ROBUST, HIGHLY DETAILED MEDICAL IMAGE SEGMENTATION

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INTRODUCTION

With steadily increasing computational power, it has become possible nowadays to perform simulations of large and complex models. Especially in the domain of BioEM, being able to simulate strongly inhomogeneous tissue distributions has opened important opportunities to gain information of previously unknown detailedness and reliability. State of the art EM/T simulation platforms, incorporating, e.g. the non-uniform Finite-Difference Time-Domain (FDTD) method, permit the simulation of highly resolved models. Therefore, in order to create realistic, elaborate models, a powerful, flexible and robust segmentation tool is needed.

OBJECTIVES

Segmentation of medical images is known to be a challenging task, and no fully automatic method exists that performs well for all purposes. Therefore, the goal was to compose a toolbox that incorporates various methods and allows the user to flexibly inter-combine them. While some of them work with nearly no user input, others require interaction. This leaves the user with the flexibility needed to segment complex, low quality image data.

The toolbox should satisfy the following objectives:

- work with all common types of medical image data (CT, MRI, etc.)
- simple to use
- offer robust segmentation
- permit fast generation of detailed models
- good intrerface to TCAD (Fig. 2)

OPTIONS FOR SEGMENTATION

The classification of segmentation methods according to the degree of interaction they require has been mentioned. In addition, the methods can be grouped according to:

- Whether they use a homogeneity criteria (grey level, texture) to identify a region, or whether they try to identify boundaries. Homogeneity is reduced by noise and imaging artefacts (drift). Boundaries can often only be detected partially.
- Whether they use statistical prior knowledge about the object to be segmented. This results in very specialized methods and is therefore not suitable for our task.
- Whether they are static or involve differential equations for curve evolution.
- Whether they use local or global information.
- Whether they work in 2D or 3D. 3D methods are often faster, but require a lot of memory and are usually less robust.
- Whether they identify a single object or several objects competitively. Competitive methods can work with poorer image data but make interaction more difficult.

THE TOOLBOX

The tool lets the user apply various methods on a source picture. The result picture can then itself be used as a new source. The methods sometimes make use of markers and parameters and can require mouse interaction. Both source and result pictures can be stored on a clipboard stack and retrieved again. Regions of the result picture can be assigned to the various tissue-classes. Surfaces and contour lines of the tissues can be extracted and simplified before exporting them. Alternatively they can be used as input for additional methods (Fig. 1).

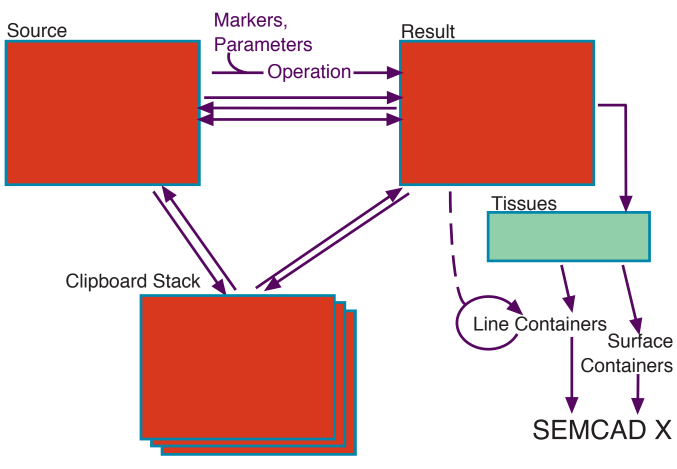

Figure 1: Design of the segmentation toolbox. Operations are applied to a source picture. Regions of the result picture are assigned to a tissue and tissue-borders extracted.

Beside segmentation techniques, the methods include operations for pre-processing (noise removal, edge enhancement, grey-level scaling, mathematical operations) and post-processing (morphological operators, outline correction, connected component analysis, hole removing, skin adding).

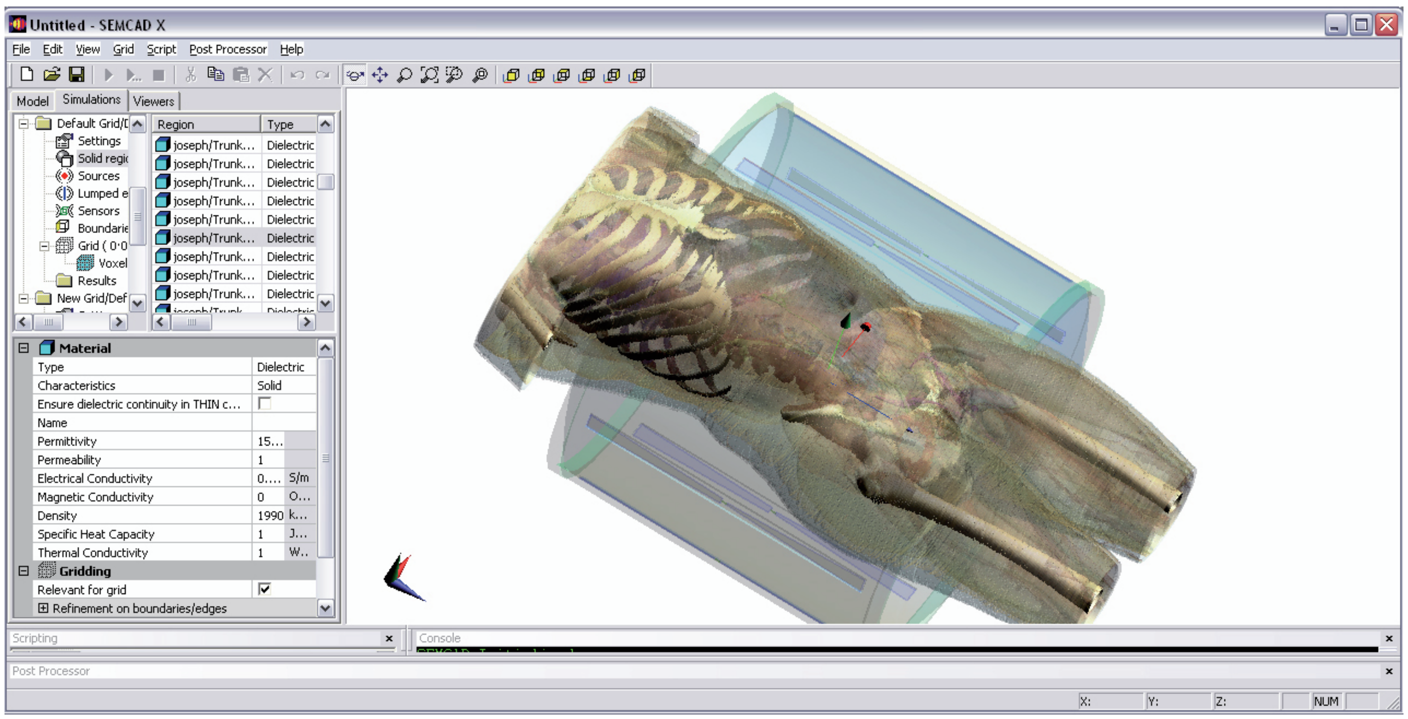

Figure 2: Segmented human trunk and a model of Sigma60-applicator in the SEMCAD X simulation environment.

SEGMENTATION TECHNIQUES

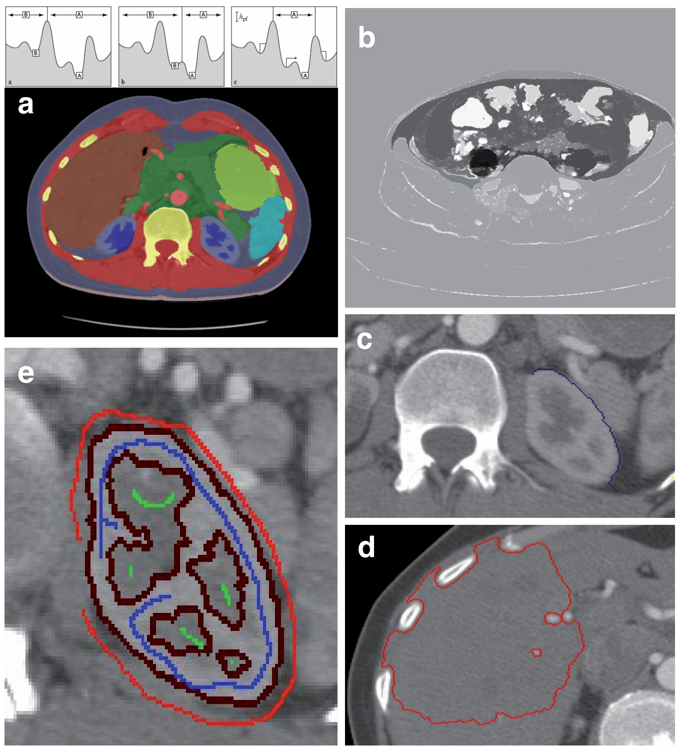

Figure 3: Samples of various segmentation techniques (see text)

The implemented segmentation techniques can be grouped as follows:

- **Thresholding**: Based on their value the pixels are attributed to a specific class. The thresholds can be set manually or automatically (based on a modal analysis of the histogram or k-means/expectation maximization techniques). Multidimensional (e.g., color/multimodal) information can be used.
- **Region Growing** (*Fig. 3e*): The region grows from starting seeds. The seeds can be found automatically (hysteretic growth). Interactive, competitive growing from many seeds/lines is possible. Limits can be manually added.
- **Fuzzy Connectedness** (*Fig. 3b*): For all the image points the probability of them belonging to the same object as a starting point is calculated using fuzzy theory.
- **Interactive Watershed Transformation** (*Fig. 3a*): Various basins are identified in the image and interactively merged using markers set by the user and image information.
- **Contouring** (Live Wire, *Fig. 3c*): The user contours the objects. The line can be made to preferentially follow object contours (incl. automatic freezing).
- **Level Set** (*Fig. 3d*): A contour evolves in time and tries to adapt to the object contour. This process is topologically flexible (contours can split/merge, holes can appear). Various image-based forces can be used.

CONCLUSIONS AND OUTLOOK

- Due to the complexity and low quality of medical image data, automatic methods rarely yield satisfactory results. While they can be used to extract simple structures (e.g., bones), they do not work when confronted with structures that lack clear borders or homogeneous characteristics. Therefore it is recommended to apply them for simple structures only (as found in the leg), while otherwise relying on interactive methods.
- Both competitive seeded methods (incl. interactive watershed transformation) and live-wire seem to be well suited for the interactive segmentation.
- Ideal segmentation routines should make use of both region and boundary information.
- Usually only 2D segmentation is reasonable.
- It is planned to couple interpolation between slices and level-set methods or live-wire, such that the interactive segmentation need not be performed on every single slice.
- The user should combine the various methods to quickly obtain satisfactory results. A standard procedure thus needs to be established which physicians can follow (e.g., 1. pre-processing; 2. automatic distinction of fat, muscle and bone; and 3. interactive methods to outline various organs, possibly using interpolation).

The implemented toolbox offers a good environment to quickly prototype new segmentation techniques and combine them flexibly. This is needed to generate very detailed patient models. The ability of the toolbox to work with various competing tissues at the same time increases its robustness. The presence of both automatic and semi-automatic, interactive methods gives the user a high degree of flexiblity. Future developments should include specialized methods to extract blood-vessels as required for thermal simulations with discrete vessels and registration methods for multimodal image data.

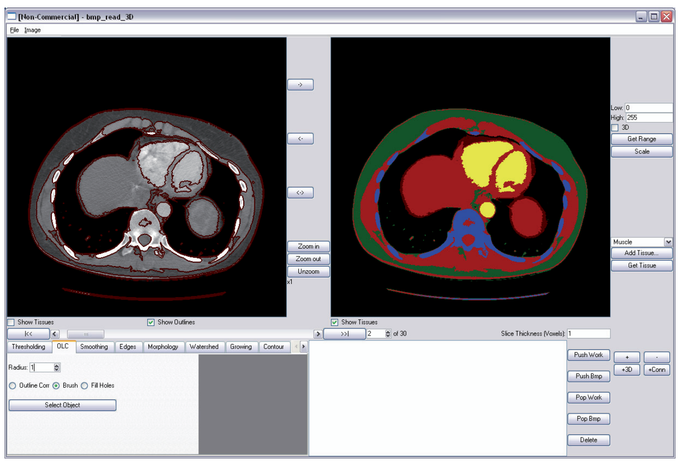

Figure 4: The front-end for the segmentation tool (alpha version).

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