



www.visceral.eu

Prototype of 3D annotation software

Deliverable number	<i>D1.1</i>
Dissemination level	<i>Public</i>
Delivery date	<i>30 April 2013</i>
Status	<i>Draft</i>
Author(s)	<i>Oscar Jiménez, Henning Müller</i>



This project is supported by the European Commission under the Information and Communication Technologies (ICT) Theme of the 7th Framework Programme for Research and Technological Development.

Grant Agreement Number: 318068

Executive Summary

This document describes the prototype of 3D software interface that is proposed for the VISCERAL project annotations of 3D structures.

The Introduction explains the objectives of the VISCERAL project regarding this tool for the creation of the gold corpus. The utilisation of such a tool is supported with a brief background on the current state of available annotation tools.

Some of these currently available medical annotation tools were reviewed in order to decide whether to base the prototype on an existing tool or develop custom built software for the VISCERAL data annotation. The final selection was taken after defining a list of selection criteria for all of the tools and choosing the tool that would be most useful for the project in regard to these criteria. Both the overview of the different tools and method implemented for the selection of the tool is explained.

The Microsoft GeoS annotation prototype is then presented with a brief description of the method used by the application to segment 3D structures and the integrated image analysis functions included in the tool. The tool's interface usage and settings are explained with some image examples of the segmented structures. The present issues in the current state of the tool are also mentioned.

Table of Contents

1	Introduction	5
2	Background.....	5
3	Annotation tool prototype selection.....	6
3.1	Evaluation criteria	6
3.2	Reviewed annotation tools.....	7
3.2.1	3D Slicer	7
3.2.2	GeoS.....	7
3.2.3	ITK-SNAP	8
3.2.4	ImageJ	8
3.2.5	M eVisLab.....	8
3.2.6	MITK	8
3.3	Tool comparison	9
4	GeoS Annotation tool.....	12
4.1	Usage	12
4.2	Prototype issues in progress	14
5	Conclusion.....	14
6	References	15

List of Abbreviations

MRI	Magnetic Resonance Imaging
CT	Computed Tomography
NIFTI	Neuroimaging Informatics Technology Initiative
DICOM	Digital Imaging and Communications in Medicine
ITK	Insight Segmentation and Registration Toolkit
VTK	Visualization Toolkit
HESSO	University of Applied Sciences and Arts Western Switzerland
MITK	Medical Imaging Interaction Toolkit

1 Introduction

This deliverable presents the prototype 3D annotation software interface for the multi-modal imaging dataset (MRI, CT) of the VISCERAL project. The objective is to propose an effective user-friendly tool that can reduce the time necessary for the annotations. It is expected that this tool allow the radiologists to annotate around 50 relevant structures in the human body. The relevant objects can then be registered between different modalities to create a multimodal image volume that reveals more specific tissue contrasts than individual images. Both individual voxels and homogenous regions are to be labelled in the 3D volumes according to the definition of relevant structures in deliverable 3.1.

The selected annotation tool needs to be able to make annotations in CT and MRI images acquired with a variety of scanners, in different MR sequences such as T1 weighted and T2 FLAIR and with a resolution of the annotated voxels of 1cm or below. These requirements demand adaptability from the proposed segmentation method to overcome differences in image contrast and resolution from the dataset.

The description and format of the annotations is described in the VISCERAL project deliverable 2.2. The NIFTI format was proposed to save image data and the resulting volume annotations. Medical raw data to be annotated are basically all in the voluminous DICOM format. The DICOM files will be converted into NIFTI format using MRICron since this is the current tool of choice in the Medical University of Vienna who is in charge of the creation of the gold corpus.

The software can be based on existing tools for 3D annotation and data curation for the competitions to be carried out efficiently and effectively. After the competitions, the evaluation infrastructure needs to remain available, so tools with a minimum support are preferred.

A brief background on the problem and available tools is presented in the next section. Different available tools were explored for the selection of the prototype that will be used in the annotation tasks of the VISCERAL project. A brief description of each of the evaluated tools medical annotation functionality is presented and the criteria used for selecting the definitive tool is shown in the following sections. The description of the methods and usage from the proposed tool is also included in this deliverable.

2 Background

With the increasing amount of patient data obtained in hospitals and the requirement to diagnose these data, tools for computerized diagnosis aid have become an important direction to increase productivity of radiologists and avoid mistakes. To train such systems for diagnosis aid, manually annotated data sets are required to train machine learning tools. In radiology, a first step for annotating data is the manual segmentation of image volumes to separate various structures in the images. Manual segmentation on the other hand demands an intensive and time-consuming labour from the radiologists. Manual segmentation of 3D structures can also lead to errors and variation in the results, depending on the observers' experience [1]. Semi-automatic segmentation methods allow the radiologists to take the final decision on the resulting 3D object and utilize segmentation tools as support tools for this task [2].

Several tools have been developed for the annotation of anatomical structures or pathologies present in medical images [1, 3, 4, 5, 6]. The implemented methods range from manual outlining in 2D cross-sections to deformable registration that finds spatial correspondences between 3D images and a

labelled atlas [1]. Some of these tools have been added to application frameworks that provide visualization and image analysis for an integral medical image computing experience.

The idea of using a web-based annotation tool for VISCERAL is foreseen so that the annotators in various places can use the tool without the installation of additional software just by typing the corresponding resource locator in a web browser and using data sets stored in a secured cloud environment. As part of HESSO's participation in the TALISMAN project a fully web-based application was developed, where the user can browse 3D high-resolution CT images and annotate regions of interest in 2D slices that can be interpolated into 3D segmentations¹. Lung segmentation is also considered in this Java Applet using a 3D region growing followed by a closing operation [7]. Unfortunately, tools developed in house are difficult to maintain. There are also available visualization frameworks that reduce the time to develop new applications through the combinations of algorithms, which is faster than writing code [8,9].

Other web-based applications with annotation functionality available like [4] and [6] are limited to a specific application or image analysis type making them unfit to be implemented for the VISCERAL project multiple structure annotation task in their current state.

3 Annotation tool prototype selection

3.1 Evaluation criteria

For the selection of the VISCERAL annotation tool prototype we evaluated a group of visualization and application frameworks that are already available as open-source programs based on their usefulness for the project. The frameworks had to contain a semi-automatic segmentation tool that can reduce significantly the time involved for making the manual annotations of the 3D structures and points of interest. Six frameworks with no license fees: GeoS [3], ITK-SNAP[†][5], ImageJ[‡], MeVisLab[§], MITK^{**} and 3DSlicer^{††} were included in the study. We selected a list of 10 criteria for comparison between the tools and evaluation of their main functionality applied to the annotation tasks needed for the creation of the data gold corpus. Other available frameworks like SciRun^{‡‡}, Osirix^{§§} and Volview^{***} were also reviewed but early discarded because of their failure to comply with some of the selection criteria. First, a general description of the frameworks' functionality in regard to the creation of the VISCERAL gold corpus is given. An overview of the compliance of the tools with the defined criteria and table with the comparison of existing tools is presented afterwards.

The criteria chosen to compare the available annotation tools is:

- ability to perform 3D annotation on CT and MRI volumes;
- flexibility to segment different structures and points of interest;

*http://www.sim.hcuge.ch/medgift/01_Talisman_EN.htm

†<http://www.itksnap.org>

‡<http://rsb.info.nih.gov/ij/>

§<http://www.mevislab.de>

**<http://www.mitk.org>

††<http://www.slicer.org>

‡‡<http://www.sci.utah.edu/cibc-software/scirun.html>

§§<http://www.osirix-viewer.com>

***<http://www.kitware.com/opensource/volview.html>

Last revision in April 2013

- usage of a user-friendly segmentation method;
- optimal visualization of segmentation and medical images;
- high effectiveness of the segmentation;
- easy interaction with the user for corrections in the semi-automatic output;
- time required for a complete structure segmentation needs to be small;
- segmentation method flexibility to data obtained from different scanners and image contrasts;
- output of the annotations according to data format defined in VISCERAL deliverable 3.1;
- Upgrading of the tool with minimum user support for its availability during and after the project has ended.

3.2 Reviewed annotation tools

3.2.1 3D Slicer

D slicer is a module based software where each module performs a particular image processing task. There are two modules that can be useful for segmenting and annotating medical 3D images. The first is called Simple Region Growing Segmentation and it is based on intensity statistics. After choosing a desired number of fiducials in the region of interest, it applies ITK filters for curvature flow and connected confidence producing a 2-class segmentation. The segmentations can be improved increasing the number of iterations, the multiplier and the neighbourhood radius options. More than one fiducial or seed is allowed for refinement of the output. The other module included is EMSegment Easy that performs a quick intensity based image segmentation on MRI. The user defines the volumes to be segmented, specifies the number of structures and can add additional sub-classes of the structures. Samples are taken from the structures of interest to define the intensity distribution and the weighting of a node in the tree. Once the algorithm is run the target images are segmented and the label map with corresponding statistics is returned.

3.2.2 GeoS

The Microsoft medical image analysis project InneEye focuses on the automatic analysis of the patients' medical scans. Its annotation tool GeoS has an algorithm to efficiently segment 3D images using a geodesic symmetric filter with contrast-sensitive spatial smoothness. Its behaviour is comparable to that of graph-cut algorithms but with a much faster implementation.

The segmentation method is based on a generalized geodesic distance transform (GGDT). A geodesic distance map is initialized from a soft seed mask. The seed region is determined interactively. It uses different brush strokes to quickly indicate a foreground object and the background that surrounds it. In this matter, geodesic distance is described as the distance between two points in an image that takes into account image content like intensity gradients.

One of the most sought after requirements is edge-sensitivity whereby the image processing system is able to change its behaviour depending on the local image contrast. This tool is able to perform contrast-sensitive image editing or processing. It shares some of the image processing tasks unifying previously diverse image techniques in such a manner that at least some processing may be shared so that computational resource requirements may be reduced.

3.2.3 ITK-SNAP

This is a software application that provides a set of tools for segmenting medical images' volumetric data. The software provides both an algorithm referred to as 'Snake evolution' and a visualization interface for 3D image segmentation. The contour evolution on which its algorithm is based uses the image gradient information and the global intensity to expand or constrain the contour with respect to user given seed points. It provides a segmentation pipeline in 3 steps with 3 modifiable parameters that influence the output of the segmentation: balloon force, curvature force and adhesion force. These three parameters regulate region growing expansion of the segmentation and the smoothness of the output borders. The framework includes a wizard for image upload and also a polygon tool that allows the user to perform freehand annotation. The freehand annotation tool can be expressed in either a continuous curve or piecewise linear with an adjustable segment length.

3.2.4 ImageJ

This tool contains several image segmentation algorithms based on intensity range thresholds. In particular, the Robust Automatic Threshold Selection (RATS) performs threshold on previously established regions using recursive quadtree architecture. It calculates the sum of the original voxels weighted by the gradient pixels. Other plugins like the watershed algorithm are available for segmenting images but they mostly rely on histogram thresholding and Gaussian modelling of the intensity values in the images, which can provide an initial estimate but has to be completed by the user with freehand 2D slice-by-slice manual annotation.

3.2.5 MeVisLab

MeVisLab is an integrated development environment with a modular framework that allows developing image processing algorithms and visualization and interaction methods. It is possible to create an end-user application with a network composed of modules based on Open Inventor scene graphs, Open GL, ITK, VTK and SDK. It supports DICOM files as well as NIFTI formats. Conversion of one format to the other is also included within the available modules. Although there are few segmentation algorithms outside those available in the ITK and VTK libraries, the user can use LiveWire combined with freehand manual annotation on a slice-by-slice basis. LiveWire is a graph-cut algorithm where the user can adjust the gradient, laplacian and directional weighting. There is also a 'bulge' module that can easily bend, expand and contract manual annotations with the mouse.

3.2.6 MITK

The Medical Imaging Interaction Toolkit (MITK) was created as a software system for development of interactive medical image processing software. It implements both ITK and VTK libraries but also offers additional development and interactive features of its own like a 3D synchronized multiviewer layout. It contains various segmentation methods based on threshold functions like the Otsu segmentation where it is possible to define a number of regions based on a Gaussian modeling of the intensity value image histograms. It is also possible to apply a region growing algorithm with a user given seed. The framework only allows one seed per region and freehand wiping, correction and filling of the created segmentation. Another option when manual 2D slice segmentations are available is to interpolate the missing slices and create a surface of a structure of interest.

3.3 Tool comparison

- Compatible 3D annotation on CT and MRI volumes

ITK-SNAP and ImageJ ask for a grey scale or RGB image when they upload and ITK-SNAP uses a wizard for loading a file. Intensity values with an intensity precision larger than 16-bit are approximated. Mevislab can upload DICOM volumes and Analyze formatted files but NIFTI files are not supported. Both MITK and 3D Slicer can upload a wide range of different image formats and contain converting format functions. GeoS does not support DICOM files but works with NIFTI files as well as other image formats like Analyze and Tagged Image File Format.

- Flexibility to segment different structures and points of interest

Tools that allow freehand annotation like Mevislab, ImageJ, and MITK can be adapted to structures with different shapes and make modifications on 2D views of the generated volumes. ITK-SNAP and region growing algorithms like the ones in 3D Slicer and Geos depend on the number of user fiducials or seeds for their adaptation to the particular shape features of the organs. All of the selected frameworks are not limited to a particular application and can perform segmentations on different organs and points of interest.

- User-friendly segmentation method usage

The semi-automatic segmentation method sought by VISCERAL annotation task should be easy to apply and must be performed in real-time in order to allow for an optimal user interaction. Segmentation methods like those used in ImageJ and ITK-SNAP require an initial trial and error user interaction to define the best values of the parameters involved. These parameters can take the users some time to understand their functionality when they are not familiarized with them, as will probably be for the annotators of the gold corpus data. The GeoS tool has a fast straightforward algorithm that can easily be implemented by the users and the default parameters given by the tool can be used without modification for most of the structures. Adding seed points in the Mevislab and 3DSlicer region growing algorithms is also a simple task once it is combined with freehand manual corrections.

- Optimal visualization of segmentation and medical images

The ImageJ framework has an independent window visualization that requires the handling of multiple open windows and manual interaction for the user to navigate in 3D medical images. MITK and Slicer 3D has a better visualization of the data with the three views visible at the same time and a multi-planar 3D representation or volume rendering that the user can zoom, rotate and navigate with the mouse. One drawback in MITK is that changing between images can cause losing the defined orientation of the image requiring the user to reset the desired image location for visualization, again. The GeoS tool has a simple easy-to-use interface with the three views where it is possible to make annotations in all of them. Unfortunately, volume rendering is still not supported and the segmentations can only be visualized in 2D in each view.

- Effectiveness of the segmentation

The purpose of selecting frameworks with semi-automatic segmentation methods is to reduce the amount of work when making the annotations and allowing the radiologists to add their experience and input in the segmentations. Since all of the selected tools are not application-oriented to a single type of anatomical structure they can obtain accurate segmentations with enough user feedback.

D1.1 Prototype of 3D annotation software interface

ImageJ and Mevislab have the least evolved segmentation methods while ITK-SNAP, 3D Slicer and Geos are the annotation tools best fitted to perform semi-automatic segmentations in medical images.

- Easy interaction with the user for corrections in the semi-automatic output

Most of the application frameworks contain the option to cut or add new voxels to the segmentation output in 2D slices if the segmentation has leakage or a part is missing. Other tools like GeoS can improve the segmentations by adding more strokes either in the background or foreground from the structure of interest. Once the algorithm is run again it provides a new segmentation incorporating user input influencing the full 3D volume of the segmentation. This is useful for rapid visual inspection of the results and little user interaction in any of the views for corrections in the output. Updating small changes however still requires the algorithm to be run fully, even though it has a fast implementation for the whole structure and no freehand correction tool is available in the current GeoS version.

- Time required for a complete structure segmentation

The GeoS annotation tool is the fastest tool for segmenting a complete structure because of its ‘lazy annotation’ implementation and good data visualization and annotation in the three views at the same time. ITK-SNAP and multiple seed algorithms like those in Mevislab and 3D Slicer can also provide quick segmentations that may need user interaction to correct some leakage or missing parts in the segmented volume. For the other available options there are efficient algorithms to start the segmentation process but eventually they require manual freehand improvements to refine the segmentations and this can take some time especially for structures with low intensity contrast and soft edges.

- Segmentation method flexibility to data obtained from different scanners and image contrasts

Some of the segmentations methods that involve thresholding can be very sensitive to image noise and full image contrast of the different structures. A more local definition of the contrast is desired particularly in MRI where field inhomogeneities are common and intensity values can change significantly even within the same structure. An advantage of the GeoS tool and the ITK-SNAP methods is their local approach that limits the expansion of the segmentations to a specific region. One limitation in the ITK-SNAP method is that it is limited to changes in the image gradient and it can also be affected by image noise and poor soft tissue contrast.

- Output format of the annotations

Mevislab generates contour segmentation object lists from the segmentation results that have to be converted to a different format for their inclusion in the annotation analysis backend. With 3D Slicer the user can decide the label of each structure and add sub-classes of it. Only in the GeoS tool and MITK framework, the output of the segmentations can be saved in a NIFTI format without additional plugins in accordance to the data format definition for the gold corpus annotation for VISCERAL. In addition, RadLex terminology is expected to already be included in the final version of the GeoS prototype, which would make the annotations comparable and provide a better setup for long-term use of the annotations.

- Upgrading of the tool with minimum user support for its availability during and after the project has ended

Thanks to the close collaboration with Microsoft and their interest in supporting medical imaging projects, the GeoS tool is expected to comply with the VISCERAL description of work for the annotation tool prototype. Its web-based full application and inclusion of RadLex terminology is

D1.1 Prototype of 3D annotation software interface

expected to be ready before the end of April 2013 when the annotators will start working on the gold corpus creation for the benchmark. Other frameworks like MITK, 3DSlicer, and ImageJ can be upgraded using plugins freely available. However, their maintenance and specific adaption for the VISCERAL first organ-detection benchmark with RadLex terms and full web-based application is at the moment not foreseen.

GeoS	ImageJ	ITK-SNAP	MeVisLab	MITK	3DSlicer	Evaluation Criteria
+	+	+	+	+	+	Annotation on 3D volumes (CT and MRI)
+	-	+	+	+	+	Semi-automatic segmentation method different shapes flexibility
+	-	o	+	o	+	Segmentation user-friendly usage
o	o	+	+	+	+	Optimal image visualization of segmentation
+	-	o	+	+	+	Effectiveness in VISCERAL data of the segmentation method
+	+	+	+	+	+	Interactive output corrections
+	o	+	-	o	o	Semi-automatic algorithm time reduction vs. manual annotation
+	-	o	-	+	+	Local image contrast flexibility
+	o	o	-	+	o	Output annotation format
+	-	-	-	o	o	Upgrading of the tool

+: Satisfactory o: Insufficient -: Missing

Table 1 : Evaluation criteria report for each of the frameworks or annotation tools.

The decision was made in collaborations with physicians checking different tools and comparing their usefulness. The Microsoft GeoS annotation tool is proposed mainly because of its efficiency and accuracy in the segmentations, which require only a few brush strokes from the user to run segmentations in 3D volumes respecting strong edges. Other advantages over the remaining tools are the tool simplicity and easy-to-use annotation interface with the learning of only a few keypads needed to start using the tool for annotations. MITK and 3DSlicer are also good alternatives that can reduce the time for the manual annotation. However, they comply less with the selected evaluation criteria and lack the focused implementation for the VISCERAL project that the GeoS tool has because of the developer's involvement in the implementation of the tool with the necessary requirements of the proposed prototype. Microsoft made the tool available to us without any license fees and in a collaboration in which they also plan to support medical imaging projects.

A description of the tool's segmentation method and its usage is shown in the following sections.

4 GeoS Annotation tool

4.1 Usage

The GeoS tool interface is divided into five parts as shown in Fig. 1. It has a simple design with traditional sagittal, coronal and axial views. To select the view in the central and larger part of the screen the user can simply click on the arrow in the top left corner of the view. The user has also access to all the available tools in the lateral parts in the main screen. On the top left side of the screen, icons are available to add a new segment label, load label settings from the disk and save all segments in one volume to the disk. Below these icons the labels for the segments are added. Each label can be visualized with a different colour and saved independently with a user name. Some instructions and keystrokes are available by holding F1 (Fig. 2).

Figure 1 Segmentation method: With only a foreground stroke for the kidney (yellow) and two background strokes for the surrounding organs (left image), an initial segmentation of the kidney is obtained (right image). This segmentation can be further refined with more strokes.

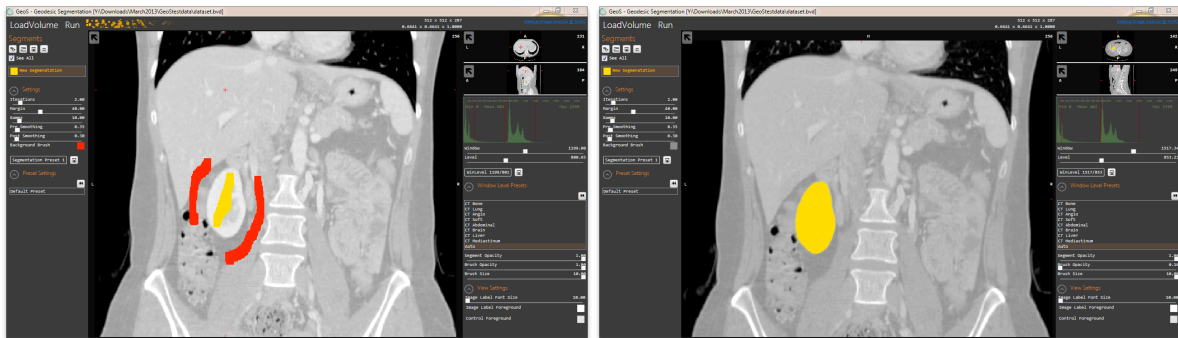
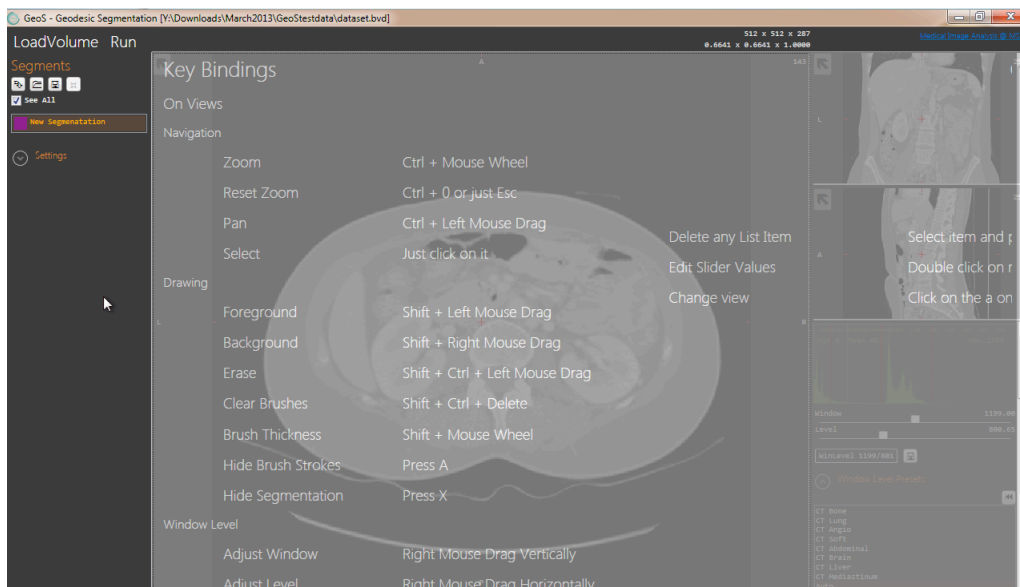


Figure 2: I Key bindings shown when F1 is pressed.



By clicking 'LoadVolume' on the initial screen the user can select the desired image file to be annotated. The segmentation can be started with only a few strokes in the desired structure (foreground) pressing Shift and a left mouse drag. To limit the extension of the segmentation, strokes outside the structure (background) can be created with Shift and right mouse drag. The strokes can be made in any of the views. To run the segmentation press F5.

D1.1 Prototype of 3D annotation software interface

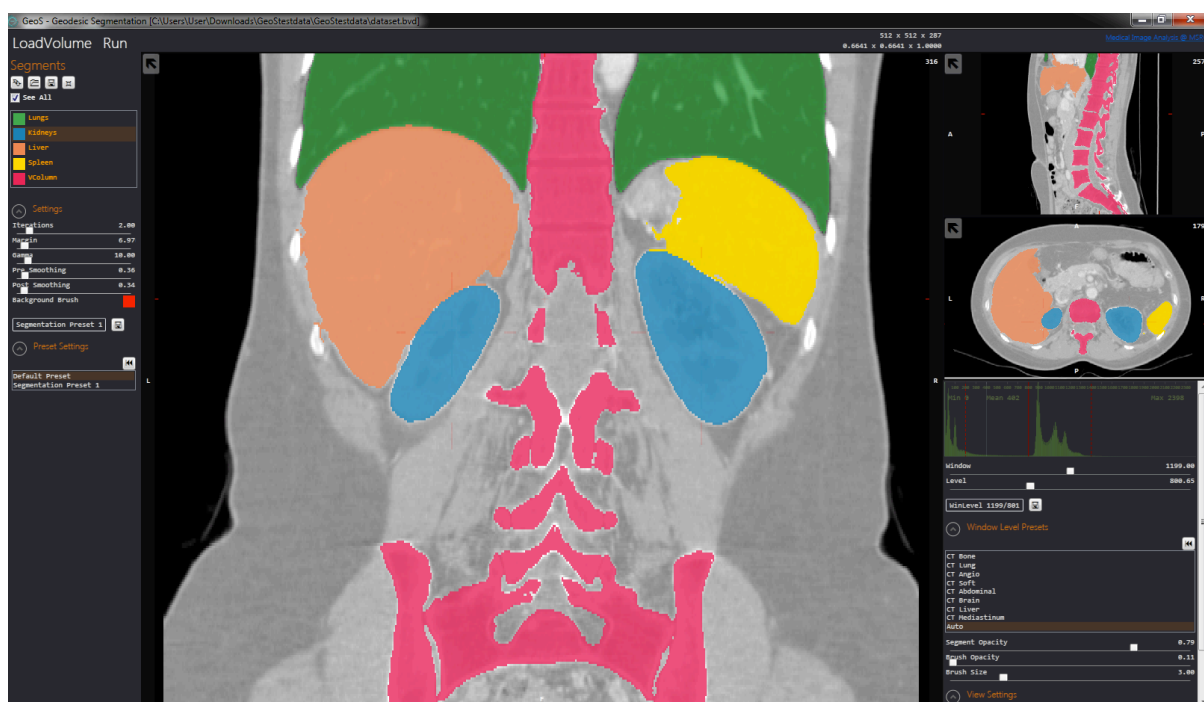
The created segment can be improved by adding more strokes in the structure and in the background. It is possible to erase previous strokes by pressing both Shift and Ctrl in the keypad and clicking with the mouse over the strokes. The size of the brush can be modified with the scroll wheel from the mouse.

On the left side of the screen the image settings offer a set of tools like zoomcontrol, scroll contrast, or scroll brightness. These tools are important for the radiologists since they can see the behaviour of the organs in different conditions. Image settings are also available for adjustment of the window and level values of the greyscale mapping, panning and zooming of the image.

The segmentation algorithm tool has 5 modifiable parameters: iterations, margin, gamma, pre-smoothing and post smoothing. The number of algorithm iterations re-evaluates in each iteration the output of the segmentation and its compliance with the priority seed given with the brushes. More iterations produce a segmentation with a better correspondence of the image contrast edges but take more time to perform. Gamma and particularly the margin parameter influence the distance maps from where the segmentations are then created. The margin is responsible for the extension of the segmentation with lower values producing a smaller output and bigger values expand the segmentation in spite of a wider range of voxel intensity values. Pre-smoothing and post-smoothing parameters can be modified to perform a smoothing filter to either the original image in the pre-smoothing or the resulting segmentation in the post-smoothing filter for an output with a smoother surface depending on the structure of interest original shape. The user can always go back to the default preset of the parameters by clicking the 'default' option.

The annotations are saved in separate NIFTI files without modifying the original images. The tool has been tested with 3D CT and MR images. Images obtained from different scanners, in various thicknesses, with and without contrast gave efficiently accurate segmentations with enough input from the user. A few examples of segmented annotations from various organs are shown in Fig.3 and their created masks are available in Fig. 4.

Figure 3: Annotation example of different structures in an abdominal CT.

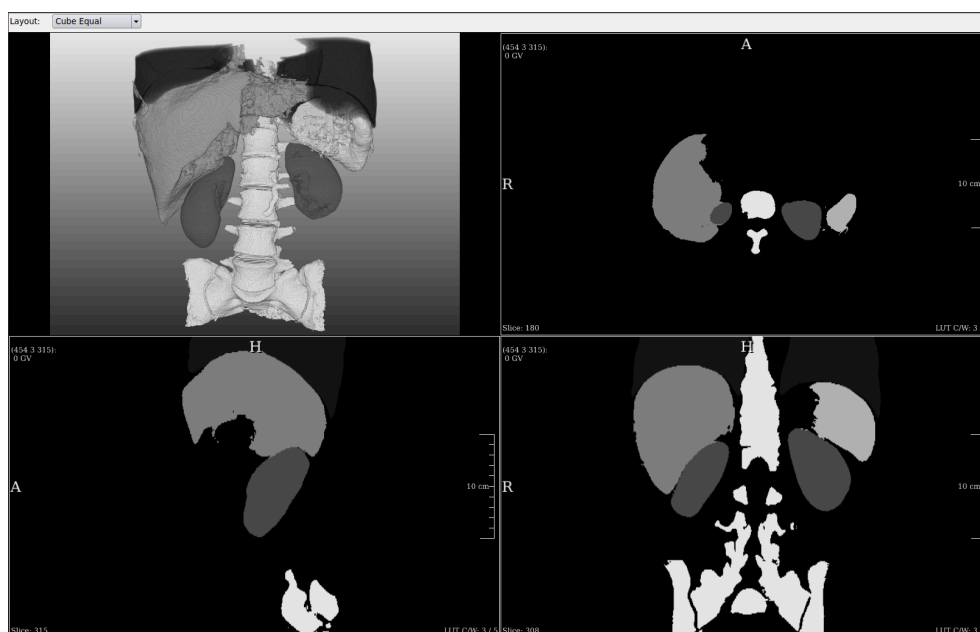


4.2 Prototype issues in progress

The objective in the VISCERAL project is to choose a user-friendly high-quality annotation tool for 3D structures. It is also stated that the tool should be a fully web-based application. This would make the annotation tool easily accessible in different locations (with data also being available in the cloud only) within the web browser without the additional installation of tools by the users. In its current state, the tool is not yet available as a web-based application, however its implementation as a web-based tool is in progress.

Currently, it is not possible to load DICOM files in the annotation tool. NIFTI files are proposed as an alternative and are validated in the data format definition for Competition 1. MRICron is the conversion tool of choice from the TUW and has been selected to convert the original DICOM volumes to the NIFTI files.

Figure 4: Masks obtained from the segmented organs in Fig.3.



The tool only allows for the segmentation of 8 different structures in the same annotation volume. With the final definition of the number of annotated structures and landmarks that will be used for Competition 1 in the VISCERAL project, the masks can be created independently with a specific configuration in mind.

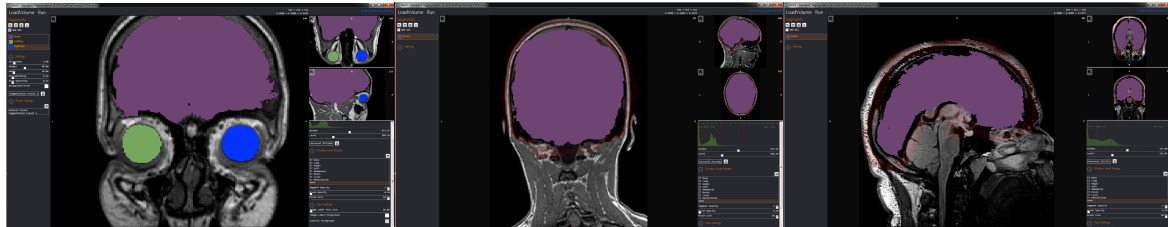
It is expected to include RadLex terms for the labelling of the anatomical parts. This is a common annotation metadata format that allows associating labels within the image data with this ontology. This inclusion to the tool is also of advantage for the annotation backend analysis considered in the VISCERAL Deliverable 3.1 for the creation of the gold corpus.

5 Conclusion

The proposed annotation tool provides fast efficient and reliable annotations to significantly reduce the amount of time required when compared to slice-by-slice manual annotations. The tool allows annotating, segmenting and visualizing 3D medical images such as CT and MRI. It respects the edges

when segmenting 3D volumes and it is easy to use with only a few brush strokes required from the user to start an annotation.

Figure 5: Annotation examples in different MRI sequences. Left and center images have T1 weighted contrast and the right image has T2 weighted contrast.



6 References

- [1] Neeraj Sharma, Lalit M. Aggarwall: Automated medical image segmentation techniques. Journal of Medical Physics, vol. 35, no.1, pp. 3-14 (2010)
- [2] Ralph L. Engle: Attempts to use computers as diagnostic aids in medical decision-making: a thirty-year experience. Perspectives in Biology and Medicine, vol.35 no.2, pp. 207-219 (1992)
- [3] Antonio Criminisi, Toby Sharp, Andrew Blake: GeoS: Geodesic image segmentation. 10th European Conference on Computer Vision, Proceedings Part I, pp. 99-112 (2008)
- [4] Brian E. Chapman, Mona Wong, Claudiu Farcas: Annio: A web-based tool for annotating medical images with ontologies. Healthcare Informatics, Imaging and Systems Biology, 2012 IEEE Second Conference on, pp. 147 (2012)
- [5] Paul Yushkevich, Joseph Piven, Heather Cody, Sean Ho, James C. Gee, GuidoGerig: User-guided level set segmentation of anatomical structures with ITK-SNAP. The Insight Journal (2005)
- [6] Christian Mata, Arnau Oliver, Albert Torrent, Joan Martí: MammoApplet: An interactive java applet tool for manual annotation in medical imaging. Bioinformatics & Bioengineering (BIBE), 2012 IEEE 12th International Conference on, pp. 34-39 (2012)
- [7] AdrienDepeursinge, Alejandro Vargas, Frédéric Gaillard, Alexandra Platon, Antoine Geissbuhler, Pierre-AlexandrePoletti, Henning Müller : Case-based lung image categorization and retrieval for interstitial lung diseases : clinical workflows. International Journal of Computer Assisted Radiology and Surgery, vol. 7, issue 1, pp. 97-110 (2012)
- [8] Jesus J. Caban, Alark Joshi, Paul Nagy : Rapid development of medical imaging tools with open-source libraries. Journal of Digital Imaging, vol.20 (suppl 1), pp. 83-93 (2007)
- [9] Ingmar Bitter, Robert Van Uiter, Ivo Wolf, Luis Ibáñez, Jan-Martin Kuhnigk : Comparison of four freely available frameworks for image processing and visualization that use ITK. Visualization and Computer Graphics, IEEE Transactions on, vol. 13, no. 3, 483-493 (2007)