Creating a high-resolution spatial/symbolic model of the inner organs based on the Visible Human

Andreas Pommert [a] Karl Heinz Höhne [a] Bernhard Pflesser [a]
Ernst Richter [b] Martin Riemer [a] Thomas Schiemann [a]
Rainer Schubert [a] Udo Schumacher [c] Ulf Tiede [a]

[a] *Institute of Mathematics and Computer Science in Medicine (IMDM)*
University Hospital Hamburg-Eppendorf, Hamburg, Germany

[b] *Dept. of Pediatric Radiology*
University Hospital Hamburg-Eppendorf, Hamburg, Germany

[c] *Institute of Anatomy*
University Hospital Hamburg-Eppendorf, Hamburg, Germany

Abstract

Computerized three-dimensional models of the human body, based on the Visible Human Project of the National Library of Medicine, so far do not reflect the rich anatomical detail of the original cross-sectional images. In this paper, a spatial/symbolic model of the inner organs is developed, which is based on more than 1000 cryosections and congruent fresh and frozen CT images of the male Visible Human. The spatial description is created using color-space segmentation, graphic modeling, and a matched volume visualization with subvoxel resolution. It is linked to a symbolic knowledge base, providing an ontology of anatomical terms. With over 650 three-dimensional anatomical constituents, this model offers an unsurpassed photorealistic presentation and level of detail. A three-dimensional atlas of anatomy and radiology based on this model is available as a PC-based program.

Key words: Visible Human, three-dimensional body model, anatomical atlas, color-space segmentation, volume visualization

1 Introduction

While in classical medicine, knowledge about the human body is represented in books and atlases, present-day computer science allows for new, more powerful and

Email address: pommert@uke.uni-hamburg.de (Andreas Pommert).

Article published in Med. Image Anal. 5 (3), 221-228, 2001

versatile computer-based representations of knowledge. Their most simple manifestations are multimedia CD-ROMs containing collections of classical pictures and text, which may be browsed arbitrarily or according to various criteria. Although computerized, such media still follow the old paradigm of text printed on pages accompanied by pictures. This genre includes impressive atlases of cross-sectional anatomy, notably from the photographic cross-sections of the Visible Human Project (Ackerman, 1991; Spitzer et al., 1996).

In the past years, however, it has been shown that spatial knowledge, especially about the structure of the human body, may be much more efficiently represented by computerized three-dimensional models (Höhne et al., 1995). These can be constructed from cross-sectional images generated by computer tomography (CT), magnetic resonance imaging (MRI), or histologic cryosectioning, as in the case of the Visible Human Project. Such models may be used interactively on a computer screen or in virtual reality environments. If such models are connected to a knowledge base of descriptive information, they can even be interrogated or disassembled by addressing names of organs (Höhne et al., 1995; Brinkley et al., 1999; Golland et al., 1999). They can thus be regarded as a “self-explaining body”.

Until now, the Visible Human Project has not reported three-dimensional models that reflect the rich anatomical detail of the original cross-sectional images. This is largely due to the fact that, for the majority of anatomical objects contained in the data, the cross-sectional images could not be converted into a set of coherent realistic surfaces. If we succeed in converting all the detail into a 3D model, we gain an unsurpassed representation of human structure that opens new possibilities for learning anatomy and simulating interventions or radiological examinations.

2 Earlier Work

Building a comprehensive model of the inner organs of the Visible Human requires both a spatial description consisting of three-dimensional objects, which are displayed using methods of volume visualization, as well as a linked symbolic description of relevant anatomical terms and their relations.

In general, volume visualization may or may not include a segmentation step. In *volume rendering*, transparency values are assigned to the individual voxels according to the intensity values and changes at the object borders (Levoy, 1988). In the case of the Visible Human, this method yields semitransparent views, which are suitable e.g. for visualization of the outer surface and the musculoskeletal system (Stewart et al., 1996; Tsiaras, 1997). This way, impressive animations could be created (Gagvani and Silver, 2000; Tsiaras, 2000). It fails, however, to display internal structures properly. In addition, organ borders are not explicitly indicated, thus making the removal or exclusive display of an organ impossible.

Segmentation, i. e. the exact determination of the surface location of an organ, is therefore crucial for building a realistic model. So far, complete automatic segmentation using methods of computer vision is suitable for very special application areas only, and could not be used to build an extensive model of the human body. The brute force approach to segmentation is manual outlining of objects on the cross-sections (Mullick and Nguyen, 1996; Seymour and Kriebel, 1998). Besides the fact that this procedure is tedious and very time consuming, it is largely observer-dependent and, even more important, does not yield exact and continuous surfaces. Furthermore, despite the high resolution of the dataset, important details such as nerves and small blood vessels cannot be identified clearly, because their size and contrast is too small.

So far, no symbolic description of the inner organs which is suitable for our purposes is available. A general discussion of the problems arising, focusing on the thorax, may be found elsewhere (Rosse et al., 1998).

3 Methods and Materials

We therefore aimed at a method that yields surfaces for the segmentable organs that are as exact as possible and textured with their original color. In order to arrive at a complete model, we decided to model non-segmentable objects like nerves and small blood vessels artificially on the basis of landmarks present in the image volume. Even though none of the methods presented here is entirely new, building a complex model required a number of substantial improvements.

3.1 Data

The original dataset of the male Visible Human consists of 1871 photographic cross-sections with a slice distance of 1 mm and a spatial resolution of 0.33 mm (Figure 1, left). For reasons of data storage and computing capacity, resolution of the cross-sections was reduced to 1 mm by averaging 3×3 pixels. From 1049 such slices, an image volume of $573\times330\times1049$ voxels of 1 mm^3 was composed, where each voxel is represented by a set of red, green and blue intensities (*RGB-tuple*). The Visible Human dataset also includes two sets of computer tomographic images of 1 mm slice distance, one taken from the fresh, the other (like the photographic one) from the frozen cadaver. Both were transformed into an image volume congruent with the photographic one, using an interactive, landmark-based registration (Schiemann et al., 1994). Since the frozen body was cut into four large blocks before image acquisition, all these parts had to be aligned individually, leaving some noticeable gaps in the data volume.

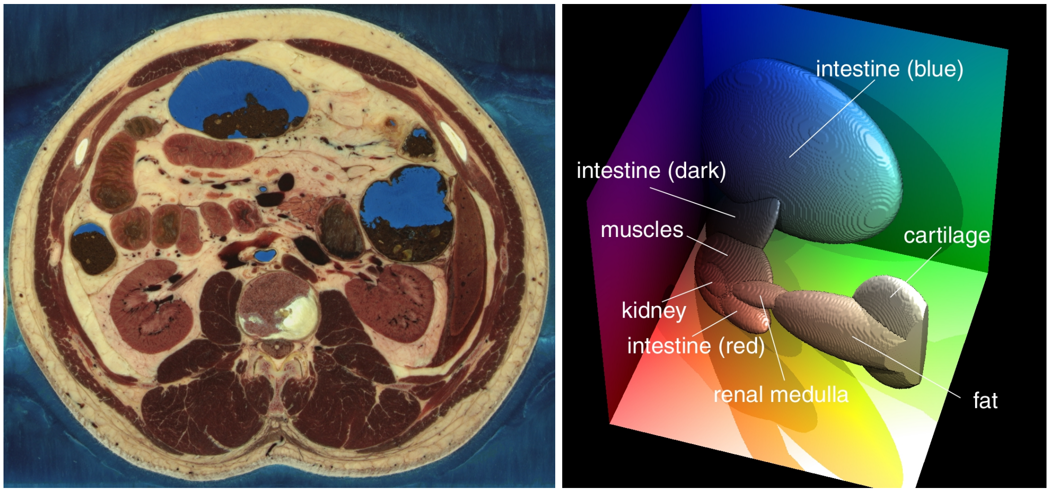

Fig. 1. *Left: Photographic cross-section of the abdomen of the male Visible Human. Right: Parameterized ellipsoids in color-space, used for classification of various tissue types in the abdomen. Many objects show similar colors, resulting in overlapping ellipsoids.*

3.2 Segmentation

The image volume thus created was segmented with an interactive tool, based on classification in color-space (Schiemann et al., 1997). It can be summarized as follows: On one or several cross-sections, an expert marks a typical region of the organ under consideration. All voxels in the volume with similar RGB-tuples are then collected by the program and shown as a painted three-dimensional *mask*. This mask usually needs to be refined by repeating this procedure in order to discriminate the target organ from the surrounding structures more clearly.

A cluster thus defined in color-space usually has an ellipsoidal shape, due to the correlation of the color components. Since a set of tuples is difficult to handle during subsequent visualization, this cluster is approximated by a parameterized *ellipsoid*, which is described by its center and three axis vectors. In general, there are other regions present in the volume which also match this color-space description. If they are not connected to the target organ, it can be isolated easily by a 3D connected component analysis. If not, borders are manually sculptured using a volume editor.

The result of this procedure is a description of an object in terms of an ellipsoid in color-space and a set of voxels, which are marked by object membership labels. Some of the ellipsoids defined for segmentation of the abdomen are shown in Figure 1 (right). As can be seen, there are anatomical constituents like the intestine which could not be described using one ellipsoid only; in this case, actually seven ellipsoids were required. On the other hand, the same ellipsoid may be valid for (parts of) various anatomical constituents, such as small intestine and colon, or even for hundreds of muscles.

As a general strategy, we applied our segmentation procedure going from simple to difficult tasks. This way, borders already defined could be used to facilitate segmentation of other objects. As a first step, several tissue classes such as fat, muscles, cartilage etc. were defined, for which the ellipsoids could be easily determined within a few minutes. For segmentation of bone, it proved easier to use the frozen CT dataset, applying a threshold value.

Since many objects show similar colors, the resulting ellipsoids are often overlapping (Figure 1, right). Therefore, some regions such as the anterior parts of the lung or the pericardium could not be segmented this way. In case of the lung, the missing parts could be determined using the frozen CT dataset and a threshold. For the pericardium and similar cases, the volume editor was used.

3.3 Graphic modeling

For several small constituents such as nerves and blood vessels, which were considered essential for a comprehensive anatomical model, our color-space segmentation proved impossible. As regards nerves, this is mostly due to very low contrast between nervous and fat tissues, while many small arteries are collapsed as a post-mortem artifact. Both problems also appear for the full resolution data.

For these cases, we developed a *tube editor* which allows us to include tube-like structures into the model (Figure 2). Ball-shaped markers of variable diameter are imposed by an expert onto the landmarks still visible on the cross-sections or on the 3D image. These markers are subsequently automatically connected using Overhauser splines (Yamaguchi, 1988). If one of the markers is moved, these splines will cause only local changes, which makes them easy to handle. Unlike the segmented objects, which are represented as sets of voxels, objects modeled with the tube editor are represented as polygon surfaces.

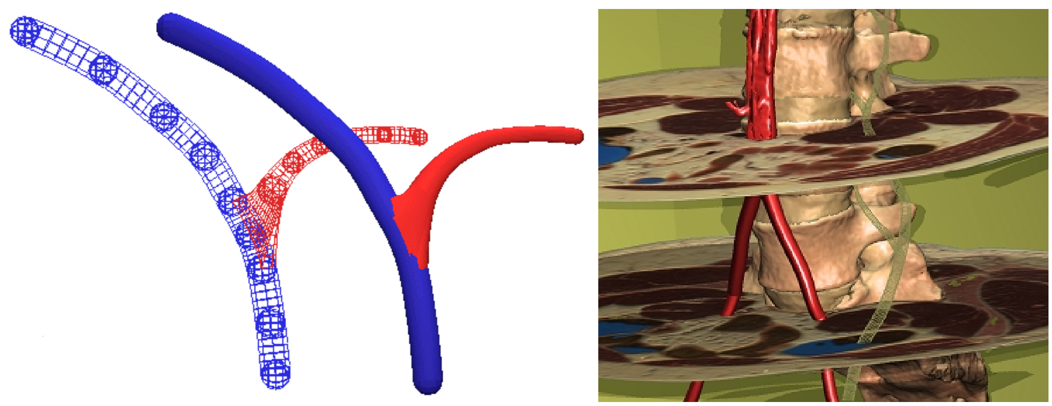

Fig. 2. *Small nerves or arteries which could not be segmented were interactively modeled using a tube editor. Tubes are defined by placing spheres of varying diameter into the volume, which are connected by interpolating splines.*

3.4 Volume visualization

The volume visualization algorithm we developed is characterized by the fact that it renders surfaces from volume data, using a ray casting approach (Tiede et al., 1998). Local surface texture (color) and inclination, as needed for surface shading, are calculated from the RGB-tuples at the segmented border line.

A decisive quality improvement is achieved by determining the surface positions with subvoxel resolution. This is done by considering both the ellipsoids (or thresholds, for CT) and the object membership labels. If a surface was created using labels only, it would appear blocky, especially when zooming into the scene. On the other hand, if only the ellipsoids were used, objects usually could not be identified without ambiguity.

In order to avoid these problems, ellipsoids and labels are combined using a color-driven algorithm (Schiemann et al., 1997; Tiede et al., 1998). Depending on the RGB-tuple found at a sampling point on a viewing ray, all ellipsoids enclosing this tuple in color-space are collected, defining a set of “object candidates”. In a second step, it is tested whether a matching object label is present in the vicinity of the sampling point. In that case, an object has been found. Its subvoxel surface position is determined by interpolating the color at the sampling point (inside the ellipsoid) and the color at the previous sampling point on the viewing ray (outside the ellipsoid), such that the color at the surface is representing the object border (on the surface of the ellipsoid). Since this approach considers colors (or intensities, for CT) before labels, a smooth, continuous surface is obtained, which is not limited by voxel size.

The objects modeled with the tube editor are visualized with standard computer graphics methods within the context of the segmented objects. The visualization program, an extended version of the VOXEL-MAN system (Höhne et al., 1995), runs on Linux workstations. Because of the size and resolution of the model, computation of a single image may take several minutes, even on a high-end workstation.

3.5 Knowledge modeling

While segmentation and graphic modeling provide a spatial description of anatomical objects, a comprehensive model also requires a linked symbolic description regarding anatomical terms and their relations. For this purpose, we developed a knowledge base system, using a semantic network approach (Pommert et al., 1994; Höhne et al., 1995). Among others, an object is described by

- names (preferred terms, synonyms, colloquial terms) in various languages

- pointers to related medical information (texts, histological images, references etc.)
- segmentation and visualization parameters (ellipsoid or threshold, object label, shading method, etc.)

For choosing anatomical terms, we built on standardized nomenclature wherever available (Federative Committee on Anatomical Terminology, 1998).

The knowledge base describes not only elementary parts found in the spatial model (e.g. *left rib 3*), but also compositions of these objects (e.g. *true ribs, ribs, thoracic skeleton, thoracic wall, body wall, body*), thus building a part hierarchy. This ontology is composed of several subnets, modeling various “views” commonly used in anatomy. For example, the kidneys can be seen according to structural or functional criteria:

- **regional anatomy**
  in this view, the kidneys are shown as part of the abdominal viscera
- **systemic anatomy**
  in this view, the kidneys are shown as part of the urogenital system
- **relation to peritoneum**
  in this view, the kidneys are shown as part of the primary retroperitoneal organs.

Views are represented as attributes of relations. Besides the “part of” relation type, our model also contains a “branching from” type, modeling the arterial blood flow.

As was pointed out earlier, an anatomical constituent may be a combination of several segmented objects, each with an individual name, ellipsoid, and object label. In order to hide these rather technical objects from a user, a relation type “hidden part of” was introduced, which is extending the part hierarchy. For a user, an anatomical constituent constructed of several hidden parts appears as one single entity.

4 Results

Using the methods described above, we built a model of the inner organs of the male Visible Human. It contains more then 650 three-dimensional anatomical constituents and more than 2000 relations between them. The size of segmented anatomical constituents varies between 3.8 million voxels (or mm^3, equivalent to 3.8 liters) for visceral fat and 124 voxels for the cystic duct. Preparation of the model using the described methods involved up to 10 people and required about 5 man years. Figure 3 gives an impression of image quality and the level of detail (see also the movie in the electronic annex - available via www.elsevier.com/locate/media).

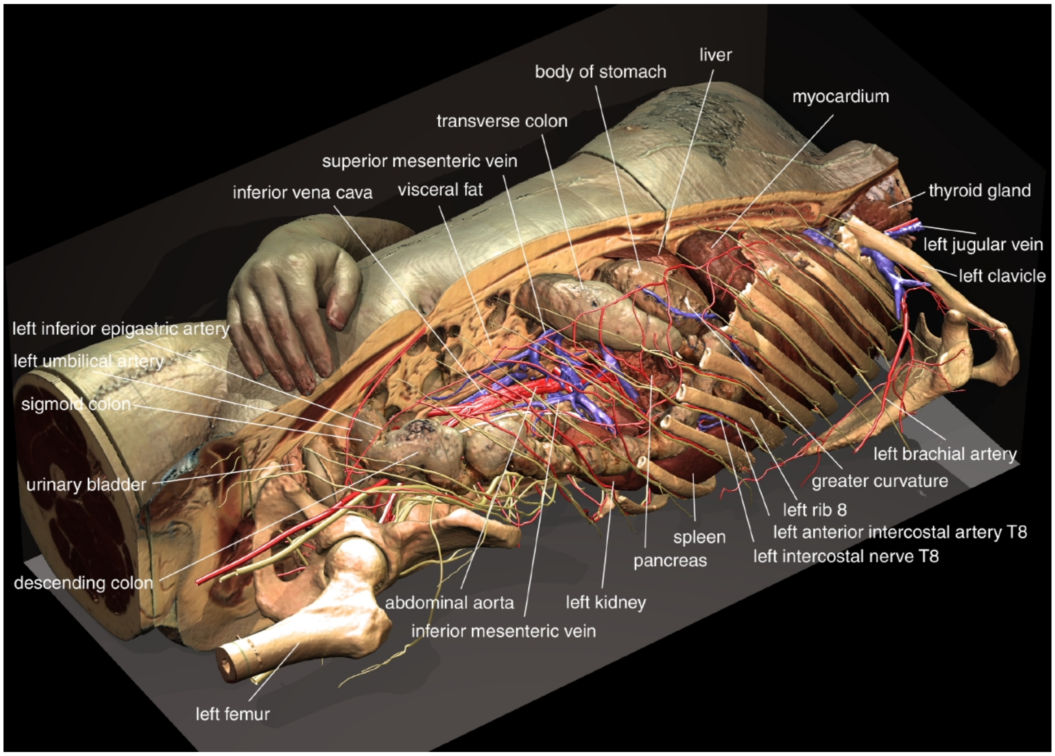

Fig. 3. *The model of the inner organs contains more than 650 anatomical constituents, with a spatial resolution of 1* mm^3. *It can be viewed from any direction, cuts may be placed in any number and direction, and objects may be removed or added. Annotations may be called by mouse click.*

Since the model is volume-based, cut planes, which can be placed in any number and direction, show the texture of the original photographic images and thus look realistic. This virtual dissection capability not only allows an interactive dissection for learning purposes, but can also be used for the rehearsal of a surgical procedure. In addition, the image of a "self-explaining body" allows us to inquire about complex anatomical facts. The more traditional way of annotating structures of interest is demonstrated within the user-specified scene in Figure 3. These annotations can be obtained simply by pointing and clicking with the mouse on the structure of interest. Likewise, objects may be painted. Pressing another button of the mouse will call several popup menus, which provide structured knowledge about anatomy and function (Figure 4). Such information is available because every voxel, and therefore any visible point of any user-created 3D scene, is linked to the knowledge base.

Vice versa, the user may navigate through the contents of the knowledge base, going to more general or more specific terms in systemic or regional part hierarchies. Images may be composed by selecting terms from the knowledge base (Figure 5).

A special feature of the model involves the possibility of simulating radiological examinations. Since the absorption values for every voxel are available in the orig-

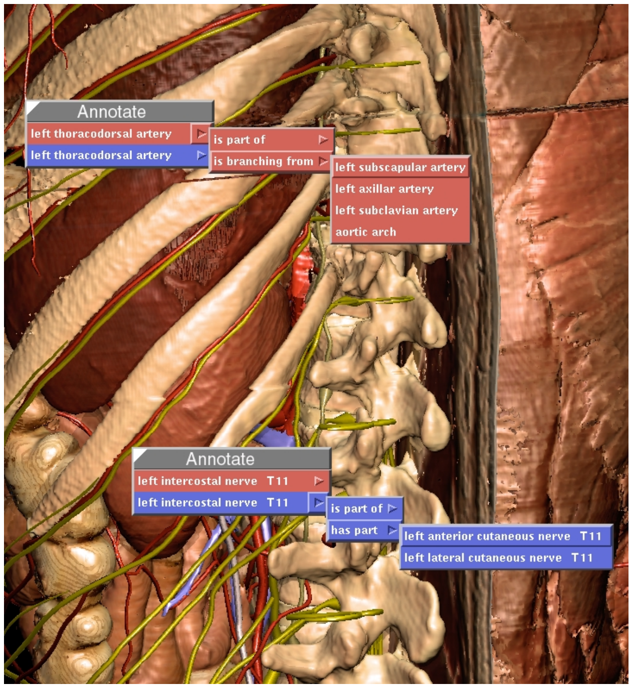

Fig. 4. *Exploring the semantic network behind the spatial model. The user has clicked onto a blood vessel and a nerve and received information about systemic (red) and regional (blue) anatomy.*

Fig. 5. *Visualization of various terms, selected from the knowledge base. Left to right: cardiovascular system; nervous system (with skeleton and iliopsoas muscles); thoracic organs; abdominal viscera.*

inal tomographic data, artificial X-ray images from any direction can be computed (Figure 6, left; see also the movie in the electronic annex). Based on the information of the model, both the contributing anatomical structures and the extent of their contribution to the final absorption can be calculated. Similarly, the information present in computer tomographic images can be clarified by presenting them in the corresponding context of 3D anatomy (Figure 6, right). For an improved spatial impression, stereoscopic views can also be created.

5 Conclusions

In this paper, we presented an approach for creating a high-resolution model of the inner organs, based on the Visible Human data. The following features of this model represent innovations:

- Because of the exact, color-space segmentation and the matched visualization method, the visual impression is one of unsurpassed realism.
- There is, to date, no computer model of the inner organs that contains and describes so many three-dimensional anatomical constituents.
- The model is space-filling, i. e. any voxel is labeled as an element of a three-dimensional object.
- The integrated formal organization of spatial and symbolic information allows a virtually unlimited number of ways of using the model.

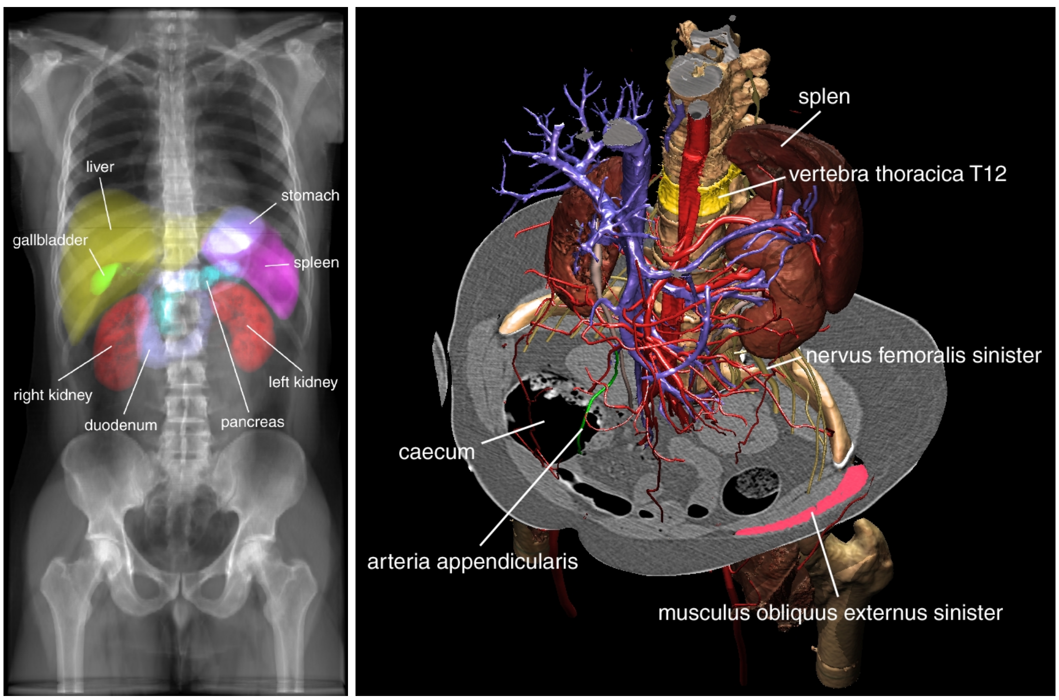

Fig. 6. *Different viewing modes such as X-ray imaging (left) or computer tomography (right) may be chosen from any direction and for any part of the model.*

The model is a general knowledge representation of gross anatomy, from which all classical representations (pictures, movies, solid models) may be derived via mouse click. The versatility of the approach makes it suitable for anatomy and radiology teaching as well as for simulation of interventional procedures. While the general principle was reported earlier (Höhne et al., 1995), the model we describe is the first to offer sufficient detail and comprehensiveness to serve these purposes seriously. A three-dimensional atlas of anatomy and radiology based on this model, called *VOXEL-MAN 3D-Navigator: Inner Organs*, is available as a PC-based program (Höhne et al., 2000).

Yet there are still improvements to be made. First of all, from an anatomist's point of view, an even more detailed segmentation would be desirable for many applications. Currently, improvements are under way. A more serious limitation is the fact that the data is derived from one single individual. The inter-individual variability of organ shape and topology in space and time is thus not yet part of the model. Inclusion of variability into three-dimensional models is a difficult problem not yet generally solved. So far, most progress has been achieved for 3D atlases of the brain (Mazziotta et al., 1995; Styner and Gerig, 2001).

However, the current model should be an excellent basis for further developments. One such development is the inclusion of physiology, e. g. the modeling of blood flow or propagation of electrical fields throughout the body (Spitzer and Whitlock, 1998). Applications such as the computation of body surface potential maps (Sachse et al., 2000) should profit from the increased level of detail. Furthermore, because of the more detailed characterization of tissues, a more realistic surgical simulation involving cutting (Pflesser et al., 2000) and soft tissue deformation (Cotin et al., 1999) can be achieved. This approach is thus an important, albeit early step towards computer models that not only look real, but also act like a real body.

Acknowledgements

We thank Victor Spitzer and David Whitlock, University of Colorado, and Michael Ackerman, National Library of Medicine (US), for providing the Visible Human dataset. We are also grateful to Jochen Dormeier, Jan Freudenberg, Sebastian Gehrmann, Stefan Noster, and Norman von Sternberg-Gospos, who substantially contributed to the segmentation and modeling work. The tube editor was implemented by Klaus Rheinwald. The movie in the electronic annex was produced by Andreas Petersik. The knowledge modeling work was supported by the German Research Council (DFG) under grant number Ho 899/4-1. An earlier version of this work was presented at *The Third Visible Human Project Conference*, Bethesda, MD, October 2000.

References

Ackerman, M. J., 1991. Viewpoint: The Visible Human Project. J. Biocommun. 18, 14.

Brinkley, J. F., Wong, B. A., Hinshaw, K. P., Rosse, C., 1999. Design of an anatomy information system. IEEE Comput. Graphics Appl. 19 (3), 38–48.

Cotin, S., Delingette, H., Ayache, N., 1999. Real-time elastic deformations of soft tissues for surgery simulation. IEEE Trans. Visualization Comput. Graphics 5 (1), 62–73.

Federative Committee on Anatomical Terminology (Ed.), 1998. Terminologia Anatomica: International Anatomical Terminology. Thieme, Stuttgart.

Gagvani, N., Silver, D., 2000. Animating the Visible Human Dataset (VHD). In: Banvard, R. A. (Ed.), The Third Visible Human Project Conference Proceedings. National Library of Medicine (US), Office of High Performance Computing and Communications, Bethesda, MD, (CD-ROM, ISSN 1524-9008).

Golland, P., Kikinis, R., Halle, M., Umans, C., Grimson, W. E. L., Shenton, M. E., Richolt, J. A., 1999. AnatomyBrowser: A novel approach to visualization and integration of medical information. Comput. Aided Surg. 4 (3), 129–143.

Höhne, K. H., Pflesser, B., Pommert, A., Priesmeyer, K., Riemer, M., Schiemann, T., Schubert, R., Tiede, U., Frederking, H., Gehrmann, S., Noster, S., Schumacher, U., 2000. VOXEL-MAN 3D Navigator: Inner Organs. Regional, Systemic and Radiological Anatomy. Springer-Verlag Electronic Media, Heidelberg, (3 CD-ROMs, ISBN 3-540-14759-4).

Höhne, K. H., Pflesser, B., Pommert, A., Riemer, M., Schiemann, T., Schubert, R., Tiede, U., 1995. A new representation of knowledge concerning human anatomy and function. Nat. Med. 1 (6), 506–511.

Levoy, M., 1988. Display of surfaces from volume data. IEEE Comput. Graphics Appl. 8 (3), 29–37.

Mazziotta, J. C., Toga, A. W., Evans, A. C., Fox, P., Lancaster, J., 1995. A probabilistic atlas of the human brain: Theory and rationale for its development. NeuroImage 2 (2), 89–101.

Mullick, R., Nguyen, H. T., 1996. Visualization and labeling of the Visible Human dataset: Challenges and resolves. In: Höhne, K. H., Kikinis, R. (Eds.), Visualization in Biomedical Computing, Proc. VBC ’96. Vol. 1131 of Lecture Notes in Computer Science. Springer-Verlag, Berlin, pp. 75–80.

Pflesser, B., Tiede, U., Höhne, K. H., Leuwer, R., 2000. Volume based planning and rehearsal of surgical interventions. In: Lemke, H. U., Vannier, M. W., Inamura, K., Farman, A. G., Doi, K. (Eds.), Computer Assisted Radiology and Surgery, Proc. CARS 2000. Vol. 1214 of Excerpta Medica International Congress Series. Elsevier, Amsterdam, pp. 607–612.

Pommert, A., Schubert, R., Riemer, M., Schiemann, T., Tiede, U., Höhne, K. H., 1994. Symbolic modeling of human anatomy for visualization and simulation. In: Robb, R. A. (Ed.), Visualization in Biomedical Computing 1994, Proc. SPIE 2359. Rochester, MN, pp. 412–423.

Rosse, C., Mejino, J., Modayur, B., Jakobovits, R., Hinshaw, K., Brinkley, J. F., 1998. Motivation and organizational principles for anatomical knowledge representation: The Digital Anatomist symbolic knowledge base. J. Am. Med. Inform. Assoc. 5 (1), 17–40.

Sachse, F. B., Werner, C. D., Meyer-Waarden, K., Dössel, O., 2000. Development

of a human body model for numerical calculation of electrical fields. Comput. Med. Imaging Graph. 24 (3), 165–171.
Schiemann, T., Höhne, K. H., Koch, C., Pommert, A., Riemer, M., Schubert, R., Tiede, U., 1994. Interpretation of tomographic images using automatic atlas lookup. In: Robb, R. A. (Ed.), Visualization in Biomedical Computing 1994, Proc. SPIE 2359. Rochester, MN, pp. 457–465.
Schiemann, T., Tiede, U., Höhne, K. H., 1997. Segmentation of the Visible Human for high quality volume based visualization. Med. Image Anal. 1 (4), 263–271.
Seymour, J., Kriebel, T. L., 1998. Virtual Human: Live volume rendering of the segmented and classified Visible Human Male in a CD-ROM product for PCs. In: Banvard, R. A., Pinciroli, F., Cerveri, P. (Eds.), The Second Visible Human Project Conference Proceedings. National Library of Medicine (US), Office of High Performance Computing and Communications, Bethesda, MD, (CD-ROM, ISSN 1524-9808).
Spitzer, V. M., Ackerman, M. J., Scherzinger, A. L., Whitlock, D. G., 1996. The Visible Human Male: A technical report. J. Am. Med. Inform. Assoc. 3 (2), 118–130.
Spitzer, V. M., Whitlock, D. G., 1998. The Visible Human data set: The anatomical platform for human simulation. Anat. Rec. 253 (2), 49–57.
Stewart, J. E., Broaddus, W. C., Johnson, J. H., 1996. Rebuilding the Visible Man. In: Höhne, K. H., Kikinis, R. (Eds.), Visualization in Biomedical Computing, Proc. VBC '96. Vol. 1131 of Lecture Notes in Computer Science. Springer-Verlag, Berlin, pp. 81–85.
Styner, M., Gerig, G., 2001. Medial models incorporating object variability for 3D shape analysis. In: Insana, M. F., Leahy, R. M. (Eds.), Information Processing in Medical Imaging, Proc. IPMI 2001. Vol. 2082 of Lecture Notes in Computer Science. Springer-Verlag, Berlin, pp. 502–516.
Tiede, U., Schiemann, T., Höhne, K. H., 1998. High quality rendering of attributed volume data. In: Ebert, D., Hagen, H., Rushmeier, H. (Eds.), Proc. IEEE Visualization '98. IEEE Computer Society Press, Los Alamitos, CA, pp. 255–262.
Tsiaras, A., 1997. Body Voyage. Time Warner, New York, NY.
Tsiaras, A., 2000. Volumetric imaging for the media. In: Banvard, R. A. (Ed.), The Third Visible Human Project Conference Proceedings. National Library of Medicine (US), Office of High Performance Computing and Communications, Bethesda, MD, (CD-ROM, ISSN 1524-9008).
Yamaguchi, F., 1988. Curves and Surfaces in Computer Aided Geometric Design. Springer-Verlag, Berlin.