even in cases where the amount of noise is greater than any previous approach can deal with. Although in most of our experiments we had to estimate the method's parameters empirically, the algorithm resulted in a correct reconstruction even if sampling conditions for γ -value were not fulfilled. Nevertheless thinned- (α, β) -shape-reconstruction is not robust to undersamplings, since the thinning algorithm strictly requires a sufficiently dense sampling of the whole surface.

In the following section we discuss the problems of the thinned- (α, β) -shape-reconstruction and give propositions for future work.

4.11 Discussion and Future Work

The aim of the work introduced in this section is to define the most weak sampling conditions for a reconstruction method. The weaker the sampling conditions the more topological and geometrical artifacts the reconstruction method has to handle. Here we list and discuss three kinds of topological noise which results from excessive amounts of noise. The handling of these problems includes limitations of the sampling conditions - particularly on the deviation of sampling points from the boundary - or extensions of the reconstruction method.

¹Stanford University Computer Graphics Laboratory in http://graphics.stanford.edu/data/3Dscanrep/

²3D Model Retrieval in http://3d.csie.ntu.edu.tw/~dynamic/cgi-bin/DatabaseII_v1.8/index.html



Fig. 4.17: Noise-free and noise-corrupted reconstruction



Fig. 4.18: (a) The $\alpha + q$ -dilation $\partial \mathcal{R}^{\oplus}$ (light gray) of the space partition covers the union of α -balls \mathscr{U} (the union of gray and dark gray balls). \mathscr{U} covers $\partial \mathcal{R}$ (black curve), $\partial \mathcal{R}$ has the same number of components as \mathscr{U} (one connected component only in this case; but a circle is one connected component too). (b) (α, β) -shape-reconstruction is the α -shape (union of edges and dark gray triangles) with filled not- (α, β) -holes (union of thin edges and gray triangles)

4.11.1 Connected Components Problem

According to Theorem 4.6 the (α, β) -shape-reconstruction preserves connectivity and neighborhood relations and defines a one-to one-mapping between original regions and the reconstructed space partition if (1) $p < \alpha \leq r-q$, (2) $\beta = \alpha + p + q$ and (3) every region r_i contains an open γ -disc with $\gamma \geq \beta + q > 2(p+q)$.

Consider a very dense and very noisy (p, q)-sampling as shown in Figure 4.18 (a) and let r be 1. The sampling allows very great sampling point deviation i.e. q = 0.53. Since the sampling is very dense p < 0.1r, we can chose α -value according to (1) $\alpha = 0.21r$. Then β is equal to (0.21 + 0.1 + 0.53)r and the sampling conditions are valid since every original region contains a γ -ball with $\gamma > 1.4$.

We observe that there can be α -balls at greater distance than α from the boundary, but be still contained in $\alpha + q$ -dilation of the boundary. It follows that the corresponding α -balls do not intersect the boundary and therefore do not necessarily intersect any other α -ball connected to the boundary. Such a constellation is demonstrated in Figure 4.18 (a) (a group of points with corresponding α -balls enclosed in a circle). The consequence is: this group of points results in a connected component in the (α, β) -shape-reconstruction which is not connected to the shape which overlays the boundary. It follows that (α, β) -shape-reconstruction has more connected components than the original boundary which disagrees with statement I in the proof of Theorem 4.6.

Definition 4.9 (Connected Components Problem). Let S be a (p,q)-sampling of a r-stable space partition \mathcal{R} . Let $\mathsf{D}_{\alpha,\beta}^{\oplus}$ be the (α,β) -shape-reconstruction of \mathcal{R} such that (1) $p < \alpha \leq r - q$, (2) $\beta = \alpha + p + q$ and (3) every region r_i contains an open γ -disc with $\gamma \geq \beta + q > 2(p+q)$. If $\alpha < q$ then $\mathsf{D}_{\alpha,\beta}^{\oplus}$ can have more connected components than $\partial \mathcal{R}$.

In Figure 4.18 (b) we notice that the (α, β) -shape-reconstruction consists of two connected components but the original boundary is only one connected component. The consequence is, there is a string of edges in the reconstruction which does not contribute to the division of different regions and which is completely contained in the q-dilation of the boundary. Since it is a string but not a region, the filling of not- (α, β) -holes has no effect on it. The thinned- (α, β) -shape-reconstruction preserves this string. In step 4 of the algorithm all simple cells, which will include this string, are deleted.

The additional connected components problems are generally covered by the q-dilation of the boundary. Since the distance values around the boundary are less than or equal to p, the greatest cell in regions covered by q-dilation will not exceed the size of $q + p < \beta$. It follows: if such a problematic additional component encloses a region then it is a not- (α, β) -hole which is filled in the (α, β) -shape-reconstruction and thinned in the post-processing step.



Fig. 4.19: 3D Projection of a 4D "Klein Bottle"

4.11.2 "Klein Bottle" Problem

The (α, β) -shape-reconstruction fills the too small holes in the α -shape resulting in a shape which is a one-to-one mapping to the original space partition. The consequence of a very great amount of noise is the topological artifacts which are either the not- (α, β) -holes or, in 3D, sets of simplices which do not separate two different reconstructed regions. We introduced the later topological distortions in Section 4.7.2 as *tunnels, handles* or *cavities*.

In fact different topological distortions can occur in the q-dilation of the boundary if q is great and the sampling is dense enough. One problem, which we observed on the reconstructed boundary, can only be descriptively introduced here since any illustration is only schematic and, from our point of view, not helpful. This problem is known as a 3D projection of a 4D "Klein Bottle".

A 4D "Klein Bottle" is a non-orientable 2D manifold surface which does not enclose any region. On both sides of the surface is the same adjacent region. The 4D "Klein Bottle" is the equivalent of the "Möbius strip". The 3D projection of the "Klein Bottle" is not manifold. The surface intersects itself. But in the 3D projection the thinner "pipe" goes through the surface of the thicker part of the "bottle". So, the pipe is closed. We remove this surface part which closes the thinner "pipe". The result is: on both sides of the "Klein bottle" surface is now the same region. The surface of the 3D "Klein bottle" became non-orientable nonmanifold. In the following we call such construction simply "Klein bottle".

The surface of a "Klein Bottle" does not have a boundary. The corresponding simplicial approximation does not have any simple simplex and since the surface does not enclose any 3D region, it cannot be filled by (α, β) -shape-reconstruction. Consequently, the problem remains even after topology preserving thinning.

Definition 4.10 ("Klein Bottle" Problem). Let S be a (p,q)-sampling of an r-stable space partition \mathcal{R} and $\partial \mathcal{R}$ be its boundary. Let each point in $\partial \mathcal{R}$ be a boundary point for at least two different regions of \mathcal{R} .

Let $\mathsf{D}_{\alpha,\beta}$ be the result of thinned- (α,β) -shape-reconstruction method. If there is a Delaunay triangle in $\mathsf{D}_{\alpha,\beta}$ which has the same adjacent reconstructed region on both sides, then we say $\mathsf{D}_{\alpha,\beta}$ has a "Klein Bottle" problem. For p < 3q, $\mathsf{D}_{\alpha,\beta}$ can have a "Klein Bottle" problem.

There are different ways to detect a "Klein bottle" in our combinatorial structure. Consider one of the examples illustrated in Figure 4.19. The boundary is broken through by a "pipe". The α -shape has to leave the boundary but carve out the "interior" of the "Klein bottle". So, the radius of the "pipe" and around it has to be greater than α . The surface may be shared with the surface of an (α, β) -hole. Consequently, the development of a "Klein Bottle" is possible if $q > 3\alpha$.

The parameters depending on the sampling density and sampling points deviation to detect a "Klein bottle" are not investigated further in this work and remain a question for future work.

4.11. DISCUSSION AND FUTURE WORK

How can we solve the "Klein bottle" problem? To detect the "Klein bottle" problem we use the fact that its surface is non-orientable. So, starting with any Delaunay triangle and its adjacent region and traversing to the neighbors of the triangle, we sooner or later will have to return to the starting triangle. If such a case occurs then the reconstructed boundary has a "Klein bottle" problem, and the set of neighbors of the starting triangle having the same region on both sides is the surface of the "Klein bottle".

Further we use the fact that the "Klein bottle" is a topological artifact and is covered by q-dilation of the boundary. The filling of the (α, β) -shape-reconstruction does not help since a "Klein bottle" is not a hole. But starting on the detected surface we can fill it out with Delaunay tetrahedrons less than β and their faces. The result is then thinned by the topology-preserving step of the algorithm.

Conjecture 4.11 ("Klein Bottle" Detection). Let $D_{\alpha,\beta}$ be the result of thinned (α,β) -shape-reconstruction method and let σ be a boundary triangle with the same reconstructed region on both sides. Let a neighbor be the first boundary triangle which can be reached by circulating on one of the edges of the triangle. Further, let neighbor be a neighbor of a neighbor. Let D_{σ} be the set of all neighbors of σ having the same adjacent region on both sides. If D_{σ} contains σ , then $D_{\alpha,\beta}$ has a "Klein bottle" problem and D_{σ} is the surface of the "Klein bottle".

Filling by values less than β is safe for not- (α, β) -holes since it is known that they are covered by q-dilation of the boundary. However, a "Klein bottle" is not a region. "Filling" the "Klein bottle" means to extend the surface by tetrahedrons on both sides of the surface triangles. Which results in a "region" with a greatest tetrahedron of size less than β but envelopes an underlying space of up to 2β . What we need to ensure is the resulting region has to be contractible. We assume that this is the case for β less than r.

Definition 4.12 (Extended β -Filling). Let $\mathsf{D}_{\alpha,\beta}$ be the result of thinned- (α,β) -shape-reconstruction method. Let $\mathsf{D}_{\alpha,\beta}$ have a "Klein bottle" problem and D_{σ} be the surface of the "Klein bottle". Then the post-processing β -Filling is defined as enriching D_{σ} by neighboring simplices with circumradius less than β , where a neighboring simplex is also a neighbor simplex of a neighbor.

Conjecture 4.13 (Contractible Extended β -Filling). Let S be a (p,q)-sampling of an r-stable space partition \mathcal{R} . Let $\mathsf{D}_{\alpha,\beta}$ be the result of thinned- (α,β) -shape-reconstruction method with a "Klein bottle" problem and D_{σ} be the surface of the "Klein bottle". Let $\mathsf{D}_{\sigma}^{\oplus\beta}$ be an extended β -Filling. Then $\mathsf{D}_{\sigma}^{\oplus\beta}$ is contractible if β is less than r

The last step to remove the "Klein bottle" problem is to contract the extended β -filling by elementary collapse. Notice that the contractible extended β -filling is enclosed by simple triangles since the circumradius of a triangle is less than or equal to the circumradius of its adjacent tetrahedrons.

4.11.3 Singular Edges Problem

Thinning on simple simplices results in a reconstruction where all triangles have no adjacent tetrahedron and edges have either zero or at least two adjacent triangles. A hole in the surface, being a removed set of triangles, leaves the boundary of the hole in the reconstructed surface as a set of simple edges. The thinning then collapses the whole surface such that no corresponding region remains.

Another case develops if a surface has more than one hole. The thinning will at some step meet a triangle with two simple edges. A collapse on such a triangle leaves one singular edge. So, after the thinning procedure we expect at least one chain of linked singular edges. In case of three holes, the resulting chain of singular edges would intersect in one vertex.

The chains of linked singular edges are either attached to the boundary of a reconstructed region developing an "ear" on the boundary, or can "hover" in space. In any case the chain of singular edges is the boundary of some set of triangles. What we need to investigate now is, if this chain of singular edges is the result of correct reconstruction, or an artifact. Correct reconstruction may develop such a chain for example in the case of two cones touching at their ends. No sampling known to us can guarantee to place a point exactly on the peak of the cones. So, most probably the reconstructed surfaces of the cones will be connected by one or a chain of edges which are crucial for the correct topology.

While the "ear" on the boundary is the topological noise the connection between two reconstructed cones is essential for correct reconstruction. Removing the chain of singular edges results in first case in a correct 2D boundary but in the second destroys the topology. We call this the *singular edges problem*.

Definition 4.14 (Singular Edges Problem). A reconstructed boundary has the singular edges problem if the reconstructed boundary contains singular edges with non-simple adjacent vertices.

Taking (α, β) -shape-reconstruction as an example we propose to fill the chains of singular edges by a set of triangles in such a way that no additional singular edges occur and all singular edges become simple. Obviously, we want the smallest triangles possible.

Definition 4.15 (Minimal Expansion). Let $D_{\alpha,\beta}$ be the result of thinned- (α,β) -shape-reconstruction method with singular edges problem and D_0 be the set of singular edges. Then minimal expansion of $D_{\alpha,\beta}$ is the minimal reconstruction which does not contain any singular edges and all simple edges are in D_0 .

We expect the minimal extension of the boundary to fill the boundary "ears" with triangles less than β , and relevant connections between reconstructed regions by triangles greater than β since this extension would have to cross the erosion of the original region. So, the next thinning step is to collapse on simple edges if the extension consists of triangles less than β and to drop the extension in other cases.

Conjecture 4.16 (Contraction on Minimal Expansion). Let $\mathsf{D}^+_{\alpha,\beta}$ be the minimal expansion of a result of thinned- (α, β) -shape-reconstruction method. If all simplices in $\mathsf{D}^+_{\alpha,\beta}$ are less than β then $\mathsf{D}^+_{\alpha,\beta}$ is covered by q-dilation of the original boundary.

Notice that the "ears" on the boundary may be knotted. The minimal expansion of the chain of singular edges is then a non-manifold 2D surface. Contraction of the minimal expansion does not necessarily solve all problems discussed previously. So, we do not state in Conjecture 4.16 that topologically-correct reconstruction results. In fact the expected result is a *reducible reconstruction*. Consult Section 2.4.5 for introduction.

4.12 Conclusion

The framework introduced for thinned- (α, β) -shape-reconstruction defines classes of shapes which can be handled by the algorithm in terms of a value (r), which stands for the maximum dilation radius of the boundary which does not change the original homotopy type. This value is called "weak feature size" [Chazal and Lieutier, 2005b].

On the basis of the class of the shape the sampling conditions are defined and conditions on the inner parameter settings of the algorithm are given.

Thinned- (α, β) -shape-reconstruction is based on α -shapes and can therefore handle data sets which fulfill a uniform sampling criterion for each point of the surface. The post-processing steps handle topological noise of the α -shape and result in a correct one-to-one mapping between the original and reconstructed regions if the original was *r*-stable.

The approach does not handle excessive sample point deviation from the boundary. We propose to tackle the problems by extra computational steps or to limit the noise - the maximal sample point deviation from the boundary. Reducing the allowed noise amount is a justified step in real applications, since the assumed amount is only a theoretical worst case.

Experiments were performed both on well-known real data sets and on artificially made data sets, comparing and visualizing the performance of various methods which underlined the advantages of the method.

The presented algorithm is theoretically and experimentally a solid and fundamental result which to our knowledge outperforms all related Delaunay triangulation-based methods. The theoretical framework extends the limits of admissible shapes to non-manifolds and handles great amounts of noise.

4.12. CONCLUSION

In the next chapter we introduce locally adaptive sampling criterion as a generalization of the sampling conditions defined for thinned- (α, β) -shape-reconstruction as well as a new reconstruction method to handle this new sampling condition.

Chapter 5

Refinement Reconstruction

5.1 Introduction

In real data sets, the sampling density often varies spatially. For instance, a laser scan captures data only where the laser "touches" the object's surface. Which means that this data acquisition device does not "see" the concavities in the surface. It follows that, even though the sampling density is globally-set, the resulting data set will have gaps in concavities of the original surface.

The thinned- (α, β) -shape-reconstruction introduced in Chapter 4 extends the concept of α -shapes in order to result in a one-to-one mapping between reconstructed regions and the original space partition. The underlying sampling conditions are expected to be globally uniform. This condition is necessary to guarantee a correct parameter-setting for the reconstruction. The provided sampling parameters are used to set up the size of the boundary simplices as well as the minimal region size.

Our new reconstruction method is based on the 3D extension of the "Gabriel graph" first introduced in [Gabriel and Sokal, 1969]. The Gabriel graph can be computed by removal of edges from the Delaunay complex if their circumcircle contains further Delaunay vertices. As shown in [Edelsbrunner, 2003] this imitates the "flow curves". The resulting set of Delaunay edges separates all discrete distance maxima. As described in Section 2.4.10, the "Geomagic WRAP[©]" algorithm [Edelsbrunner, 2003] results in the 3D extension of the Gabriel graph. Originally, the method separated the infinite background from the interior of the original shape, assuming that the original surface is manifold. The result of the algorithm is the set of minimal boundary triangles. In [Edelsbrunner, 2003] no guarantees on original topology preservation are given, but it is proven that the result is manifold and the reconstructed shape is contractible.

Methods like "Crust" [Amenta et al., 1998] or "Cocone" [Amenta et al., 2000a] or any of their derivatives use the fact that the sampling is very dense and the maximal sample point deviation from the boundary is very low for proving topology preservation. The required sampling conditions may vary according to the curvature of the original surface, but the ratio between the sampling density and the distance to the medial axis is constant and positive. Taking a small fraction of this ratio ensures all sampling points to lie very much closer to and much denser around the boundary than their distance to the original medial axis. This is only possible for smooth shapes.

Although the medial axis is a complete shape descriptor, only a subset of it is required to preserve topological properties. For local maxima separation (cf. WRAP), the relevant subset is the set of local maxima. For homotopy preservation, the subset is the homotopy axis. The local region size and local homotopical feature size (as introduced in Section 2.2.5) are greater than zero even for non-smooth

surfaces. Now, in order to ensure the sampling density and maximal sampling point deviation to be smaller than the distance values in the region's interior, we relate the sampling conditions to a feature size which is strictly greater than zero. So, in Section 5.3 we define locally variable sampling conditions which are finite for non-smooth surfaces.

In Section 5.2, we introduce the local maxima separation as a *refinement*. A refinement correctly separates the original local maxima on the continuous distance transform. We apply the WRAP algorithm to all discrete local maxima. If the underlying sampling ensures the sampling density to be less than the distance value of the nearest local continuous maximum, the outcome of the WRAP algorithm is a refinement.

We define corresponding sampling conditions in Section 5.4. These new sampling conditions require that the original local maxima are surrounded by sampling points in such a way that The sampling density between the points is demanded to be higher than the continuous distance values on the original local maxima. This guarantees that, starting on original local maxima and following the steepest ascends on the discrete distance transform, we reach local discrete maxima without crossing the original boundary. We call these discrete maxima *associated*. Our new sampling conditions ensure the associated maxima to be correctly separated, which - as we prove in Section 5.5 - is equivalent to the statement: each original maximum is associated with a centered Delaunay cell and the circumcenter of this cell is inside the original region. So, deleting centered cells from the Delaunay complex we hit each original region at least once.

There are different ways to correctly separate the local maxima. For our framework we require the boundary of the refinement to be minimal. As we define in section Section 5.6, a minimal refinement separates the local maxima by smallest boundary simplices. In Section 5.7, we prove that the WRAP applied on every discrete local maximum results in minimal refinement.

In our framework the reconstruction is a refinement of the original space partition. A refinement is a special case of *oversegmentation* which preserves the correct local maxima separation. Still, the reconstruction may be an oversegmentation. Consider a shape with a narrowing: The interior consists of two local maxima in the same original region. The refinement reconstruction subdivides the space separating the associatives of these maxima. In Section 5.8 we introduce a criterion which rejects boundary simplices which are inappropriate to separate regions. Deleting such edges results in merging reconstructed regions and - as we prove - still in minimal refinement. We call this region-merging step the *refinement reduction*.

The sampling conditions defined according to local region size may lose the information which local maxima belong to the same region. Furthermore, the sampling is too sparse to guarantee that removal of certain boundary simplices reduces the refinement to a topological equivalent of the original space partition. In Section 5.9 we introduce a new stability definition. A refinement is *stable* if its boundary does not intersect the original homotopical axis. A refinement is *reducible* if it is a superset of a stable refinement.

In Section 5.11, we prove that refinement reconstruction results in reducible refinement if the sampling is defined using the local homotopical feature size. We introduce the new sampling conditions in Section 5.10. In Section 5.12, we undertake the particular reconstruction steps on three different samplings of the same 2D shape.

The evaluation of the new reconstruction method is done in three steps. In Section 5.13, we compare the sampling conditions and the underlying shapes. The experimental results are presented in Section 5.14. We evaluate the new reconstruction method on well-known laser range scan data from "The Stanford 3D Scanning Repository" and on data sets resulting from X-ray computed tomography imaging (using 3D Canny edge detection to extract a point cloud). In Section 5.15, we discuss the effects of the very sparse sampling conditions and too large amounts of noise which can be handled by our algorithm and make propositions for future work and in Section 5.16, we summarize our new results.

Refinement reconstruction is both theoretically and experimentally solid and gives a fundamental result which has advantages even over thinned- (α, β) -shape-reconstruction. The underlying shapes are assumed to be non-manifold multiregional surfaces. The method results under guarantee in reducible refinement, even if the sampling is very sparse and noise corrupted. The approach expects sampling

parameters which are required for internal settings. However, the reconstruction with estimated sampling parameters covers all sampling conditions defined in related work.

5.2 Refinement

In Section 4.2, we introduced a new class of shapes called r-stable shapes. r-stability is defined by homotopy preserving dilation of the boundary, where the dilatation value does not exceed r. The result of the reconstruction is a one-to-one mapping between reconstructed regions and the original. The reconstructed boundary is homotopy equivalent to the original.

A topologically correct space partition does not require the regions to be geometrically similar to the original ones. The famous example of topological equivalence between a coffee cup and a donut demonstrates this with two objects of completely different geometry.

In the case of reconstruction, one expects the reconstructed region to lie somewhere where the original region is and most probably to overlap it in some definite common interior points. The set of such invariant common points is interesting for our new framework. The equivalent expectation is also given for boundary reconstruction. Even if the boundary of the reconstructed regions deviates from the original, one again expects it to lie in some certain environment of the original. The reconstructed boundary of the thinned- (α, β) -shape-reconstruction necessarily lies inside $\alpha + q$ -dilation (compare Section 4.6).

In [Dey et al., 2005] the authors formalize these expectations by requiring the reconstruction to separate the critical points of a shape. Critical points are the points in space where the gradient value - defined on distance function to the sample points - is zero. The separation ensures the critical points to lie either near the boundary or near the original medial axis. So, the computed interior critical points are clearly separated from the critical points of the background region as well as from the boundary representing critical points.

What does that have to do with boundary or surface reconstruction and topological properties of the shape? The critical points belong to the medial axis. The medial axis is homotopy-equivalent to its open set or, as we call it, the region (proof in [Lieutier, 2004]). So, proving the homotopy equivalence between the medial axes suffices as the proof for the homotopy equivalence between the corresponding regions and their boundaries.

Here we investigate the stability of reconstruction in cases of very sparse and non-uniform sampling conditions. The aim is again to separate the regions by preserving the neighborhood relations and topological properties. If the reconstruction problem is scaled down to critical points separation the question arises, what is the relation between the reconstructed critical points and what is the correspondence to the original?

Consider for example two non-intersecting balls (2D illustration in Figure 5.1). The centers (\oplus) of these balls are also the maxima of the distance function. The critical point separation ensures the separation of these two maxima, which can be done by a plane dividing the space into two half-spaces each containing a maximum. The criticals are correctly separated but the reconstructed boundary is never our wanted boundary of two balls.

Here we ignored the maximum which corresponds to the infinite region. So, to separate these two maxima from the infinite one we need to envelope the two maxima and then to separate them from each other. Now the result is three regions correctly separated from each other with intersecting boundary of the balls.

The simplest geometrical primitive to envelope a point in 3D, separating it from its environment, is a tetrahedron. Consequently, we need at least four non-planar sample points to separate one maximum from the infinite space and at least two tetrahedrons to correctly separate two maxima in space. Obviously, these tetrahedrons may have one, two or three points common corners. This means that we would need at least five sample points to separate two maxima in space.

However, how do we compute the correspondence between the original maxima and the tetrahedrons. Obviously, the correspondence is given if the tetrahedrons contain the original maxima. In cases of very noisy sampling conditions this expectation cannot be fulfilled. We need to establish a correspondence between the circumcenter of the tetrahedrons and the maxima.



Fig. 5.1: The thick line is the boundary of the original space partition \mathcal{R} : two 2D balls and the background. The triangles separate the centers of the 2D balls from each other and the background.

Associated Discrete Maximum

In our framework, we require the sample points to be placed in such a way that the circumcenter of the corresponding tetrahedron is reachable by a simple increasing path on the distance transform of the sample points. But following the increasing path we do not necessarily stop in the circumcenter of the tetrahedron, because it is not necessarily a local maximum of the distance function. A tetrahedron which does not contain its own circumcenter is such a case. Here, the increasing path passes though the circumcenter in the direction of an infinite maximum (compare the introduction in Section 2.4.8). To avoid this problem, we also require the corresponding tetrahedron to contain its own circumcenter which is then a local maximum. This requirement establishes a correspondence between the original local maxima and the local maxima of the distance transform defined on the sample points. We call the discrete local maximum reachable by steepest path starting on an original maximum the *associated maximum*:

Definition 5.1 (Associated Discrete Maximum). Given the space partition \mathcal{R} , the continuous distance transform $d_{\mathcal{R}}$ on \mathcal{R} , the set of points S, and the discrete distance transform d_{S} on S, let x be the local maximum of $d_{\mathcal{R}}$ and $\mathbf{H}(S, x)$ be its set of reachable local maxima on d_{S} . Then, we call $y = \arg \max_{u' \in \mathbf{H}(S,x)} d_{S}(y')$ the associated discrete maximum of x.

The associated maximum is the greatest reachable maximum, where the set of maxima reachable by steepest paths is given by Definition 2.33.

Now, let us consider our original scene containing two balls in space. The reconstruction is said to separate the local maxima correctly, if for any two originally separated local maxima their associated maxima are also separated. We call such reconstruction a *refinement*.

Definition 5.2 (Refinement). Given two space partitions \mathcal{R} and \mathcal{R}' with two distance transform functions $d_{\mathcal{R}}$ and $d_{\mathcal{R}'}$ defined respectively on \mathcal{R} and \mathcal{R}' . \mathcal{R}' is called a refinement of \mathcal{R} , if for any two local maxima x_i, x_j of $d_{\mathcal{R}}$ lying inside different regions R_i, R_j of \mathcal{R} , the discrete maxima x'_i, x'_j being associated to x_i, x_j lie in different regions R'_i, R'_j of \mathcal{R}' .

According to the new defined notation, the original space partition consists of three regions: two open balls and the infinite background space. The boundary of the two tetrahedrons which envelopes the original maxima partitions the space into three regions, too. The associates of the original maxima are correctly separated, so, the new space partition is a *refinement* of the original.



Fig. 5.2: The thick line is the boundary of the original space partition \mathcal{R} . The edges of the triangles divide the space into a refinement of \mathcal{R} . The two most left continuous maxima are associated with the same discrete maximum. The maxima corresponding to the dotted circles are not associated with any continuous maximum.

The definition of *refinement* does not make any statements about the possibility of regions with two or more local maxima. Let us extend our scene for example by adding a new local maximum and connecting the balls to a simplified shape of a "barbell".

In the 2D illustration presented in Figure 5.2 the thick line is the boundary of the original scene. The boundary divides the space into two regions: the interior of the barbell and the infinite background. The distance transform defined on the boundary has three local maxima denoted by \oplus and, obviously, the maximum of the infinite background. The edges of the triangles divide the space into a refinement of the original space partition. The distance transform defined on the points has four local maxima denoted by \boxplus plus the infinite maximum. The two left continuous maxima \oplus are associated with the same discrete maximum. The discrete maxima corresponding to the dotted circles are not associated with any continuous maximum.

We notice, that by Definition 5.2 for each continuous maximum there exists exactly one discrete maximum, but this mapping is neither injective nor surjective.

5.3 (ψ, ρ) -Sampling

In the previous chapter on thinned- (α, β) -shape-reconstruction we introduced sampling conditions based on globally set parameters p and q (compare Definition 4.2). The parameters p and q control sampling density and maximal sample point deviation from the boundary. p is the maximal distance between any boundary point and its nearest sampling point, and, q is the maximal distance between any sample point and its nearest boundary point.

Here we generalize the concept for locally adaptive sampling conditions. Analogously to (p, q)sampling we want parameters to control density and noise amount, but now they should be locally adaptive. The local adaptation is done by a feature size (f(.)) defined for every point of the boundary. The feature size may vary depending on curvature, size of the adjacent regions or a metric of a shape descriptor like distance to the medial or homotopical axis. Notice, the distance to the homotopical axis is another measure of curvature for smooth shapes. This property is partly lost for non-manifold shapes, see Section 2.2.5.

The feature size is scaled by parameters which correspond to p and q. The maximal sample point deviation depends on the sampling density. The greater the sample point deviation the denser has to be the sampling. This dependence is modeled by scaling parameter ρ . The greater ρ the sparser is the sampling and the less noise is allowed. The ψ parameter is an auxiliary parameter for the



Fig. 5.3: Dependency between the $\psi \rho$ -sampling parameters with r as the local feature size. The sample points are in the $(1 - \rho)$ dilation of the *r*-circle. The maximal distance values on the boundary of the *r*-circle are $\psi \rho r$.

sampling density only and lies in the interval (0, 1). ψ is used in our reconstruction method for definition of simplices which are too great to belong to the boundary, which we call *undersampled* (compare Definition 5.10).

Definition 5.3 (Non-Uniform (ψ, ρ) -Sampling). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} and let $f : \partial \mathcal{R} \to \mathbb{R}$ be a function which maps any point on the boundary to its feature size. Let $S \subset \mathbb{R}^3$ be a finite set of points. Then S is said to be a (ψ, ρ) -sampling of $\partial \mathcal{R}$, if

$$\begin{array}{rcl} \forall b \in \partial \mathcal{R} : & \mathrm{d}_{\mathsf{S}}(b) \leq \psi \rho f(b) \quad \mathrm{and} \\ \forall s \in \mathsf{S} \, \exists b \in \partial \mathcal{R} : & ||b - s|| & = & \mathrm{d}_{\mathcal{R}}(s) \leq (1 - \rho) f(b) \end{array}$$

Notice, in the definition Definition 5.3 $d_{\mathsf{S}}(b)$ is the distance between a boundary point b and the set of sample points S , whereas $d_{\mathcal{R}}(s)$ is the distance between a sample point s and the continuous boundary of the space partition $\partial \mathcal{R}$.

In Figure 5.3 we find an equivalent illustration to Figure 4.3 introduced for (p, q)-sampling. Here we see again an *r*-ball (thick circle). We simplify the shape to a ball, so the feature size is *r* for each point of the boundary. The *r*-ball is dilated (gray in the illustration) by the maximal sampling point deviation $(1 - \rho)r$ defined by f(b) = r for each boundary point *b*.

For two points on the boundary we visualize the maximal distance to the nearest sampling point. The distance is $\psi \rho r$ and is also visualized in the center of the *r*-ball. The maximal distance to the nearest sampling point $\psi \rho r$ necessarily is less than ρr . The circumcenter of the *r*-ball is the local continuous maximum of the region. The $\psi \rho r$ ball is inscribed into the $(1 - \rho)r$ -dilation of the *r*-ball.

The consequence of the (ψ, ρ) -sampling conditions is, the discrete distance value on the local maximum is enveloped by lesser distance values in the dilation. This is the quintessence of our work and the basis for the guarantees of the reconstruction method.

5.4 Sampling Conditions for Refinement Reconstruction

As introduced in Section 5.2 a refinement correctly separates the associatives of the local maxima. The concept generalizes the shapes. The regions are represented by their greatest maximum. This concept can also be used for reconstruction if the result of maxima separation is the aim of the reconstruction i.e. if the regions provably contain one local maximum each.

An illustration of a shape with exactly one maximum (\oplus) for each region is given in Figure 5.4. The feature size, which measures for every boundary point the adjacent region size, is the *local region size* (Irs compare Definition 2.35). The local region size for a boundary point is defined as the minimal distance value of all reachable maxima starting on this point.

Now, our intention is to separate the local maxima correctly. Using the local region size we can measure the maximum which we are going to separate from the rest. So, we define the sampling density



Fig. 5.4: (a) Space partition consisting of 15 regions and the background as the result of five intersecting circles. Each resulting region consists of one local maximum only. The local region size for every point on the boundary is the smallest maximum value of the adjacent regions. The sampling points fulfill the conditions of the region stable sampling with $\psi = 0.5$ and $\rho = 1$ the corresponding $\psi\rho$ Irs-balls are centered on sample points. (b) Fish, region stable sampling with $\psi < 0.5$, $\rho < 0.5$. The union of balls contains $\psi\rho$ Irs-balls with radius ≈ 0.25 Irs and $(1 - \rho)$ Irs-balls with radius ≈ 0.5 Irs.

for each point on the boundary in such a way, that the discrete distance values around the boundary are less than the discrete distance values on the minimal reachable maximum. To do so we use the (ψ, ρ) -sampling with local region size.

 (ψ, ρ) -sampling implements the (p, q)-sampling conditions for locally adaptive cases. The idea is to make the sampling density around the boundary dependent on the maximal sample point deviation, the noise. The more noise is expected, the denser must be the boundary sampling. Or vice versa, the sparser the sampling density is, the less noise can be handled. In our case the feature size varies from point to point so we use non-uniform definition of sampling conditions induced by local region size:

Definition 5.4 (Region Stable (ψ, ρ) -Sampling). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} and let Irs be the local region size defined on $\partial \mathcal{R}$. Let $S \subset \mathbb{R}^3$ be a finite set of points. Then S is said to be a region stable (ψ, ρ) -sampling of $\partial \mathcal{R}$, if S is a (ψ, ρ) -sampling with $\forall b \in \partial \mathcal{R} : f(b) = Irs(b)$

The sampling conditions defined in [Stelldinger and Tcherniavski, 2009b] for guaranteed refinement reconstruction are a special case of a region stable (ψ, ρ) -sampling with $\psi \approx 1$ and $\rho \approx 0.5$. Even if the noise amount does not depend on sampling density, the sampling conditions can be expressed by (ψ, ρ) -sampling conditions. The locally adaptive noise free sampling with $\psi \approx 0.5$ and $\rho \approx 1$ is illustrated by dots in Figure 5.4 with corresponding $\psi\rho$ lrs-balls centered on sample points.

In Figure 5.4 (b) we illustrate region stable sampling on a more complicated example "fish". In this case the sampling is highly noise-corrupted with $\psi \approx 0.5$ and $\rho \approx 0.5$ which results in maximal sample point deviation from the boundary of $(1 - \rho)$ lrs ≈ 0.5 lrs. The union of balls is divided into $\psi\rho$ lrs balls and $(1 - \rho)$ -balls to illustrate the sampling conditions. The nearest boundary point of the center of a $(1 - \rho)$ -ball dictates the local region size and so the maximal distance to the boundary. We observe that some of $(1 - \rho)$ -balls are as distant from the boundary as possible but still do not contain any local maximum. Notice, the ψ , ρ lrs-balls do not have to completely cover the boundary. This is due to the fact that even so a boundary point b is sampled by a sampling point s but the nearest boundary point b' to s is not b. The local region size on b' could then be less than the local region size on b.

5.5 Centered Tetrahedron Condition

In Section 5.2 we introduced a local maximum separation called *refinement* The boundary of the refinement correctly separates the local maxima associated with the local maxima of different regions of the original space partition. In Section 5.4 we defined sampling conditions to envelope the local maxima with sample points. Now we establish a correspondence between the local maxima of the space partition and the local maxima of discrete distance transform defined on the sample points.

Our sampling conditions ensure the discrete distance values in closer environment of the local maxima to be greater than around the boundary which results in elevations on discrete distance transform in the interior of the continuous region. Consult Figure 2.15 for illustration. As introduced in Section 2.4.9, due to the duality to the Voronoi graph, the Delaunay triangulation reproduces the properties of the distance transform. The maxima of the distance transform are circumcenters of Delaunay cells which intersect their dual Voronoi cells. We call them the *centered* Delaunay cells (see Section 2.4.8.

Notice, we use the term *cell* for the simplex of greatest dimension. In our case of 3D reconstruction we have the 3D Delaunay triangulation. A Delaunay cell corresponds to a Delaunay tetrahedron - the 3-simplex.

The first step of the new reconstruction algorithm is adjusting the correspondence between the local continuous maxima and the maxima of elevations of the distance transform which, as we prove, are the circumcenters of centered Delaunay cells.

Lemma 5.5 (Centred Simplex Condition for Region Stable (ψ, ρ) -Sampling). Let $R \in \mathcal{R}$ be a region of a space partition \mathcal{R} . Let S be a region stable (ψ, ρ) -sampling of the boundary $\partial \mathcal{R}$ with $0 \leq \psi < 1$ and $0 < \rho \leq 1$, and let D be the Delaunay triangulation of S. Then there exists at least one centered simplex of D with its center lying inside R.

Proof: Due to the definition of the local region size, there exists a point x inside R, where the continuous distance transform $(d_{\mathcal{R}})$ is greater than or equal to $r = d_{\mathcal{R}}(x) \ge \mathsf{lrs}(b)$ for all $b \in \partial R$. Let d_S be the discrete distance transform built on S. According to the definition of region stable (ψ, ρ) - sampling, $d_{\mathsf{S}}(x) \ge r - (1 - \rho)r = \rho r$.

By ascending the discrete distance transform starting in x one finally arrives in a local maximum of the discrete distance transform with distance value greater than or equal to $d_{\mathsf{S}}(x)$. The traversed path can not intersect ∂R , since $\forall b \in \partial R : d_{\mathsf{S}}(b) \leq \psi \rho | \mathsf{rs}(b) \leq \psi \rho r$ and $\forall \psi \in [0,1), \rho \in (0,1] : \psi \rho r < \rho r \leq d_{\mathsf{S}}(x)$. Thus the discrete distance transform admits a local maximum inside R. This maximum is the circumcenter of a Delaunay tetrahedron τ .

To show that this tetrahedron is centered, let us assume the opposite: the circumcenter m lies outside τ . Then there exists a plane containing m, such that τ lies completely on one side of this plane. Then by moving m along the orthogonal away from the plane by a sufficiently small distance, the value of the discrete distance transform increases, which is in contradiction to the assumption of being a local maximum.

In Figure 5.5 (a) we illustrate on our fish example the associated discrete maxima on a highly noisy region stable sampling from Figure 5.4 (b). Recall, the region stable sampling is induced by local region size. The Delaunay triangulation in Figure 5.5 (a) lacks in centered triangles (white) associated with local continuous maxima. The associated triangles accidentally contain their corresponding continuous maxima but this is not always the case.

Associated Centered Cells Due to Lemma 5.5 and the general position assumption, a local continuous maximum can uniquely be mapped to a centered Delaunay cell - not necessarily the cell which contains the local maximum. This centered cell is located in such a way that its circumcenter is necessarily in the same original region as the continuous maximum. So, the associatives of the local continuous maxima are circumcenters of central Delaunay cells. Deleting centered cells from the Delaunay triangulation leaves a space partition with thick boundary and regions of shape of centered cells. The centered cells contain their own circumcenter which are local maxima of the discrete distance transform. So, the resulting



Fig. 5.5: (a) Delaunay triangulation (gray triangles and thin edges). The white triangles are associated to the local continuous maxima (\oplus). Notice the associated triangles or their circumballs do not always contain the corresponding continuous maxima. (b)Delaunay triangulation without centered (acute) triangles. By deleting all centered triangles we necessarily hit the associated ones.

regions contain either exactly one associated discrete maximum or none. It follows that deleting all centered cells from Delaunay triangulation results in a refinement of the original space partition.

The local maxima are not known in the reconstruction process, but by deleting all centered cells we necessarily hit the associated ones and, consequently, we hit each region at least once. The Delaunay triangulation without centered cells (triangles) is shown in Figure 5.5 (b). But deleting all centered cells from the boundary results in a space partition which consists of too many regions which correspond to the same original region. Lemma 5.5 guarantees that, if two or more continuous maxima are associated with the same discrete maximum, all continuous maxima lie inside the same continuous region. We call the *oversegmentation*, which correctly separates the associated maxima, a *refinement*. The question now is how to thin the reconstructed boundary preserving the topology and how to appropriately merge the reconstructed regions?

5.6 Minimal Elementary Refinement

As we discussed earlier, deleting centered cells from Delaunay triangulation guarantees to hit a region at least once and if two or more continuous maxima are associated with the same discrete maximum and consequently with the corresponding centered cell, then these continuous maxima lie in the same continuous regions. Deleting the centered cells as illustrated in Figure 5.5 (b) results in a space partition with thick boundary (gray polygons containing Delaunay cells). The original boundary is thin. In 3D it is a 2D surface embedded in 3D space. In 2D it is a contour. Our aim is to reconstruct a thin boundary. In 3D it is a union of triangles. In 2D it is a union of edges.

Consider such a point b on the original boundary that its three nearest sampling points are equidistant to b. Let the three sampling points build a triangle. The line through b and the circumcenter of the triangle contains a Voronoi Edge dual to this triangle. Consequently, this triangle is a Delaunay triangle. The *normalized mesh* ([Attali, 1997]) is the union of all such triangles. It defines a thin boundary which separates different regions from each other. According to the definition of the normalized mesh, and since sampling of each boundary point defines a minimal density, we state that the simplices in the reconstructed boundary do not exceed some definite size. We say, the simplices have to fulfill the locally required sampling density.

Obviously the boundary is not known in the reconstruction process and therefore we can not derive the normalized mesh by just knowing the sampling points, as is possible for 2D [Attali, 1997]. In 3D the normalized mesh fails even for smooth surfaces [Attali, 1997, Stelldinger, 2008c]. So, our aim is to get a boundary reconstruction with its triangles being as *small* as possible. In order to mimic the behavior of



Fig. 5.6: (a) Elementary refinement resulting by region growing on smallest edge. (b) Minimal elementary refinement resulting by region growing on not Gabriel edge.

the discrete distance transform, the size of a simplex is measured by maximal distance value . Consult Section 2.4.11 for discussion and size computation .

Definition 5.6 (Minimal Elementary Refinement). Given a space partition \mathcal{R} and a set of points S. Let the underlying space R of a complex partition \mathcal{D} built on S be a refinement of \mathcal{R} . Then R is called elementary refinement if every reconstructed region of R contains exactly one local maximum of the discrete distance transform built on S.

Two refinements R, R' are called compatible, if there exists a one-to-one mapping of their reconstructed regions, such that every reconstructed region is mapped onto a reconstructed region containing both local maxima of the discrete distance transform which are associated to exactly the same local maxima of the continuous distance transform.

For compatible refinements R, R' we define an ordering relation < in the following way: Let $T := (\tau_1, \tau_2, \ldots, \tau_m)$ and $T' := (\tau'_1, \tau'_2, \ldots, \tau'_n)$ be the lists of all boundary triangles of R, resp. R', ordered descending by their size. Then we say R is smaller than R', R < R' if T < T' regarding lexicographic order. A refinement R is called minimal, if there exists no compatible refinement R', such that R' < R.

According to Definition 5.6, a refinement is defined by discrete local maxima. It follows that the definition of a refinement assumes a construction on a set of points. This limitation is suitable for our framework, but the definition obviously can be generalized to local maxima of any distance transform.

Consider again the result of centered cells (triangles in 2D) deletion from the Delaunay complex in our 2D example in Figure 5.5 (b). The gray polygons separate the reconstructed regions (white triangles). Between some regions there is more than just one edge. The boundary is thick. It contains triangles. There are several possibilities to thin out the boundary between two neighboring regions. Nevertheless in each case the resulting refinement correctly separates the local maxima.

According to Definition 5.6, the thinned boundaries are compared by ordered lists of the simplices contained in the reconstructed boundary. The minimal refinement minimizes the size of the simplices in the boundary. Notice, the compatible refinements are compared by lists of simplices which separate two different regions. Two compatible refinements have a "head" - or a sublist - of simplices, which is equal for both, and a "tail" of simplices, which starts with first occurrence of a different simplex. The refinement is smaller if its first simplex in the tail is smaller. Notice that the tail may contain simplices which are not compared at all.

In Figure 5.6 two different elementary refinements demonstrate maxima separation with thin boundaries. In (a) the regions of Figure 5.5 (b) are expanded on smallest edge first. In (b) the originally thick boundary is thinned on edges which are opposite to an obtuse angle. The circumball of such edges is not free of points. Simplices with no point-free circumsphere are called *equivocal* or *not Gabriel*. (compare Definition 2.41). Both refinements correctly separate the local maxima. The regions of both refinements contain one local maximum each. But only the elementary refinement in Figure 5.6 (b) is minimal. In the following we prove the result.

5.7 Elementary Thinning

The minimal elementary refinement correctly separates the associated local maxima. The separation of local maxima is already done by deletion of centered cells. As we have seen in Figure 5.6 the order of simplex removal affects the underlying space of the resulting region. Now we introduce the boundary thinning procedure which results in the same local maxima separation but the refinement boundary is thin and minimal.

The result of reconstruction depends on the quality of the sampling, and the sampling conditions depend on the geometrical and topological properties which have to be preserved in the digitization process. If the input of the reconstruction is a region stable sampling (Definition 5.4) then it is assumed that the correct local maxima separation is of interest and not the correct homotopy of the regions.

Region stable sampling guarantees the discrete distance values on the original local maxima to be greater than the discrete distance values on the boundary. The original local maxima lie in the mountains of the discrete distance transform whereas the original boundary is the valley. The associated local maxim is one of the nearest peaks of the mountains which is reached without descending. The steepest path is given by flow curves on the distance transform.

"Flow relation" (compare Section 2.4.9) imitates the behavior of flow curves. "Constructive retraction" ("WRAP") algorithm, as introduced in Section 2.4.10, collapses on equivocal simplices removing its unique predecessor. So, the constructive retraction algorithm follows the flow relation.

Equivocal simplices have a unique predecessor (compare [Edelsbrunner, 2003] Claim 8.). The distance values on the predecessor are less than on its successor. So, following the flow relation starting on an equivocal and ending on its unique predecessor, we follow the flow curve on the steepest path uphill.

WRAP step removes in each step an equivocal simplex and its predecessor in such a way descending in the flow relation. According to Theorem 2.65, the order in which the equivocals are chosen for deletion is irrelevant. It follows that the result of constructive retraction is minimal and, since no reconstructed regions are merged, the result is also elementary.

The WRAP algorithm ensures each step to result in the homotopy equivalent open set. So, after performing the WRAP on each reconstructed region we obtain a set of homotopy equivalent reconstructed regions. Since all centered cells have been removed in the first step of the algorithm, no further regions can be contained in the thick boundary surrounded by the faces of inconsistent cells.

WRAP stops on inconsistent cells. As introduced in Section 2.4.9 inconsistent cells consist of two equivocal faces such that the cell has more than one successor. That means that removing the equivocals merges two ancestor sets. The ancestor sets of a centered cell correspond to reconstructed regions. Merging two ancestor sets implies the possibility of merging two different regions. So, to undergo the inconsistency but to achieve the thin boundary we, in contrast to WRAP, perform the collapsing step on the greater inconsistent face and then resume the algorithm procedure.

Algorithm 5.7 (Elementary Thinning). Let D be a Delaunay triangulation. Let $D_E = D$.

- 1. Remove all centered cells from D_E .
- 2. If possible perform any constructed retraction on D_E . Continue with 2.
- 3. Else if there are simple inconsistent simplices in D_E collapse on the greatest. Continue with 2.
- 4. Return D_E .

Lemma 5.8. The result D_E of elementary thinning algorithm is a minimal elementary refinement.

Proof: Let x_1, x_2 be two maxima of the continuous distance transform lying inside different continuous regions $R_1 \in \mathcal{R}$ and $R_2 \in \mathcal{R}$ and let y_1, y_2 be their associated maxima of the discrete distance transform. Due to Lemma 5.5, it follows that $y_1 \neq y_2$. Thus y_1 and y_2 are circumcenters of different centered tetrahedra, which implies that they lie inside different reconstructed regions. Thus D_E is a refinement. Since each centered tetrahedron defines a separate region, D_E is an elementary refinement. Thus it remains to show that D_E is minimal. Let us now assume the opposite. Then it follows that there is a compatible refinement $D'_E < D_E$ which is minimal, ie.T' < T, where T, T' are the corresponding lists of boundary triangles σ'_i respectively σ_i ordered descending by their size. Let i be the position on which the first difference between T' and T appears: $\sigma'_i < \sigma_i$. Without loss of generality let σ_i be the boundary triangle between two reconstructed regions $|D|'_1, |D|'_2$ with their central tetrahedra τ_1, τ_2 . Then σ_i is smaller than all triangles lying on a collapsing path from τ_1 or τ_2 to a coface of σ_1 . Since every elementary refinement separates the centered tetrahedra from each other, the triangle σ'_i must lie on one such collapsing path, which is in contradiction to the assumption $\sigma'_i < \sigma_i$. Thus D_E is a minimal elementary refinement.

In 3D a tetrahedron either contains its own circumcenter and is by definition centered, or it does not contain its own circumcenter and is confident. In the latter case there is a proper face - a triangle of the tetrahedron whose affine expansion separates the tetrahedron from its circumcenter. This face is equivocal. It follows that the Delaunay tetrahedrons are either deleted in the first step of the elementary thinning algorithm, or they have at least one proper equivocal face and are deleted in step two or three. So, the elementary thinning algorithm processes all tetrahedrons of the complex. Due to this, the subcomplex remaining after the elementary thinning algorithm is thin, i.e. it contains no tetrahedrons.

5.8 Refinement Reduction

To reduce a given refinement means to merge the reconstructed regions which are associated with the same original region or are not associated with any original region at all. The merge is done by deletion of a boundary triangle and is then followed by collapsing on simple edges. How do we know which boundary triangle is appropriate for deletion? The answer can be given if the underlying sampling conditions are region stable. In such a case a triangle may be too *big*. Which means the ratio between the size of the triangle and the reconstructed region is too great. The size of a reconstructed region is the circumradius of its greatest centered tetrahedron. The size of a triangle is its maximal distance value.

The region stable sampling conditions ensure the sampling points near the boundary to be much denser than in the interior of the original region. Simply speaking each original maximum is surrounded by very small distance values around the boundary and correspondingly by small triangles. The maximal sample point deviation reduces the possible minimal discrete distance values on original maximum is surrounded by distance values around the original boundary which are less than ρr . The ψ -value gives the upper bound for maximal distance value. So, the original maximum is surrounded by boundary points with discrete distance values less than $\psi \rho r$. It follows that the corresponding triangles are less than $\psi \rho r$ with $\psi < 1$.

Obviously, the original maxima and their distance values are not known during the reconstruction process. But, if a discrete local maximum m' is associated with an original one and since we know that its discrete distance value r' is greater than r we can conclude the maximum size of boundary triangles. r' is greater than ρr then $\psi r'$ is greater than $\psi \rho r$. It follows that knowing the greatest distance value r' of a reconstructed region we also know that it can be correctly separated by boundary triangles smaller than $\psi r'$.

Well, it is almost as easy as that. Before the merge of reconstructed regions can be performed it has to be ensured that such boundary triangles are still in the reconstruction. Consider our 2D example in Figure 5.6 (a). The reconstructed eye is a triangle bounded only by edges which are greater than at least half of the circumradius of the triangle. By previous considerations this region can be merged to its neighbor if $\psi \approx 0.5$ which would destroy the original neighborhood relation. The reason is, the



Fig. 5.7: (a)Minimal elementary refinement resulting from Elementary Thinning. (b) Refinement Reduction in lexicographically increasing order: the greatest undersampled in the smallest region first.

refinement although elementary is not minimal. The reconstructed eye could be separated by edges in the denser sampled environment of the original boundary but the edges have been removed in the previous procedure.

To ensure that the reconstruction contains the boundary simplices which are small enough to correctly separate the associated regions we demand the reconstruction to be a minimal refinement. Elementary thinning results in minimal elementary refinement and so is the appropriate preprocessing step.

Constructed retraction in the elementary thinning algorithm as well as the collapsing on an inconsistent simplex removes an equivocal face and its unique predecessor. The procedure follows the flow curves uphill. Thus by construction, there are monotonically increasing paths starting on remaining boundary triangles and ending in circumcenters of centered tetrahedrons without passing through further boundary simplices. Consequently, finding a simplex in the boundary which is greater than ψ of the greatest distance value in the region, we also find a path of distance values too great to pass through the original boundary. So, merging the reconstructed regions we connect two discrete maxima which are either associated with the same region or not associated at all.

Lemma 5.9 (On Simplex Deletion in Minimal Refinement). Let D_R be a minimal refinement constructed on a region stable (ψ, ρ) -sampling of a space partition \mathcal{R} . Let σ be in the boundary between two reconstructed regions R_i and R_j . Let R_i be less than R_j and let r_i be the radius of the greatest simplex in R_i . R_i and R_j are associated with the same continuous region if the circumradius of σ is greater than ψr_i .

Proof: If there is no continuous maximum associated with any maximum in R_i or R_j then the proof is trivial, σ can be deleted and R_i and R_j can be merged.

Let $x_i \in R_i \in \mathcal{R}$ and $x_j \in R_j \in \mathcal{R}$ be the continuous local maxima respectively associated with the greatest discrete local maxima y_i, y_j in R_i and R_j . According to the definition of (ψ, ρ) -sampling and the construction in Lemma 5.5, $r_i = d_{\mathsf{S}}(y_i) > d_{\mathsf{S}}(x_i) > d_{\mathsf{R}}(x_i) - (1-\rho)d_{\mathsf{R}}(x_i) = \rho d_{\mathsf{R}}(x_i)$.

Since by construction of minimal refinement all previously deleted simplices are greater than σ , there exists a path between $y_i y_j$ and, according to Lemma 5.5, a path π between x_i and x_j through σ , which is everywhere greater than or equal to the greatest distance value in σ . Consequently, $\forall t \in [0, 1]$: d_s($\pi(t)$) $\geq \psi r_i$.

Let us consider π intersects the boundary in b, then $d_{\mathsf{S}}(b) \ge \psi r_i > \psi \rho d_{\mathcal{R}}(x_i)$. Then from definition of (ψ, ρ) -sampling $\forall b' \in \partial \mathcal{R} : d_{\mathsf{S}}(b') < \psi \rho | \mathsf{rs}(b')$ follows $\psi \rho | \mathsf{rs}(b) > \psi r_i > \psi \rho d_{\mathcal{R}}(x_i)$ which is a contradiction since x_i is maximal for $R_i : \forall b' \in \partial R_i : |\mathsf{rs}(b') \le d_{\mathcal{R}}(x_i)$.

According to Lemma 5.9 a boundary simplex is too great if its distance values exceed ψ of the circumradius of the greatest simplex in the region. The underlying space of such a simplex is not

supported by enough sample points, or in other words, is sampled with insufficient density. So, we introduce the following definition:

Definition 5.10 (ψ -Undersampled). Let R be a reconstructed region and σ be in its boundary. Let $r_{\rm R}$ be the circumradius of the greatest simplex in R and r_{σ} be the circumradius of σ . Then σ is called a ψ -undersampled simplex of region R if $r_{\sigma} \geq \psi r_{\rm R}$

We call the processing step which merges two reconstructed regions by removing the undersampled simplex the ψ -undersampled merge.

Definition 5.11 (Top ψ -Undersampled Merge). The ψ -undersampled merge is a processing step which deletes a simplex σ fulfilling the following properties: there exists a reconstructed region R with at least one ψ -undersampled simplex of region R, and σ is the greatest boundary simplex of R.

The top ψ -undersampled merge is a ψ -undersampled merge on the greatest ψ -undersampled simplex.

According to Lemma 5.9 the result of ψ -undersampled merge is still correct separation of original local maxima. The aim of the algorithm is to result in a boundary reconstruction which correctly separates the local maxima and which oversegments the regions as little as possible. In other words we want to merge as many reconstructed regions as possible preserving the correct separation. The precondition for ψ -undersampled merge is a minimal refinement.

Theorem 5.12 (Result of Top ψ -Undersampled Merge is Minimal Refinement). Let D_R be a minimal refinement and let σ be the greatest ψ -undersampled simplex. Let D'_R be the result of top ψ -undersampled merge on σ then D'_R is minimal refinement.

Proof: According to Lemma 5.9 D'_R is a refinement. Assume D'_R is a not minimal. Then there is a compatible refinement D''_R which is minimal. But D''_R contains σ in its boundary, so D'_R is less than D''_R which is a contradiction.

Using the construction of top ψ -undersampled merge we propose the following algorithm.

Algorithm 5.13 (Sorted Refinement Reduction). Let D_E be the result of elementary thinning. $D_R = D_E$. Let $Q_{\partial D_R}$ be a priority queue of pairs of ψ -undersampled simplices and their smallest adjacent regions lexicographically sorted in decreasing order according to the size of ψ -undersampled simplices.

- 1. While $Q_{\partial \mathsf{D}_R}$ is not empty:
 - (a) Let (σ, τ) be the top element of $Q_{\partial \mathsf{D}_{\mathsf{B}}}$. Pop $Q_{\partial \mathsf{D}_{\mathsf{B}}}$.
 - (b) If σ is deleted or is not ψ -undersampled on smallest adjacent region, then continue with 1.
 - (c) If τ is not the greatest cell of the adjacent region, then push τ', σ into $Q_{\partial \mathsf{D}_R}$ where τ' is the greatest cell of the smallest adjacent region of σ , then continue with 1.
 - (d) Perform the ψ -undersampled merge on σ .
 - (e) Collapse on all simple simplices, then continue with 1.
- 2. Return D_R .

In refinement reduction the ψ -undersampled merge is performed on one boundary simplex only. After deletion of that simplex the adjacent regions are merged and the boundary may consist of simple simplices. The subsequent elementary collapsing on all simple simplices deletes among others the ψ undersampled simplices. So, we need to check in Algorithm 5.13 1.b if the current ψ -undersampled simplex is still in the boundary.

Merging regions means to join one reconstructed region with a greater one. The greatest cell of the first region is updated to the greatest cell of the second. So, the ψ -undersampled condition for the simplices of the first region is no longer valid. Therefore in step 1.b the test is performed if the simplex is ψ -undersampled according to the smallest adjacent region. The smallest adjacent region might have been merged to a greater on which would change its size.



Fig. 5.8: (a) Refinement Reduction in lexicographically increasing order: the greatest undersampled in the smallest region first. (b) Refinement Reduction in arbitrary order: the greatest undersampled with respect to any region. The empty boxes are vertices of the merging graph. Each empty box is the greatest maximum of a reconstructed region after elementary thinning. The connecting edges through a thin Delaunay edge demonstrate a merge of reconstructed regions on the undersampled edge (the Delaunay edge crossing the graph edge). The brighter the color of the edge the earlier the merge was performed. The black box is the root of the graph.

Notice, the refinement reduction algorithm is order-independent according to the choice of the reconstructed region. The priority queue is sorted according to the size of the undersampled simplices only to ensure the result to be minimal refinement. The undersampled merge connects two regions on an undersampled simplex. Considering the elementary regions as knots, and the pairs of connected elementary regions as edges, we obtain a graph. The graph is a set of trees with the greatest region cells after refinement reduction as roots and the elementary regions as leaves.

Since the initial boundary for each ψ -undersampled merge is the minimal refinement, we can consider the ψ -undersampled merge as joining of two trees. Since the root and the greatest undersampled simplex in the corresponding region are unique there is only one possibility for the merge. So, the reconstruction graph is unique for any choice of join of trees.

In Figure 5.8 we demonstrate the different orders of refinement reduction by a reconstruction graph. The resulting boundary reconstruction is the thick line corresponding to Figure 5.7.

The thin lines are the boundary simplices of elementary thinning. The empty boxes are the maxima of elementary regions. The black boxes are the greatest maxima of resulting reconstructed regions after refinement reduction. The black boxes are the roots of the graph trees.

The graph edges between the boxes are Voronoi edges dual to simplices in the unique flow relation between the nearest maximum and the undersampled edges. Since for any reconstructed region the greatest undersampled edge is unique, the construction of a merge in a graph requires for any undersampled edge only the connection of the nearest reachable maxima.

The graph edges in Figure 5.8 are colored according to the order in the sequence of the undersampled merges. The earlier the undersampled merge is, the lighter is the gray color of the graph edge. In Figure 5.8 (a) the undersampled edges are lexicographically sorted in increasing order according to the size of the undersampled edge. So, the greatest undersampled of the smallest region is processed first. The lighter graph edges start on smaller regions. The darker graph edges connect greater regions. In Figure 5.8 (b) the choice of a region is random. The lighter graph edges demonstrate earlier merges.

The condition of the minimal refinement is proven by top undersampled merge. The list of simplices to delete is already sorted to ensure minimal result. According to this construction the proof is straight forward. But the undersampled merge is a merge of two trees. The smaller root becomes a branch of a greater tree. For this root the undersampled simplex is unique, as we indicated previously, so we conjecture that the refinement reduction results in minimal refinement order independently.



Fig. 5.9: (a): original surface; (b): irreducible refinement; (c): stable refinement

Conjecture 5.14 (Result of Order Independent ψ -Undersampled Merge is Minimal Refinement). Let D_R be a minimal refinement and let σ be the greatest ψ -undersampled simplex. Let D'_R be the result of ψ -undersampled merge on σ then D'_R is minimal refinement.

Assuming Conjecture 5.14 to be true, the refinement reduction allows highly parallel implementation of the algorithm.

5.9 Reducible Refinement

As we may see in Figure 5.2 even if the boundary does separate the associated maxima correctly the resulting space partition is not homotopy-equivalent to the original. Furthermore the regions containing maxima associated with continuous maxima of one and the same region cannot be joined without loosing the refinement property. Opening any triangle by deletion of an edge joins the regions and the infinite maximum is no longer separated from the maximum of the triangles.

In Figure 5.9 we see the problem in 3D. The original shape (a) is a donut with one swallowed and one shrunk side. The original shape has only one local maximum in its interior as well as the refinement in (b). But the refinement in (b) is not homotopy-equivalent to the original and any further deletion of edges or triangles either destroys the refinement property or the connectivity of a region. The refinement in (c) is homotopy and even topology-equivalent space partition.

Separating maxima only is not enough for shapes with necks or narrowings. Neck or narrowing corresponds to a saddle on the distance transform. Our next aim is the correct separation of all criticals. The criticals which belong to the same original region are then associated with discrete criticals which belong to the same reconstructed region. The minimal homotopy equivalent subset of the medial axis containing all criticals and the steepest paths connection them is the *homotopical axis* (see (see Definition 2.24)). . So we demand from the refinement to preserve the connectivity of the homotopical axis.

Definition 5.15 (Stable Refinement). Given a space partition \mathcal{R} , let \mathcal{R}'' be the refinement of \mathcal{R} . Let HA be the homotopical axis of \mathcal{R} . Then \mathcal{R}'' is called a stable refinement of \mathcal{R} , if the underlying space of its boundary $\partial \mathcal{R}''$ does not cut HA.

Definition 5.16 (Reducible Refinement). Let \mathcal{R}' be a refinement of \mathcal{R} . \mathcal{R}' is a reducible refinement if there is a stable refinement \mathcal{R}'' of \mathcal{R} such that the boundary of \mathcal{R}'' is a subset of the boundary of \mathcal{R}' .

A stable refinement of our barbell example in Figure 5.10 now divides the space in such a way that the homotopical axes of different original regions are separated. The refinement containing the dashed edge is *reducible* to a stable refinement by joining the regions by deletion of the dashed edge. Obviously the topological equivalent in Figure 5.9 (c) is a stable refinement.

Reduction vs. Enhancement to a Topological Equivalent Notice, that a donut is a stable


Fig. 5.10: The thinner line is the boundary of the original space partition \mathcal{R} . The thick line connecting \oplus is the homotopical axis of \mathcal{R} . The union of thick edges the space into a stable refinement of \mathcal{R} . The union of thick edges with the dashed edge partitions the space into a refinement which can be reduced to a stable refinement.

refinement of a ball but is not reducible to the topological equivalent by deletion of some subsets of its boundary. In this case the loop of the donut must be cut. In other words we have to enlarge the boundary to cut the interior region or to reduce the interior region and simplify its topology.

To reduce a refinement we delete some boundary subset. This boundary subset is a connected component resulting from boundary intersection. Deletion of this boundary intersection joins the regions and the boundary subset becomes subset of their interior. Obviously in cases of a region whose boundary intersects itself (compare Figure 5.9 (b)) no regions are joined, but the intersection becomes a subset of the region's interior.

The region reduction like in case of a donut does not lead to refinement reduction. In fact by deletion of interior subsets we enlarge the boundary and/or add new regions to the space partition. Which means that we enhance the refinement instead of reducing it.

5.10 Sampling Conditions for Reducible Refinement

The boundary of a stable refinement does not intersect the homotopical axis. The homotopical axis is homotopy-equivalent to its open set and contains all critical points of the continuous distance transform but also all the steepest paths connecting them. Reconstructing the homotopical axis, we reconstruct the homotopy type of the space partition.

Let us consider a non-smooth non-manifold shape of a multi-regional space partition in Figure 5.11 (a). The contour of a fish is one of the simplest examples to demonstrate a region with at least two local maxima and a saddle between them. The two fins are two further regions as well as the eye of the fish. This shape illustrates also a saddle of even lesser distance value between the fish and the eye boundary. Between the bottom fin and the fishtail the distance value of the maximum is only slightly greater than of the neighboring saddle. The tips of the fins and the fishtail are non-smooth points on the boundary as well as the meeting points between the fin, the background and the fish contour.

The homotopical axis (dashed line in Figure 5.11 (a)) of the whole space partition consists of five connected components. The connected components, or in other words the homotopical axis, in the fins and the eye consist of one single local maximum. Obviously we illustrate only a cutout of the homotopical axis corresponding to the infinite background containing the infinite maximum and the connection between the saddle and the maximum between the bottom fin and the tail. The homotopical axis in the fish interior consists of two maxima connected by steepest paths starting on the saddle and a loop which are two steepest paths starting on the smallest saddle and ending in the same greatest



Fig. 5.11: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denote the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b) Local homotopy sampling with $\psi = 0.5$ and $\rho = 1$

maximum.

Our aim now is to define the sampling conditions in such a way that the homotopical axes of different regions are separated by an envelope with lesser discrete distance values than in the close environment of the homotopical axis. In fact we define the sampling conditions to obviate the possibility of starting a steepest increasing path on the homotopical axis and pass through the boundary of a stable refinement.

The local homotopical feature size (lhfs compare Definition 2.36) measures for every point the distance to the homotopical axis and compares it to the local region size on this point. The lesser value is the local homotopical feature size. If we consider a very thin and high pyramid we notice that the homotomopical axis consists of one local maximum only. But the distance between the tip of the pyramid and the maximum is inappropriately large to be used for sampling conditions.

We use again the idea of the (p, q)-sampling and define non-uniform sampling conditions induced by local homotopical feature size:

Definition 5.17 (Local Homotopy Stable (ψ, ρ) -Sampling). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} and let lhfs be the local homotopical size defined on $\partial \mathcal{R}$. Let $S \subset \mathbb{R}^3$ be a finite set of points. Then S is said to be a region stable (ψ, ρ) -sampling of $\partial \mathcal{R}$, if S is a (ψ, ρ) -sampling with $\forall b \in \partial \mathcal{R} : f(b) = \mathsf{lhfs}(b)$

A noise free local homotopy stable sampling (dots) of the fish example is presented in Definition 2.36 (b). The corresponding circles demonstrate the $\psi \rho | \text{hfs-balls}$ with $\psi \approx 0.5$ and $\rho \approx 1$.

The sampling conditions defined for refinement reconstruction in [Tcherniavski et al., 2012] are a special case of a local homotopy stable (ψ, ρ) -sampling with $\psi \approx 1$ and $\rho \approx 0.5$.

Local homotopical feature size is the smaller value between the distance value of the minimal reachable local maximum which is the local region size, and the distance to the homotopical axis. It follows that the local homotopical feature size is always less than or equal to the local region size and implies:

Corollary 5.18 (Local Homotopy Stable (ψ, ρ) -Sampling is Region Stable). Let $\partial \mathcal{R}$ be the boundary of a space partition \mathcal{R} and let lhfs be the local homotopical size and lrs be the local region size defined on $\partial \mathcal{R}$. Let $S \subset \mathbb{R}^3$ be local homotopy stable (ψ, ρ) -sampling of $\partial \mathcal{R}$. Then S is region stable (ψ, ρ) -sampling

Proof: Since $\forall b \in \partial \mathcal{R} : \mathsf{lhfs}(b) \leq \mathsf{lrs}(b)$ is valid it follows:

$$\begin{array}{rcl} \forall b \in \partial \mathcal{R} : & \mathrm{d}_{\mathsf{S}}(b) & \leq & \psi \rho \mathsf{lhfs}(b) & \leq & \psi \rho \mathsf{lrs}(b) & and \\ \forall s \in \mathsf{S} \exists b \in \partial \mathcal{R} : & \mathrm{d}_{\mathcal{R}}(s) & \leq & (1-\rho) \mathsf{lhfs}(b) & \leq & (1-\rho) \mathsf{lrs}(b) \end{array}$$

For simplicity in following we call a sampling which is a region stable (ψ, ρ) -sampling a region stable sampling, and a sampling which is local homotopy stable (ψ, ρ) -sampling a local homotopy stable sampling. Obviously, since Corollary 5.18 is valid all further statements and guarantees proven for a region stable sampling also hold for a local homotopy stable sampling.

5.11 Reducible Refinement Reconstruction

The aim of our work is to investigate the sampling conditions and to present methods for reconstruction of topological properties. In this chapter, we assume multi-regional space partitions. In this way the refinement reconstruction algorithm is a method which results in a space partition which, under guarantee, separates the local continuous maxima. But the separation of local maxima is insufficient for objects consisting of waists or narrowings in their boundary. In this section, we prove that the result of refinement reduction on homotopy stable sampling is a reducible refinement.

The main idea of the proof is based on two facts. First, according to Corollary 5.18 the homotopy stable sampling is region stable. So, the result of the refinement reconstruction is a minimal refinement. In other words, all maxima are correctly separated and all decreasing paths starting on the homotopical axis meet the reconstructed boundary. Second, increasing paths starting in the homotopical axis stay in the homotopical axis. So after we have outlined the arising trivial cases in **I**, in **II** we cover the case of the homotopical axis cutting the reconstructed boundary. We show that all increasing paths from the cutting point to maxima of different reconstructed regions belong to the homotopical axis of one original region.

So, removing the cutting simplex will preserve the topological properties of the original region. Assuming the opposite will lead to a contradiction. The result of **III** is that every path to the different original region goes through the boundary and needs to be partly decreasing. In contradiction, **IV** shows that there is an increasing path between the cutting point and the maximum of the neighboring region, which falsifies the assumption.

Theorem 5.19 (Stability of the Minimal Refinement on (ψ, ρ) -Locally Stable Sampling). Let D_R be a minimal refinement constructed on (ψ, ρ) -locally stable sampling of a space partition \mathcal{R} . Then the boundary ∂D_R of D_R contains the boundary of a stable refinement.

Proof: We need to show that removing all simplices of ∂D_R which cut or touch the homotopical axis results in a space partition which is still a refinement.

I Obviously, if D_R is a stable refinement, the theorem holds. So let D_R not be a stable refinement. Let $|\partial \mathsf{D}_R|$ be the underlying space of $\partial \mathsf{D}_R$ and HA be the homotopical axis of $\partial \mathcal{R}$, then $|\partial \mathsf{D}_R| \cap \mathsf{HA} = X \neq \emptyset$.

Let R_i and R_j be two reconstructed regions such that there is an $x \in X$ in the common boundary of R_i and R_j . There are two cases to consider: First, at least one reconstructed region contains no continuous maximum: then merging the reconstructed regions does not destroy the refinement condition. Thus, we only have to consider the second case: each reconstructed region contains at least one continuous maximum.

II All continuous local maxima are also local maxima of MAT (Observation 2.22) and so are in HA. Let $x_i \in \mathbf{R}_i$ and $x_j \in \mathbf{R}_j$ be two nearest local maxima on HA reachable by steepest paths starting on x. We have to show that there is a path π_i in \mathbf{R}_i between x and x_i and a path π_j in \mathbf{R}_j between x and x_j with π_i, π_j entirely contained in HA.

III Let us assume that there is no such path π_i . Since for each continuous region R the intersection $\mathsf{HA} \cap R$ is continuous (Corollary 2.28), x and x_i must belong to different continuous regions. It follows that any path between x and x_i must cross $\partial \mathcal{R}$. Therefore, for all paths π' between x and x_i there is a t such that $\pi'(t) = b \in \partial \mathcal{R}$ and by definition of (ψ, ρ) -locally stable sampling $d_{\mathsf{S}}(b) < \psi \rho \mathsf{lhfs}(b)$.

IV Let b be the nearest boundary point to x, then, since $x \in HA$, $d_{\mathcal{R}}(x) \geq \mathsf{lhfs}(b)$ and $d_{\mathsf{S}}(x) \geq \mathsf{lhfs}(b) - (1 - \rho)\mathsf{lhfs}(b) = \rho\mathsf{lhfs}(b)$. But by construction of the refinement reduction algorithm, the circumradius of the previously deleted simplices in D_R are greater than $\mathsf{d}_{\mathsf{S}}(x)$, and so there exists a path π between x and x_i through the circumcenters of the deleted simplices which fulfills $\forall t \in [0, 1]$: $\mathsf{d}_{\mathsf{S}}(\pi(t)) \geq \mathsf{d}_{\mathsf{S}}(x) \geq \rho\mathsf{lhfs}(b)$, which contradicts the previous paragraph.



Fig. 5.12: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denotes the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b) Dots are the noise-free homotopy stable sampling with $\psi = 0.5$ and $\rho = 1$, the thick line is the result of refinement reconstruction.

Obviously the same is valid for π_j and for all $x \in X$ which are also in the boundary of R_i and R_j . Since π_i and π_j exist, there is a continuous path between x_i and x_j in HA. Consequently, the local maxima of the continuous distance transform lying inside R_i and R_j lie in the same continuous region. Then, after removing the simplex containing x, no local maxima lying in different continuous regions will lie in one reconstructed region, and the resulting discrete space partition is still a refinement.

The refinement reconstruction is a method to separate the original local maxima, not to separate the connected components of the original homotopical axis. With the result of Theorem 5.19, we guarantee that the outcome of the algorithm on homotopy stable samplings can be reduced to a boundary which correctly separates the connected components of the homotopical axis.

The result of the refinement reconstruction on noise-free homotopy stable sampling is presented in Figure 5.12 (b). The reconstructed contour (thick line) correctly separates the local maxima. The contour also contains an edge which cuts the original homotopical axis. We observe, that removing the edge does not destroy the property of refinement. The increasing paths on discrete distance transform starting in the cutting point stay in the interior region.

5.12 Algorithm

In this section, we summarize the reconstruction steps and illustrate the results of the algorithm on three examples. Each example is a sampling of our non-manifold 2D example "fish" (see Figure 5.13 (a)). In (b) we demonstrate a very sparse noise-free homotopy stable sampling. The example in (c) is a very dense homotopy stable sampling which has been corrupted by high amounts if noise without losing the sampling stability conditions. The sparse sampling in the last example (d) lost its stability conditions as the consequence of noise.

5.12.1 Sampling Conditions

Obviously, the sampling sets in Figure 5.13 are artificial and the sampling parameters are known. In real applications, the sampling parameters are not always known in the reconstruction procedure and have to be determined or estimated.

Consider the illustration of noise-free sampling conditions in Figure 5.13 (b). The sampling points are on the boundary. The dark gray balls surrounding the sample points represent the $\psi \rho lhfs$ value on this point. So, we want to assume that for each boundary point in this ball the nearest sample point is



Fig. 5.13: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denotes the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b) Noise-free homotopy stable sampling with $\psi < 0.5$. (c) Homotopy stable sampling with $\psi < 0.5$ and $\rho < 0.2$. (d) Homotopy stable sampling with $\psi < 0.5$ and $\rho < 0.2$. (d) Homotopy stable sampling with $\psi < 0.6$, $\rho < 0.8$ which has been corrupted by huge amount of noise ($\rho < 0.2$). (b,c,d) the gray circles represent the $\psi \rho hfs$ on the boundary point where the center is the corresponding sample point. (c,d) the gray dilation is the $(1 - \rho) hfs$ -dilation of the boundary.

the center of this ball and since the distance to it is less than $\psi\rho$ lhfs, then the sampling conditions are fulfilled. But the local homotopical feature size (lhfs) is not constant on the boundary. So, taking for our consideration the greatest dark gray ball we conclude that the lhfs on boundary points to the right of the sampling point is decreasing and is increasing to the left of the sample point. The ball containing the boundary points for which the center is the nearest sample point fulfilling the sampling conditions should actually be an "egg" shape. However, for simplified illustration we chose the circular balls with variable radius. In our illustration the union of balls covers the boundary and is covered by the $\psi\rho$ lhfs boundary dilation. In such a way we ensure the sampling conditions to be fulfilled. Notice, that in the examples (c) and (d) the irregular light gray envelope of the boundary is not the $(1 - \rho)$ lhfs-dilation, but the illustration of the lhfs distribution.

So, the first example is noise-free. That implies that $\rho = 1$. Observing the radii of the gray balls, we state that the radii are less than 0.5lhfs. So, we estimate $\psi \approx 0.5$. The second example (c) is highly noise corrupted. But there is a dense point set around the boundary such that the distances between the boundary points and the nearest sample points are less than 0.1lhfs. The sample point deviation from the boundary is in the 0.8lhfs-dilation of the boundary. So, we estimate the parameters with $\rho < 0.2, \psi < 0.5$.

The last example is a sparse sampling which has been corrupted by noise in the same way as in the previous example. The $\psi \rho$ lhfs balls have the radii of 0.5 lhfs with estimated ψ -value of 0.5 and,



Fig. 5.14: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denotes the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b,c,d) The results of elementary thinning (thick line).

consequently $\rho \approx 1$ which does not allow any sample point deviation from the boundary. But the balls overlap and their centers are not exactly on the boundary. Furthermore the local homotopical feature size is equal to the distance to the nearest maximum in only a few points. The maximal deviation on such points is critical for reconstruction. The initially sparse sampling denoted by dark gray balls might have been fulfilling the sampling conditions but is now corrupted by huge amount of noise with maximal deviation of 0.8lhfs. So, we expect the reconstruction to lose topological properties. We observe furthermore that the regions which correspond to "fins" are represented by a soup of almost uniformly distributed sample points.

5.12.2 Elementary Thinning

The first step of our method is to build a refinement on the Delaunay triangulation by deleting all centered cells. The holes in the triangulation are the reconstructed regions of the first step. The boundary between the regions may be thick and consist of further Delaunay cells. The constructive retraction method applied on the simple simplices thins the boundary leaving the compatible reconstructed regions bounded by minimal simplices.

As stated previously the reconstructed regions contain at this step of the algorithm one discrete local maximum which makes the refinement elementary. It follows that since maxima are separated by minimal simplices the refinement is minimal.

The results of elementary thinning on our three examples is presented in Figure 5.14. The recon-

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struction is an oversegmentation which correctly separates the local maxima. The reconstructed contour in (a) is a good approximation of the original boundary especially in curve segments with low curvature. Unintentionally the sampling met the corners of "fins", so, the contour is less erroneous in the sharp angles.

The results in (c) and (d) are built on point sets consisting of equal subsets. So, the reconstruction may consist of equal structures and, so, look similar. But in (c) the points near the boundary are much denser than in (d). Both reconstructions seem to consist of a soup of triangles especially in the areas of fins and the fishtail. But the ratio between the greatest triangles inside the fins and the edges around the original boundary is much higher in (c) than in (d). In (d) the size of triangles inside the fins and the fishtail is the same as the size of triangles around the boundary. That means that the distance values along the paths through the original region do not change significantly, which makes the separation between the maxima impossible.

5.12.3 Refinement Reduction

The last step of our algorithm reduces the oversegmentation by appropriate merging of reconstructed regions. Appropriate regions for a merge are reconstructed regions which belong to the same original region. Consider for example the two greatest empty areas in Figure 5.14 (c) or (d). The two areas belong to the same original region - the interior of the fish - and are separated by a slim triangle which for itself is a reconstructed region of the same original region. Breaking through the slim triangle and so to join the three areas into one is the appropriate merging.

The results of refinement reduction on our three examples are presented in Figure 5.15. In all examples we see, why the reconstruction is only a refinement and cannot guarantee the topological correctness. The narrowing between the eye and the fish boundary is a saddle on the distance transform. The refinement reconstruction algorithm was built to separate the local maxima, but not all critical points. The guarantee of homotopical stability in the sampling ensures that the simplices cutting the homotopical axis (dashed line) may be removed from the reconstruction without destroying the topological correspondence. In our example we observe an edge cutting the dashed line. The circumcenter of that edge is a saddle point on the discrete distance transform. Deleting the edge results in a loop in the reconstructed region which corresponds to the loop of the original homotopical axis.

In (b) we observe that even though the sampling achieved data points on the sharp tips of the corners the reconstruction cut them off. Let us consider the reconstructed region containing the tip in its boundary. The sharp corner is a tip of a triangle with nearly equal sides and a very small angle between them. The edge opposite the acute angle is the smallest. Since the method pursues smaller boundary simplices, the smallest edge of the triangle is preferred to separate regions. So, merging of reconstructed regions containing this triangle in the boundary results in deleting the greater edge and, so, in cutting off the sharp tip of the region. The goal of our reconstruction method is the simplest way and conditions for preservation of topological properties. The result with cut off sharp tips and the result with sharp corners in the boundary are topologically equivalent, so the reconstruction problem is solved in both cases.

The result in (c) demonstrates the stability of the algorithm on a highly noisy data set. In (d), as already presumed, some of the reconstructed regions are lost in the reconstruction. Since the ratio between the local maximum of the reconstructed region and its boundary simplices is too small, the regions are assumed to belong to the same original region and, so, are merged in the reconstruction process. The interior of the fish does contain a discrete local maximum with distance value which is much greater than the sampling rate on the boundary. The result is, the interior region is surrounded by small enough simplices and, so, the reconstructed region is recognized as a discrete region corresponding to a different original region.

In (d) we also illustrated the result of the reconstruction (thin line) on a data set before it was corrupted by high amounts of noise as in (c). The boundary is sampled such that the distances between the boundary and the sample points are less than 0.5lhfs. The sampling is done with $\psi \approx 0.6$ and $1 > \rho > 0.8$. Here we also demonstrate robustness of the algorithm due to the choice of the reconstruction parameter ψ . The sampling parameter ψ is expected to be passed to the reconstruction method. But it is



Fig. 5.15: (a) Space partition consisting of 4 regions and the background. Thick line is the boundary, \oplus denotes the local continuous maxima, \otimes denotes a saddle, the dashed line is the homotopical axis and the dotted line is the medial axis extension. (b,c,d) The results of refinement reduction with $\psi = 0.5$ (thick line). (d) The refinement reconstruction on data set (with $\psi < 0.6$, $\rho < 0.8$) which was not corrupted by noise with $\rho < 0.2$

not always exactly measurable. Here the original parameter was $\psi = 0.6$. In the reconstruction method the parameter was set to $\psi = 0.5$. In this case the underestimated parameter delivers a refinement with a reduced oversegmentation. The result is a correct separation of the local maxima. Why is that so?

The minimal density of the points depends on the maximal sample point deviation from the boundary. Consider the sampling of a circle. If the maximal sample point deviation is allowed to be up to 0.8r where r is the radius of the original circle then the points might be placed so unfortunately that inside the circle develops the greatest triangle with circumradius approximately 0.2r. Our reconstruction method requires then the local maximum to be surrounded by simplices less than ψ times 0.2r.

Such an unfortunate constellation does not occur in our case. The maximum inscribing ball corresponding to the greatest continuous local maximum of the interior region touches the boundary in three points only. The distance to the homotopical axis at these points is less than the distance value of the maximum. So, even with the sample point deviation of 0.2lhfs the points do not land too close to the local maximum. The greatest inscribing balls in the fins and the fishtail also touch the boundary in three points each. But the sample points do not reach the 0.2 closure of the maxima and so, the greatest sample point deviation is less than 0.2. Summing up, even if, the sampling simulation parameters are set to $\psi < 0.6$, $\rho < 0.8$ the resulting data set can be modelled with $\psi \approx 0.5$ and $\rho \approx 0.9$.

5.13 Comparison to Other Approaches

The methods used for surface reconstruction which are relevant for our context are based on Delaunay triangulation. So, the worst case complexity is $O(n^2)$. The results of the reconstructions are different and depend on the sampling conditions required to guarantee the outcome. We use the (ψ, ρ) -sampling parameters as a unique measure for all approaches for appropriate comparison of the sampling conditions.

The uniform sampling conditions can be represented by (p, q)-sampling parameters as it is done in Section 4.9. In the following we express the global (p, q)-sampling parameters by locally adaptive (ψ, ρ) sampling parameters and use the result to unify the results of thinned- (α, β) -shape-reconstruction with an extension of our refinement reconstruction. Equivalently we approach the locally adaptive sampling conditions for manifold surface reconstruction methods to compare the results and the requirements.

5.13.1 Uniform on (p,q)-Sampling Sets

The refinement reconstruction method is developed to handle locally adaptive sampling sets. The thinned- (α, β) -shape-reconstruction method is distinguished by its guarantee to result in a one-to-one mapping between the original and the reconstructed regions. Our algorithm lacks this ability. In this section we investigate the result of refinement reconstruction on uniformly parameterized (p, q)-sampling sets and discuss the extension of the algorithm if the parameters also required by thinned- (α, β) -shape-reconstruction method are known during the reconstruction process.

Lemma 5.20 ((p,q)-Sampling is Local Homotopy Stable). Let S be a (p,q)-sampling of a r-stable space partition with p < 0.5r and q < r - 2p, then S is a (ψ, ρ)-sampling with $\psi = \frac{p}{r-q}$ and $\rho = 1 - \frac{q}{r}$ such that $\rho > \frac{2p}{r}$ and $\psi\rho < 0.5$.

Proof: The (p, q)-sampling conditions for r-stable space partition \mathcal{R} are

$$\forall b \in \partial \mathcal{R} \, \exists s \in \mathsf{S} : \quad ||b - s|| \le p < 0.5r \\ \forall s \in \mathsf{S} \, \exists b \in \partial \mathcal{R} : \quad ||b - s|| \le q < r - 2p$$

Let $\psi \rho = \frac{p}{r}$ and $(1 - \rho) = q$, then $\rho = 1 - \frac{q}{r}$ which implies $\psi = \frac{p}{r-q}$. It follows that:

$$\forall b \in \partial \mathcal{R} \exists s \in \mathsf{S} : \quad ||b-s|| \le p = \psi \rho r < 0.5r \le 0.5 \mathsf{lhfs}(b) \\ \forall s \in \mathsf{S} \exists b \in \partial \mathcal{R} : \quad ||b-s|| \le q = (1-\rho)r < r-2p = (1-\frac{2p}{r})r \le (1-\frac{2p}{r})\mathsf{lhfs}(b)$$

According to Lemma 5.20 the sampling conditions required for correct thinned- (α, β) -shape-reconstruction are local homotopy stable which implies that the result of refinement reconstruction algorithm on a (p,q)-sampling is a minimal reducible refinement. In the following we call the data set which fulfills the sampling conditions for correct thinned- (α, β) -shape-reconstruction (consult Section 4.3) the (p,q)-sampling.

Corollary 5.21 (Refinement Reconstruction on a (p, q)-Sampling is a Minimal Reducible Refinement). Let S be a (p, q)-sampling of an r-stable space partition \mathcal{R} with p < 0.5r and q < r - 2p. Then the result of refinement reconstruction on S is a minimal reducible refinement of \mathcal{R} .

Proof: The proof follows from Lemma 5.20 and Theorem 5.19.

Let us consider the result of refinement reconstruction on a (p, q)-sampling of an *r*-stable space partition. As discussed previously the algorithm is developed for locally adaptive sampling methods and, so, chooses a boundary simplex for deletion and resulting merge of reconstructed regions by ratio between the size of the region and the size of the boundary simplex. The size of a reconstructed region is the circumradius of its greatest simplex. A boundary simplex is deleted by refinement reduction if its size is greater than ψ times the size of the adjacent region. Obviously, since the refinement reduction is a

locally adaptive method, the region's size may be much greater than r. Consequently, the ψ -fraction of that region's size may be greater than α -parameter of the thinned- (α, β) -shape-reconstruction method. We conclude that our algorithm in its original form does not recognize all undersampled simplices in the boundary and so leaves some reconstructed regions unmerged.

Furthermore, consider boundary simplices corresponding to saddles - as the edge in the reconstruction of our 2D example in Figure 5.15, between the eye and the boundary of the interior of the fish. An equivalent example is in the boundary of a 3D donut reconstruction in Figure 5.9 (c). The illustration demonstrates the boundary after the boundary inside the donut was reduced by breaking through the set of simplices inside the donut building a "membrane" in the tightest narrowing of the donut. The result is, the interior of the donut became a loop. Such a membrane in the donut or the edge in the fish is the consequence of reconstruction built on a ratio between the region size and the size of boundary simplices. The too great regions may be separated even by too great boundary simplices.

In the case of a uniform sampling, such a disadvantageous choice of a boundary simplex can be recognized since all boundary simplices do not exceed a global parameter α .

According to Theorem 4.6 (α, β) -shape reconstruction is a correct one-to-one mapping between the original regions and (α, β) -holes. The thinned- (α, β) -shape-reconstruction uses the fact that the distance values in *p*-dilation of the boundary are less than the value α but the values outside the *p*-dilation are greater than α . It follows that the holes in the α -shape which correspond to the original regions are surrounded by distance values less than α . Using this fact and according to the duality between Voronoi and Delaunay the simplices separating the holes have lesser size than α .

 α -exposed simplices have greater circumradius than α and empty circumballs. Deletion of α -exposed simplices results in holes in the α -shape. Since all holes in the α -shape are surrounded by simplices which are not α -exposed the α -holes correspond to local maxima and so to reconstructed regions in our context. Notice, α -holes may contain several discrete local maxima. The corresponding elementary regions in our context are separated by α -exposed simplices.

Lemma 5.22 (α -shape is a stable refinement). Let \mathcal{R} be r-stable and S be a (p,q)-sampling of the boundary of \mathcal{R} with $p < \frac{1}{2}r$ and q < r - 2p. Then the α -shape \mathscr{S}_{α} with $p < \alpha < r - q$ is a stable refinement of \mathcal{R} .

Proof:

Refinement Let \mathscr{U} be the union of α -balls centered on points in S. Since $\alpha > p$ and $\forall b \in \partial \mathcal{R} \exists s \in S : ||b-s|| , <math>\mathscr{U}$ covers $\partial \mathcal{R}$. Consequently, the continuous local maxima are correctly separated by \mathscr{U} . By definition of a (p,q)-sampling for each point b on a boundary: $d_S(b) < p$, consequently no increasing path starting on a continuous local maximum intersects $\partial \mathcal{R}$, and since the discrete distance values on the associates is greater than or equal to the discrete distance values on the continuous local maxima and their associates are in the same components of \mathscr{U}^c and according to Theorem 2.50 in the same α -holes. So \mathscr{S}_{α} is a refinement

Stability By definition of r-stability r is the distance between the boundary of \mathcal{R} and the set of criticals on the distance transform. So, r is the smallest distance between boundary and criticals and so the smallest distance to the homotopical axis HA. Since $\alpha + q < r$ no α -ball centered on any point in S intersects HA. So, the union of balls does not touch or intersect HA. According to Theorem 2.50 the \mathscr{S}_{α} is homotopy equivalent to the union of α -balls centered on points in S. It follows, that \mathscr{S}_{α} does not touch or intersect HA

According to Lemma 5.22 the α -shape is a stable refinement. So, there is a reconstruction without α -exposed simplices which correctly separates local maxima and does not cut the homotopical axis. We want to use the α -parameter to achieve an equivalent result. Obviously, the simplices with size greater than or equal to α are α -exposed., and since the distance values in the *p*-boundary are smaller than α the minimal boundary simplices are smaller than α . It follows that the simplices with size greater than α correctly separate reconstructed regions.

Lemma 5.23 (Reducible Refinement without Simplices greater than α is Stable). Let \mathcal{R} be an r-stable space partition and S be an (p,q)-sampling of its boundary with $p < \frac{1}{2}r$ and q < r - 2p. Let D_R be the

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result of refinement reconstruction on S. Let D_{α}^{c} be the subset of D_{R} consisting of simplices less than α . Then $D_{R} \setminus D_{\alpha}^{c}$ is a stable refinement.

Proof:

Refinement The boundary simplices of D_R are minimal. It follows that for every boundary simplex there are increasing paths on the discrete distance transform starting in the points with greatest distance value on the simplex and ending in the local maxima of the adjacent reconstructed regions. So, if a boundary simplex is greater than α then there are paths starting on that simplex with distance values on all points of the paths greater than α . This implies that the paths do not intersect the *p*-dilation of the boundary and the adjacent reconstructed regions correspond to one original.

Stability According to Corollary 5.21 D_R is reducible. Due to Lemma 5.22 not α -exposed simplices do not cut HA. It follows that $D_R \setminus D_{\alpha}^c$ does not cut HA.

Using the result of Lemma 5.23, we can achieve a stable reconstruction which is already an advantage compared to the guaranteed results on locally adaptive (ψ, ρ) -samplings. However the reconstruction does not cut the homotopical axis, it still contains to many regions which do not correspond to original ones. In the discussion on thinned- (α, β) -shape-reconstruction method the complement of an α -shape is divided into components which are either big enough to correspond to original regions or small enough to correspond to topological artefacts in the q-dilation of the boundary. The measure taken into account for this separation is the β -parameter. An α -hole corresponds to an original region if and only if the α -hole is greater than β . Compare Theorem 4.6. The deletion of not (α, β) -holes ensures the one-to-one mapping between the reconstructed and original regions.

Lemma 5.24 (Deletion of not- (α, β) -Holes results in Stable Refinement). Let \mathcal{R} be an r-stable space partition and S be a (p,q)-sampling of its boundary with $p < \frac{1}{2}r$ and q < r - 2p. Let $p < \alpha \leq r - q$ and $\beta = \alpha + p + q$. Let each region of \mathcal{R} contain a γ -ball with $\gamma \geq \beta + q$. Let D_R be a minimal stable refinement of \mathcal{R} and $\partial \mathsf{D}_R$ be its boundary without simplices greater than or equal to α . Let $\partial \mathsf{D}_{\alpha,\beta}$ be the subset of $\partial \mathsf{D}$ which partitions the space into a set $\mathsf{D}_{\alpha,\beta}$ of reconstructed regions greater than β . Then $\mathsf{D}_{\alpha,\beta}$ is a stable refinement.

Proof:

Refinement Since all original regions contain a γ -ball and each erosion of an original region is contained in a single α -hole, for each continuous local maximum there has to be a path with discrete distance value greater than r-q ending in a local discrete maximum with discrete distance value greater than or equal to $\gamma - q \geq \beta$.

Consider a reconstructed region whose greatest local discrete maximum has the distance value less than β . The reconstructed region is separated by boundary simplices less than α . So, there are no paths inside the reconstructed region with discrete distance values greater than r - q which end in a discrete local maximum greater than β . It follows that there is not a continuous local maximum associated with the reconstructed region and any merge of it results in a refinement.

Stability The stability of D_R is preserved since no simplices have been added to the boundary which cut the homotopical axis.

The (α, β) , p, q and γ parameters are assumed to be known during the (α, β) -reconstructed. So, the requirement for Lemma 5.24 is justified as an appropriate extension of refinement reconstruction.

Now, knowing the parameters, the result of refinement reconstruction can be reduced even further to a stable reconstruction containing only such reconstructed regions which are big enough to correspond to original ones. Since all sampling points are in the q-dilation of the boundary, we infer that there is no reconstructed region which does not correspond to an original. It follows that all reconstructed regions necessarily contain a connected component of the original homotopical axis and the reconstructed regions. The stable refinement but is also a one-to-one mapping between the original and reconstructed regions.

Theorem 5.25 (Stable Refinement is a One-To-One Mapping). Let \mathcal{R} be an r-stable space partition and S be a (p,q)-sampling of its boundary with $p < \frac{1}{2}r$ and q < r-2p. Let $p < \alpha \leq r-q$ and $\beta = \alpha + p + q$.

Let each region of \mathcal{R} contain a γ -ball with $\gamma \geq \beta + q$. Let D_R be a minimal stable refinement of \mathcal{R} and $\partial \mathsf{D}_R$ be its boundary without simplices greater than or equal to α and no reconstructed region is less than β . Then there is a one-to-one mapping between the reconstructed regions of D_R and original regions of \mathcal{R} .

Proof: The proof follows from Lemma 5.23 and Lemma 5.24 and since all sampling points are in the q-dilation of the boundary of \mathcal{R} .

As a result of Theorem 5.25, it follows that knowing the parameters of thinned- (α, β) -shape-reconstruction we can extend the refinement reconstruction such that the result is equivalent to the result of thinned- (α, β) -shape-reconstruction. The extension requires only a further check of the size of the boundary simplices and a further check of the size of regions and can be done in linear time.

5.13.2 Methods using Locally Adaptive Sampling Conditions

The well-known surface reconstruction algorithms such as "crust" [Amenta et al., 1998], "power crust" [Amenta et al., 2000b, Amenta et al., 2001] or "co-cone" [Amenta et al., 2000a] result in a guaranteed outcome if the underlying point set is a locally adaptive ϵ -sampling. Compare Definition 3.4. There are numerous derivatives of the methods weakening the requirements or extending the results which are based on ϵ -sampling conditions or some diversion of it.

Finding Common Notation To compare the results on ϵ -sampling we first show that the ϵ -sampling conditions are local homotopy stable. The consequence is, the guaranteed results of refinement reconstruction are also valid on ϵ -sampling.

Corollary 5.26 (ϵ -Sampling is a Local Homotopy Stable (ψ, ρ)-Sampling). Let S be an ϵ -Sampling then S is a (ψ, ρ)-Sampling with $\rho < 1, \psi > \frac{\epsilon}{\rho}$, so S is (ψ, ρ)-locally stable.

Proof: Since $\forall b \in \partial \mathcal{R}$: $\mathsf{lfs}(b) \leq \mathsf{lhfs}(b)$ and $\forall b \in \partial \mathcal{R} \exists s \in \mathsf{S} : \mathsf{d}_{\mathsf{S}}(b) ||b - s|| \leq \epsilon \mathsf{lfs}(b)$, it follows that $\forall b \in \partial \mathcal{R} : \mathsf{d}_{\mathsf{S}}(b) \leq ||b - s|| \leq \epsilon \mathsf{lfs}(b) \leq \frac{\epsilon}{\rho} \rho \mathsf{lhfs}(b) < \psi \rho \mathsf{lhfs}(b)$. Since all sample points are in $\partial \mathcal{R}$, $\forall s \in \mathsf{S} \exists b \in \partial \mathcal{R} : \mathsf{d}_{\mathcal{R}}(s) = 0 < (1 - \rho) \mathsf{lhfs}(b)$.

The "Modified Power Crust" method results in a correct reconstruction on noisy sampling points. The definition of ϵ -sampling conditions is extended to handle sample point deviations from the boundary by an ϵ -fraction of the local feature size.

Corollary 5.27 (Noisy ϵ -Sampling by [Mederos et al., 2005] in "Modified Power Crust" is (ψ, ρ) -Locally Stable). Let S be a noisy ϵ -sampling as defined in Definition 3.3, then S is (ψ, ρ) -locally stable for all $\rho < (1 - k\epsilon)$ and $\psi > \frac{(1+k+k\epsilon)\epsilon}{\alpha}$.

Proof: Let S' be the *projection* (see Definition 3.2) of S onto $\partial \mathcal{R}$ and let S' be an ϵ -sampling of $\partial \mathcal{R}$ such that $\forall s \in S \exists s' \in S' : ||s - s'|| \le k \epsilon \mathsf{lfs}(s')$. Since $\mathsf{S'} \subset \partial \mathcal{R}$, $\forall s \in S \exists b \in \partial \mathcal{R} : ||s - b|| \le k \epsilon \mathsf{lfs}(b)$. $\rho < (1 - k\epsilon)$ implies $k\epsilon < (1 - \rho)$. It follows $\forall s \in S \exists b \in \partial \mathcal{R} : ||s - b|| \le k \epsilon \mathsf{lfs}(b) < (1 - \rho) \mathsf{lfs}(b) \le (1 - \rho) \mathsf{lfs}(b)$.

Since S' is an ϵ -sampling of $\partial \mathcal{R}$: $\forall b \in \partial \mathcal{R} \exists s' \in S' : ||b - s'|| \leq \epsilon \mathsf{lfs}(b)$. s' is a projection of a sample point $s \in \mathsf{S}$ onto $\partial \mathcal{R}$, then $||s - s'|| \leq k \epsilon \mathsf{lfs}(s')$. It follows that $\forall b \in \partial \mathcal{R} \exists s \in \mathsf{S} : ||b - s|| \leq \epsilon \mathsf{lfs}(b) + k \epsilon \mathsf{lfs}(s')$, where s' denotes the projection of s onto $\partial \mathcal{R}$.

Since lfs is 1-Lipschitz, $\forall b, s' \in \partial \mathcal{R} : ||\mathsf{fs}(b) - |\mathsf{fs}(s')| \le ||b - s'|| \le \epsilon \mathsf{lfs}(b)$. It follows $\forall b, s' \in \partial \mathcal{R} : \mathsf{lfs}(s') \le (1 + \epsilon)\mathsf{lfs}(b)$ and $\forall b \in \partial \mathcal{R} \exists s \in \mathsf{S} : ||b - s|| \le \epsilon \mathsf{lfs}(b) + k\epsilon(1 + \epsilon)\mathsf{lfs}(b) = (1 + k + k\epsilon)\epsilon \mathsf{lfs}(b)$.

 $\forall \rho < (1 - k\epsilon), \psi > \frac{(1 + k + k\epsilon)\epsilon}{\rho} : (1 + k + k\epsilon)\epsilon < \psi\rho.$ It follows: $\forall \rho < (1 - k\epsilon), \psi > \frac{(1 + k + k\epsilon)\epsilon}{\rho} : (1 + k + k\epsilon)\epsilon < \psi\rho.$ It follows: $\forall \rho < (1 - k\epsilon), \psi > \frac{(1 + k + k\epsilon)\epsilon}{\rho} : (1 + k + k\epsilon)\epsilon < \psi\rho.$

Let's consider an example for Corollary 5.27. The bound for k is for example given by condition $\psi < 1$ (in case of $\psi \ge 1$ undersampled merge see Definition 5.11 is trivial) and consequently $\frac{(1+k+k\epsilon)\epsilon}{1-k\epsilon} < 1$. The resulting bound for given ϵ is then $k < \frac{1-\epsilon}{\epsilon^2+2\epsilon}$. So, let $\epsilon = 0.1$ and k = 2 < 4.2857, then $\rho < (1-k\epsilon) \Rightarrow$ $\rho \leq 0.8$ and $\psi > \frac{(1+k+k\epsilon)\epsilon}{\rho} \Rightarrow \psi > \frac{0.32}{\rho}$. So, a not very noisy sampling is i.e ($\psi = 0.46, \rho = 0.7$)-locally stable.

The condition on ψ requires ρ to be greater than $(1 + k + k\epsilon)\epsilon$, so, for $\epsilon = 0.1$ and k = 2 the following is valid: $0.32 \leq \rho \leq 0.8$. Consequently, the most tolerable amount of noise is $\rho = 0.32$ and the most noisy sample is (1, 0.32)-locally stable.

The results in [Dey and Goswami, 2004] limit the noisy ϵ -sampling conditions. So, it follows from Definition 3.3 that the noisy ϵ , k-sampling conditions are also local homotopy stable.

Corollary 5.28 (Noisy ϵ , k-Sampling by [Dey and Goswami, 2004] in "Robust Co-Cone" is (ψ, ρ) -Locally Stable). Let S be a noisy ϵ , k-sampling as defined in Definition 3.5, then S is (ψ, ρ) -locally stable for all $\rho < (1 - k\epsilon)$ and $\psi > \frac{(1+k+k\epsilon)\epsilon}{\rho}$.

Proof: Since the first two conditions in Definition 3.5 correspond to the conditions in Definition 3.3 and the third condition is only limiting, the proof follows from Corollary 5.27.

Notice, that the original definition of noisy ϵ , k-sampling in [Dey and Goswami, 2004] uses instead of our k the notation κ . In our context we exchanged the notations to avoid ambiguity with the definition in [Chazal and Lieutier, 2008].

Corollary 5.29 (Noisy ϵ, κ -Sampling by [Chazal and Lieutier, 2008] in "Noisy, Non-Uniform Approximation" is (ψ, ρ) -Locally Stable). Let S be a noisy ϵ, κ -sampling as defined in Definition 3.6, then S is (ψ, ρ) -locally stable for all $\rho < (1 - \kappa \epsilon)$ and $\psi > \frac{(1 + \kappa + \kappa \epsilon)\epsilon}{\rho}$.

Proof: Since $\kappa > 0$ and $\forall b \in \partial \mathcal{R} \exists s \in S : ||b - s|| < \epsilon |\mathsf{lfs}(b) < (1 + \kappa + \kappa \epsilon) \epsilon |\mathsf{lfs}(b), S$ is noisy ϵ, k -sampling with $k = \kappa$ as defined in Definition 3.5 and the proof follows from Corollary 5.27

Listing the Results The result of previous considerations brings the sampling conditions to a common notation of a local homotopy-stable (ψ, ρ) -sampling which in our context guarantees the reducible refinement reconstruction. Obviously, further limitations on the sampling conditions or the assumed shapes allow the underlying algorithms to guarantee further topological results.

We collected some of the well known methods in Table 5.1. Notice, that the sampling conditions required for topological guarantees are based on ϵ -sampling. The methods in question are the first five which guarantee a topologically correct reconstruction of an originally smooth manifold surface. The numbers in the columns " ψ " and " $1 - \rho$ " show the upper bounds. The approaches limit the sampling density or the maximal sampling point deviation by further parameters which have to be known during the reconstruction process. In [Mederos et al., 2005] the authors introduced further parameters which limits the maximal curvature. Nevertheless the upper bounds of the ϵ -sampling are also valid for the method, which justifies our simplification.

The framework in [Chazal and Lieutier, 2008] is only theoretical. The interior and the exterior boundaries of the union of balls are proven to be topologically equivalent to the original smooth manifold surface. The proof of homotopical equivalence of the union of balls and its dual shape is successfully used to prove the results of (α, β) -shape reconstruction. Even though the results in [Chazal and Lieutier, 2008] are not used in our framework, they present a significant intermediate step towards the topologically equivalent reconstruction.

Obviously, the sampling density in our framework depends on the maximal sampling point deviation. The upper bounds of our sampling conditions serve only for demonstration. For specific values consult Section 5.10.

Result of the Comparison We defined the sampling conditions in such a way that limitations weaken with the increasing values. The approaches which guarantee the topologically equivalent outcome require the highest sampling density. The results on noise-corrupted point sets limit the maximal curvature and require the appropriate parameter settings.

method	ψho	1- ho	comments			
topologically equivale	ent sm	ooth ma	nifold reconstruction			
"crust"	0.06	0	parameter free			
[Amenta et al., 1998]						
"power crust"	0.1	0	parameter free			
[Amenta et al., 2000b, Amenta et al., 2001]						
"co-cone"	0.06	0	parameter free			
[Amenta et al., 2000a]						
"Modified Power Crust"	0.1	0.1	parameter: smallest lfs			
[Mederos et al., 2005]						
"Robust Co-Cone"	0.1	0.1	not parameter free			
[Dey and Goswami, 2004]						
topologically equivalent						
"Noisy, Non-Uniform Approximation"	0.1	0.1	wfs, not parameter free			
[Chazal and Lieutier, 2008]			no reconstruction method			
			proof for union of balls only			
limited topological guarantees						
"Refinement Reconstruction"	< 1	< 1	refinement reconstruction,			
[Stelldinger and Tcherniavski, 2009b]			topologically correct on (p, q) -sampling sets			
[Tcherniavski et al., 2012]			the greater noise, the denser sampling			

 Table 5.1: Comparison of different surface reconstruction algorithms based on locally adaptive sampling conditions

Our method also requires the ψ -parameter to be set. However for higher sampling densities or lower amounts of noise the parameter may arbitrarily be set to a guaranteed overestimated value and so ensure the guaranteed outcome. The usual value in our practical experiments is $\psi = 0.5$. The setting limits the sampling density but is still a great advantage over the results in related work.

5.14 Experiments

The experimental evaluation of the refinement reconstruction algorithm is performed in three steps. First we present the results on well-known data sets coming from a dense 3D scanner. Second we evaluate the algorithm on volumetric data sets which are products of X-ray computed tomography imaging with post-processing 3D Canny edge detection to produce point sets. The experiments on sparse locally adaptive sampling sets require a new theoretical framework and are presented in Chapter 6.

5.14.1 Real Data Sets from Laser Range Scanner

Following the experiments in Section 4.10 we present here the results of refinement reconstruction on two well known data sets: "Armadillo" and "Dragon" taken from "The Stanford 3D Scanning Repository"¹.

The presented illustrations in Figure 5.16 demonstrate the power of the method on dense data sets taken from smooth manifold shapes. The reconstructions in the two top illustrations are the expected results. Notice in (b) the opening between the tail of the dragon and its body is closed. This is the oversegmentation effect of a refinement. The triangles in this *membrane* are small enough for the adjacent regions. Both adjacent regions are the same infinite background space. To break through the membrane the reconstruction method would need additional information of the original shape.

¹Stanford University Computer Graphics Laboratory in http://graphics.stanford.edu/data/3Dscanrep/

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The results in (c) and (d) demonstrate the advantage of refinement reconstruction over related methods. The data sets are here corrupted by outliers: the *salt-and-pepper noise*. More than 10% of points in the armadillo data set are outliers. In the dragon data set more than 20% are salt-and-pepper noise. The number of points and times are collected in Table 5.2. Time in sec. is the elapsed time including loading of points, reconstruction and saving the mesh into a text-file. Notice, no α -shape-based method is able to obtain a comparative result as is demonstrated in (c) and (d).

data set	points	noise	time (s)	comments
Armadillo	172974	0	30.43	smooth manifold reconstruction
Armadillo	192974	> 10%	31.91	more than 10% outliers
Armadillo	34006	0.361r	6.81	globally set density and sample point deviation
Dragon	437645	0	118.58	smooth manifold reconstruction
Dragon	528575	> 20%	119.77	more than 20% outliers
Dragon	28395	0.12r	3.86	globally set density and sample point deviation

 Table 5.2: Comparison of reconstruction parameters on "Armadillo" and "Dragon" data sets. (See Figure 5.16 for illustration) First is a very dense noise-free sampling. Second is salt-and-pepper noise-corrupted sampling. Third is a sampling with globally set minimal density and maximal sampling point deviation.

The last experiment in (e) and (f) serve as comparison to the result of thinned- (α, β) -shape-reconstruction. The data sets are sparse and the sampling points deviate from the boundary. The density and the maximal sample point deviation are uniformly set for the whole shape according to the *r*-stability value.

5.14.2 Volume-Based Sampling Sets

Volume-based methods enable insight into the object. The data acquisition device samples the scene at any point. The result is a sampled 3D interval, for example, with a regular grid. The typical examples are X-ray computed tomography (CT) and magnetic resonance imaging (MRI). The interior of the object can be subdivided into two or more regions which can have common boundaries.

We present our results on two similar data sets. Two different walnuts are scanned by computed topography resulting in a sequence of 2D gray color images. Using the 3D Canny edge detection algorithm² (compare [Bähnisch et al., 2009]), point sets are extracted which contain volumetric information on outer surface as well as boundaries between interior regions.

data set	points	ψ	ρ	time (s)	comments
Sparse Walnut	156198	0.5	0.5	39.26	arbitrary set (ψ, ρ) -parameters
Dense Walnut	2362275	0.5	0.5	824.86	arbitrary set (ψ, ρ) -parameters

 Table 5.3: Comparison of reconstructions of two similar shapes. (top) Sparsely and nearly noise-free sampling of a walnut. (bottom) Dense and noise-corrupted sampling.

In Figure 5.17 (a) and (e) we illustrate the data sets. The first line demonstrates results of refinement reconstruction on a sparse nearly noise-free data set illustrated in (a). The example in (e) is a very dense strongly noise-corrupted data set. The second image in the set demonstrates the outer shell of the walnut. The third image is the combination of the underlying point set and the extracted kernel. The extracted kernel, which is one of the interior regions of the walnut, is presented in the image on the extreme right of the sequence. In Table 5.3 we give the running time parameters. Notice that we assumed the (ψ, ρ) parameters to be unknown for both reconstructions. The default setting is $\psi = \rho = 0.5$.

The reconstruction on walnut data sets results in 8 regions on sparsely sampled walnut and 21 regions on dense data set. The reconstructed regions are the thin outer shell (the boundary between the walnut and the infinite background), the kernel, the thick outer shell (the walnut shell has certain spatial

²Implementation in the scope of Deutsche Forschungsgemeinschaft (DFG) project STI 147/2-1



(b)





Fig. 5.16: Noise-free, "salt-and-pepper-corrupted" and noise-corrupted reconstruction. Left: Armadillo. Right: Dragon. Compare the reconstruction parameters in Table 5.2

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Fig. 5.17: Refinement Reconstruction of two different walnut shapes. (top) sparse nearly noise-free data set. (bottom) dense noise-corrupted data set. (a) (e) sampling points. (b) (f) reconstruction of the outer shell. (c) (g) combination of points and kernel. (d) (h) kernel reconstruction

expansion), the seed coat (interior layer which envelopes the kernel preventing rancidity), and the region corresponding to the hollow of the walnut. The specified regions are subdivided. The kernel consists of two regions in the sparse data set and of three regions in dense data set. The seed coat consists of the most regions and is not reconstructed properly since the sampling is insufficient. In Figure 5.17 we extracted the most relevant to us and most illustrative boundary reconstructions.

The dense sampling of a walnut in the bottom illustration in Figure 5.17 is very noisy. The data set consists of a great amount of outliers as well as of sampling point displacements. The reconstruction performs excellently on outliers (see the kernel extraction and the outer shell) but the systematic sample point displacements result in inaccurate constructions.

Observe the kernel boundary illustration in Figure 5.18. The left image shows salient spurious features. The displaced points correspond to the sampling of the seed coat. The density of displaced points is higher than the density of sample points near the boundary. The corresponding but even more illustrative spurious feature is demonstrated in the right image. The kernel is merged with a part of the seed coat. The narrowing between the kernel and the seed coat itself is insufficiently sampled. The sample points of the seed coat are dense enough to build a boundary. However the size of boundary triangles is related to the size of the kernel which results in satisfactory ratio. The narrowing is tighter than the sampling density of the boundary. Since the reconstruction is minimal we obtain an equivalent result for different (ψ, ρ) settings.

In Figure 5.19 we demonstrate the refinement reconstruction result on volume-based sampling of an orange. The reconstruction consists of 17 regions: 10 slices (two of them are merged couples as can be seen in the right image), two seeds and the rind. The rind is not sufficiently sampled and consequently is subdivided into several regions. The transparent outer boundary of the orange and the reconstructed slices - one of the slices is selected - are illustrated in the right image.

data set	\mathbf{points}	ψ	ρ	time (s)	comments
Orange	260215	0.5	0.5	84.35	arbitrary set (ψ, ρ) -parameters

Table 5.4: Reconstruction settings on orange data set.

The presented experiments enable us to compare the results of the refinement reconstruction to the thinned- (α, β) -shape-reconstruction as well as to present advantages over related methods. The great



Fig. 5.18: Effects of insufficient sampling on dense walnut data set. Parts of the seed coat region is merged to the kernel.



Fig. 5.19: Reconstruction on "orange" data set. (a) point set (b) surface of the orange slices. (c) transparent boundary between the rind and slices.

amount of the salt-and-pepper noise is not processable by thinned- (α, β) -shape-reconstruction, and no surface-based method results in the reconstruction of the interior regions of the object.

However the samplings used for experiments are uniform, i.e. the density does not vary on the boundary. The locally adaptive samplings, known to us from related works, are very dense ϵ -samplings of smooth surfaces with $\epsilon < 0.1$. To demonstrate the advantage of refinement reconstruction over related results we need to ensure the data set to be sufficiently sparse. In Chapter 6 we introduce new criteria for data set decimation, according to which the resulting data set preserves topological properties and is local homotopy stable.

5.15 Discussion and Future Work

In this section we discuss open problems in solving the reconstruction problem and briefly outline possible ideas how this can be tackled in future work.

In Section 5.15.1 we discuss the insufficiency of the sampling conditions defined for our framework. The one data set is a valid local homotopy sampling for two shapes with completely different topology. The consequence is, the refinement cannot be reduced to stable refinement without further knowledge of a shape. This information is not contained in the data set. We propose a combination of homotopical axis extension introduced in Section 5.15.2 and a global limitation of noise introduced in Section 5.15.3 to overcome the problem.

5.15. DISCUSSION AND FUTURE WORK

In Section 5.15.4 we discuss the definition of the refinement property. We show that a donut shape can be regarded as a stable refinement of a ball while the surface of a donut cannot be reduced to the surface of a ball. So, we imply that the refinement property can be insufficient for homotopy type preserving surface reconstruction. However in Section 5.15.4 we argue that there is no consequence for our method since the outcome is always reducible.

5.15.1 Insufficiency of the Sampling

To solve the reconstruction problem as defined in our framework we define sampling criteria and an algorithm, which reconstructs a topologically equivalent space partition.

In Section 5.11 we have shown that our new sampling criterion based on the homotopical feature size enables us to use the refinement reduction algorithm to get a reconstruction which is *reducible* to a space partition which correctly separates the connected components of the original homotopical axis. However in general, the result is still the problem of oversegmentation.

So, the question arises whether it is possible to use the local homotopy stable sampling criterion in order to reconstruct the true topology of the shape by adequately changing the reconstruction algorithm. Unfortunately, it is easy to show that relevant topological information can be lost in the sampling.

In Figure 5.20, two shapes with different topology are given, together with a set of sampling points that is local homotopy stable for both. So, both shapes are not distinguishable from this sampling. We call the inability to distinguish between the shapes by the local homotopical axis the *dissolution problem*:



Fig. 5.20: A manifold shape (a) and a non-manifold shape (c). Shape (c) differs from (a) only by a contour segment which bridges the narrow part of the contour in the middle of the shape. In (a) the homotopical axis is the thin line connecting its criticals. The distance values b of the maxima (\oplus) in (a) are denoted by circles with the radius b. The distance value a of the saddle \otimes in (a) is denoted by the smaller circle with the radius a. In (c) the homotopical axis is only the union of the two maxima (\oplus) . For both shapes the set of sampling points (b) is local homotopy stable.

Definition 5.30 (Dissolution Problem). Let \mathcal{R} and \mathcal{R}' be two space partitions with different topological properties. If there is a sampling set S which is (ψ, ρ) local homotopy stable for both \mathcal{R} and \mathcal{R}' then we call the problem of differentiating the shapes by the point set S as dissolution problem.

One may argue, that this problem can be fixed by increasing the sampling density, i.e. by using $\gamma \cdot \text{lhfs}$ for locally stable sampling with $\gamma > 0$ being a sufficiently small factor. However, it is also easy to show that for any such γ it is always possible to find two shapes and a corresponding set of points which is again a local homotopy stable sampling for both. For any given $\gamma > 0$ choose either a > 0 sufficiently small or b > 0 sufficiently great for the two shapes given in Figure 5.20. Then, a sufficiently dense set of sampling points lying on the boundary of the shape (a) is again a locally stable sampling for both shapes.

Notice, in Figure 5.20 sampling points lie on the boundary of the shapes. Which implies that this problem occurs even in the absence of noise. We conclude that the restriction of the maximal sample points deviation to a global parameter or even 0 does not necessarily solve the dissolution problem.

Corollary 5.31 (No Solution with Noise-Free Sampling). The dissolution problem cannot be solved by restricting the maximal sample points deviation to a > 0.

Further note that the two shapes can be distinguished by using data sets based on global parameter settings such as is the case in samplings based on the weak feature size or r-value in r-stable sets. The shape in (a) has smaller r-value than in (c). So, using the r-value for (p, q)-sampling to digitize the shape (a), the sampling with equal parameters would place sample points onto the line segment which makes the shape different from (c). On the other hand the r-value in case (c) is too great to be used for sampling the shape in (a).

It appears as if the homotopical axis does not deliver enough information to handle the problem in cases of non-manifold shapes.



Fig. 5.21: (a): shape with its critical which also forms the homotopical axis. (b): placing a small circle in the dilation of (a) already forms a shape which cannot be distinguished from (a) if the shown set of sampling points is given.

However, we can show that in general a topologically correct reconstruction is not possible even if only manifold shapes are allowed. Figure 5.21 gives an illustrative counterexample. Left shape is a circle. The right shape is two circles. The sampling is noisy. Local homotopy stable sampling conditions restrict the sample points to be enveloped by the dilation denoted by thick gray line in both illustrations (a) and (b) in Figure 5.21. Notice that the dilation in (a) encloses the group of points corresponding in (b) to the smaller circle. In (a) the group of points is noise. But in both cases the sampling points lie in the $\psi \rho lhfs$ -dilation with $\psi = 0.5$ and $\rho < 0.9$.

The sampling points are taken by an even more restricted global condition based on the stability r-value of the right shape. The sampling is then still local homotopy stable for both shapes and with the same (ψ, ρ) -parameters. The two shapes are still not distinguishable if the r-value is not given.

The 3D extension of the dissolution problem can be seen on a sampling of a ball and topologically a donut geometrically similar to the ball: one side is greatly swollen. In Figure 5.22 (a) we illustrate this example. The outer dark gray ball partly contains the ball with a handle. The handle is hollow. We call the ball with the handle shape the *donutball*.

The dark gray ball and the donutball are the two shapes with the same local homotopy stable sampling. The refinement reconstruction of this sampling is the boundary of the donutball in Figure 5.22 (a). Notice, for simplicity the original donutball shape is not illustrated.

This example is the 3D extension of the example in Figure 5.21. The sampling points corresponding to the tighter side of the donut (in our example a "handle") are effects of the noisy local homotopy stable sampling of the ball shape.

In Figure 5.22 (b) we zoomed the handle to illustrate the result of refinement reconstruction. For better illustration we cut the reconstructed boundary in the direction of handle's expansion and then zoomed it.

Let us consider the infinite space to have one infinite point only such that all paths extending into infinity end in this point. Then the homotopical axis of the interior and the exterior of the donutball are two chain links. Each is topologically equivalent to a circle. So, the donutball is topologically a donut. In other words, we can push a finger through the handle as we know it from the cut and we can push a finger through the interior of the handle as we know it from a tunnel. To avoid disambiguation let

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Fig. 5.22: Donutball reconstruction. (a) The greater transparent ball is the original shape of a ball. The inner ball with a handle is the reconstructed boundary of both: noisy sampled ball and donutball. (b) The zoomed cutout of the handle in donutball shape. The dashed edged membranes ensure the interior of the shape to be homotopically equivalent to a ball. The boundary is not reducible to a topological equivalent of a ball.

us call the inside of the handle reachable from the interior of the ball the handle *tunnel* (dashed edged ellipse in Figure 5.22 (b)) and the inside of the handle reachable from the infinite space the handle *bridge* (dashed edges half-ellipse in Figure 5.22).

Since the donutball interior as well as the infinite point have considerably greater distance values than the distance values inside the handle, the discrete distance transform has two saddles in the handle: in the tunnel and in the bridge. The elementary thinning step leaves the tunnel and the bridge closed by a group of Delaunay simplices forming a *membrane*. Since the membranes are in the dilation of the ball the corresponding simplices are not undersampled. It follows that the refinement reconstruction necessarily results in a boundary which cuts the original homotopy axis. But as we know from Theorem 5.19 the reconstruction can be reduced to a stable refinement.

The boundary reconstruction as it is shown in Figure 5.22 (b) is a reducible refinement for both initial shapes with different topology. Since the given sampling did not contain the crucial information to differentiate between the two shapes, obviously, the information is lost for the reconstruction.

5.15.2 Extended Homotopical Axis

As we have seen in Figure 5.21 the sampling loses crucial topological information. In Figure 5.23 we reintroduce the 2D-illustration of the barbell example. Simply speaking the shape consists of two connected circles. In our example the connection is a small linear edge between the two circles. The ends of this edge are non-manifold.

In Figure 5.23 we also show the medial axis schematically illustrated by dashed line. The homotopical axis, as it is defined in our framework, only consists of two local maxima of these two circles. The consequence is the local homotopical feature size on non-manifold points as well as on the edge which divides the circles is too high.

The solution of the dissolution problem (compare Definition 5.30) is to ensure that the sampling places data points on or close to the common boundary of the two circular regions. Let us call this linear part of the common boundary the "edge". To achieve this result the homotopical axis has to be extended by a further subset of the medial axis.

Consider in our example (Figure 5.23) the medial axis (dashed line) and its subset (continuous line) which does not extend to the corners. Since the example is symmetrical consider only one of the dotted circles. This circle is centered on the meeting point of two steepest paths starting in the two



Fig. 5.23: Proposition for new subset of medial axis to define locally adaptive boundary feature size

non-manifold contour points. This circle is the first maximum expanding circle on the descending path on the medial axis starting in the local maximum which touches the contour in three points. The center of that circle is the non-manifold point in the medial axis.

We propose to extend the current homotopical axis definition by the steepest increasing paths starting on non-manifold points in the medial axis.

Proposition 5.32 (Extended Homotopical Axis). Let X be a set of non-manifold points in the medial axis. The Extended Homotopical Axis is then the union of the homotopical axis and all steepest increasing paths starting in X.

The local homotopical feature size measured using the extended homotopical axis is significantly lower on the edge. It does carry the topological information needed to partly solve the dissolution problem as it was described in Figure 5.23. The sampling conditions based on the extended homotopical axis necessarily increased density on the common boundary between the two circular regions and placed data points on it. So, the sampling of the shape with two circular regions with common boundary differs from the sampling of the shape with one region with waist.

5.15.3 Local Homotopy Stable q-Sampling

The dissolution problem is not generally solved by the extended homotopical axis as it was proposed in the previous section. Consider the second example in Figure 5.21. There are no non-manifold points in the medial axis of both shapes. To differentiate the original shapes by the data sets, an additional knowledge of the maximum sampling point deviation is required. Here the dissolution problem is an effect of noise. Limiting noise by a global parameter sorts out all regions less than this global parameter.

The 3D example in Figure 5.22 can also be considered as an effect of topological noise. The irreducible non-manifold boundary reconstruction is a topological artifact based on a too great amount of noise. Notice, the interior of the ball is homotopically equivalent to a sphere and so is a correct reconstruction. Limiting here the absolute bound for the maximal point deviation removes the possibility of such topological noise for a donutball: the boundary is a donutball if the maximal sampling point deviation is nearly 0.

As we concluded in Section 5.15.1 limiting the noise amount by a global parameter does not generally solve the dissolution problem either. So, for a general reconstruction problem we propose a combination of sampling density based on extended homotopical axis and limitation of maximum sampling point deviation.

Proposition 5.33 (Local Homotopy Stable q-Sampling). Let hfs_{EHA} be local homotopical feature size measured on extended homotopical axis EHA. Then local homotopy stable q-sampling with globally set maximal sampling points deviation q is defined as follows:

$$\forall b \in \partial \mathcal{R} \exists s \in \mathsf{S} : \mathrm{d}_{\mathcal{R}}(s) < \psi \rho \mathsf{lhfs}_{\mathsf{EHA}}(b) \\ \forall s \in \mathsf{S} \exists b \in \partial \mathcal{R} : \mathrm{d}_{\mathcal{R}}(s) < \min\left((1-\rho)\mathsf{lhfs}_{\mathsf{EHA}}(b), q\right)$$

The refinement reconstruction results in a minimal refinement which is reducible to a stable refinement. The method, as it was originally defined, does not consider global noise limitation and consequently stops without guarantee of a one-to-one mapping between regions. The involvement of a global noise limit sorts out the spurious regions. So, we conjecture that there is a one-to-one mapping between the original regions and the resulting space partition of refinement reduction on local homotopy stable q-sampling without regions less than q.

Conjecture 5.34. Minimal Refinement with One-To-One Mapping to Original Space Partition

Let D_R be the result of refinement reduction on local homotopy stable q-sampling of a space partition \mathcal{R} . Let D_R not contain any region less than or equal to q. Then there is a one-to-one mapping between the reconstructed regions and \mathcal{R} .

Notice, the post-processing removal of regions less than q does not necessarily result in a stable refinement with stability defined by extended homotopical axis. The measure of the region size during the reconstruction is obviously insufficient to enable us to decide whether a boundary simplex cuts the axis. This question is partially answered by local homotopical feature size estimation in Chapter 6.

5.15.4 Insufficiency of the Refinement

Here we discuss two problems. First we introduce the problem resulting from refinement reconstruction method. Then we state the problem of the concept and mathematical framework "refinement".

Let us consider again the example in Figure 5.22 (b) discussed above and let us assume that the original shape is a ball denoted by the dark gray circle in Figure 5.22 (a) which partly envelopes the donutball. The vertices of the donutball are the noisy local homotopy stable sampling. Which implies that the result of the refinement reconstruction is a reducible refinement. Furthermore we previously observed that the boundary of the donutball closes the handle tunnel and bridge. The resulting space partition is homotopy equivalent to the original. The interior of the donut ball with the membranes (darkened surface patches denoted by dashed contour) closing the tunnel and the bridge is topologically a ball as well as the exterior infinite region.

But the membranes which close the handle tunnel and the bridge are orthogonal. The reconstructed boundary is not manifold and cannot be reduced to a topological equivalent of the original boundary of a ball. Deletion of any further simplex of the boundary destroys the refinement property and the topology of the reconstruction. According to this example we state the following problem:

Definition 5.35 (Boundary Reduction Problem). Let the reducible refinement D_R be a result of refinement reconstruction of the original space partition \mathcal{R} . The boundary of D_R is not necessarily reducible to a topological equivalent of the boundary of \mathcal{R} .

Consider further we would push through the tunnel membrane. The outer region does not change. The inner region is topologically a donut. The boundary of a donut is not reducible to a boundary of a ball. The interior correctly separates the local maxima and even the connected components of the homotopical axis. Which implies that the donut is a stable refinement of a ball.

In contrast to the boundary reduction problem where the stable refinement was homotopically equivalent to the original, we have here a stable refinement with not reducible boundary, and furthermore the associated regions are not necessarily homotopically equivalent.

Definition 5.36 (Refinement Problem). Let \mathcal{R} be a space partition and \mathcal{R}' be its stable refinement. \mathcal{R}' is not necessarily homotopy equivalent to \mathcal{R} .

However the refinement problem only occurs if no restrictions on the refinement are given. In our framework the result of reconstruction is restricted by the sampling which carries certain topological information. In the example of the donut and a ball there is no way for our method to result in a donut shape if the original shape is the ball. Assuming general position, the distance transform on a sampling taken from a ball boundary leads to saddles. Corresponding to these saddles, the elementary thinning necessarily divides the reconstructed regions.

Claim 5.37. The result of refinement reconstruction is not a refinement problem.

We conclude that the formal definition of the refinement is not an equivalence relation to reducibility condition but an implication: If a reconstruction is reducible then it is a refinement.

The boundary reduction problem is an effect of noise and cannot be handled by our algorithm without fundamental changes on the framework. The minimality condition has to be reconsidered in order to obtain a manifold boundary in the case of a donutball instead of a non-manifold minimal refinement as is the outcome of our method.

5.16 Conclusion

The framework of this chapter defines classes of space partitioning which result from our algorithm. The new sampling conditions are based either on local region size or on local homotopical feature size. The reconstruction method results in an oversegmentation of the original space partition preserving correct separation of local maxima or is reducible to an oversegmentation preserving correct separation of connected components of the original homotopical axis.

The new sampling conditions combine and extend the locally adaptive sampling conditions based on local feature size with the uniform (p, q)-sampling conditions defined for *r*-stable sets. However the new sampling conditions present insufficiency in non-manifold noise-free case and in manifold multiregional noisy cases: the sampling is equal for shapes with different topology. The propositions are made to resolve the problem.

The reconstruction method applies the WRAP algorithm ([Edelsbrunner, 2003]) on each previously deleted Delaunay tetrahedron containing its own circumcenter and proceeds with region merging on measurably undersampled simplices. The undersampled simplices are measured according to the ratio between the simplex size and the size of the minimal adjacent region. The algorithm steps are experimentally demonstrated on an illustrative 2D example.

The evaluation shows that the refinement reconstruction results in an equivalent space partition on a (p,q)-sampling if the parameters provided for thinned- (α, β) -shape-reconstruction are given. Furthermore the theoretical evaluation shows that the new sampling conditions cover the existent definitions, and so uniform factors can be computed for comparison.

Refinement reconstruction is theoretically and experimentally a solid and fundamental result which has advantages over related works and thinned- (α, β) -shape-reconstruction. The underlying shapes are assumed to be non-manifold multiregional surfaces. The method results under guarantee in reducible refinement even if the sampling is very sparse and noise-corrupted. The approach expects sampling parameters which are required for internal settings. However the reconstruction with estimated sampling parameters covers all sampling conditions defined in related works and even so delivers correct results.

The experiments are done on well known points sets "Armadillo" and "Dragon" which are uniform very dense and nearly noise-free samplings. To compare the results to the thinned- (α, β) -shapereconstruction the data sets are enhanced by salt-and-pepper noise, are decimated and the resulting points replaced to model sample points deviation from the boundary. Furthermore the experiments are done on volume-based data sets which result from 3D Canny edge detection [Bähnisch et al., 2009]. The original shapes are multiregional with non-smooth boundary. The data sets are noise-corrupted.

The known locally adaptive sampling sets fulfill conditions based on medial axis and local feature size. We want to evaluate the refinement reconstruction on sparser local homotopy stable sampling sets. In the next chapter we present a framework for data set generation which is under guarantee too sparse to be an ϵ -sampling but dense enough to fulfill local homotopy stable sampling conditions.

Chapter 6

Experiments on Decimated Point Sets

6.1 Introduction

Most of our examples used until now are 2-dimensional. This simplifies the illustration of notations as well as the consequences of the algorithm steps. However, our goal is the reconstruction in the 3dimensional domain. The result of reconstruction in our framework is a 2-dimensional non-manifold surface embedded into a 3-dimensional space. The surface is the boundary of a space partition which consists of more than two regions. Consequently, the boundary may consist of more than one connected component.

We use Delaunay triangulation as the combinatorial structure to imitate the behavior of continuous flow on the distance transform. Although in 3 and higher dimensions there is a very intriguing phenomenon which makes the correspondence not possible. So, the abstraction from 2D into 3D is not sufficient for evaluation of our algorithm.

In Section 5.14 we presented the results of refinement reconstruction on real data sets acquired from very dense laser range scanners as well as volume-based sampling sets. The volume based point sets result from 3D interval scanning with a regular grid followed by 3D edge detection algorithm to obtain a point cloud.

The results on laser scan data demonstrate the performance of the algorithm on very dense sampling sets and the advantage of the method on very noise-corrupted data sets. The results on volume-based data illustrate the ability of the algorithm to reconstruct multi-regional space partitions with nonmanifold boundary. In this chapter, we demonstrate the advantage of the refinement reduction over the thinned- (α, β) -shape-reconstruction handling samplings with locally variable density.

The known locally adaptive point sets are the results of mesh simplification algorithms which reduce the density of the point set and enlarge the size of polygons connecting them. The criterion to preserve the topology and geometrical properties is the curvature or the local feature size. The methods as introduced for example in [Lindstrom and Turk, 1998], [Garland and Heckbert, 1997] or [Dey et al., 1999] iteratively delete one point and all its adjacent simplices of the mesh and rebuild the mesh without that point.

In this chapter, we derive an approach similar to the method proposed in [Dey et al., 2001]. We assume a function which maps each point to a value of maximal distance to the nearest neighbor and

delete all points having a distance smaller than that value. The deletion is performed on the list of points sorted in increasing order according to the mapping value.

The function estimates the local homotopical feature size. So, the resulting data set is local homotopy stable. In Section 6.3, we propose a computation method which approximates the discrete homotopical axis defined on discrete critical points.

The stability of critical points is a research subject dual to surface reconstruction and has been studied in numerous related works. We introduce the subject in Section 6.2 and present our results on stability of critical points on low quality sampling sets.

In Section 6.6, we present arguments for the assumption that a subset of the discrete homotopical axis is homotopy equivalent to the original. Whereas the computed homotopical axis is homotopy equivalent to the discrete. According to these statements, and using a scaling factor derived in Section 6.4, we argue that the estimated local homotopical feature size underestimates the original in worst case. Consequently, the point set decimation in worst case is oversampled but local homotopy stable.

We also discuss the feature size estimation on not stable critical points and steepest paths connecting them. The computation overestimates the feature size. However, we claim that the overestimation is done on not relevant parts of the homotopical axis such that the homotopical axis without these parts is homotopy equivalent to the original. So, we claim the result of the reconstruction to be a refinement reducible to a space partition which is homotopy equivalent to the original.

In Section 6.7 we demonstrate the power of the refinement reconstruction algorithm on sparse locally adaptive sampling sets.

6.2 Stability of Critical Points

Our intention in this chapter is to decimate a point set. Decimation is done by feature size which is defined on sample points. We assume that the feature size in the original boundary is not known during the reconstruction, so, the value has to be estimated.

The local feature size is estimated by local maxima. Refinement reconstruction correctly separates the local maxima. So, using the reconstructed regions we can measure the local region size. The measurement can be overestimated and has to be scaled.

The local homotopical feature size depends on the homotopical axis. The homotopical axis is the smallest set of steepest paths between critical points on the medial axis. So, to measure the local homotopical feature size we have to compute the medial axis. However, the correct discrete medial axis computation is not trivial and can be seen as a reconstruction problem dual to correct surface reconstruction.

In the following we investigate the relation between the reconstructed medial axis and the original by given sampling conditions. In [Dey et al., 2005] the relation is proven by unique separation of the discrete critical points: the critical points are either very close to the original medial axis or to the original boundary. In [Chazal et al., 2009] it is proven that for small perturbations on the surface the discrete critical points are in the small environment of the original ones.

Our research extends the bounds of sampling conditions. We require the reconstruction to guarantee the preservation of topological properties on samplings of low quality. Here we investigate how we can imply the location and the distance value of the original critical points by discrete critical points which do not correspond to the given reconstructed boundary.

Critical Points Separation

In [Dey et al., 2005] the critical points are correctly separated if the criticals may be uniquely mapped either to the criticals on the discrete medial axis or to the criticals on the surface reconstruction. The proof for ϵ -sampling (compare Definition 3.4) is given by stating that the critical points are either in $\epsilon/3$ neighborhood of the smooth manifold original surface or in the $\epsilon/3$ -neighborhood of the original medial axis. Then a critical point c belongs to the discrete medial axis if the angle between the vector between c and the sample point s whose dual Voronoi cell contains c, and the estimated normal on s is less than $\pi/4$ or greater than $3\pi/4$. The normal on a sample point is computed by poles.

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The argumentation in [Dey et al., 2005] is intuitively followed from the *co-cone* (compare Figure 3.3 in Section 3.2.4 and originally in [Amenta et al., 2000a]) statement since the computed normal is nearly collinear to the original and the nearest sample points are in the co-cone of the current sample point. So, the vector to nearest sample points is almost orthogonal to the normal. It follows that since the criticals of the medial axis are much farther away from the sample point, the angle between the direction to the medial axis critical and the normal is highly acute.

Stability of Criticals for Small Perturbations on the Surface

The results presented in [Chazal et al., 2009] use the points in space where the norm of the gradient does not exceed μ : $\|\nabla_K(x)\| \leq \mu$. Such points are called μ -critical points. In this framework it is proven that for two compact sets, with Hausdorff distance less than a scalar value ϵ between them, in a small environment of each μ -critical point of the first compact set there is a μ' critical point of the other compact set. In other words, for small perturbations on the surface the critical points stay in a small certain environment of the original.

The stability of criticals in [Chazal et al., 2009] implies the convergence of the μ -medial axis which is a set of all points with gradient norm less than μ . Which means that small perturbations on the surface do not change the topology of the medial axis and decreasing perturbations on the surface result in decreasing perturbations on the medial axis. The results are valid for noisy, uniform κ, μ -sampling (compare Definition 3.7) of a not necessarily smooth manifold surface.

There are related results on λ -medial axis in [Chazal and Lieutier, 2005a]. Let the reversed distance function map any point of an open set to the boundary points which are touched by the maximal inscribing ball centered on this point. Then the function which maps any point of an open set to the radius of the minimal ball enclosing the touching points defines the λ -medial axis. The λ medial axis is the subset of the open set on which this function is greater than λ (compare Definition 2.23). Since the reversed distance function maps any point not on the medial axis to one single boundary point, the minimal enclosing ball of this point has a zero radius. It follows that λ -medial axis is a subset of the medial axis.

According to Theorem 2 in [Chazal and Lieutier, 2005a] the λ -medial axis has the same homotopy type as the open set if λ is less than weak feature size which is the Hausdorff distance between the boundary and the critical points. The λ -medial axis remains stable under small perturbation on the boundary as stated in Theorem 3 in [Chazal and Lieutier, 2005a]. For each point on the deviating λ' medial axis, at a certain distance there is a point on the original medial axis if the boundaries deviate by a value significantly smaller than λ . So, the deviating λ' -medial axis is in a homotopy equivalent dilation of the original. This implies the stability and separation of critical points of the open set.

There is a one-to-one mapping between the critical points of the open sets. Further, since only a thin dilation of the original λ -medial axis is considered, the critical points of the boundary approximated by sample points are correctly separated. The sampling is then required to be a noisy ϵ -sampling of the original boundary. By this condition the approximated boundary does not deviate from the original by a greater value than ϵ .

As stated in Lemma 5.2 in [Chazal and Lieutier, 2005a] the approximated λ -medial is contained in the Voronoi diagram. The 2D λ -medial algorithm adds a Voronoi cell to the result if its dual Delaunay cell has a greater circumradius than λ . The λ -medial axis approximation converges toward the original for a series of noisy ϵ samplings with decreasing Hausdorff distance.

Low Quality Sampling Sets

In cases of low quality sampling sets there is no guarantee that the reconstruction is topologically correct. However, using the framework developed for refinement reconstruction, we can make certain statements. Here we assume that the sampling sets are local homotopy stable.

Consider Figure 6.1. The continuous line represents a cut-out of the original boundary. The dots are the sample points. Gray thick line denotes the $(1 - \rho)$ lhfs-dilation with $\rho \approx 0.5$. The sampling is local homotopy stable. In the left picture the cut-out of the homotopical axis is a thin line containing one maximum (\oplus) and one saddle (\otimes). Obviously, there is a "bottle neck", a narrowing in the original



Fig. 6.1: left: unstable maximum, right: pseudo-maximum

boundary. However, the conditions of the sampling device did not establish the equivalent bottle neck in the data points. The discrete distance transform continuously increases and, so, the cut-out does not contain any discrete critical points. The continuous local maximum \oplus cannot be reached by an increasing path on continuous distance transform starting on its associate. Anticipatory, we can say that the discrete maximum associated with \oplus is an associate of several continuous maxima. The original maximum seems to vanish. We call such continuous local maxima *unstable*. So, we can define a *stable* continuous local maximum by:

Definition 6.1 (Stable Maximum). Let \mathcal{R} be a space partition, $d_{\mathcal{R}}$ be the continuous distance transform on \mathcal{R} and x be a local maximum on $d_{\mathcal{R}}$. Let S be a point set and d_S be the discrete distance transform defined on S. Let x' be a discrete local maximum on d_S associated with x. x is stable for point set S if and only if x is reachable by an increasing path on $d_{\mathcal{R}}$ starting on x'.

In the right picture, on the other hand, the continuous distance function continuously increases inside the contour. So, no continuous critical points are visible in the cut-out. However, the sample points develop a discrete local maximum (\boxplus) in the discrete distance transform and a discrete saddle (\boxtimes). The discrete local maximum \boxplus is not reachable on any increasing path on the continuous distance transform starting on any point of the original homotopical axis. So, we call a discrete maximum, which is not associated with any original maximum, the *pseudo-maximum*. Notice, the notation *stable* and *unstable maximum* are referred to continuous local maximum, whereas the notation *pseudo-maximum* denotes a discrete local maximum.

Definition 6.2 (Pseudo-Maximum). Let \mathcal{R} be a space partition, HA be its homotopical axis. Let S be a point set and d_S be the discrete distance transform defined on S. Let x' be a discrete local maximum on d_S . For all points x on HA: x' is called a pseudo-maximum if and only if x' is not reachable by an increasing path starting on x.

In the following we prove that a local continuous maximum is stable for all local homotopy stable samplings if this is the only maximum in the continuous region or if the distance value of the corresponding saddles is sufficiently small. According to Definition 2.17, we recall that $\mathbf{F}_{\beta}(\mathcal{R})$ is the set of points of a space partition with gradient value less than β and, correspondingly, $\mathbf{F}_0(\mathcal{R})$ is equal to $\lim_{\beta\to 0} (\mathbf{F}_{\beta}(\mathcal{R}))$. As defined in Definition 2.33, $\mathbf{F}^{\infty}(\mathcal{R}, x)$ is the set of all critical points reachable by steepest paths starting on an arbitrary point x.

Claim 6.3 (Stable Maxima). Let x_m be a local maximum on a continuous distance function $d_{\mathcal{R}}$ and $X \subseteq \mathbf{F}_0(\mathcal{R})$ be the set of all critical points such that $\forall x \in X : x_m \in \mathbf{F}^{\infty}(\mathcal{R}, x)$.

 x_m is a stable maximum for all locally stable (ψ, ρ) -samplings if $\forall x \in X : \mathbf{F}^{\infty}(\mathcal{R}, x) = \{x_m\}$ or for all increasing paths π consisting of sequences of steepest paths starting and ending in $\mathbf{F}^{\infty}(\mathcal{R}, x)$ with $\pi(1) = x_m : \exists t \in \mathbb{R} : (2 - \rho) d_{\mathcal{R}}(\pi(t)) < \rho d_{\mathcal{R}}(x_m)$

Proof: Consider the opposite. There is a locally stable sampling S with the associate discrete maximum x'_m on d_s to x_m such that there is no increasing path between x_m and x'_m . Since the local maxima are correctly separated by refinement, so x_m and x'_m are in the same continuous region. Consequently, the

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local continuous maximum $y_m \neq x_m$ reachable by steepest path starting on x'_m is in the same continuous region too. It implies that there has to be a saddle x_s between y_m and x_m on $d_{\mathcal{R}}$. Since a saddle is a minimum on two steepest paths between criticals the following is valid: $(2 - \rho)d_{\mathcal{R}}(x_s) < \rho d_{\mathcal{R}}(x_m)$.

Since x'_m is the associated maximum there is a steepest increasing path π' in d_s with $\pi'(0) = x_m$ and $\pi'(1) = x_m$.

Starting in each point of the path π' there has to be a steepest path on $d_{\mathcal{R}}$ to HA. Since the steepest paths starting on $\pi'(0)$ and $\pi(1)$ end in different maxima, there has to be a t, such that a steepest path starting on $\pi'(t)$ ends in x_s .

Since $\forall t \in (0,1]$: $d_{\mathsf{S}}(\pi'(t)) \ge d_{\mathsf{S}}(x_m)$ it follows that $(2-\rho)d_{\mathcal{R}}(x_s) > d_{\mathsf{S}}(x_s) > d_{\mathsf{S}}(x_m) > \rho d_{\mathcal{R}}(x_m)$, which is a contradiction.

The union of steepest paths ending in a local maximum is its corresponding stable manifold. The saddles, from which the local maximum is reachable, are on the boundary of this stable manifold. The saddles are also minima on the boundary of the stable manifold. Consequently, if the possible maximal discrete distance values on the minima on the boundary of the stable manifold are even smaller than minimal discrete distance value on the local maximum, then the associated discrete maximum will lie in the stable manifold. It will not be possible for the increasing path on the discrete distance transform starting on the local continuous maximum to pass through the boundary of the stable manifold.

According to this argumentation, it follows that, if the discrete distance values on the boundary of the stable manifold are less than the discrete value of the corresponding continuous local maximum, then no increasing path on the discrete distance transform passes though the boundary of the stable manifold.

Corollary 6.4 (Stable Maximum for a Point Set). Let x_m be a local maximum on a continuous distance function $d_{\mathcal{R}}$ and $X \subseteq \mathbf{F}_0(\mathcal{R})$ be the set of all critical points such that $\forall x \in X : x_m \in \mathbf{F}^{\infty}(\mathcal{R}, x)$.

 x_m is a stable maximum for a locally stable (ψ, ρ) -sampling S if $\forall x \in X : \mathbf{F}^{\infty}(\mathcal{R}, x) = \{x_m\}$ or for all increasing paths π consisting of sequences of steepest paths starting and ending in $\mathbf{F}^{\infty}(\mathcal{R}, x)$ with $\pi(1) = x_m : \exists t \in \mathbb{R} : d_{\mathsf{S}}(\pi(t)) < d_{\mathsf{S}}(x_m)$

Consider now a simple homotopical axis consisting of two local maxima connected by two steepest increasing paths starting on a saddle. This is the homotopical axis of a barbell shape. The saddle is a 2-critical point corresponding to the neck in the barbell. If the distance values of the saddle do not differ much from the distance values of the maxima, the local maxima are *unstable*. The consequence is, the reconstruction may consist of one maximum only. The second continuous local maximum is associated with the same discrete maximum as the first. The second local maximum and the saddle seem to vanish. So, we can say, the saddle is *unstable*. To generalize the stability concept for all critical points we define:

Definition 6.5 (Stable Saddle). Let \mathcal{R} be a space partition, $d_{\mathcal{R}}$ be the continuous distance transform on \mathcal{R} and x be a saddle on $d_{\mathcal{R}}$. Let S be a point set and d_S be the discrete distance transform defined on S. x is stable for point set S if and only if all reachable maxima on $d_{\mathcal{R}}$ are stable for S.

The homotopical axis is the union of critical points and the minimal set of steepest paths connecting them. If all critical points are stable, we imply that all associated discrete local maxima are in the stable manifolds of the original maxima. Furthermore, the local homotopy stable sampling restricts the discrete distance values on the boundary to be less than $\psi\rho$ lhfs, with $\psi < 1$. Let b be the boundary point touched by the maximal inscribing ball centered on the local continuous maximum. Since the discrete distance value on the continuous maximum is at least ρ lhfs(b), and the discrete distance value on its associate is necessarily greater than ρ lhfs(b), the steepest path between the local continuous maximum and its associate does not cross the ρ lhfs-dilation of the boundary. Since the equivalent consideration is valid for stable saddles too, we conclude that the associated critical points and the steepest increasing paths on the discrete distance transform between them are in an *envelope* (HA[⊕]) of the original homotopy axis which does not intersect the ρ lhfs-dilation of the original boundary.

The envelope HA^{\oplus} of the original homotopical axis is the union of steepest increasing paths on the discrete distance transform starting in the original homotopical axis. Since HA^{\oplus} does not cross the

 ρ -dilation of the original boundary, there is an increasing path between the original saddle and each of the associated maxima of all its reachable continuous maxima. Consequently, HA^{\oplus} cannot have more connected components than the original homotopical axis.

The refinement reconstruction guarantees correct local maxima separation. According to previous consideration we also know that the stable saddles are correctly separated too. So, no different original regions are joined in the reconstruction and, consequently, no corresponding different components of the original homotopical axis can be connected. We imply, that the number of connected components of the original homotopical axis and its envelope HA^{\oplus} is the same. In the following we use this result to compute for point set decimation.

The point set decimation, as we use it for evaluation, requires for each sample point the estimated feature size of the corresponding boundary point. The feature size estimation is done on the homotopical axis which is a subset of the medial axis. For dense samplings the reconstructed medial axis is in the dilation of the original. Consequently, the discrete distance values on the reconstructed medial axis deviate by a fraction of the original. The fraction is computable by given sampling density and sampling point deviation.

The low quality sampling sets cause pseudo and unstable critical points. The associates of stable critical points and the corresponding subset of the homotopical axis are in an envelope of the original homotopical axis. The envelope encloses the steepest increasing paths which start on the stable subset of the original homotopical axis. So, here again the discrete distance values are a fraction of the original.

The computation of the medial axis is not the subject of this work and is assumed as given in following sections. However the stability of the reconstructed medial axis can be investigated by results of this section.

6.3 Homotopical Axis Approximation

The data set decimation is done on sample points for which the local homotopical feature size is known. The question is, how do we measure the local homotopical feature size by given sample points? The definition given in Definition 2.36 is done on boundary points in a continuous domain. Assuming the sample points to lie on the boundary, the continuous local homotopical feature size on sample points is the value on the underlying boundary point. But in our framework the sample points deviate from the boundary. However, the sample points are taken from the boundary points and we assume that the sampling conditions are fulfilled for each boundary point. So, we have to estimate the original homotopical feature size on boundary points by their given discrete representatives.

Let us first assume that the sample points lie on the boundary and that the topology is given by a polygonal approximation of the original boundary. The local homotopical feature size is defined by the homotopical axis of the space partition. In our case a polygonal approximation separates the space into polytopes. The polygonal approximation is done on sample points. The homotopical axis is a subset of the medial axis. The medial axis on sample points is the Voronoi diagram. So, the medial axis of the polytopes is a subset of the Voronoi diagram and so is the homotopical axis. So, the definition and implementation of the homotopical axis in the discrete domain is done using the discrete medial axis which is a subset of the Voronoi diagram on the sample points. We follow the Definition 2.24 to define the discrete homotopical axis:

Definition 6.6 (Discrete Homotopical Axis). Let S be a set of points and ∂D_R be the boundary of a discrete space partition with $S \subset \partial D_R$. Let MA_R be the medial axis of D_R . Let \mathbf{F}_R be the set of critical points such that $\mathbf{F}_R \subseteq MA_R$ with $\mathbf{F}_R = \mathbf{F}_0(D_R)$ and $\mathbf{F}_\beta(D_R) = \{x \in D_R \mid ||\nabla(x)|| \leq \beta\}$ such that $\lim_{\beta \to 0} (\mathbf{F}_\beta(D_R)) = \mathbf{F}_0(D_R)$. The discrete homotopical axis HA_R is then defined as

$$\mathsf{HA}_{R} = \lim_{\beta \to 0^{+}} \mathbf{G}_{\beta}(\mathsf{D}_{R}) \quad \text{where}$$
$$\mathbf{G}_{\beta}(\mathsf{D}_{R}) = \{ x \in \mathsf{D}_{R} | \ \exists t \in \mathbb{R}^{+} \exists y \in \mathbf{F}_{\beta}(\mathsf{D}_{R}) : x = \mathfrak{C}(t, y) \}.$$

6.3. HOMOTOPICAL AXIS APPROXIMATION

In Definition 6.6 we again use the extended definition of the gradient ∇ as it is introduced in [Lieutier, 2004] (compare also Definition 2.17). In addition now, ∇ is defined on the polygonal approximation of the original boundary. ∇ gives the direction of the steepest ascent, i.e. the direction which maximizes the growth of discrete distance transform d_{D_R} . The steepest ascent is a curve of the continuous flow \mathfrak{C} which is the result of the gradient integration. So, the discrete homotopical axis is the union of critical points and the set of points reachable by steepest ascent starting on critical points on the discrete medial axis.

In our framework we assume that the discrete medial axis is given. For secondary literature consult [Amenta et al., 2001], [Dey and Zhao, 2002], [Dimitrov et al., 2003] or [Sud et al., 2007]. The discrete medial axis MA_R is a subset of the Voronoi diagram and consequently can be represented by a set of dual Delaunay simplices D_{MA} .

According to Section 2.4.9 (compare: [Edelsbrunner, 2003]) the Delaunay simplices can be ordered in a strict relation ($\prec \subseteq D \times D$) which imitates the behavior of the flow lines. A critical point on the medial axis corresponds to the intersection point between a Voronoi simplex and its dual Delaunay simplex. It implies that the Delaunay simplices corresponding to criticals are centered. Centered Delaunay simplices have no successors in the flow relation ({ $\sigma \mid \sigma \in D_{MA} \land \neg \exists \sigma' \in D_{MA} : \sigma \prec \sigma'$ }).

The homotopical axis is the union of steepest increasing paths - the flow lines - on the medial axis starting on critical points. Correspondingly, in the set of Delaunay simplices D_{MA} dual to the discrete medial axis we follow the flow relation starting on centered Delaunay simplices. The discrete homotopical axis is the join of ancestor sets of centered simplices.

We propose to construct the discrete homotopical axis equivalently to "Elementary Thinning" in Section 5.7. We delete the centered cells from D_{MA} and perform elementary collapsing on equivocal simplices.

Elementary collapsing on equivocal simplices defines a tree with a centered cell as the root, the equivocal facets as the edges and the visited Delaunay cells as knots and leaves. The Delaunay simplices in the tree are the descendant set of the centered cell. We call a path starting in the root of the tree and ending in a leaf, such that each simplex in the path has exactly one successor or none, a *deletion path*.

Definition 6.7 (Deletion Path). Let $\pi_{MA}(\tau_0) = \tau_0 \prec \sigma_0 \prec \tau_1 \dots \sigma_{n-1} \prec \tau_n$ be a path in flow relation consisting of cells and facets in D_{MA} such that τ_0 is centered and each facet in $\pi_{MA}(\tau_0)$ is equivocal. Let τ_n be a Delaunay cell in D_{MA} such that there is no equivocal facet σ_n with $\tau_n \prec \sigma_n$. Then we call $\pi_{MA}(\tau_0)$ a deletion path.

We delete the simplices of two deletion paths if their leaves share a Delaunay triangle in D_{MA} . Then we perform elementary collapsing on simple edges in D_{MA} and subsequently remove all singular edges in D_{MA} . The set of Voronoi simplices dual to deleted Delaunay simplices is the computed homotopical axis.

Algorithm 6.8 (Homotopical Axis Approximation). Let D_R be a reconstructed space partition. Let $MA_R \subset V$ of D_R be the discrete medial axis, where V is the Voronoi diagram and let D be the Delaunay complex dual to V.

- 1. Compute set $D_{MA} \subset D$ of Delaunay simplices dual to MA_R .
- 2. Compute all deletion paths on centered cells in $\mathsf{D}_{\mathsf{MA}}.$
- 3. For each pair π_i, π_j of deletion paths: delete the simplices in π_i and π_j if the last cells in π_i and π_j share a Delaunay triangle in D_{MA} .
- 4. As long as a simple edge $v D_{MA}$ can be found perform elementary collapsing on v.
- 5. Delete all singular edges in D_{MA} .
- 6. Return the set HA_R of Voronoi simplices dual to the deleted simplices in D_{MA} .

The Homotopical Axis Approximation in Algorithm 6.8 terminates since there is only a finite number of deletion paths and the already delete simplices are not deleted again.

Consider now four nearly coplanar points. The tetrahedron with these four points as vertices is called *flat*. Consider a flat tetrahedron which contains its own circumcenter. This flat tetrahedron is centered and corresponds to a local maximum on the discrete distance transform.

Unfortunately, flat tetrahedrons are a frequent phenomenon in surface reconstruction especially on dense noise-free samplings. The circumcenter of a flat tetrahedron is a critical point and consequently a point on a homotopical axis. The associated discrete local maximum is always greater than the original. Since we assume the sampling to be at least local homotopy stable (ψ, ρ) -sampling (compare Definition 5.17), the boundary simplices are at most ψ, ρ lhfs. The local homotopical feature size in the case of the flat tetrahedron is at most the continuous distance value on the original local maximum and consequently less than the discrete distance value of its associate.

In our case we assume the sampling even for noise-free cases ($\rho = 1$) to be dense enough: $\psi < 0.5$. However, at least one triangle of the flat tetrahedron is greater than half of its circumradius. It follows that the flat tetrahedron cannot be associated with an original and so is a *pseudo-maximum*.

Knowing ψ and ρ parameters we can sort out pseudo-maxima. Consider a deletion path, which is not necessarily in the discrete medial axis. Let τ_0 be the starting centered cell and let τ_i be the last simplex in the path in the discrete medial axis and let a leaf of the path contain a boundary simplex. This boundary simplex has to be less than $\psi\rho$ lhfs. The local homotopical feature size is defined by a distance value on a point x on the original homotopical axis. The discrete distance value on x is at least $(1 - \rho)$ lhfs. The associated point in the discrete homotopical axis has a greater distance value than x. It follows that the circumradius of the boundary simplex has to be less than $\frac{\psi\rho}{1-\rho}$ of the circumradius of τ_i otherwise the circumcenter of τ_0 is a pseudo-maximum.

6.4 Feature Size Estimation

In Section 6.2 we learned that stable points on the original medial axis have an associate on the discrete medial axis. In Section 6.3 we proposed an algorithm to approximate the discrete homotopical axis. So, for each sampling point we can compute the reachable discrete maxima in the discrete distance transform and the nearest point on the discrete homotopical axis. These points are associates of points on the original homotopical axis.

In this section we assume that all points on the original medial axis are stable and learn how to estimate the position and distance value of points on the original homotopical axis by their discrete associatives. So, for each sampling point we estimate the local homotopical feature size on their corresponding boundary point.

Consider a boundary point b. The local homotopical feature size is defined either by a distance value on minimal reachable maximum or by distance to the homotopical axis. Let x be the point on the homotopical axis with distance value which minimizes these two values. So, the distance value on x is the local homotopical feature size lhfs(b) on b. The sample points of b are distributed around it by at most $(1 - \rho)lhfs(b)$. The same is valid for all boundary points with the same local homotopical feature size. It follows that the maximal inscribing ball touching at least one of the sample points of b has a radius in the interval $d_s(x) \in (\rho lhfs(b); (2 - \rho) lhfs(b))$. The circumcenter of the maximal ball inscribed into the sample points is a point on the discrete homotopical axis reachable by steepest path from x. We conclude that, knowing the circumradius of the maximal inscribing ball touching a sample point, we can estimate the bounds of the local homotopical feature size of the corresponding boundary point:

Corollary 6.9 (Infs-Estimation on Stable Homotopical Axis). Let b be a boundary point and $s \in S$ be its sample point of a local homotopy stable sampling. Let the nearest point x on the homotopical axis be stable. Let y be the first point on the approximated homotopical axis reachable by steepest path on discrete distance transform starting on x. Then the local homotopical feature size on b is less than $\frac{1}{2-\rho}d_S(y)$

The given boundary reconstruction defines the discrete homotopical axis. The distance between each sample point and the discrete homotopical axis, as well as the distance value of the minimal discrete maximum define the discrete local homotopical feature size. This value is the discrete distance value of the first point reachable by steepest path starting on a point which defines the continuous local homotopical feature size on a boundary point. So, using the result in Corollary 6.9 we can associate each sample point with a boundary point and estimate the original local homotopical feature size.

6.5 Point Set Decimation

Point Set Decimation is a process to reduce the point density while preserving the topological properties of the data set. The advantage in this context is that we do not need to preserve the topology of the mesh but the topology of the point set. The mesh construction on the decimated point set is then the reconstruction of the original mesh. Related mesh decimation procedures iteratively delete one point and subsequently re-establish the connections in the resulting data set by newly generated simplices. Each iteration guarantees the correct topology of the resulting mesh. For secondary literature consult [Lindstrom and Turk, 1998], [Garland and Heckbert, 1997], [Dey et al., 1999]. We skip that procedure and concentrate our attention on the density of the points. A similar procedure is proposed in [Dey et al., 2001].

Using the result of Corollary 6.9 we can estimate the original local homotopical feature size on the boundary by given sample points even for low quality and highly noise-corrupted data sets as long as the input is local homotopy stable (compare Definition 5.17). The result is a function which maps each sample point to an estimated local homotopy feature size.

Here we assume that the local homotopical feature size is known. Further, we consider the original mesh to represent the continuous boundary. Then the vertices of the mesh are considered as boundary points and the data set is assumed to be dense enough to contain "almost" every boundary point.

Consider a ball centered on a boundary point b with radius plhfs(b) such that the boundary points in the ball have the local homotopical feature size greater than or equal to the local homotopical feature size on b. Consider further a sample point in the center of this ball, in other words a sample point on b. Then the distance between any boundary point b' in the ball and the sampling point is less than or equal to plhfs(b), which is less than p times the local homotopical feature size on b'. So, leaving the sample point in b, we may delete all sample points in the ball, preserving for all boundary points in the ball the property of minimal distance to the nearest sample point. We do not need to be concerned about the second condition on maximal sample point deviation since no new points are added to the data set and original points are assumed to be on the boundary. In the following we call the deletion of points under such conditions the *local homotopy stable decimation step*.

Definition 6.10 (Local Homotopy Stable Decimation Step). Let \mathcal{R} be a space partition and $\partial \mathcal{R}$ be its boundary. Let S be a local homotopy stable sampling of \mathcal{R} such that for $|S| \to \infty$, $S \to \partial \mathcal{R}$. Let $s \in S$ be a sampling point and b be its nearest boundary point such that $||s-b|| \to 0$ and let $\forall s' \in S : \mathsf{lhfs}(s) \leq \mathsf{lhfs}(s')$. Let $\rho \to 1$. Let \mathcal{B}_o be an open sphere centered on s with radius $\psi \mathsf{lhfs}(b)$. Then $S' = S \setminus S \cap \mathcal{B}_o \cup \{s\}$ is a local homotopy stable sampling and the procedure which reduces S to S' is the local homotopy stable decimation step.

The Decimation algorithm reduces the originally oversampled data set to a point set preserving the local homotopy properties. In other words, the algorithm performs the local homotopy decimation step until no such steps are possible. The straightforward implementation is to perform the decimation step on the list of points sorted in increasing order according to its local homotopical feature size.

Algorithm 6.11 (Local Homotopy Stable Point Set Decimation). Let S be a noise-free local homotopy stable (ψ, ρ) -sampling set. Let \mathcal{L} be a list containing S sorted in increasing order according to the local homotopy feature size on the points in S.

- 1. Let S' be an empty set of points.
- 2. Let s be the first sampling point in \mathcal{L} .
- 3. Push s into S'.

- 4. In \mathcal{L} delete all sample points with distance less than $\psi \mathsf{lhfs}(s)$ to s.
- 5. If \mathcal{L} is not empty go to 2.
- 6. Else return S'

The Algorithm 6.11 terminates since in 4. the number of elements in the list of points is decreased by at least one and the algorithm stops with an empty list. One of the possible implementations of step 4. is the range search on a kD-tree [Bentley, 1975]. A kD-tree uses O(dn) space for the data structure and solves a d-dimensional range query in worst case time of $O(n^{1-\frac{1}{d}} + m)$, where m is the number of output points. In a 3-dimensional case the worst case complexity of a query is then $O(n^{\frac{2}{3}} + m)$.

The construction of Algorithm 6.11 implies:

Fact 6.12 (Decimation Correctness). *The output of the* local homotopy stable point set decimation *is a local homotopy stable sampling.*

The occurrence of unstable critical points (compare Definition 6.5) in low quality data sets causes underestimation of local homotopy feature size. The consequence for the decimation is undersampling of the boundary with the resulting reconstruction intersecting the original homotopical axis. It follows that the result of reconstruction on a decimated data set is a refinement of the original space partition.

Corollary 6.13 (Result of Decimation is a Refinement). Let S be a local homotopy stable sampling set of the space partition \mathcal{R} and let D_R be a stable refinement reconstruction of \mathcal{R} . Let S_R be the result of data set decimation with estimated local homotopical feature size. Then the result of refinement reconstruction on S_R is a refinement.

However, we expect the result of reconstruction on a decimated set to preserve certain original topological properties. Consider a torus. The homotopical axis is a ring consisting of non-stable critical points only. Consider further the boundary of the torus to be sampled according to local homotopy stable sampling conditions. Then according to Theorem 5.19 the result of refinement reconstruction is reducible to a stable refinement. It follows that the homotopical axis of the stable refinement preserves the original homotopy. We imply that even though the original critical points are unstable the discrete homotopical axis preserves the topological properties. So, the computation of the local homotopical feature size and consequently the point set decimation considers the correct homotopy. We conclude that the refinement reconstruction may cut the homotopical axis, but there is a subset of the reconstructed boundary with a discrete homotopical axis which is homotopy equivalent to the original.

6.6 Discussion and Future Work

The aim of the framework in this chapter is to produce data sets with variable density for evaluation of our refinement reconstruction algorithm. So, the intention is to experimentally show the stability of the algorithm on sparse locally adaptive sampling sets.

The first experimental framework presents most interesting insights into and questions on stability and reconstruction of critical points on low quality data sets. Many of the insights we give in this chapter are not yet proven, however, do propose arguments and ideas to prove the statement made on stability of critical points and data set decimation.

As introduced in Section 6.3 we differentiate between the discrete homotopical axis and the computed homotopical axis. The discrete homotopical axis is defined by continuous flow on discrete distance transform. The computed homotopical axis is the result of an algorithm. The algorithm uses the flow relation to imitate the continuous flow. The computed homotopical axis approximates the discrete homotopical axis.

We discuss the topological correspondence between the discrete homotopical axis and the original homotopical axis defined on the continuous boundary in Section 6.6.1 and argue in Section 6.6.2 that the approximated homotopical axis is homotopy equivalent to the discrete homotopical axis. In Section 6.6.3

we use the arguments together with the results of feature size estimation made in Section 6.4 to derive an expectation on homotopy equivalence between the result of refinement reconstruction on decimated point sets and the original space partition.

6.6.1 Homotopy Type of Discrete Homotopical Axis

The results on critical points separation on dense sampling sets and stable critical points deliver an envelope of the original homotopical axis which necessarily contains the discrete homotopical axis. So, feature size can be estimated using the bounds of this envelope. In Section 6.2 we also propose an argumentation that there is a one-to-one mapping between the connected components of the discrete homotopical axis and original. Here we discuss the homotopy type of the discrete homotopical axis on low quality data set.

Not stable critical points disappear on discrete distance transform. Consider for example a cone shape but let the tip be swollen. This swelling corresponds to a local maximum on the distance transform which is much less than the local maximum corresponding to the ground of the cone. The homotopical axis is a line segment connecting these two local maxima passing through a 2-saddle. Let the distance value on this saddle be not much greater than the distance value of the small maximum. Then the small maximum is unstable.

Consider a noisy local homotopy stable sampling such that the data set contains one local maximum only. The associates of the small and great continuous maxima is this one great discrete maximum. Consequently the discrete homotopical axis consists of this great maximum only. Now, assuming the distance between the original maxima to be arbitrary great, the associate of the small original maximum is then arbitrary far away. But the discrete homotopical axis is homotopy equivalent to the original.

Consider now a donut shape. The homotopical axis is a circle. Consider further three local maxima on the homotopical axis. Let the three local maxima have nearly equal distance values. Assume two of them to be unstable. There is a saddle between these two maxima. Since all reachable local maxima are unstable the saddle is not stable.

According to Theorem 5.19 the refinement reconstruction on a local homotopy stable sampling is reducible. So, the reconstructed boundary can be reduced to a boundary which does not intersect the original homotopical axis. The result is a stable refinement.

Consider such reduction step. The boundary of the reducible reconstruction contains a simplex which intersects the original homotopical axis. The reduction step connects the ends of the approximated homotopical axis by steepest path crossing the circumcenter of the simplex. It follows that the continuous saddle can uniquely be mapped to a discrete saddle. The discrete homotopical axis is homotopy equivalent to the original.

According to the previous examples and using the result of Theorem 5.19 we have an argument to conjecture:

Conjecture 6.14 (Homotopy Type of Discrete Homotopical Axis). Let S be a local homotopy stable sampling of a space partition \mathcal{R} and let $HA_{\mathcal{R}}$ be the homotopical axis of \mathcal{R} . Let D_R be a stable refinement of \mathcal{R} built on S. Then there is a subset $HA'_{D_R} \subseteq HA_{D_R}$ of the homotopical axis HA_{D_R} of D_R which is homotopy equivalent to the original homotopical axis $HA_{\mathcal{R}}$.

To compute the discrete homotopical axis we use an equivalent procedure as for refinement reconstruction in Section 5.12. In the following section we use again the result of Theorem 5.19 to argue that the computed homotopical axis is homotopy equivalent to the discrete homotopical axis. Then using Conjecture 6.14 we imply that the computed homotopical axis contains a subset which is homotopy equivalent to the original.

6.6.2 Homotopy Type of the Approximated Homotopical Axis

The discrete homotopical axis is a subset of the discrete medial axis which is a subset of Voronoi diagram. The discrete homotopical axis is defined by steepest ascents on the discrete distance transform which start on critical points. The discrete homotopical axis is the union of stable manifolds of the

critical points. The result in Lemma 2.25 (compare [Chazal and Lieutier, 2005a]) implies the homotopy equivalence between the discrete homotopical axis and the discrete medial axis.

The ancestor sets defined by the flow relation (compare Section 2.4.9) of centered cells imitate the stable manifolds. In contrast to stable manifolds the ancestor sets may have a non-empty intersection. In the intersection the flow relation forks. However, refinement reconstruction solves the problem. So, we expect the approximation of the discrete homotopical axis to be homotopy equivalent to the discrete medial axis.

Conjecture 6.15 (Homotopy Type of the Approximated Homotopical Axis). The result of homotopical axis approximation in Algorithm 6.8 is homotopy equivalent to the discrete medial axis.

The algorithm operates only on Delauanay simplices which correspond to medial axis. So, assuming the opposite, the approximated homotopical axis is not homotopy equivalent to the discrete medial axis, then there has to be a simplex which is not visited or not deleted by the algorithm. In other words, there has to be a simplex which is not reachable by elementary collapsing on equivocal simplices starting on deleted centered simplices. We expect this assumption to lead to a contradiction.

6.6.3 Stability of Reconstruction on Decimated Point Sets

For the point set decimation in 6.5 we assumed the local homotopical feature size on sample points to be known. Assuming the given values to be the local homotopical feature size of the corresponding boundary points, the result of decimation is a local homotopy stable sampling.

As discussed in Section 6.6.1 we expect the discrete homotopical axis to contain a subset which is homotopy equivalent to the original. In Section 6.6.2 we argued that the computed homotopical axis is homotopy equivalent to the discrete homotopical axis. We imply that the computed homotopical axis contains a subset which is homotopy equivalent to the original homotopical axis.

In Section 6.4 we discussed how the local homotopical feature size can be estimated on stable critical points and the steepest paths connecting them. But according to previous considerations certain unstable critical points are preserved in the homotopy equivalent subset of the computed homotopical axis. So, there is a guarantee that the homotopy equivalent subset of the computed homotopical axis is in the *envelope* of the original. Which means that following the steepest path on the discrete distance transform starting on the original homotopical axis, the first point on the computed homotopical axis has the discrete distance value not greater than $(2 - \rho)$ of the original. The factor $(2 - \rho)$ results from the bounds in Corollary 6.9.

Using the bounds of feature size estimation and the arguments for the homotopy equivalence of the subset of the computed homotopical axis, we infer that, though the refinement reconstruction on a decimated point set does intersect the original homotopical axis, the boundary is reducible to a subset with a discrete homotopical axis which is homotopy equivalent to the original. Simply speaking, the point set decimation is too sparse on certain sampling points but preserves the correct homotopy type of the reconstruction.

Conjecture 6.16. The result of refinement reconstruction on a decimated point set is reducible to a space partition which is homotopy equivalent to the original.

An interesting experiment to evaluate the stability of decimation is to apply the decimation algorithm a number of times on a decimated point set. We expect the outcome to be the same point set as the original decimated set.

6.7 Experiments

The point set decimation, as we introduced it in this chapter, results in a very sparse data set with locally variable point density. The aim is to evaluate the refinement reconstruction algorithm. Notice, point set decimation is not an issue of this work and so, we deal with the results only experimentally.


Fig. 6.2: (a) nonmanifold shape; (b) Refinement reconstruction on decimated data set

In Section 5.14 we have already presented the results of refinement reconstruction on real data sets. The results demonstrate the performance of the algorithm on very dense or highly noise-corrupted sampling sets as well as the ability of the algorithm to reconstruct multi-regional space partitions with non-manifold boundary. Here we demonstrate the advantage of the refinement reconstruction to handle samplings with locally variable density.

Reconstruction of Nonmanifold Shape on Locally Adaptive Sampling

Using the results of this chapter we created a non-manifold shape in Figure 6.2 (a) consisting of two donuts stuck together. Each donut was initially compressed on one side to obtain one stable maximum. The transparent illustration in Figure 6.3 (a) shows the interior of the shape. The space partition consists of three regions. The data set is noise-free with sample point density of 0.5lhfs.

In Figure 6.2 (b) we see a decimated mesh reconstruction with locally variable density. The density and consequently the size of triangles depends on the distance to the computed homotopical axis. We may also infer that the computed homotopical axis needs further pruning: the surface around the inclusion of the donuts is densely sampled, which is explained by its close proximity to the homotopical axis. The computed homotopical axis extends too far to the boundary.

The mesh in Figure 6.2 (b) is the result of refinement reconstruction on a decimated point set. As we can observe on the transparent mesh in Figure 6.3 (d) the reconstruction is a reducible refinement of the original space partition. Unfortunately not evident in the illustration is the membrane in the compressed side of the donuts. This narrowing corresponds to a stable saddle. Removing the membrane we obtain a surface reconstruction topologically equivalent to the original shape.

No method depending on global parameter setting like " α -shapes"-based algorithms, or approaches based on a globally set sampling density, like λ -medial axis, can cope with this data set. Since the original shape in Figure 6.2 is nonmanifold and the sampling is very sparse, no locally adaptive methods based on lfs or assuming *r*-regular shapes can reconstruct a nonmanifold surface. So, we present here a fundamental result and show the advantage of the refinement reconstruction over all methods known to us.

Well Known Data Set Decimation

As the final experiment we apply the decimation procedure onto well known data sets "Stanford



Fig. 6.3: (a) nonmanifold shape; (b) Refinement reconstruction on decimated data set

Bunny" and "Angel". In Figure 6.4 we present the results of refinement reconstruction on both data sets: the original very dense sampling and the decimated locally adaptive point set.

"Stanford Bunny" data set with originally 34824 points was reduced to a set of 1972 points. "Angel" was reduced from 237018 points to 3902. Notice that the resulting point density depends on the quality of homotopical axis approximation. The less is the difference between the computed homotopical axis and the discrete homotopical axis the greater is the distance between the points and the axis, and the smaller is the resulting data set.

According to the argumentation in Section 6.6.2 the computed homotopical axis is homotopy equivalent to the discrete homotopical axis. It follows that, since the discrete homotopical axis is the minimal set of steepest paths between the critical points, the computed homotopical axis is in the worst case the superset of the discrete. Consequently, in the worst case we have an oversampled but local homotopy stable boundary.

6.8 Conclusion

In this chapter we successfully completed the evaluation of the refinement reconstruction. The experiment requires a local homotopy stable sampling set which is sparser than the local feature size based ϵ -samplings provided by related algorithms. To provably meet the demands on the sampling we derived a stability criterion on the critical points and discrete homotopical axis.

The computation of the discrete homotopical axis is derived from the flow relation framework which is also an underlying step in refinement reconstruction. The stability of the computed homotopical axis provides feature size estimation on data points and consequently the lower bounds for the sampling. The estimated feature size defines the maximum distance to the nearest neighbor, so all points with lesser distance are not required in the data set. Successive deletion of points sorted in increasing order according to the estimated value provably results in a local homotopy stable sampling.

The framework on stability of critical points and homotopical axis experimentally developed in this chapter extends the results on boundary reconstruction and offers a basis for further research on homotopy equivalence of reconstructed space partitions. We provided arguments for homotopy type preservation in the discrete homotopical axis computation deriving the stability of the reconstruction on decimated data sets.



Fig. 6.4: left: original mesh, right: reconstruction from the decimated local homotopy stable point set \mathbf{F}

The experiments provide a nonmanifold multi-regional shape which is non-uniformly sampled according to the framework on data set decimation derived in this chapter. The underlying shape is nonmanifold, not smooth and multi-regional which makes reconstruction with all related computational topology based approaches known to us not possible. The thinned- (α, β) -shape-reconstruction handles nonmanifold multi-regional shapes but does not process locally adaptive samplings which is successfully carried out by refinement reconstruction. So, we developed an experiment which shows the advantage of refinement reconstruction over thinned- (α, β) -shape-reconstruction and all related computational topology based approaches known to us.

Chapter 7

Conclusion and Outlook

The main goal of this work was to define locally variable sampling conditions and a reconstruction method which results in a digital representation of a given real world scene provably preserving original topological properties. The starting point for our research was theoretical framework and reconstruction method for non-manifold 3D-surface reconstruction originally introduced for 3d in [Stelldinger, 2008b]. This framework requires the sampling parameters to be globally set for the whole scene.

The real world scene in [Stelldinger, 2008b] is divided into a set of disjoin open regions called space partition. It is assumed that the space partition consists of more than two regions and that the boundary of more than two regions can intersect. It follows that the boundary of the assumed space partition is a non-manifold 2D-surface embedded into a 3D Euclidean space. The research aim in [Stelldinger, 2008b] is then the topology preserving reconstruction of the non-manifold 2D-boundary. This research on sampling fosters questioning what the most sparse sampling conditions are and which amount of noise can be handled by the reconstruction method.

The sampling conditions are defined in such a way that the homotopy-equivalent and geometrically similar subsets of the original regions are enveloped by sampling points denser than the tightest narrowing in the subsets. In other words the discrete distance value on the original boundary is always less than the discrete distance value on the critical point with smallest continuous distance value.

The sampling density serves as a parameter to adjust the α -parameter of the reconstruction algorithm. The α -shape already separates the relevant homotopy-equivalent regions correctly but contains spurious holes. The maximal sample point deviation is then used to detect the holes which do not correspond to any original regions. The regions less than the internal parameter β , which is computed using the maximal sample point deviation, are filled and the resulting thick boundary is then thinned by a topology-preserving post-processing step.

The sampling conditions defined in [Stelldinger, 2008b] ensure even the tightest narrowing to be sufficiently sampled. But the sampling density is then constant for the whole boundary. In our framework we explore the idea of limiting the sampling density and - depending on the sampling density - to limit the maximal sample point deviation. But our requirement for the sampling is to ensure all steepest increasing paths on discrete distance transform - starting in the relevant subsets of the original regions - to stay in these relevant parts. This renders possible to define locally adaptive sampling conditions.

The framework developed in [Edelsbrunner, 2003] defines a strict relation called "flow relation" on Delaunay simplices which mimics the steepest increasing paths. The result of the reconstruction method called "Geomagic Wrap[©]" (applied on each Delaunay tetrahedron containing its own circumcenter) is the 3D extension of the Gabriel graph [Gabriel and Sokal, 1969]. We call this reconstruction step on samplings fulfilling our conditions the Elementary Thinning.

The result of elementary thinning is a correct separation of local maxima, where the discrete local maxima are uniquely associated with continuous local maxima. The separation is called *correct* if the associated discrete local maxima of the continuous local maxima being in different original regions are in different discrete regions.

The original regions may contain more than one local maximum. But the result of elementary thinning is the separation of all maxima. Such separation corresponds to an oversegmentation of the original scene. Since the oversegmentation naturally carries boundary elements which may be removed to merge different regions while preserving correct separation, we call such separation a *refinement*.

The Wrap algorithm follows the steepest decreasing path in the discrete distance transform and successively deletes Delaunay simplices from the complex which it passes through. The remaining Delaunay simplices have then the smallest discrete distance values in the relation. We call such boundary reconstruction *minimal refinement*.

The medial axis [Blum, 1967] is a complete shape descriptor, but only a subset of the medial axis is necessary to represent the homotopy type of the shape or, as we call it, the *region*. Contractible regions have star-like medial axes. The homotopy type can be represented by one point only. The *local region size* measures for each point on the boundary the minimal distance value of the local maxima reachable by steepest ascent on the continuous distance transform. This value gives the lower bound of the largest inscribing ball of the region. Thus the local maxima only are relevant for definition of the local region size.

Our new sampling conditions limit the ratio between the discrete distance value on the boundary and the local region size. The result is, the discrete distance value on the associate local maximum is at least a fraction of the continuous distance value on the original local maximum. Since the reconstructed boundary is minimal, by scaling the discrete distance value by the reciprocal of the fraction we obtain a value of the maximal boundary simplex. Thus all boundary simplices which exceed this value cannot separate different regions and can be deleted. We call such region merging on too large simplices the *refinement reduction*.

In this work we show that the sampling conditions defined by local region size are insufficient in order to obtain a reconstruction which can be reduced by further deletion of boundary simplices to a homotopical equivalent of the original space partition. So, we defined a new subset of the medial axis - the minimal superset of all discrete critical points. As proven in [Chazal and Lieutier, 2005a], this subset of the medial axis, in our framework called the *homotopical axis*, is homotopy-equivalent to the medial axis and, as we implied, the homotopical axis is homotopy-equivalent to the space partition.

The *local homotopical feature size* is the minimum between the local region size and the distance to the homotopical axis. The local homotopical feature size measures the distance to the critical points and to the steepest paths between the critical. So, the sampling conditions defined by local homotopical feature size ensure a denser sampling in narrowings. The result of refinement reduction is then a boundary reconstruction which is reducible to a space partition with a boundary which does not cut the original homotopical axis. So, the result is reducible to the correct separation of connected components of the original homotopical axis.

As we have shown, the our algorithm for refinement reconstruction has advantages over all reconstruction methods based on a computational geometry approach known to us, including the "Thinned- (α, β) -Shape-Reconstruction" published in [Stelldinger, 2008b]. In summary:

- The class of shapes which can be handled by our new refinement reconstruction has been extended to space partitions consisting of multiple regions with non-manifold boundary. So, the assumed shapes generalize *r*-regular, *r*-halfregular, non-smooth and *r*-stable objects. (Note that in [Stelldinger, 2008b] the multi-regional space partitions with non-manifold boundary are classified by the value of maximal boundary dilation which does not change the homotopy type.)
- The assumption of multi-regional space partition enables the reconstruction for volume-based samplings such as in computer tomography or magnet resonance imaging.

7.1. CONTRIBUTIONS

- The refinement reconstruction handles locally non-uniform and highly noisy sampling. To our knowledge the sampling conditions generalize the requirements made in [Stelldinger, 2008b] as well as the sampling conditions defined for all topology preserving reconstruction methods based on a computational geometry approach.
- The method handles noise arising from blurring which is here defined as excessive sample point deviation from the boundary, as well as a large amount of outliers (over 20% in our experiments).
- Given the sampling conditions and parameters as defined in [Stelldinger, 2008b], the refinement reconstruction results in an equivalent boundary approximation.

However our method reconstructs a reducible refinement only. The result preserves the original topological properties but needs further processing and knowledge to be reduced to a homotopy-equivalent space partition.

7.1 Contributions

In our ambition to make this work self-contained lucid we achieved theoretical, experimental and empirical contributions. In the introduction of theoretical concepts we presented:

- The proof that the local maxima of the distance transform are the local maxima of the corresponding medial axis.
- The definition of the homotopical axis as the smallest superset of critical points and steepest increasing paths between them and derivation of the homotopical equivalence to the space partition.
- The definition of the local region size as a function which maps each boundary point to the smallest distance value of the local maxima reachable by steepest increasing paths.
- The definition of the local homotopical feature size as the minimum between the local region size and the distance to the homotopical axis.
- The proof of equivalence between the concepts of equivocal and "Not-Gabriel" simplices which is needed to combine the concepts in the framework of refinement reconstruction.
- Observations and proved claims for geometrical dependence between certain Delaunay simplices.
- A discussion on comparison of Delaunay simplices and introduction of a new *size* of a simplex as the largest distance value in the simplex which corresponds to the flow defined on discrete distance transform.
- A proposition on how to compute the size of a simplex and a discussion when the computation is necessary.

The evaluation of the framework developed for thinned- (α, β) -shape-reconstruction contributed in the following respect:

- Unification of sampling conditions and comparison to other approaches showed that the thinned- (α, β) -shape-reconstruction has advantages over all other reconstruction methods known to us before we developed refinement reconstruction.
- Experiments on laser range scan data sets with nearly noise-free dense as well as blurred data, which demonstrate equivalent results achievable with previous reconstruction methods as well as the advantage and robustness of the algorithm on blurred data sets with excessive sample point deviation.

- Experiments with samplings taken from non-manifold boundary of multi-regional space partitions demonstrating the ability of the method to reconstruct homotopy-equivalent surfaces.
- Discussion of problems of thinned- (α, β) -shape-reconstruction due to excessive noise corruption and propositions to overcome these. The excessive noise corruption causes topological distortions on the reconstructed boundary which can be removed only under further assumptions. We propose an extension of the algorithm to detect certain topological artifacts such as chains of singular edges or surface patches without boundary which do not separate two different regions and have the same region on both sides.

Taken together the main contribution of our work is the introduction of the theoretical framework, the derivation of guarantees or, respectively, proofs, and the evaluation of the refinement reconstruction. The theoretical framework includes:

- Introduction of unique association between local maxima on distance transform defined on original boundary and the local maxima on distance transform defined on sample points.
- Definition of a refinement as the correct separation of associated local maxima.
- Definition of a minimal refinement consisting of minimal Delaunay simplices according to steepest decreasing paths starting on local maxima.
- Definition of locally adaptive sampling conditions which generalize all sampling conditions known to us and contain information on local homotopy.
- Proof that application of the constructed retraction algorithm on Delaunay tetrahedrons containing own circumcenter results in a minimal refinement.
- Proof that minimal refinement can be reduced by merging of regions on boundary simplices which exceed a certain value. This value can be computed by the largest circumradius of all Delaunay simplices in the region.
- Proof that the result of refinement reconstruction is reducible to a stable refinement which correctly separates the connected components of the homotopical axis.

The evaluation of the reconstruction algorithm resulted in the following new results:

- Given the sampling parameters as required for thinned- (α, β) -shape-reconstruction, the result of refinement reconstruction is homotopy-equivalent.
- The sampling conditions defined for refinement reconstruction generalize all sampling conditions defined for previous reconstruction methods known to us.
- Refinement reconstruction handles the most sparse sampling and the largest amount of noise of all methods known to us.
- Refinement reconstruction results in a reducible refinement on samplings of non-manifold boundaries of multi-regional space partitions.
- Our method handles large data sets from laser range scanners. Even if we cannot guarantee that the result is homotopy-equivalent, in practice for very dense sampling sets we observed no need of reduction.
- Our new method reconstructs the non-manifold boundary of a multi-regional space partition which has been sampled by a volume-based approach such as computer tomography post-processed by 3D Canny edge detection algorithm for point cloud extraction.

7.2. FUTURE WORK

To experimentally demonstrate the advantage of the refinement reconstruction over thinned- (α, β) shape-reconstruction we introduced a framework for data set decimation which results in a *local homotopy* stable sampling set. The sampling is *local homotopy* stable if it is a (ψ, ρ) -sampling based on local homotopical feature size. For the resulting data set we required the most sparse sampling density to additionally show the superiority of refinement reconstruction over reconstruction methods based on ϵ -samplings. The contributions from the evaluation on locally non-uniform very sparse data sets are:

- Stability of critical points in low quality data sets. Here we introduced a new definition on stability. A continuous local maximum is stable if the distance value on the discrete distance transform on the discrete local maximum reachable by steepest ascent on the discrete distance transform is guaranteed to be whithin a certain interval of the original continuous distance value. A saddle is stable if all reachable local maximum are stable.
- Proof that a continuous local maximum is stable if the distance values on all saddles reachable by steepest ascent are sufficiently small.
- Definition of the discrete homotopical axis based on extended gradient and the continuous flow defined on discrete distance transform.
- Proposition to compute the homotopical axis which approximates the discrete homotopical axis.
- Local homotopical feature size is estimated on data points given the discrete homotopical axis.
- The definition of a data set decimation method which results in a *local homotopy stable* sampling.
- The experiments demonstrate refinement reconstruction results on sparse *local homotopy stable* data sets. The underlying data sets are laser range scan data from "Stanford 3D Scanning Repository" as well as artificially generated data sets to demonstrate the strength of the reconstruction and the decimation methods on the non-manifold boundary of a multi-regional object.

However this work has left open questions and issues which motivate further research.

7.2 Future Work

Extensions for Thinned- (α, β) -Shape-Reconstruction The evaluation of the thinned- (α, β) -shapereconstruction indicated some open problems according to excessive amount of noise. The reconstruction method results in a homotopy-equivalent boundary only under the assumption that the boundary cannot consist of singular edges and does not contain non-orientable 2D surface patches on the boundary which we call "Klein bottle" surfaces. We propose several ways to overcome the topological artifacts:

- Limiting the internal parameter α to be less than the largest sample point deviation promises to solve the problem of surface patches which do not correspond to the original boundary.
- The processing step to detect non-orientable surface patches and the reconstruction step to fill them. The final topology preserving thinning which is already a processing step of the algorithms removes the distortion.
- The chains of singular edges connected to the boundary enclose surface patches which are covered by q-dilation of the boundary with q being the maximum sample point deviation. The expansion containing the smallest Delaunay triangles according to their circumradii results in a surface without singular edges chains. The final contraction on simple simplices contracts the distorted surface.

Topologically Correct Boundary Reconstruction The ambition of our work has been to find both the weakest conditions on the sampling and the most effective method to reconstruct the topology of the original object. Even though in our research we succeeded in presenting results on locally adaptive boundary reconstruction the defined conditions are too weak to find an unique object representation.

As we have seen in the evaluation, sampling based on the homotopical axis loses relevant topological properties. Differentiating between shapes of different topology can become impossible. So, we propose to:

- Extend the definition of the homotopical axis which respects the non-manifold boundary points and
- Limit the upper bound of the sample point deviation from the boundary.

The two extensions strengthen the sampling conditions, but first, the resulting sampling conditions still generalize the requirements of previously proposed methods known to us, and second, we expect this to solve the problem of shape dissolution in the sampling.

Parallelization The construction of the first step of our algorithm and the property of strict relation between Delaunay simplices specified in [Edelsbrunner, 2003] enables parallel thinning processing. Each thinning process performes "Geomagic WRAP[©]" on deleted Delaunay tetrahedrons which contain their own circumcenters.

The refinement reduction step as introduced in our work is performed on a sorted list of boundary simplices. However we expect the process to be order-independent which again enables parallel implementation of the algorithm.

Application to Shape Matching The medial axis together with the distance values uniquely describes a shape. Consequently, two shapes with equal medial axes and corresponding distance values are equal. Two shapes with equal medial axes but different distance value mapping on the medial axis are homotopy-equivalent. Two shapes with homotopy-equivalent medial axes are also homotopy-equivalent.

In [Chazal and Lieutier, 2005a] a homotopy-equivalent subset of the medial axis is presented called λ -Medial axis. Two shapes with homotopy-equivalent λ -medial axes are homotopy-equivalent.

The homotopy axis is a homotopy-equivalent subset of the medial axis and is a subset of λ -medial axis. Two shapes with homotopy-equivalent homotopy axes are homotopy-equivalent. So, using the robust approximations of homotopy axes shapes can be compared.

Finding similar shapes in a data base is a resource consuming procedure. Since the homotopy axis is a very reduced form of a topologically similar shape we propose to use it to simplify the search. The representation of the homotopy may then be computed and coded in the most simple way. We propose to compute the homotopy by the method of *topological persistence* introduced in [Edelsbrunner et al., 2002] and already successfully applied in [Chazal and Lieutier, 2005b] for computation of *homology groups*.

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List of Symbols

\mathbb{R}	Set of real numbers	20
\mathbb{R}^3	Three dimensional Euclidean space	20
\mathcal{A}	Affine Expansion	20
\mathcal{R}	Space partition	20
R	Continuous region	20
rd	Distance Transform	21
d	Distance Transform	21
MA	Medial Axis	23
MAT	Medial Axis Transform	24
B_{mc}	maximal closed ball	24
\mathcal{B}_o	Open Ball	24
S	Finite Set of Sampling Points	24
HA	Homotopical Axis	25
lfs	Local Feature Size	26
wfs	Weak Feature Size	27
lrs	Local Region Size	28
lhfs	Local Homotopical Feature Size	29
\mathcal{K}	any simplicial complex or later Delaunay	34
\mathcal{D}	Simplicial Complex Partition	34
D	Delaunay complex	35
R	Reconstructed Space Partition, subset of Delaunay	37
R	Reconstructed Region	37
D	Interior of a reconstructed region	37
D	Reconstructed Region	37
V	Voronoi diagram	41
D_{lpha}	α -complex	42
\mathscr{S}_{α}	α -shape	42
U	Union of Balls	83
$H_{\alpha,\beta}$	(lpha,eta)-hole	85
\mathscr{H}_{lpha}	Union of α -Holes	85
H_{α}	Set of α -Holes	85
H_{α}	α -Hole - One Connected Component in the Union of α -Holes	85
$H_{\alpha,\beta}$	(α, β) -Hole - α -Hole greater than β	85
D_{α}	α -Hole - subset of Delaunay Complex	85
$D_{\alpha,\beta}^{\oplus}$	(α, β) -shape-reconstruction	86
$D_{\alpha,\beta}$	Result of (α, β) -Complex Thinning	92
$\mathscr{S}_{\alpha,\beta}$	Shape of Thinned- (α, β) -Shape-Reconstruction	92
D_E	Result of Elementary Thinning, Minimal Elementary Refinement	123
D_R	Result of Refinement Reduction Complex	125
D_R	Discrete Space Partition	158

Index

 (α, β) -shape-reconstruction, 86 α -complex, 42 α -hole, 86, 139 α -shape, 42, 84, 138 λ -medial axis, 155 μ -critical, 102 μ -critical point, 155 μ -reach, 31 r-regular, 81, 84 r-stable, 80 ancestor set, 123, 164 associated centered cell, 121 axis discrete homotopical axis, 158 extended homotopical axis, 150 homotopical axis, 128 homotopical axis approximation, 159 canny 3D canny edge detection, 143 cell centered cell, 120 inconsistent, 47 circumball, 35 circumcenter, 35 circumradius, 35 coface, 35 collapse, 60, 92, 98, 123 collapsible pair [Edelsbrunner, 2003], 50 compatible (α, β) -hole, 95 computed tomography, 143 condition centered cell condition, 120 constructive retraction, 123 critical reachable critical, 28 critical function, 31 critical point μ -critical point, 30, 102, 155 Delaunay, Voronoi, 42

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