Guided Structure-Aligned Segmentation of Volumetric Data

Michelle Holloway[1], Anahita Sanandaji[2], Deniece Yates[2], Amali Krigger[5],
Ross Sowell[4], Ruth West[3], and Cindy Grimm[2]

[1] Washington University in St. Louis
[2] Oregon State University
[3] University of North Texas
[4] Cornell College
[5] University of the Virgin Islands

Abstract. Segmentation of volumetric images is considered a time and resource intensive bottleneck in scientific endeavors. Automatic methods are becoming more reliable, but many data sets still require manual intervention. Key difficulties include navigating the 3D image, determining where to place marks, and maintaining consistency between marks and segmentations. Clinical practice often requires segmenting many different instances of a specific structure. In this research we leverage the similarity of a repeated segmentation task to address these difficulties and reduce the cognitive load for segmenting on non-traditional planes. We propose the idea of guided contouring protocols that provide guidance in the form of an automatic navigation path to arbitrary cross sections, example marks from similar data sets, and text instructions. We present a user study that shows the usability of this system with non-expert users in terms of segmentation accuracy, consistency, and efficiency.

1 Introduction

Revealing useful knowledge from 3D/4D biological imaging usually starts with a segmentation of the structure(s) of interest. Segmentation is critical in a wide range of applications such as rendering visualizations, quantitative analysis, treatment planning, and virtual simulations. Thus, effective segmentations need to be accurate, consistent, and created efficiently. When segmentation becomes a bottleneck in the data-to-knowledge pipeline, it hinders research and could even result in health risks in clinical practice [4].

A variety of research in automatic segmentation techniques is ongoing. While these methods are becoming more reliable [16], many segmentations are still created manually to ensure the necessary quality and accuracy. Manual segmentation entails marking the boundary of the structure throughout the volume commonly done by drawing contours on multiple 2D slices. In standard practice, the slicing planes are either parallel along, or orthogonal to, the scanning direction of the image data. Delineating enough contours to create an accurate

segmentation can be both difficult and time intensive, depending on the shape of the structure and the size and quality of the image data.

In many settings the same type of structure is repeatedly segmented (e.g. patient livers, mitochondria in cells, etc.). In this work we leverage the fact that the same general shape is segmented in each instance in order to define a *protocol* to guide segmentation of a specific class of structures. This can help to reduce navigation time as well as help users maintain consistency both in how and where they place marks from one instance to another. A protocol is useful in the traditional parallel or orthogonal contouring approach, but more importantly it supports using arbitrarily-oriented contouring planes that can be placed to follow the global structure of the shape — for instance, tracking a tubular structure as it curves in space. The primary finding of this paper is that we can support these structure-specific contouring planes (which reduces both time and error in the segmentation process) without unduly increasing the cognitive load over more traditional contouring methods.

Specifically, we present the first stage of a new conceptual approach for working with volume data – guided 3D segmentation through structure-aligned contouring protocols – and design a novice friendly interface for evaluating this approach.

Contributions of this paper include:

1. A guided, structure-aligned approach to segmentation that reduces the cognitive burden of using non-traditional contouring planes.
2. A real-time visualization of location in a 3D volume in parallel with drawn contours and segmentation surface.
3. Verification that experts can utilize structure-aligned planes to create segmentations comparable to their traditional parallel segmentations.
4. A user study to show that this guided approach allows novices to produce segmentations of comparable quality to experts.
5. Identification of factors that influence segmentation time and quality, enabling comparison of different contouring protocols.

2 Related Work

2.1 Manual 3D Image Segmentation

Manually creating accurate segmentations in an efficient manner is a non-trivial task. Biological tissues are often not clearly separated, in addition to image noise and lack of sufficient resolution and contrast. Within volumetric imaging, this is further compounded by difficulties in maintaining orientation and structural awareness in the data. Therefore, in practice usually only domain experts with years of training in inspecting their specific imaging modality for their specific structures perform segmentation.

Traditionally, experts mark boundaries on parallel slices throughout the volume. Many systems also allow marking contours on orthogonal intersecting slices,

as generally less marking is needed and they can better capture surface curvature extrema. Orthogonal contouring has spawned various interactive systems that take user contour input and reconstruct a surface using splines or implicit functions [1, 6]. The work in [5] makes use of the live-wire technique for drawing contours on orthogonal planes and for interpolating between the contours. These methods, however, are all dependent on the user's ability to choose planes to contour on and do not provide guidance in this regard. Additionally, methods that rely on detecting boundaries may lead to undesirable results or require more input when the boundaries are unclear.

2.2 Segmentation Guidance

The main difficulty in any interactive segmentation system is navigating and choosing where to mark boundaries. Thus new research has explored using guidance in segmentation systems. The work in [9] uses the random walks algorithm in a seed-based semi-automatic segmentation system where users place marks inside the structure instead of drawing boundary contours. The random walk probability is used to direct users to areas where more seeds could be placed.

Contour-based guidance approaches aim to automatically choose planes to mark contours on. In [13] the authors extend the work in [5] to arbitrary planes, and use the live-wire cost of the segmentation result to suggest planes that need marking. Similarly in [14] the authors have users provide drawn contours to seed the random walks algorithm, and in turn actively suggest new arbitrary planes with high uncertainty in the segmentation. Both of these methods require some initial contour(s) to find an initial segmentation to use as training data. There is little contouring consistency between similar data sets as the algorithms' choices depend on the training input and uncertainty probabilities.

These automatic plane selection methods are quite useful and our work fits nicely in tandem with them. We don't require initial input since we instead define structure specific protocols that encode a preset automatic navigation path to contouring planes. This path encourages consistency, so our protocols could be used to provide consistent training data to these other methods. Additionally, experts could use these methods to aid in protocol creation.

3 Methods

3.1 Motivation

Two major challenges posed by manual volume segmentation are the cognitive strain of free-form data navigation and knowing where to draw contours. It is for these reasons that many segmentation systems limit the selection of planes to only parallel or orthogonal placement. However, arbitrarily placed planes can offer more useful views of the data that are aligned to the structure's shape and capture known features more efficiently [15]. Our approach leverages prior knowledge of the structure's general shape in order to use arbitrary planes without increasing the segmenter's cognitive load to complete the task.

To address 3D free-form navigation we propose to remove the need for large-scale manual navigation. Navigation in 3D data is difficult for domain experts let alone novices unfamiliar with biological structures. Our approach provides a navigation path to a relative set of structure-aligned planes to draw contours on for a given structure. Here "relative" means the planes shift according to the initial position of the first plane placed in the volume. Plane locations incorporate structure shape knowledge, and they describe a set path that increases predictability from data set to data set. In this work we side step the larger problem of choosing the best set of planes for a given structure and have an expert manually choose a reasonable structure-aligned sequence of planes.

In [10] it was shown that references images can substantially improve contour drawing consistency for novice users for a single, arbitrary plane. Thus, to address difficulties knowing where to draw on a given plane, we provide visual cues in the form of images of example expert-drawn contours from similar data sets along with text instructions. Using reference visuals transforms a complex perceptual and cognitive task requiring domain expertise to, essentially, a pattern matching task that can be performed by novices. This allows us to use knowledge of the structure while still taking advantage of people's abilities to adapt to the data.

3.2   Contouring Protocol Definition

The *guided contouring protocol* incorporates a preset navigation path of arbitrary planes within the volume, images of example contours from similar data sets for each plane in the navigation path, and text instructions. It is essentially step-by-step instructions for drawing a set of contours that result in a segmentation surface for a specific type of structure.

The navigation path is defined as a set of successive 3D transformations between the chosen planes in a temporal order. For each step, the system automatically navigates to a plane by means of a smooth animated transition. Text instructions and a small set of expert-drawn example contours from a similar data set provide guidance for drawing the new contour. Additionally, users can make local plane navigation adjustments to better match the example images before drawing. A surface is constructed and progressively refined after the addition of each contour to provide immediate visual feedback. We utilize [8] for surface reconstruction for its speed and reliability in producing a surface with partial or distorted input.

3.3   Interface

Our contouring protocols could easily be implemented into any standard segmentation interface. For novice testing we built an interface, inspired by [10]'s design, that focused on 1) supporting clear orientation and enhancing structural awareness, and 2) exposing all functionality through in-screen elements to minimize required clicks. Fig. 1 depicts the four areas of the interface.
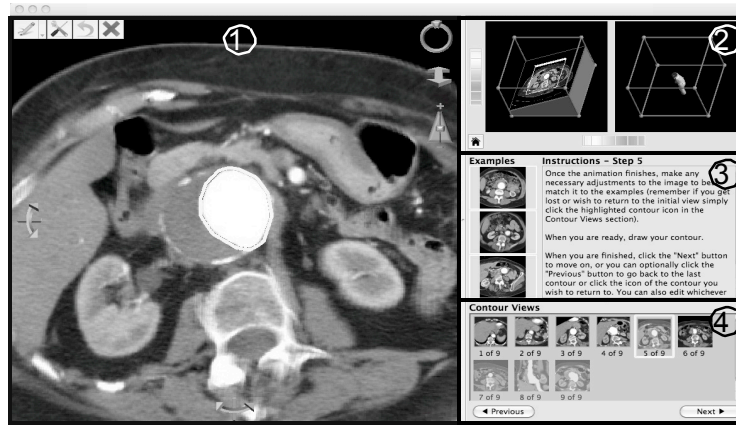
Fig. 1. Interface layout. Area 1 is the main window, 2 is the 3D volume localization, 3 is the protocol instructions, and 4 is the navigation path visualization.

1) Main Window: The primary focus for interaction that shows the current slice, drawn contours, and if desired, the surface. Includes standard navigation and free hand drawing tools.

2) Localization: The pair of linked views visualizes the current slice's position in the volume (left) and the location of all drawn contours and the segmentation surface (right). They are presented as YAH (You-Are-Here) cubes, inspired by [7, 12]. Turntable controls rotate the cubes to find a useful view of the volume without losing global orientation.

3) Instructions: Provides both the image-based and text-based information. Each of the example image icons can be clicked to view it in the main window.

4) Navigation Path: The navigation path is visualized as a sequence of thumbnails. The user navigates using the next and previous buttons or by clicking on a thumbnail in the enforced order. The thumbnail for a completed step shows their drawn contour; thumbnails for uncompleted steps are grayed out and filled with an example image. The navigation path provides a simple method for "scanning" through the volume and shows the progression through the protocol.

4 User Study

To demonstrate that our system is suitable we tested it with expert users from radiation oncology. To demonstrate that novices are able to complete a valid segmentation using the guided contouring protocol, we conducted a study with novice users and compared the results to expert segmentations. The four hypotheses we tested are:

H1 Given sufficient guidance in the form of example images and predetermined contouring planes, novices can reliably produce valid segmentations for relatively complex structures.

H2 Using a set of structure-aligned planes increases segmentation accuracy and consistency compared to a set of parallel or orthogonal planes with the same amount of work.

H3 Total contouring time is dependent on contour length and curvature and the number of contours.

H4 Experts can produce comparable segmentations and in less time using non-parallel contouring to those using the traditional parallel approach.

For H1, we compare novices both pairwise and to ground truth expert segmentations. For H2 we compare the accuracy, consistency, and completion time for three types of protocols used on a single dataset where each protocol requires approximately the same amount of drawing. For H3 we look at novice completion time and contour drawing times in contrast to their length and curvature. For H4 we examine expert completion time and the inter-expert consistency of segmentations produced using parallel contouring and our guided approach. For mesh comparisons we use Dice's coefficient (DC) [3] and the mean percent distance (MPD), which is the mean distance [2] normalized by the structure size.

4.1   Study Design

Participants: We recruited 20 volunteers from the Washington University in St. Louis community to segment three different data sets using structure-aligned protocols. Only 20% were moderately familiar with medical images and only 10% claimed to be moderately or highly experienced with image segmentation. Additionally we recruited 8 volunteers from the Oregon State University community to segment one of the data sets using parallel and orthogonal protocols. Only 1 user claimed to be highly experience with image segmentation.

Image Data: We used CT scans of a liver, an aorta, and a ferret brain. The selected data sets enable us to evaluate our approach sufficiently to demonstrate validity. They range from simple (aorta) to complex (ferret) with differing image/contrast quality representative of data encountered in real segmentation tasks. Fig. 2 shows example images from each data set and an expert segmentation. The contours show the planes used in the structure-aligned protocols. Since the aorta is a tube we had users segment slightly more than the expert and then clipped the results.

Training: Users received a verbal introduction and explored the interface using a data set not included in the study. The training averaged 15 to 20 minutes.

Procedure: The first 20 users used structure-aligned protocols to segment the three data sets in a random order determined pseudo-randomly such that the six orderings were evenly represented. The number of protocol planes were eight for the liver, nine for the aorta, and ten for the ferret brain. The 8 additional users segmented only the liver using both a parallel and orthogonal protocol in a random order consisting of seven and eight planes respectively. The planes for the parallel and orthogonal protocols were chosen such that they required about the same total amount of drawing as the structure-aligned protocol. We only allowed free-hand drawing for comparison purposes. No user failed to complete
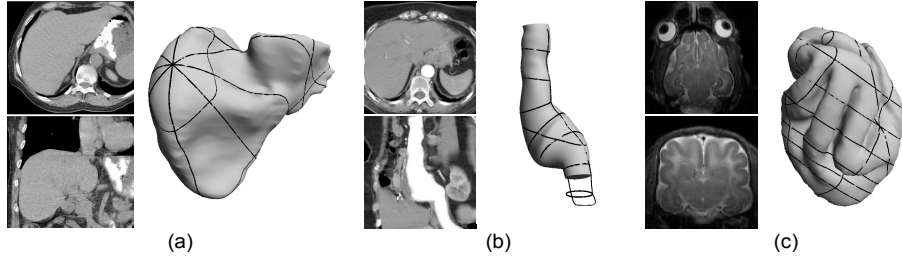
Fig. 2. Example images and segmentations from the three data sets: (a) liver (b) aorta (c) ferret brain.

any tasks. A questionnaire was administered at the completion of the tasks to gauge user background and opinions on the task.

4.2 Expert Evaluation

We invited 7 experts to complete segmentations of only the liver using their traditional parallel contouring and using our structure-aligned guided contouring protocol. The training and comparison metrics were the same as the novice study. The procedure was similar, except they did parallel contouring first followed by the guided approach (using the same interface), and did not complete a questionnaire. Inter-expert consistency was higher for the guided approach versus the traditional one (DC: 0.92 ± 0.016 vs 0.87 ± 0.138, and MPD: 1.62 ± 0.45 versus 1.86 ± 1.71), and overall completion time was faster (469 ± 186 seconds vs 804 ± 113 seconds) confirming H4. For more details see thesis [11].

4.3 Novice Results and Discussion

Accuracy: We evaluate the accuracy of novice segmentations by comparing to a ground truth expert segmentation for each structure (Fig. 3 Top). The liver ground truth was the average of the expert segmentations from Sec 4.2, while the aorta and ferret brain ground truths were provided to us with the data.

Users were able to construct reasonably accurate segmentations for the three structure-aligned data sets. The ferret brain was least accurate due to its complexity. Much of the expert boundaries don't fall on strong gradients, shown with the solid line in Fig. 4, and many users tended to follow the stronger boundaries, shown with the dotted lines. The variance in the aorta was because some planes had a second visible boundary that some chose to follow, as shown in Fig. 4. For reference, we show the liver results from Sec 4.2 as dashed lines in Fig. 3 and can see that the novice accuracy is close to the variance seen among expert liver segmentations. These results indicate that using our guided contouring protocol novice users are capable of producing segmentations of comparable quality to expert segmentations, confirming H1.
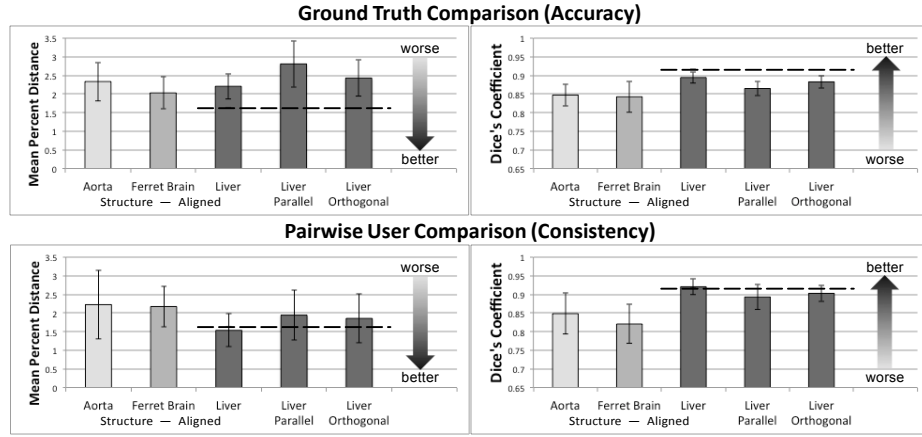
Fig. 3. Top: The average MPD and DC between novice segmentations and the ground truth. Bottom: The average MPD and DC between all pairwise novice segmentations. The dashed line indicates the results from 4.2.
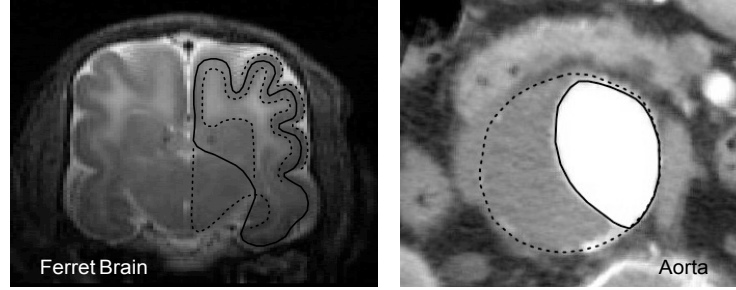
Fig. 4. Examples of ambiguous boundaries. The solid outline is the expert segmentation, and the dotted lines show boundaries that some novices followed instead.

For the liver cases, the structure-aligned protocol produced a significantly (T-Tests MPD: $p=0.00007 \leq 0.05$, DC: $p=0.00016 \leq 0.05$) more accurate segmentation compared to the parallel protocol confirming H2. And while the structure-aligned results were slightly more accurate than the orthogonal, they were not significantly so (T-Tests MPD: $p=0.1015 \geq 0.05$, DC: $p=0.0836 \geq 0.05$).

Consistency: We evaluate the consistency of the novice segmentations by performing pairwise comparisons among all users for each protocol (Fig. 3 Bottom).

Users were reasonably consistent for the three structure-aligned cases. The ferret brain and aorta had more variation for the same reasons discussed in the accuracy section. Looking at the dashed line, the novice liver segmentations were as consistent as the experts, which shows that novice users can reliably produce similar segmentations using our protocols, confirming H1. The protocol approach

encourages consistency because it enforces a defined contouring scheme so that segmentations are performed in a relatively uniform manner.

For the liver cases, the structure-aligned protocol produced significantly more consistent segmentations than both the parallel (T-Tests MPD: p=0.00001 $\leq$ 0.05, DC: p=1.19144$E-8 \leq$ 0.05) and orthogonal (T-Tests MPD: p=0.00024 $\leq$ 0.05 ,DC: p=0.00005 $\leq$ 0.05) protocols, confirming H2.

Efficiency: We evaluate the efficiency of our guided contouring protocol by computing the average completion time for each protocol. We also examine contouring time in terms of contour length and curvature.
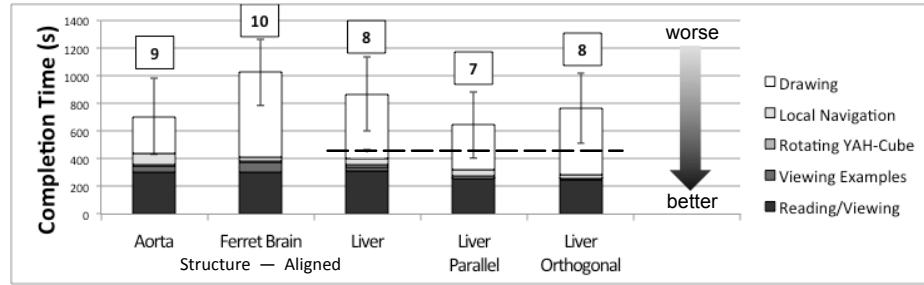

Fig. 5. Average completion time broken down by user actions. The number of protocol planes is shown above each bar. The dashed line on the indicates the results from 4.2.

The average completion time for each protocol was between 10-15 minutes (Fig. 5) with the exception of the ferret brain due to its complexity. For the liver, novice users took less than double the expert time for the liver on average. We feel that these results are compelling considering the users had little to no prior experience. Using our protocols the segmentation time is firstly dominated by time spent drawing contours and secondly by time spent idling (i.e. reading/observing), confirming H3; little time is used for manual navigation.

For the liver cases, the completion time for the three protocols were very similar since they were designed to have approximately the same amount of drawing. The parallel case was slightly significantly faster than the structure-aligned (T-Test: p=0.04914 $\leq$ 0.05) but it was also less accurate, meaning that more parallel contours are needed which would increase the time.

Because segmentation time is now mostly dependent on the time taken to draw contours, we consider two contour length and curvature, and their influence on drawing time. In Fig. 6 that the general trend shows that as the length or curvature increases so does the drawing time, confirming H3. The aorta contours all have similar length and curvature, so we see them clustered together in both plots. The liver contours have similar curvature but vary in length. The complex ferret brain contours varied fairly equally on both factors.
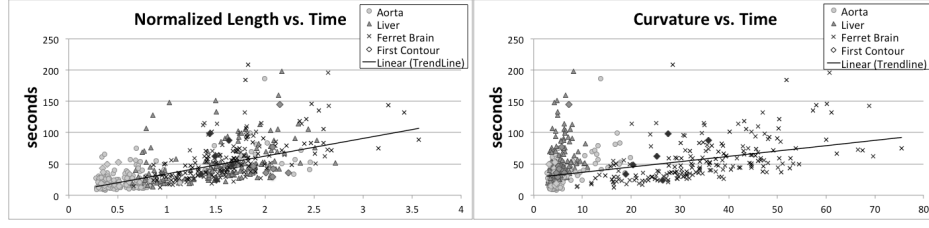
Fig. 6. Scatter plots of contour length and curvature versus drawing time. The contour length was normalized to a unit square drawing window. The curvature for each contour was measured as the sum of the absolute curvature across all contour points.

From these results we can represent the approximate time, T, needed to draw n contours as a function of the contours' length and curvature, plus an uncertainty factor, as shown in Equation 1 below.

$$T = \sum_{i=1}^{n} \alpha L_i + \beta C_i + U_i \tag{1}$$

For each contour, i, L_i is its length, C_i is its curvature, and U_i is an estimate of the time needed for its uncertainty. We normalize curve length by mapping the visible window to a unit square, and the curvature is the sum of the absolute curvature across the contour. We fit a linear polynomial surface to our novice 3D data points of contour length vs. curvature vs. time (with outliers removed) to find α as 23.85 and β as 0.3135 for our examples.

5 Conclusions

Segmentation quality is defined by what the domain expert deems as useful. This notion drives the usefulness and flexibility of expert designed protocols that is more powerful than an arbitrary "gold standard". Future work will develop tools for protocol creation with automatic plane selection to easily choose the best structure-aligned planes. To further improve accuracy we will make use of our structure protocol knowledge in conjunction with surface reconstruction.

Acknowledgment

References

1. de Bruin, P., Dercksen, V., Post, F., Vossepoel, A., Streekstra, G.: Interactive 3D segmentation using connected orthogonal contours. Computers in Biology and Medicine 35, 329–346 (2005)
2. Cignoni, P., Rocchini, C., Scopigno, R.: Metro: Measuring error on simplified surfaces. Computer Graphics Forum 17, 167–174 (1998)
3. Dice, L.R.: Measures of the amount of ecologic association between species. Ecology 26(3), 297–302 (July 1945)
4. Foppiano, F., Fiorino, C., Frezza, G., Greco, C., Valdagni, R.: The impact of contouring uncertainty on rectal 3D dose-volume data: results of a dummy run in a multicenter trial. Int J Radiat Oncol Biol Phys 57(2), 573–9 (2003)
5. Hamarneh, G., Yang, J., McIntosh, C., Langille, M.: 3d live-wire-based semi-automatic segmentation of medical images. In: SPIE Medical Imaging. vol. 5747, pp. 1597–1603 (2005)
6. Heckel, F., Konrad, O., Hahn, H.K., Peitgen, H.O.: Interactive 3D medical image segmentation with energy-minimizing implicit functions. Computers & Graphics: Special issue on Visual Computing for Biology and Medicine 35(2), 275–287 (2011)
7. Khan, A., Mordatch, I., Fitzmaurice, G., Matejka, J., Kurtenbach, G.: Viewcube: a 3d orientation indicator and controller. In: Proceedings of the 2008 symposium on Interactive 3D graphics and games. pp. 17–25. I3D '08, ACM (2008)
8. Macedo, I., Gois, J., Velho, L.: Hermite interpolation of implicit surfaces with radial basis functions. In: Computer Graphics and Image Processing (SIBGRAPI), 2009 XXII Brazilian Symposium on. pp. 1–8 (Oct 2009)
9. Prassni, J.S., Ropinski, T., Hinrichs, K.: Uncertainty-aware guided volume segmentation. Visualization and Computer Graphics, IEEE Transactions on 16(6), 1358–1365 (Nov 2010)
10. Sowell, R., Liu, L., Ju, T., Grimm, C., Abraham, C., Gokhroo, G., Low, D.: VolumeViewer: an interactive tool for fitting surfaces to volume data. In: SBIM '09: Proceedings of the 6th Eurographics Symposium on Sketch-Based Interfaces and Modeling. pp. 141–148. ACM (2009)
11. Sowell, R.T.: Modeling Surfaces from Volume Data Using Nonparallel Contours. Ph.D. thesis, Washington Univ. in St. Louis (2012)
12. Stoakley, R., Conway, M.J., Pausch, R.: Virtual reality on a wim: interactive worlds in miniature. In: Proceedings of the SIGCHI conference on Human factors in computing systems. pp. 265–272. CHI '95, ACM (1995)
13. Top, A., Hamarneh, G., Abugharbieh, R.: Active learning for interactive 3d image segmentation. In: Proceedings of the 14th International Conference on Medical Image Computing and Computer-assisted Intervention - Part III. pp. 603–610 (2011)
14. Top, A., Hamarneh, G., Abugharbieh, R.: Spotlight: Automated confidence-based user guidance for increasing efficiency in interactive 3d image segmentation. In: Medical Computer Vision. Recognition Techniques and Applications in Medical Imaging, Lecture Notes in Computer Science, vol. 6533, pp. 204–213 (2011)
15. Weiss, E., Richter, S., Krauss, T., Metzelthin, S.I., Hille, A., Pradier, O., Siekmeyer, B., Vorwerk, H., Hess, C.F.: Conformal radiotherapy planning of cervix carcinoma: differences in the delineation of the clinical target volume. A comparison between gynaecologic and radiation oncologists. Radiother Oncol 67(1), 87–95 (2003)
16. Wirjadi, O.: Survey of 3D image segmentation methods. Tech. Rep. 123, Fraunhofer ITWM (2007)