# Visualization of Vasculature with Convolution Surfaces: Method, Validation and Evaluation

Steffen Oeltze and Bernhard Preim

Abstract—We present a method for visualizing vasculature based on clinical CT- or MR data. The vessel skeleton as well as the diameter information per voxel serve as input. Our method adheres to these data, while producing smooth transitions at branchings and closed, rounded ends by means of convolution surfaces. We examine the filter design with respect to irritating bulges, unwanted blending and the correct visualization of the vessel diameter. The method has been applied to a large variety of anatomic trees. We discuss the validation of the method by means of a comparison to other visualization methods. Surface distance measures are carried out to perform a quantitative validation. Furthermore, we present the evaluation of the method which has been accomplished on the basis of a survey by 11 radiologists and surgeons.

*Index Terms*—vessel visualization, convolution surfaces, implicit modeling, vessel reconstruction method.

## I. INTRODUCTION

N medical education as well as in therapy planning, the visualization of vasculature is crucial. It is desirable that the topology of vascular trees can be correctly inferred from the visualization. Moreover, the curvature and the diminution of the diameter towards the periphery should be depicted correctly. Traditional methods of medical volume visualization, such as direct volume rendering, threshold-based isosurface rendering, or MIP are not well-suited for the above-mentioned goals. Due to image noise and the limited resolution of computed tomography (CT) or magnetic resonance imaging (MRI) conventional methods produce noisy 3d visualizations. Also, the visual separation of contrast-enhanced vascular structures and other high-intensity structures, such as bones, might be very difficult. Artifacts and discontinuities in the visualization distract the viewer. For educational purposes and therapy planning, vascular structures should be reconstructed based on the radiological data and some model assumptions as to the shape of vasculature (Gerig et al. [1]). Furthermore, reconstructed visualizations are useful in the vessel analysis stage because segmentation errors become obvious.

We describe a new method for vessel visualization which originates from implicit modeling. This method produces smooth surfaces even at endpoints and branchings. The vessel skeleton serves as the input for the visualization process. It is represented as a directed graph [2]. Edges of this graph are approximated by line segments connecting adjacent voxels. Each segment is described by its two endpoints and one associated radius (the radius of the largest circle completely

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enclosed by the segmentation result), respectively. The visualization method applied here is based on *convolution surfaces* introduced by Bloomenthal and Shoemake [3]. As a difference to previous applications of convolution surfaces we shall faithfully represent the radius distribution given by the vessel analysis.

We investigate surface distances between our visualization and other visualization methods. In particular, we compare isosurface renderings of the vessel segmentation result with convolution surfaces. An evaluation with 11 experienced medical doctors suggests that our method is especially useful for close-up views.



Fig. 1. Close-ups of a liver vessel tree generated by isosurface rendering, concatenation of truncated cones [4] and convolution surfaces (from left to right).

## II. PRIOR AND RELATED WORK

Following the pioneering work of Gerig et al. (recall [1]) several attempts have been made to develop special visualization techniques for vascular trees. Our visualization technique is based on the model assumption that cross sections of non-pathologic vessels have a circular shape, as discussed in [5]. Masutani et al. fitted cylinders along the skeleton to visualize vascular structures. The drawback of this method is that discontinuities at branchings arise where cylinders with different diameters coincide. A special problem, the visualization of cerebral structures, has been tackled by Puig et al. [6]. She modeled typical bifurcations and pathologic situations and fitted these models to the patient specific data at hand. The focus of her work is on the geometric continuity and on realistic shading.

In [4] a vessel visualization pipeline has been introduced. The skeleton and the local vessel diameter determined in the image analysis stage are smoothed with a (121) binomial filter. Special care is taken at branchings to weight the incident branches. In the mapping step, truncated cones are used to represent the diminutions of the vessel diameter faithfully. However, the fitting of primitives along the skeleton does not generate smooth transitions between vessel segments at branchings. In [7], branchings are treated separately to avoid rendering discontinuities and the construction of structures inside the geometric model. Along straight parts, a vessel

S. Oeltze and B. Preim are with the Department of Simulation and Graphics, Otto-von-Guericke University of Magdeburg, P.O. Box 4120, 39016 Magdeburg, Germany (email: {stoeltze|preim}@isg.cs.uni-magdeburg.de)

segment is approximated by four quadrilateral patches. The method is based on the iterative refinement of a rough, initially constructed base mesh by means of subdivision surfaces.

An advanced method for vessel visualization is *Curved Planar Reformation* (CPR) [8]. Given the vessel skeleton, a curved plane is generated by moving a line - aligned parallel to the horizontal axis of the viewing plane - along the skeleton. A 2d-image of the vessel is eventually obtained by flattening the curved plane and displaying all voxels located close to it. A comprehensive survey of methods for vessel visualization is given in [9].

## A. Reconstruction of Vessels for Interaction

Not much effort was spent so far on the exploration of vascular structures. The exploration is crucial because vascular trees are often complex. Facilities to restrict the visualization are essential to support the understanding. In [10] vessels have been segmented and analyzed in order to selectively hide them. The subdivision of vessels by placing and moving balloons with the goal to interact with such parts of vascular structures is described in [11].

## III. MODELING OF TREE-LIKE STRUCTURES WITH IMPLICIT SURFACES

Implicit surfaces offer an alternative to explicitly constructing the surface of an object by a set of polygons or parametric patches. They describe the surface by an equation which is often more compact than its parametric counterpart. Especially in modeling smooth, deformable objects, implicit surfaces unfold their full strength. James F. Blinn introduced implicit surfaces in computer graphics. He developed *Blobby Molecules* to visualize electron density fields [12].

#### A. Implicit Surfaces: a Brief Introduction

A classical example for an implicit equation is the description of a sphere with radius r:  $x^2 + y^2 + z^2 - r^2 = 0$ . This formula represents all points p(x,y,z) in space which are on the surface of a sphere with radius r. Furthermore, it facilitates point classification by simply checking the sign of the resulting scalar value. With  $F(p) = x^2 + y^2 + z^2$  and  $Iso = r^2$  the equation of a sphere can be generalized as Eq. 1:

$$F(p) - Iso = 0 \tag{1}$$

F(p) is called the *scalar field function* because a scalar value may be computed for each point p. *Iso* denotes the *isovalue* for generating an *isosurface* which represents the surface where the implicit equation is zero.

The scalar field function employed for modeling 'blobs' [12] is given in Eq. 2:

$$F(p) = be^{-\sigma \|c - p\|^2}$$
(2)

where c is the center of an electron. Eq. 2 describes a Gaussian bump centered at c, having height b and standard deviation  $\sigma$ . In order to create more complex objects, several

blobs might be specified whose scalar fields overlap if close enough. Then the scalar value at p can be calculated as Eq. 3:

$$F(p) = \sum_{i} b_{i} e^{-\sigma_{i} ||c_{i} - p||^{2}}$$
(3)

Note that only scalar fields around point primitives were considered so far.

## B. Convolution Surfaces

Bloomenthal and Shoemake extended the concept to skeletal primitives of theoretically any kind, e.g. line segments, polygons, or planar curves [3]. This enhancement overcomes a major drawback of point primitives namely their deficiency in describing flat surfaces and smooth generalized cylinders. They introduce *convolution surfaces* to model the surface of an object around its skeleton. In the following, S denotes a skeleton and s refers to a single point on the skeleton.

With *convolution surfaces* the scalar value is calculated according to Eq. 4:

$$F(p) = f(S, p) = \int_{S} \left( e^{\left(\frac{-\|s-p\|^2}{2}\right)} \right) ds \tag{4}$$

where f(S, p) is the convolution of a skeleton with a three-dimensional Gaussian filter. In contrast to other implicit surfaces, the value is computed considering *all* points of the skeleton by integration. The resulting surface does not show creases and is bulge-free for non-branching skeletons.

Convolution surfaces utilize a concept which is well known from signal processing namely the modification of a signal by a filter. For a Gaussian filter function with height 1 and standard deviation 1/2, Eq. 4 may be rewritten as

$$F(p) = f(S, p) = (h \otimes S)(p)$$
(5)

where S is the signal, h is the filter function and  $\otimes$  denotes the convolution operator. For the visualization of vasculature, the vessel skeleton corresponds to the signal. The selected filter function should smooth this signal and thereby letting high frequencies gently drop off in the neighborhood. The resulting field around the skeleton corresponds to the scalar field mentioned earlier. By constructing an isosurface through this field the convolution surface is formed.

For the understanding of bulge-free blending it is necessary to elaborate on the superposition property of convolution:

$$h \otimes (S_1 + S_2) = (h \otimes S_1) + (h \otimes S_2) \tag{6}$$

This guarantees that two abutting segments produce the same convolution as does their union [13]. Furthermore, superposition has an impact on implementation issues and the modeling process. It permits the convolution of a complex object primitive by primitive in an arbitrary order instead of considering the skeleton as a whole.

## C. Filter Selection

An appropriate filter function should be continuous and monotonic. Furthermore, it should have finite support (or be negligible beyond a certain distance), and exhibit zero or near zero gradient at this distance. These requirements restrict the filter selection to low-pass filters, such as the Gaussian. Numerous other kernels have been published. [14] includes an analysis of widespread functions with respect to computational complexity and the types of modelling primitive. For the visualization of vasculature each of the surveyed kernels is applicable. However, the scope of eligible filter functions is strongly reduced when a given radius distribution should be faithfully represented.

Initially, the convolution surface along a line segment has a fixed radius. In [14], the creation of a surface that resembles a tapered cylinder by using linear profiling functions is described. The use of Bezier curves with two control points for representing linear radius distributions is introduced in [15]. Both methods are convenient when interactive radius modification is required. However, they are inadequate for modeling surfaces that exactly converge against a given radius. As far as we know, solely in [13] and [16] approaches have been published that concentrate on this problem.

In [13] a Gaussian function is utilized for convolution:

$$h(p) = e^{-d(p,S)^2\omega}, \ \omega = \ln 2, \ d(p,S) > 0$$
 (7)

where  $\omega$  is referred to as the *width coefficient* which equals  $1/(2\sigma^2)$ . The distance between point p and the line segment skeleton S is denoted by d(p, S).

In [16] the use of two other filter functions is discussed with regard to the correct representation of a linear radius distribution. However, both the suggested inverse cubic function  $(1/d(p, S)^3)$  as well as an alternative function  $(r^2/d(p, S)^2)$ , where r equals the varying radius along the line segment) decrease more slowly to near zero compared to the Gaussian.

Discussion: Computational speed determined our choice of a filter function. By definition of the convolution surface (Eq. 4), the entire skeleton needs to be considered when calculating the scalar value at a point p. For the visualization of vascular structures this means a prohibitively high computational effort. To improve the performance, we will restrict the computation of the scalar field using bounding volumes along line segments. The tightness of a suitable bounding volume strongly depends on the filter function (in particular on the distance from the center to where the function value is negligible). We choose the Gaussian because it drops much faster to zero than the other two kernels discussed in [16]. It therefore allows tight bounding volumes and fast computation. In [17], the filter selection is discussed in more detail.

#### D. Correct Representation of the Radius Distribution

According to [13], the computation of the convolution integral in Eq. 4 may be simplified by separating it into the product of the *integration filter* and the *distance filter*. Whereas the first term requires solving a one-dimensional integral the second is simply a single evaluation of the kernel:

$$h(p) = e^{-(d(p,H))^2\omega},$$
 (8)

where d(p, H) is the distance between point p and its projection H on the line which proceeds through the considered line segment (if p is near the end of the segment, H might be beyond the segment). The separation of the computation into two filters is crucial for the evaluation of the implicit function. Instead of the 3d integration (Eq. 4) we have to solve a 1d integral which can be precomputed and stored in a lookup table. We use the same lookup table as [13] with 10000 entries.

For adapting the radius of the resulting convolution surface, d(p, H) is divided by radius r(H). The latter is determined with linear interpolation between the radii at the segment endpoints. In order to let the convolution surface converge against a desired radius, an appropriate isovalue and a width coefficient  $\omega$  must be selected. Bloomenthal employed an isovalue of 1/2 so as to let the convolution surface pass through the segment endpoints. Now, let us consider the convolution surface of a sufficiently long cylinder and a point p which is located exactly on the surface and in the middle of it. Here, the integration filter equals 1 since the kernel is fully subtended by the segment. With the constraint that d(p, H) = r(H) for point p on the convolution surface it follows from Eq. 1 and Eq. 8:

$$e^{-(r(H)/r(H))^2\omega} - 1/2 = e^{-\omega} - 1/2 = 0$$
(9)

Thus,  $\omega = \ln 2 \approx 0.6931$ .

## IV. BLENDING

The creation of smooth transitions between simple objects, forming a complex organic shape, is a strength of implicit surfaces. Here, so-called *blends* are used instead of parametric free-form surfaces. For convolution surfaces, blending corresponds to an integration of the filter along the skeleton. At the skeleton joints, the scalar fields of adjacent primitives overlap. The convolution surface constructed through the resulting field forms a smooth envelope of the underlying joint. In an implementation, each primitive may be convolved separately due to the superposition property of convolution. Blending may also have negative effects for a faithful visualization of anatomic tree structures which are discussed in the following.

#### A. Blending Strength at Branchings

With the initial filter design in [13], the transitions at branchings were very smooth but deviated strongly from the skeleton. Discussions with an experienced radiologist showed that this is undesirable and may even hamper the interpretation of the topology. We propose a narrower filter kernel which results in a surface which tracks the skeleton more faithfully.

#### B. Unwanted Blending

For precise modeling of complex shapes it is essential to control the blending between certain parts of the object. Concerning vascular structures, segments whose skeleton is not connected should not blend with each other. In [18] a *restricted blending graph* was suggested to overcome this problem. Unfortunately, this solution does not ensure  $C^1$ continuity of the shape. As an alternative, *local convolution*  was introduced [19]. This concept is based on defining a portion of the skeleton for computing the scalar value at a certain point in space. It prevents blending even between small folds of the skeleton and facilitates the generation of a  $C^{1}$ -continuous shape.

## C. Bulging

Convolution surfaces are bulge-free for non-branching line segment skeletons due to the superposition property of convolution. However, as shown in [13], they do exhibit bulges at branchings. This effect is disturbing for the visualization of vascular structures since a bulge might be easily mistaken for a pathological variation, e.g. an aneurysm. Even though our visualization method is not targeted at supporting vascular diagnostics, we shall minimize this drawback.

## D. Consequences

As a consequence of our analysis of different filters we choose the Gaussian [13] for the convolution. However, we suggest a modification to reduce the blending strength at branchings. Employing the altered filter function has an impact not only on the blending strength but also on unwanted blending as well as on bulging. Furthermore, with the modified filter function the polygonization of scalar fields might be accelerated by means of tighter bounding volumes.

## V. VISUALIZATION OF ANATOMIC TREE STRUCTURES WITH CONVOLUTION SURFACES

In this section we describe how a modification of  $\omega$  allows to solve the blending problems. We then and discuss a preprocessing of the data in order to reduce the effort to compute the convolution surface. The same vessel analysis results which have been used in [4] are the input for our method. We also employ the binomial filtering to smooth the vessel skeleton and diameter.

## A. Filter Modification

We carefully evaluated different  $\omega$  values and found that a value of  $\omega = 5ln(2)$  is suitable to considerably reduce the undesired effects such as unwanted blending and bulging (see Sec. VII-C). Note, that  $\omega$  has been increased with the effect that the filter function is narrower. In order to correctly represent the radius distribution along a line segment, a recalculation of the isovalue is required. Under consideration of our new  $\omega$  value the isovalue (*Iso*) is evaluated as follows:

$$F(p) = e^{-(r(H)/r(H))^2 5 \ln 2} - Iso = e^{-5 \ln 2} - Iso = 0$$
(10)

Hence, Iso = 1/32 = 0.03125.

To evaluate our filter function, we employ a simple skeleton with a trifurcation (4 coinciding branches). In anatomic tree structures, we never found more branches coinciding. In Fig. 2 it is illustrated how the blending strength is reduced for the simple skeleton. Also, the bulging problem is avoided with the modified filter function (see Fig. 3). To study unwanted blending, we use an S-shaped skeleton with 3 mm distance between the horizontal lines. The radius was increased until the problem occurred. With the original filter, unwanted blending appeared for a radius of 1.07 mm, whereas with the modified  $\omega$ value, it appeared at 1.37 mm. The ratio between the distance of the convolution surfaces and the distance of the centerlines determines the occurrence of unwanted blending. With the modified  $\omega$  value, we could reduce the ratio from 29% (see Fig. 4 (left)) to 9% (see Fig. 4 (right)).



Fig. 2. Transition at branching, left: convolved with original filter function  $(\omega = ln(2))$ , right: convolved with modified filter  $(\omega = 5ln(2))$ . The semitransparent visualization reveals the underlying skeleton. Note that the original filter was designed to let the convolution surface pass through the segment endpoints. With the modified filter the surface tracks the skeleton more closely.



Fig. 3. Side view of the branching in Fig. 2. The bulging problem (left) is considerably reduced with the modified filter (right).



Fig. 4. Unwanted blending. Distance between the horizontal branches of the S-shapes is 3 mm. The radius of all branches is 1.07 mm. Unwanted blending (left) is considerably reduced with the narrower filter (right).

## B. Computational Complexity

For the construction of the convolution surface it is necessary to evaluate the scalar value at numerous points in space. Each of these computations requires considering the whole tree. By contrast to previous applications of convolution surfaces with small to moderate-sized structures, vascular trees may well have more than 1000 branchings.

In order to accelerate the computation, we determine the *significant* range of the *scalar field* (SSF) about each line segment. For a point p located outside this range, F(p) is smaller than a given threshold T. We require the first three decimal places of F(p) to equal 0 (T = 0.001). For storing the SSF, a partitioning of space is necessary. The voxel grid of the underlying data may be used as a basis for the partitioning.

The preprocessing proceeds as follows: While iterating over all line segments, a cylindrical bounding volume (CBV) is constructed. The cylindrical shape of the bounding volume allows to closely approximate the shape of the convolution surface and the underlying scalar field. The radius of the CBV is based on the SSF which in turn is determined by the maximum radius along the line segment multiplied by a factor *fac*. The latter is computed with respect to the width of the convolution filter. The width influences the extension of the SSF. Although, the modified Gaussian from Sec. V-A has infinite support, it exhibits values close to zero for points beyond a certain distance from the center. This distance corresponds to *fac* and is adapted to *T*:

$$e^{-x^2\omega} < T \tag{11}$$

$$e^{-fac^2 5 \ln 2} < 0.001$$
 (12)

Thus, a factor of fac = 1.5 is adequate for enclosing the SSF. The CBV is then employed to identify those voxels contained in the SSF of the current line segment (see Fig. 5). This information is used during surface construction for determining the line segments with a significant influence on p.



Fig. 5. Axes-aligned bounding boxes (left) and cylindrical bounding volumes (right) for an artificial tree (right)

More details of the acceleration are described in [17]. As a result, the use of the CBV accelerates the whole computation by two orders of magnitude (factor 100-200).

## VI. EXPLORATION OF VASCULATURE

It is often desirable to restrict the visualization of anatomic tree structures or to focus it on certain subtrees. For example, in tumor surgery, vessel segments around the tumor are more important than more distant parts. In general, surgeons would like to know which vessel segments must be reconstructed, if they have to be cut. The vessel analysis results allow for interactions to support such visualization goals. Based on the branching graph, vessel segments which depend on a userselected branch might be highlighted or removed from the visualization. Using a region-selection (called lasso selection), an arbitrary subset of vessels might be selected based on their position in the viewport. Instead of completely removing the selected edges it is often useful to show them less focused using gray colors and/transparency (see Fig. 6). Since convolution surfaces do not produce polygons inside the vessel tree a semitransparent visualization without artifacts is enabled.

## VII. VALIDATION

A crucial aspect for any visualization technique which is intended for clinical use is its validation. The underlying data (vessel centerline and local vessel diameter) are generated with the vessel segmentation and skeletonization method described



Fig. 6. Lasso selection and defocused visualization of the selected vessel segments. Inside the semitransparent vessels the centerline is presented. (©Eurographics 2004, [17])

in [2]. The validation of these methods is beyond the scope of this paper. With respect to the visualization of the data the validation should answer the following questions:

- Are (small) branches of the tree structure suppressed in the visualization (false negatives)?
- Are there occurrences of small branches which are not represented in the data (false positives)?
- Are there occurrences where separate branches appear as one branch?
- Is the constriction of the vessel diameter represented correctly?

These questions are relevant since the implicit modeling approach is more prone to such visualization errors than explicit methods where graphics primitives are explicitly fitted along the skeleton.

## A. Qualitative Validation

We choose two different methods to answer the above questions: first we analyzed the visualization of artificial data with different branching types (e.g. with a trifurcation) and second we compared the implicit method with the method developed by Hahn et al. [4]. We refer to the first approach as convolution surface (CS)-visualization and to the latter one as truncated cone (TC)-visualization.

The tests with artificial data showed that unwanted effects could be strongly reduced. The unwanted blending problem may occur in rare cases. The comparison of both methods (Fig. 7) reveals a good correspondence. The TC-visualization produces longer branches at the leafs of the vessel tree. This is due to the construction where a half sphere is added at the end of segments.

In order to further study the accuracy of our method, we compare it with an isosurface visualization of the vessel segmentation result. Differences between the segmentation result and the CS-visualization can be expected because:

• the vessel diameter which guides the CS is the diameter of the incircle <sup>1</sup> - therefore the CS underestimates the

<sup>1</sup>The diameter of the incircle is the only value which can be reliably defined also near branchings and at strongly bended vessel segments.



Fig. 7. TC and CS are combined for a qualitative validation. The CS are rendered as wire-frame while the results of the other method are shaded. The comparison of both surfaces reveals a good correspondence. The inset illustrates that the CS forms smooth transitions which diverge slightly from the TC at branchings.

segmentation result,

- the skeleton and the vessel diameter have been smoothed and
- small side branches have been suppressed (*pruning*) during skeleton enhancement by taking into account the length of a side branch relative to the branch at the next higher level of hierarchy [4].<sup>2</sup>

## B. Quantitative Validation

Over and above the visual inspection, a quantitative analysis is needed to judge whether the underlying data (centerline and local diameter) are faithfully represented. We chose to analyze the distances between surfaces constructed by isosurface rendering of the segmentation result, TC- and CS-visualization. Distance measures are most relevant here because these visualizations are often used to assess distances (e.g. from a lesion to a vessel).

The software platform AMIRA ( $\bigcirc$  Indeed - Visual Concepts GmbH, Berlin) is applied to perform a quantitative surface comparison. We compare the CS with both the isosurface and the TC. For constructing the CS  $\omega$  is set to 5ln(2) (recall Sect. V-A). A comparison is realized such that for each vertex of one surface the unsigned distance to the closest point on the other surface is computed. From the histogram of these values the following statistical measures are calculated:

- mean distance (Ø)
- standard deviation from the mean distance  $(\sigma)$
- root mean square distance (Rms)
- minimum distance (Min)
- maximum distance (Max)
- median of the distance (Med)
- area deviation (Area): percentage of distance values that deviate more than a given threshold

Since distance measures between two surfaces are nonsymmetric, AMIRA supports a two-sided comparison. However, the computation of measures in direction from isosurface

<sup>2</sup>The amount of pruning is adjusted with caution to make sure that only discretization artifacts are avoided.

to CS distorts the overall result. Due to pruning of tiny vessel segments during skeletonization [4] these parts are missing in the CS. For some vertices of the isosurface no points exist within a small range on the CS. Hence, this comparison is disregarded as well as the comparison from TC to CS. While with the TC-visualization polygons are constructed inside the model at branchings the CS is hollow. Hence, for vertices of the inner polygons no corresponding points exist on the CS.

The averaged results of a quantitative comparison between the surfaces of 10 different vascular trees based on CT of the human liver are presented in Table I. We chose half the diagonal voxel size (VoxDiag2) as the threshold for computing the area deviation (last column in Table I). Boxplots illustrating the distribution of measured distances for each dataset are presented in Fig. 8.

## TABLE I

Averaged results of the quantitative comparison of surfaces based on 10 different datasets. Measures were computed from CS to isosurface (Iso) and from CS to TC. All length measures are in mm whereas Area is measured in %.

	Ø	σ	Rms	Min	Max	Med	Area
CS→Iso	0.37	0.32	0.49	0	3.21	0.29	8.74
CS→TC	0.09	0.11	0.14	0	1.13	0.05	0.56



Fig. 8. Boxplots of the distance measures (in mm) carried out for a comparison of CS and Isosurface based on 10 vascular trees. Each box has lines at the lower quartile, median, and upper quartile values. The whiskers extend from each end of the box to show the extent of the rest of the data. Their length equals the inter-quartile range multiplied by 1.5.

The upper value within each text box represents the percentage of data values beyond the ends of the whiskers. The lower value is the maximum distance. Thick lines indicate the VoxDiag2 values. Note that each upper quartile is consistently below its corresponding value.

With an average of 0.37mm, deviations between CS and isosurface are below a typical value for VoxDiag2. Note, also the average area overlap of 91.26% which refers to the respective value of VoxDiag2. It could be observed that high deviations (> 3mm) occur in all datasets only close to the root of the vessel tree as illustrated in Fig. 9. This effect is negligible because the root does not pertain to the intrahepatic vessel system and is therefore of less interest for surgery planning. Inside the vascular trees even distance measurements are reliable with the CS. The median of the deviation is below *VoxDiag2* for each considered dataset. The deviations along the whole vessel tree are to be expected since the CS constantly underestimates the segmentation result as described in Sect. VII-A. It could be further ascertained that smoothing the vessel skeleton has a negligibly small effect on the measurements. The CS based on their corresponding non-smoothed skeletons yielded almost the same results. Pruning of small side branches has no effect since the surface comparison is only accomplished from CS to isosurface and not vice versa.



Fig. 9. Intensity-coded visualization of the deviation from CS to isosurface. Each vertex of the CS is assigned an intensity with respect to the corresponding distance. The legend represents the correlation between intensity and magnitude of the deviation. A high intensity indicates a high deviation. The strongest deviations occur at the root of the vessel tree as depicted in the inset showing the superimposed isosurface in wire-frame mode.

As could be expected, there is a better correspondence between the two model-based approaches (TC- and CSvisualization). More than 99% of the directional distances are below VoxDiag2. The average maximum deviation between CS and TC is 1.13mm, which is less than a typical diagonal voxel size. The low deviations indicate that strong blending, unwanted blending and bulging are effectively avoided. The CS represents the vessel skeleton and diameter as faithful as the TC. The computational results reveal that the deviation from CS to TC ranges from 0mm up to 1.13mm. Minor deviations are observed at branchings which results from the smooth transitions of the CS (Fig. 10). These naturally diverge slightly from the discontinuous transitions of the polygonal model built according to the TC-visualization. Along straight parts of the vessel tree no deviations can be noticed. The highest deviations occur at the vessel ends since the TCvisualization produces longer branches at the leafs of the vessel tree (recall Sect. VII-A).

With respect to the four questions at the beginning of this section, the qualitative and the quantitative validation indicate that none of the problems discussed actually occurs.

## C. Determination of the width coefficient

The accuracy of the CS-visualization strongly depends on  $\omega$ . Therefore, within the validation we also investigated the effect of different  $\omega$  values. In order to define an appropriate default value, we created several CS, based on the same vascular tree,



Fig. 10. Intensity-coded visualization of the deviation from CS to TC. Minor deviations may be observed at the branchings. The strongest deviations occur at the vessel ends as illustrated in the inset. Here, the superimposed truncated cones caped by a hemisphere are rendered in wire-frame mode.

with multiples of the original  $\omega$  value. Then, we carried out a surface comparison (see Sec. VII-B) between each CS and the TC which served as a reference model (see Fig. 11).



Fig. 11. Influence of varying  $\omega$  on surface distances between the respective CS and the TC based on one vascular tree. Mean (diamonds), median (bars) and standard deviation (vertical lines) of the distance measures (in mm) hardly decrease for values higher than  $\omega = 5 \ln 2$ .

We found that with an increasing  $\omega$  value, the distances between the CS and the TC decrease on average. This can be expected since increasing  $\omega$  reduces the blending strength. However, with  $\omega > 10 \ln 2$  the effect of smoothing is almost leveled and the resulting surface exhibits creases at branchings (see Fig. 12, right). We chose  $\omega = 5 \ln 2$  as default value since mean, median and standard deviation hardly decrease for higher values. The difference between the mean deviation using  $\omega = 5 \ln 2$  and  $\omega = 30 \ln 2$  is only 0.03mm.

#### VIII. EVALUATION

To evaluate the benefit of the CS-visualization, we prepared a survey in order to compare it to other visualization methods. For this purpose a collection of visualization results was rated by six experienced surgeons and five radiologists (1 woman, 10 men). All participants in the study had experience



Fig. 12. Influence of varying  $\omega$  on the blending strength at branchings. The close-ups of the trifurcation from Fig. 2 where generated using  $\omega = 2 \ln 2$ ,  $\omega = 5 \ln 2$  and  $\omega = 30 \ln 2$  (from left to right). With  $\omega = 2 \ln 2$  the blending strength is barely reduced. Using  $\omega = 30 \ln 2$  the surface exhibits creases at the skeleton joint. Highlights were set to emphasize the creases.

with 3d visualizations and in particular with the visualization developed by [4].

The collection represented three liver vessel trees from CT data and consisted of 10 images per tree: one context view for better orientation showing the tree within the liver lobe and three different close-ups generated by isosurface rendering, TC- and CS-visualization, respectively. The viewing direction as well as all other visual parameters are identical (Fig. 1).

The evaluation focussed on close-up views because these are relevant for therapy and surgery planning. The evaluation criteria were:

- clarity of the visualization,
- · comprehensibility of spatial relations,
- similarity to intraoperative views
- and visual quality.

For each criterion users were asked to rate from 1 (unsatisfactory) to 5 (excellent). The results are summarized in Table II.

#### TABLE II

Subjective Comparison of vessel visualization by isosurface rendering (Iso), TC and CS. Ø denotes the mean value and  $\sigma$ represents the standard deviation. Valuations range from 1(unsatisfactory) to 5 (excellent).

	Clarity		Comprehen- sibility		Similarity to intraoperative views		Visual quality	
	(1	(n=11) (n=11)		(n=11)	(n=8)		(n=11)	
	Ø	$\sigma$	Ø	$\sigma$	Ø	$\sigma$	Ø	$\sigma$
Iso	1.8	0.69	1.9	0.85	1.6	0.7	1.7	0.69
TC	3.7	0.84	3.9	0.86	3.5	0.9	3.8	0.71
CS	4.1	0.87	4.1	0.89	4.0	0.89	4.2	0.76

Three radiologists could not compare the visualization results with intraoperative views and therefore left this field blank. Within the evaluation, the CS consistently achieves the best results, although the difference to TC is statistically not significant. Above all the similarity to intraoperative views (column 3) and the visual quality (column 4) has been emphasized by doctors under discussion.

Furthermore, the results in Table II argue for the reconstruction of a vessel model from the segmented data. The modelbased visualization (rows 2 and 3) clearly outperforms the direct visualization by isosurface rendering.

## IX. RESULTS

The CS-visualization has been applied to 25 clinical datasets so far. In Fig. 13 we compare the visual quality of the CS- visualization with the TC-visualization. Other examples for the visual quality of the visualization can be seen in Fig. 14-15. The visualizations do not exhibit any of the unwanted effects. We carefully examined the surfaces near branchings and noted that geometric continuity was achieved for all kinds of branchings and branching angles. The surfaces are terminated at leafs of the anatomic trees with a rounded appearance which is a consequence of the construction method.



Fig. 13. Close-up of a visualization with truncated cones with artifacts along the seams (left). Smooth visualization with implicit functions of the same dataset (right).



Fig. 14. Visualization of cerebral blood vessels derived from a clinical MR angiography with 149 edges.



Fig. 15. Visualization of a bronchial tree derived from a clinical CT dataset with 1504 edges.

To give an idea of the complexity of the resulting geometry and the setup time, we present some results in Table III. The setup time includes the preprocessing step. The first row corresponds to a portal vein tree of low complexity. The two middle rows represent the datasets shown in Fig. 14 and 15. The last row in Table III represents a complex anatomic tree from a corrosion cast. Interactive frame rates (>24 fps) were achieved with the first three models (rows 1-3).

## TABLE III

PERFORMANCE MEASUREMENTS FOR ANATOMIC TREE STRUCTURES CARRIED OUT ON A PENTIUM 4 CPU 3.2GHz system with 1024MB RAM.

edges	triangle	s (*1000)	setup time (s)		
	CS	Cones	CS	Cones	
136	125	55	6.14	0.11	
149	253	74	8.12	0.12	
1504	1,126	599	53.24	1.30	
3461	2,366	907	52.01	2.11	

## X. CONCLUSION

We have presented a method for visualizing vascular tree structures which adheres to the underlying data (skeleton and local vessel diameter), while producing smooth transitions at branchings. The method is based on convolution surfaces, a variant of implicit surfaces. The filter design has been finetuned to prevent irritating bulges and to represent the course of the vessel diameter faithfully. The width of the Gauss filter turned out to be the essential parameter to accomplish our visualization goals. With a preprocessing step which computes bounding volumes we can efficiently compute the convolution surface even for large vascular trees.

We compared the CS-visualization with the TCvisualization and could show the superior visual quality. We analyzed the surface differences between the methods with respect to the precision and come to the conclusion that the CS-visualization faithfully represents the underlying data. The quantitative validation indicated that the convolution surfaces deviate less than VoxDiag2 for almost the whole dataset. The directional distances between convolution surface and isosurface rendering of the segmentation result are larger, but still below a typical value for VoxDiag2.

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## LIST OF FIGURES

1	Exemplary set of close-ups used for evaluation .	1
2	Blending at branchings	4

3	Bulging at branchings	4
4	Unwanted blending between branches	4
5	Bounding volumes	5
6	Lasso selection of vessel segments	5
7	View of TC and CS superimposed	6
8	Boxplots of CS to isosurface comparison results	6
9	Deviations from CS to isosurface.	7
10	Deviations from CS to TC	7
11	Relation between accuracy and width coefficient.	7
12	Extreme values for the width coefficient	8
13	Comparing smoothness between TC and CS	8
14	Cerebral vessel tree	8
15	Bronchial tree	8

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