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Summary

For medical diagnosis, visualization, and model-based therapy planning three-dimensional geometric reconstructions of individual anatomical structures are often indispensable. Computer-assisted, model-based planning procedures typically cover specific modifications of “virtual anatomy” as well as numeric simulations of associated phenomena, like e.g. mechanical loads, fluid dynamics, or diffusion processes, in order to evaluate a potential therapeutic outcome. Since internal anatomical structures cannot be measured optically or mechanically in vivo, three-dimensional reconstruction of tomographic image data remains the method of choice. In this work the process chain of individual anatomy reconstruction is described which consists of segmentation of medical image data, geometrical reconstruction of all relevant tissue interfaces, up to the generation of geometric approximations (boundary surfaces and volumetric meshes) of three-dimensional anatomy being suited for finite element analysis. All results presented herein are generated with amira[®] – a highly interactive software system for 3D data analysis, visualization and geometry reconstruction.

Keywords

Medical image segmentation, computational geometry, virtual anatomy, finite element meshes

1. “Virtual anatomy” – 3D computer models of individual anatomy

3D geometry models of human anatomy are becoming increasingly relevant in the digital ages. Not only for entertainment or education but also for businesses where human models are involved (e.g. virtual crash tests), or in medicine with respect to patient specific computer assisted therapy planning. Research in the latter field is rapidly advancing. We can distinguish between *generic anatomy* represented by atlases, that demonstrate anatomical structures and their relationships, and *individual anatomy*, that becomes of interest in cases where pathological situations need further attention with respect to any kind of medical treatment. Generic anatomy models can be the result of careful design using modeling software, whereas patient specific anatomy models typically come as an output of an appropriate scanning device, associated with point cloud or image based reconstruction algorithms. However, corresponding sets of individual anatomy models can in turn be combined into generic models using statistical averaging of 3D shapes. Within this work we will focus on the reconstruction of individual anatomy from medical image data for computer assisted treatment planning and numerical simulations.

1.1 Medical imaging yields insight

In order to reconstruct three-dimensional geometry from medical image data appropriate imaging techniques are required. A suitable technique is tomographic imaging (CT, MRI), where a contiguous series of image slices is captured non-invasively. Each slice represents a cut through the scanned structure with a particular thickness. The pixels within each image slice are represented by scalar values that can be interpreted as intensity values (Fig. 1.1). Each intensity value within that pixel matrix is an averaged measurement of material properties at that particular location of the scanned structure. In computed tomography, for instance, the X-ray absorption rate is measured, normalized to the absorption rate of water, given in so-called Hounsfield units. Regions of homogeneous intensity values typically represent anatomical structures, whereas strong gradients are indicators of tissue boundaries. The smallest structures that can be reconstructed from such images depend on the image resolution, i.e. the pixel dimensions. Medical images are typically stored in DICOM format, and dedicated image readers are required for visualization.

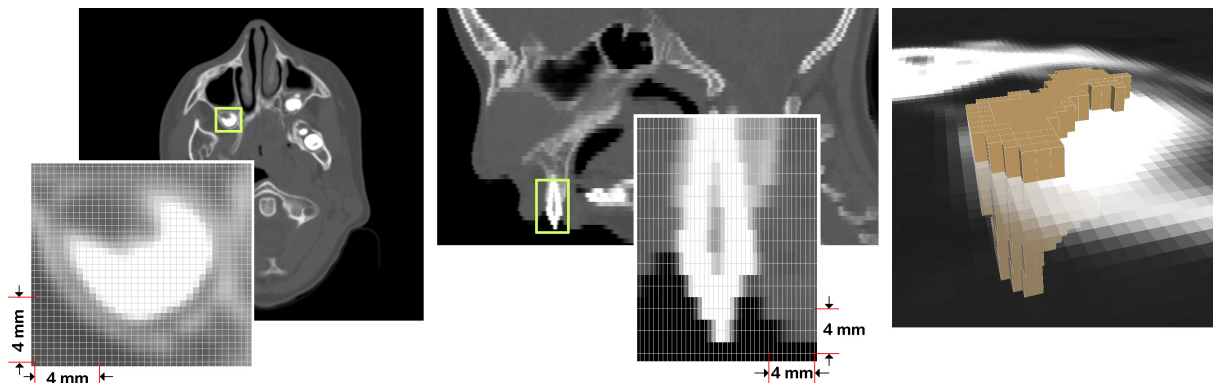


Fig. 1.1: 3D medical image data: From pixels to voxels

Image slices can be concatenated according to the slice position of the respective tomographic measurement, thus forming a three-dimensional image stack (equally or non-uniformly spaced). Anatomical structures of interest can now be traced between adjacent images (Fig. 1.1). Stacking those sliced structures on top of each other reveals an approximation of their three-dimensional shape [1]. The closer the inter-slice distance is, the more accurate will be the spatial reconstruction. Ideally, the distance between consecutive slices equals the pixel resolution. Pulling pixels and slices together we obtain a three-dimensional partition of the image space into volume elements (voxels) forming a 3D scalar field.

Though 3D scalar fields can already be visualized directly using so-called volume rendering techniques [2, 3], such data cannot be modified in an easy way and do not provide a reasonable input for FE simulation (even though finite difference or finite element methods often are applied to labeled voxel data directly due to the lack of suitable geometry reconstruction methods). The major challenge will be to recover the inherent 3D shapes of anatomical structures from 3D medical image data as accurately as possible, and to convert them into geometry. Such structures are described topographically by their boundaries, and these boundaries are implicitly given by means of the classification of voxels, after the entire data volume has been segmented into different regions. Each

voxel gets a particular tissue type assigned. Connected voxels of the same type represent tissue structures (e.g., organs). Structures can again be embedded in other structures, in total forming a complex 3D anatomy model.

2. The amira[®] geometry reconstruction pipeline

With the process of geometry reconstruction we move from 3D voxel space to 2D boundary surfaces embedded in \mathbb{R}^3 , hence extracting information and massively reducing data. The most popular methods do approximate an implicit surface (e.g., via an iso-value) from a 3D scalar field with a polygonal representation [4, 5]. Dividing a 3D scalar field on base of a grey value threshold into foreground and background voxels only works if structures of interest are separable that way. In computed tomography, bone, soft tissue and air can be roughly discriminated by characteristic scalar values. Thus, soft tissue to air interfaces (skin) as well as soft tissue to bone interfaces can be quickly computed as iso-surfaces (i.e. surfaces passing through voxels of the same scalar value). The so-called marching cubes algorithm [4] and its derivatives do reconstruct such implicit surfaces according to this principle using a fast look-up method (Fig. 2.1). As a result, boundary surfaces are represented by a rather large set of piecewise linear surface primitives, i.e. triangles, that are convenient to render since graphics hardware is optimized in this regard.

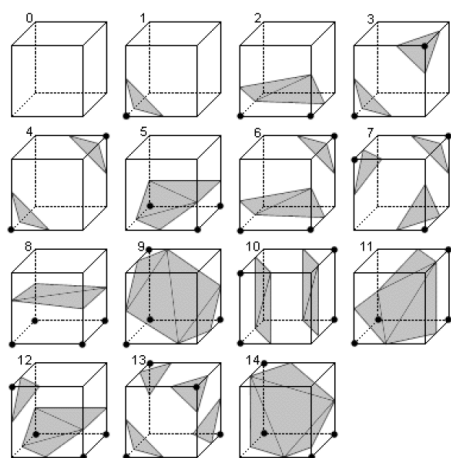


Fig. 2.1: Classical marching cubes look-up for binary classification

Although iso-surfaces are an appealing method for the analysis of 3D scalar fields, they are sensitive to noise and partial volume effects (i.e. voxels that do represent an average value of two or even more adjacent materials), thus introducing speckles or unintended holes. Also in case nested structures or multi-material components have to be reconstructed, standard iso-surface methods are unemployable, since they produce so-called manifold surfaces that do not represent material interfaces in regions where more than two materials are adjacent to each other. This, however, is not an unusual case for anatomical tissue structures and has to be modeled accordingly. In addition, imaging artifacts introduce distortions or lead to erroneous intensity values that prevent any grey-value based method from reconstructing the correct tissue boundaries automatically. Hence, more sophisticated tools and methods are needed for accurate 3D geometry reconstruction.

In the subsequent part of this article we focus on the geometric reconstruction of anatomical structures from three-dimensional medical image data, i.e. the generation of surface and volume meshes in a finite-element sense. At ZIB a dedicated software for medical image processing and geometry reconstruction is being developed, which is called amira[®] [6].¹ Sequences of medical images in DICOM format can be easily imported. The resulting 3D scalar fields can be visualized and inherent structures can be analyzed in many different ways. A commercial version of amira[®] is distributed by Visage Imaging.² Due to a technology transfer agreement between ZIB and VI new methods developed at ZIB become also part of the commercial product, and most of the functionality that is going to be presented is already available therein. Since cutting edge research problems often lead to novel sophisticated methods and to new quality enhancing features, this technology transfer continues and constantly improves the functionality of the commercial version of the software.

2.1 Medical image segmentation

The drawbacks of iso-surface reconstruction have been shortly discussed. Hence, threshold based segmentation might serve as a preprocessing step to any kind of elaborate segmentation strategy. The simplest method would be to correct the segmentation within each image slice using a brush like tool. Surprisingly this is also one of the most commonly used methods in clinical practice. Other tools, such as a *magic wand* for 2D and 3D region growing, *intelligent scissors* for semi-automatic contouring, *deformable contours* that are attracted by image gradients, up to inter-slice interpolation, wrapping, and modification of segmented structures in a 3D view, provide a reasonable support for complex image segmentation tasks. A good example for a large set of such sophisticated selection

¹ <http://amira.zib.de>

² <http://www.visageimaging.com>

tools is provided within the well known image processing software Adobe Photoshop[®]. In its latest version it is also enabled to read images in DICOM format, thus images can be easily converted into region masks that describe anatomical entities within an image slice. Such image masks can be exported to any popular image format, thus being further processed with amira[®] (as long as Adobe does not release some kind of 3D post-processing software for converting stacks of binary region masks into 3D geometry).

The constant use of the software in medical research projects at ZIB with their complex requirements led to practical experience and consequently to the development of features that are quite helpful for medical image segmentation. One is the possibility to mark and classify image areas in any of three orthogonal views with an immediate feed-back in all other views including a three-dimensional visualization (Fig. 2.2). Another is the possibility to assign a multiplicity of materials (in contrast to iso-value segmentation), thus being able to segment a data volume into a multi-material compound. A set of morphological operators such as erosion and dilation (i.e. shrink and grow), as well as smoothing, speckle reduction and consistency tests finally enable a user to create a consistent decomposition of a 3D medical image stack into anatomically meaningful segments. The segmentation result is finally represented in the form of a 3D label field.

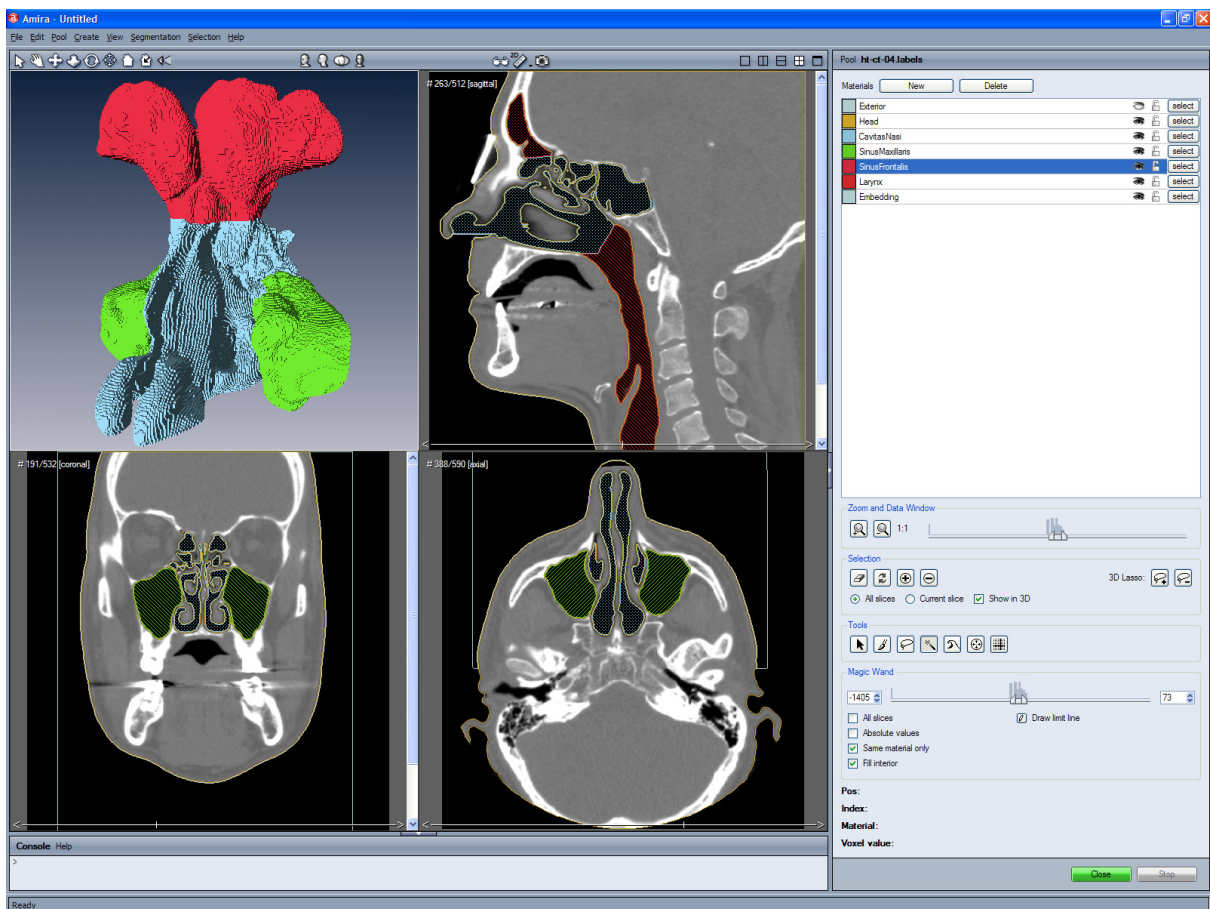


Fig. 2.2: Segmentation editor of amira[®]

With an increasing amount of image slices due to an ever increasing resolution of scanning devices, a manual segmentation approach, however, becomes a less useful option. Since the segmentation process is a rather labor intensive task, current research at ZIB is directed towards a robust and fully automated segmentation of tissue structures [7, 8].

2.2 Boundary surface reconstruction

Typically anatomical structures are of complex shape, normally smooth, and with curved boundary surfaces whose preservation is of importance. *Exterior boundaries* separate structures of interest and background. *Interior boundaries* do separate anatomical regions that have different properties, i.e. contact areas between different tissues. Keeping the complexity of anatomical shapes with all relevant details as well as its multi-material nature, and generating consistent boundary surfaces is our primary