CHAPTER 8

Conclusion

Our thesis was motivated by the need of researchers to visualize tensor fields in biomedical finite element models. Commercial software packages proved to be limited in their capabilities for tensor field visualization, were not suitable for finite element models and often required extensive knowledge of computer graphic principles and scripting languages in order to use them appropriately. Various research groups contacting us for advice in visualizing their data sets confirmed this impression. Subsequently we got offered the task to visualize the diffusion tensor field in the brain. Diffusion tensor imaging is on the forefront of current research in neuroscience because of its promise to yield in vivo information about the neuroanatomy. The results have the potential to vastly improve the diagnoses and understanding of various neurodegenerative white matter diseases.

The goal of this thesis was therefore twofold. First we wanted to create an easy to use toolkit suitable for the visualization of tensor fields in biological tissue. Secondly we wanted to analyze the stress and strain field in the heart and the diffusion tensor field in the brain. This chapter reviews our achievements and lists our contributions to the fields of scientific visualization and biomedical imaging.

8.1 Achievements & Contributions

The main contribution of our research is a toolkit for visualizing biomedical finite element models. The toolkit comprises the standard visualization icons for scalar, vector and tensor fields, including colour maps, isosurfaces, height fields, vector glyphs, streamlines, line integral convolution, tensor ellipsoids, hyperstreamlines.

In addition the toolkit incorporates several novel features. The first feature is a modular design with separate objects describing input data sets, visualization settings, rendering parameters, and visualization windows. The design facilitates the definition of powerful simultaneous visualizations of multiple models such as the simultaneous display of a sick and a healthy heart. Using the same rendering parameters ensures that both models are displayed using the same view, scaling, orientation and lighting.

The second feature is a generalized field structure. The user can define scalar fields, vector fields, and tensor fields by a FE mesh with interpolation functions, as a regular grid with a reconstruction filter or as analytic functions. New fields can be derived by using a set of predefined operators. The advantage of this construction is that fields only have to be created if they are really used and that the user can interactively construct new non-standard fields when important for a given application. Fields can also be represented with respect to both material and world coordinates.

The third novel feature of our toolkit is a global colour map control with an interface for designing new colour maps. New colour maps can be created by discretizing, exponentially stretching, or cyclically repeating a colour spectrum. Cyclical colour maps reveal isocontours and indicate gradient information without inducing visual cluttering and are useful when examining symmetry patterns and discontinuities in a scalar field. Colour map markers are a novel tool to indicate isocontours in a colour mapped domain. The width of the resulting isocontour indicates local gradient information. Another novel contribution is barycentric colour maps which are used to visualize three scalar fields simultaneously under the condition that the three fields form a barycentric coordinate system. The approach can be extended toward any number of scalar fields forming a convex sum.

As a new visualization tool we introduced filter objects. Filters can be used to define a domain for positioning visualization icons and to control a streamline integration. Filtering a point set for the placement of visualization icons introduces additional information into a visualization and reduces visual cluttering.

We also introduced an efficient and precise algorithm for computing length, area and volume measures. Regions of interest can be specified easily using a novel point, surface, and volume selection mechanism which is also used for the placement and combining of visualization icons.

In addition to the new tools explained above we implemented several useful improvements to existing icons such as a Marching Cubes algorithm for curvilinear FE meshes and a separation of tensor ellipsoids into six different coloured hexagonal sections to indicate the sign of the eigenvalues of the visualized tensors.

As a new visualization method for tensors we introduced anisotropy modulated line integral convolution (AMLIC). The technique convolves a noise texture with the major principal direction of the tensor and blends the texture with a colour map encoding the mean eigenvalue. The blending function is controlled by the ratio (anisotropy) of the eigenvalues. The direction of the major eigenvector relative to the image plane is encoded in the length of the convolution kernel.

An important issue in biomedical visualization is the perception of 3D structures. As a generalization of clipping planes we introduced a sectioning tool which allows the user to divide the model into 3D sections. Different sides of a model can be viewed simultaneously by placing mirrors into the scene. We showed that perception can be further improved by using markers, tags, raw image data and anatomical landmarks which are simple easily recognised features in a biomedical model.

An important requirement in biomedical imaging is a feature to communicate visualization results to laymen and experts at distant locations. An ideal medium to achieve this is the Internet. Our visualization package allows the user to save a visualization in Web3D (VRML) format which can be read using a standard web browser and VRML viewer which is available as a public domain browser plug-in. A visualization can be annotated using markers and name tags in order to identify features and regions of interest.

As a result of our research in the area of scientific visualization we presented a visualization schema which extends the traditional visualization pipeline by a visual interpretation step consisting of visual perception and cognition. Whereas the traditional approach represents only the encoding of data into visual attributes, visual interpretation represents a decoding of visual attributes. We also suggested a classification of visual attributes according to representational accuracy, perceptual dimension and spatial requirement. The classification supports finding suitable visual attributes for representing a given data set and hence forms the basis for mapping data onto visualization icons. As a further tool for supporting the visualization task we presented an extended classification of visualization icons by type, spatial domain, and information scope. We also provided a set of guidelines for selecting suitable visualization icons, for combining different visualization icons, and for increasing the effectiveness of a visualization.

This thesis concluded with two case studies presenting novel biomedical research. The first case study examined the deformation of the left ventricle of the human heart. The visualization of the healthy heart confirmed observations previously reported in the literature. Using tensor ellipsoids, streamlines and hyperstreamlines made it possible to visualize its complex deformation behaviour in a single image. Line integral convolution uncovered the presence of degenerate points at which the principal strains suddenly change direction. The visual information was supplemented by computing ventricular performance measures which are easily obtained from the finite element model using numerical integration. Colour mapping highlighted small continuity problems previously unknown to the developers of the ventricular model.

Visualizing a ventricle with dilated cardiomyopathy showed that the deformation of the lateral wall resembles most closely the expected motion whereas the septal wall behaved almost contrary to the expected deformation. Very large negative shear strains were recorded in the anterior-basal wall of the ventricle. The combined effect of these deformations seems to be a pumping action by shape deformation (from a circular to an ellipsoidal cross section) rather than by contraction.

The second case study introduced an incremental approach to explore the diffusion tensor field in a healthy brain. The use of various colour mapping techniques made it possible to identify several neuroanatomical structures. We also discovered an asymmetry in the diffusion anisotropy of the brain which could indicate differences in the alignment of white matter fibers. Furthermore we showed that slice images are improved by overlaying them with selected vector and tensor glyphs and that visual cluttering can be reduced by employing filters for the placing of the glyphs.

New insight into diffusion tensor data is gained by using barycentric colour maps which depict the distribution of anisotropies over a region and indicate possible fiber tract crossings. A high amount of information can be encoded into a slice image by using ellipsoid-based textures or anisotropy modulated line integral convolution. Both techniques indicate the three dimensional fiber direction and provide a visual segmentation of tissue types. Anisotropy modulated line integral convolution has the added advantage that it gives a continuous representation of the fiber tract direction and a clearer differentiation of tissue types.

Three dimensional visualizations of the fiber tracts in the brain can be created by computing streamtubes or hyperstreamlines along the maximum principal diffusion direction. In contrast to Zhang et al. [ZCML00b] we do not normalise the transverse diffusivities represented in hyperstreamlines and therefore represent additional information. We also offer more freedom for the selection of streamlines and we perform the fiber tracking using a simple, fast and flexible general purpose streamline tracking algorithm implemented within our visualization toolkit. We identified most of the principal pathways in the brain and validated the visualization by consulting a neuroanatomist. The understanding of the complicated geometry of the fiber tract visualizations is improved by inserting anatomical landmarks which are interactively generated using our visualization package.

New insight into the nerve fiber configuration was gained by applying hyperstreamlines in the direction of the minimum principal diffusion in regions of oblate diffusion anisotropy and we were are able to identify several regions with a possible planar nerve fiber arrangement.

CHAPTER 9

Future Research

Our visualization toolkit is already extremely powerful but further research is needed to improve user-friendliness, interactivity, and the range of available features. Although the toolkit contains a finite element modelling system so far no user interface has been implemented for it. In future we would like to fully integrate the finite element modelling of biological systems with their visualization. We would also like to enhance the modular design of our package such that the same visualization parameters can be applied to different models in order to compare them more easily. This would require the notion of equivalence between meshes and fields defined on those meshes.

Interactivity of our toolkit could be improved by defining new element and point selection features to identify regions of interest and by improved interaction with the visualization icons such as dragging isosurfaces through the model domain. We are also interested in improving the interactive derivation of new field data sets. More research on the user interface design is needed to make the toolkit more accessible to medical experts (e.g., [Max00]). Ideally we would like to create a visual programming interface to derive new fields and to design visualizations.

In terms of supported visualization icons we would like to implement the 3D tensor topology and examine its relevance for interpreting 3D stress and strain fields. More research is currently underway examining the use of 3D LIC for tensor field visualization. Also of interest is the application of statistical methods and artificial intelligence (data mining) techniques to explore the relationship between different fields and between field components, and to analyse the structure of a field. Cluster analysis and neural networks are promising techniques in this context.

Tools supporting comparative visualization could prove useful in order to visualize differences between healthy and diseased tissue or in order to visualize the progress of a disease. Visualization of uncertainty might be appropriate when dealing with models where the reliability of data varies over the model domain.

Our case studies so far have concentrated on examining models of healthy organs. We are interested in analysing data sets of neurodegenerative and heart diseases.

Of special interest is the detection of ischemic myocardium. It is known that small changes in the deformation behaviour of the myocardium occur before first symptoms of a cardiac infarct develop and we hope that visualizing the stress and strain field gives an indication of regions of low blood perfusion. Visualization methods such as LIC and tensor topology might be especially promising for this purpose.

We are also interested in visualizing DTI data sets of various white matter diseases. Current research indicates that DTI is superior to traditional MRI imaging modalities and employing advanced visualization methods might improve the diagnosis and the understanding of the development of various neurodegenerative diseases such as schizophrenia and multiples sclerosis. An exciting project is the simultaneous visualization of DTI data and functional MRI data. Using visualization methods similar to the ones suggested by Worsley et al. [WMN$^+$96] would make it possible to simultaneously display anatomical and functional information and to explore their relationship.

9.1 The Future of Medical Imaging

Cardiac MRI is predicted to become a comprehensive test of choice [POCD99]. An MRI toolkit for evaluating cardiac disease is progressing toward clinical reality and promises to have a major effect on the care of patients [BMM$^+$98]. Its applications include the evaluation of vascular anatomy (coronary angiography, aortic disease, aberrant vessels, vascular access), cardiac anatomy (congenital anomalies, right ventricular dysplasia, constrictive pericarditis, valvular function), myocardial perfusion, myocardial wall motion [BMM$^+$98] and visualization of metabolic processes using magnetic resonance spectroscopic imaging [SB99, p. 199]. Combining multiple MRI techniques in one examination replaces several other imaging procedures such as X-ray angiography, echocardiography, and scintigraphy and as such is cost effective and patient friendly [vR99].

Visualizing the strain field in the heart could yield even more insight if combined with the visualization of infarcted [vvd$^+$91, PNP$^+$99, LC99], ischemic and stunned myocardium [GKR$^+$98, RJH$^+$98] (using contrast MRI) and the visualization of the coronary artery tree (using MR coronary angiography) [RHH$^+$97]. Of particular importance in future will be molecular imaging which can detect organic or cellular malfunction before first anatomical changes occur [LSHP03]. Further understanding might be obtained by visualizing and analysing the complex fluid dynamics of the blood flow in the heart [KYW$^+$00].

A comprehensive future medical imaging and visualization system would communicate visualizations and diagnostic results using the internet [WK00, AG00] and might be connected to an expert system. Margulis and Sunshine [MS00] and Giger [Gig01] report that automatic diagnosis has already been achieved using neural networks and that applications such as MR treatment planning, computer assisted surgery and teleradiology are already becoming reality. Modern and future nuclear medicine workstations will network and allow incorporation into PACS with not only simultaneous viewing of US, CT, and MR images but also the option of image fusion [MS00].

9.2 Summary and Outlook

The field of medical imaging has increased rapidly in importance over the past decade. New image modalities and improved technologies allow the measurement of ever more data of the human body. Visualization packages like ours help transform this data into images which contain clearer and more accessible information. An ever closer alliance between medical imaging and scientific visualization will improve medical teaching and the understanding of the human body and its diseases. Visualizing medical data sets can enable general practitioners to perform a faster and more reliable diagnosis without consulting medical specialists. Complicated cases are already now frequently diagnosed over the internet using teleradiology [Hua01]. Much hope exists that this development will lead to faster and better treatment of patients, improved diagnostic, and lower health care costs. We are excited to participate in this development.