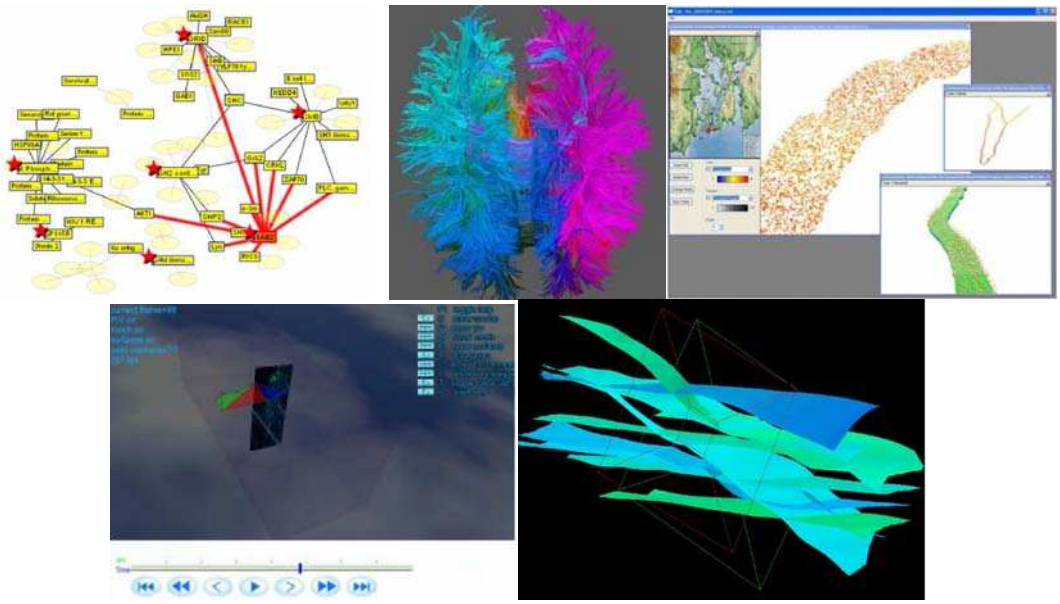
CS237
Interdisciplinary Scientific Visualization



Final Projects 2005

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Viualizing Topological Defects in Smectic Liquid Crystals

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Introduction

This work is the first visualization developed towards seeing topological defects found during the smectic phase of liquid crystals (LC). While physicists can identify the existence of layers formed by LC molecules in this phase with current visualization methods, they are unable to readily view the topological defects formed by these layers. Such irregular behavior limits the applicability of LCs in technology. In response, this novel visualization endeavors to clearly display the layers and their defects, such as merging and fusing, from molecular dynamics simulation data. The user is then able to focus on regions of interest by clipping away other layer geometry.

Previous related work includes that of Slavin et al. to visualize the topological defects in the nematic LC phase [1]. We know of no work to visualize the smectic phase.

Methods

The visualization was developed in AVS, so that we could extend the framework used in [1]. The framework includes tensor data parsing and smoothing modules and is already familiar to our physicist collaborator.

The smectic layer geometry is created by adapting the streamsurfaces technique [2]. The streamsurface layer grows orthogonal to the major eigenvectors of the LC molecules. This is accomplished by generating seed surfaces along the medium and minor eigenvectors.

Since the ultimate goal is to study defects on and between layers, we use color as a cue to show change in direction of surface curvature. The color is based on the major eigenvector (i.e. the vector normal to the surface at a particular triangular patch) information. Figure 1.

Due to surface occlusion, two clipping planes are introduced, giving the user control over how much of the visualization is actually seen.

Results

Smooth surfaces are perpendicular to the general LC molecular orientation as shown in Figure 1 and 2. Abrupt changes in surface curvature suggest areas of topological defects (Figure 2). Observing differences in layer spacing from one side of the smectic phase geometry to the other also indicate irregular behavior between layers. We note that the tensor data sampling process, in the process of smoothing data for surface generation, possibly smoothes out the explicit locations of defects as well.

In adjusting the streamsurface method to use the minor eigenvectors, we have observed problems where creases (visible in Figure 1) form in the layer geometry when the surface should be entirely continuous.

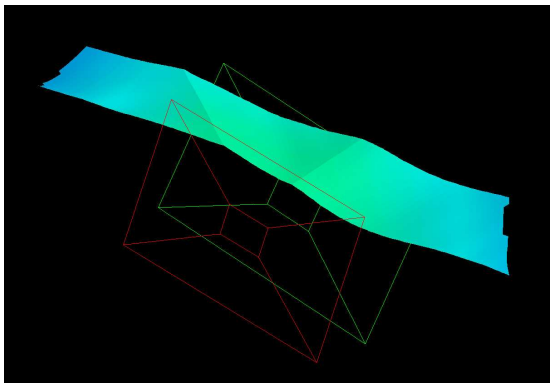

Figure 1. A sliced view of a single layer. Colorization is based on changes of major eigenvector from vertex to vertex.

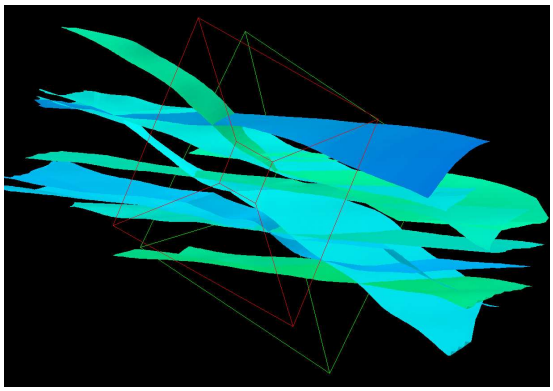

Figure 2. A sliced view of multiple smectic layers. Intersections of layers suggest locations of topological defects.

Conclusions

We have succesfully developed a preliminary visualization for layering defects in the LC smectic phase. At this stage, physicists can use this to find potential areas of topological defects and get a general idea of defect behavior by comparing one timestep data set to another.

This also serves as the first visualization generating streamsurfaces based on the minor eigenvectors. The creasing problem we discovered may help solve an algorithm issue and thus fortify the streamsurface algorithm for more applications in scientific visualization.

References

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[2] S. Zhang, C. Demiralp, and D.H. Laidlaw. Visualizing Diffusion Tensor MR Images Using Streamtubes and Streamsurfaces. IEEE Trans. On Vis. And Comp. Graph.,9(4):454-462, September 2003.

Visualization of Layering Defects in Smectic Liquid Crystals

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Introduction

Liquid crystals are a unique state of matter displaying properties of both liquids and solids. This unique blending of states makes liquid crystals (LCs) difficult for physicists to both understand and model.

Recent research has been conducted in visualizing and understanding the nematic phase of LCs due to its consumer application in liquid crystal displays [1]. However, equally important is another LC phase, the smectic phase, which has potential applications in both physics and chemistry due to its unique physical and optical properties. These properties are a result of the LC molecules forming into distinct layers. Defects within these layers limit potential applications and are therefore of prime interest to physicists and could provide a better understanding of LC properties and possible applications.

We developed a means of displaying the layers formed during the smectic phase utilizing streamsurfaces[2]. This was combined with color cues based on surface normal orientation to highlight areas of potential layering defects and provide the first visualization of layering defects in smectic LCs.

Methods

This project was developed within AVS utilizing the same framework as previous work to visualize the nematic phase of LCs[1]. This allows for many basic functions to be utilized including data smoothing and parsing of the tensor data, as well as allowing for the possibility of an all-inclusive LC visualization tool in the future.

Layers are generated orthogonal to the molecular orientation utilizing an adapted form of the streamsurfaces proposed by Zhang et al.[2]. Seed surfaces are generated along the minor eigenvectors of the tensor data. The surfaces are then extended outward by following the eigenvectors and generating polygons to curve the surface to the next tensor. The result is a smooth and continuous surface extending through the model. Coloring of the surfaces is achieved by mapping the major eigenvector to RGB. This creates a visual cue to areas of possible defects, as sharp changes in color parallel quick changes in surface contour.

Following discussion and preliminary evaluation, it was discovered that occlusion was a concern. Therefore, cropping was also enabled to allow for slices to be taken of the resulting surfaces. These slices can be manipulated by the user.

Results

As seen in Figure 1 and Figure 2, smooth and continuous surfaces are generated orthogonal to the overall orientation of the molecules. These surfaces allow the user to determine the orientation of the molecules. Areas of potential defects can be identified by sudden changes in surface curvature, cued by the changes in surface color, as well as by changes in the spaces between layers. Defects can only be implicitly identified because the sampling process necessary for surface generation smoothes the data removing explicit defects.

Problems have also been identified in the streamsurface generation algorithm. Artifacts, manifesting as linear ridges, are evident in the surfaces. Preliminary investigation shows the defects likely arise due to the use of minor eigenvectors instead of the major eigenvectors for surface generation.

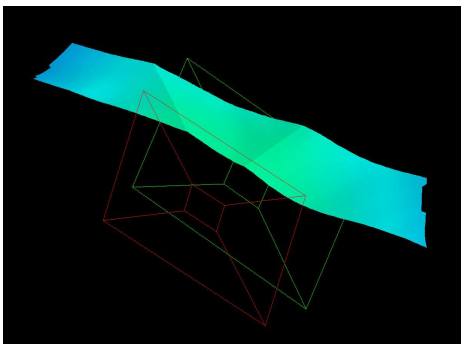

Figure 1. A slice of one smectic LC layer. Colorization is based off the major eigenvector providing cues to defects . Possible artifacts are also seen as distinct linear ridges in the surface.

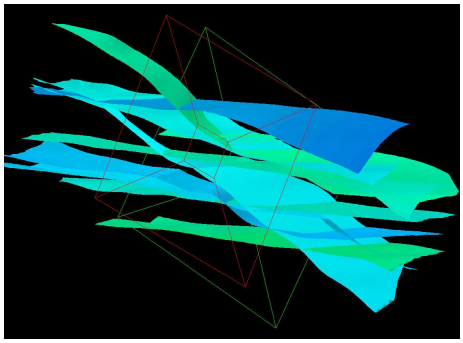

Figure 2. Multiple layers in a smectic LC model. Orientation of the molecules is evident from the average surface normal. Potential defects are present as crossing planes and sharp curves.

Conclusions

We have succeeded in developing a preliminary visualization of defects in the smectic phase of liquid crystals. This is the first visualization using streamsurfaces generated along minor eigenvectors, hopefully opening the door for further application areas. In its current state, the surfaces generated highlight areas of potential defects, which should provide physicists a general idea of the extent of defects in an LC substance. Furthermore, it should help physicists narrow down where to check for errors. Finally, the issue discovered with the streamsurface algorithms may solve an underlying problem in the algorithm and facilitate its application in other visualizations.

References

[1] V.A. Slavin, D.H. Laidlaw, R. Pelcovits, S. Zhang, G. Loriot, and A. Callan-Jones. Visualization of Topological Defects in Nematic Liquid Crystals Using Streamtubes, Streamsurfaces, and Ellipsoids. IEEE Visualization, vol. 00, no.,p. 21p, 15th, 2004.

[1] S. Zhang, C. Demiralp, and D.H. Laidlaw. Visualizing Diffusion Tensor MR Images Using Streamtubes and Streamsurfaces. IEEE Trans. On Vis. And Comp. Graph.,9(4):454-462, September 2003.

Visualization of Kinematics and Particle Image Velocimetry of Bat Flight

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We present an interactive visualization and exploration tool designed for a new kind of scientific data in order to help animal flight experts study biomechanics of bat flight. We combine bat wing motion capture data with particle image velocimetry (PIV) to obtain a simultaneous visualization of the wing membrane and the vorticity field of the flow in the wake behind the bat.

I. INTRODUCTION

Understanding the connection between wing structures and flight behavior can help gain insight into evolution of flight and biological world in general and provide an idea for implementation of complex flight mechanisms. The only flying mammals, bats feature unique wing construction properties and exhibit unconventional flight behavior, which, as pointed out in [1], can not be analyzed using a traditional rigid-plane approach.

A key element vital to studying the characteristics of bat flight is the vorticity field around the wing, especially in the wingtip regions. Essential to success of flight analysis and simulation is an efficient exploration tool that would allow researchers to display this field in conjunction with bat kinematics information.

II. METHODS AND RESULTS

Bat wing kinematics data is collected using high-speed infrared cameras that capture the positions of reflective markers attached to bone joints and wing membrane. PIV cameras capture imagery of micron-sized particles in the wake behind the flying bat, and this imagery is used to compute flow velocity field and, consequently, vorticity field.

Based on the vorticity field, a texture is generated for each PIV slice and registered to an appropriate time and position in kinematics data. A user then can control full spatial and temporal navigation of data, including playing the animation, stepping by individual frames, snapping to frames at which PIV slices were taken, etc. as well as moving a scene camera or a follow camera that provides a point of view in the coordinate frame of the bat. This allows a researcher to gain a variety of perspectives on the relationship between the wingbeat cycle and the corresponding flow structures represented by the vorticity field.

Since different bat runs involve variation of a number of conditions, all parameters for the animation, including framecount, paths to marker and PIV data files, marker indices for bone mesh connections and surface patches, can be changed in a configuration file that is read into the application, allowing the researchers full control over different data sets and visualization options.

The implementation of the project is based on G3D 3D graphics engine developed at Brown, which allows us to maintain high portability of code across operating systems and visualization platforms. A graphical user interface is written entirely using G3D components as well, which helps avoid further compatibility limits or issues.

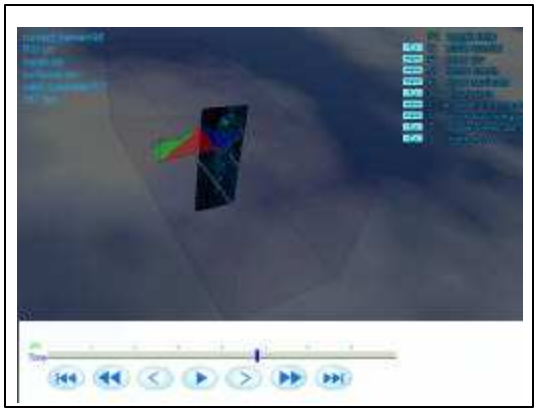

Figure 1. Meshed bat wing markers and PIV vorticity data in a visualization interface.

The application was developed in close collaboration with Dr. Sharon Swartz's bat flight research group at Brown's Dept. of Ecology and Evolutionary Biology, and Dr. Kenneth Breuer at Dept. of Engineering, and was tailored to meet their joint efforts and needs in visualizing the combined data from kinematics and PIV data collection. The tool has already helped the group uncover a calibration error present in the digitized data, and will continue to be used in visualizing and validation of capture datasets starting with the new test runs in spring of 2006 and throughout several years.

Due to flexible configuration profiles, the application can also be easily adapted to accommodate other datasets that involve similar types of data, including geometry and flow visualization for fish, birds and insects.

III. CONCLUSION

We have developed the first visualization integrating kinematic and PIV data in bat flight, and provided biologists and engineers working on analysis of animal flight research with a useful interactive tool that can help them gain valuable insight into bat flight aerodynamics. Our application is already yielding tangible contributions and is fully expected to become integrated with the bat research group's capture initiative in the future.

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A Framework for the Visualization of Bat Flight

Peter Yee Mykhaylo Kostandov David Laidlaw Sharon Swartz Kenny Breuer

Abstract

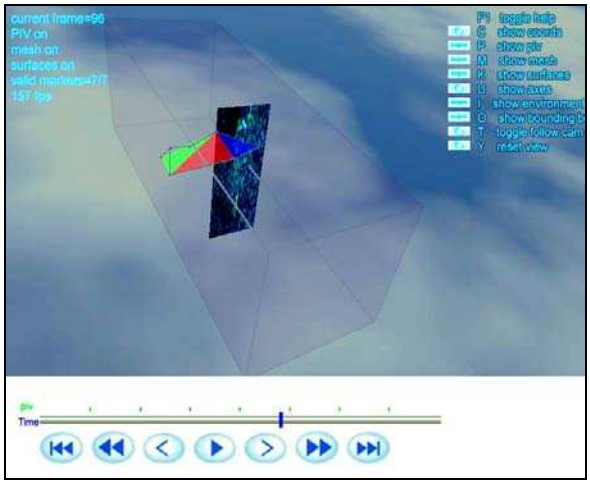
A visualization method for bat flight was developed as part of an ongoing investigation into the mechanisms of bat locomotion. Easy to use and true to actual measurements of bats flying, this visualization allows the verification of successful data capture and demonstrates the relationships between wing geometry and wake vorticity.

Introduction

Bats are the only flying mammals, and use a method of flight that is unique from any other form of locomotion yet observed. Judging from the physiology and metabolism of bats, this method of flight not only allows a high degree of maneuverability, but it is also highly efficient [1]. Unfortunately, humans have yet to replicate or even understand the dynamics of bat flight, due to the complexity of the bat movement and wake pattern; in order to be able to replicate bat flight, knowledge about the forces exerted on the wings is needed. These forces cannot be measured directly, and we must resort to running simulations in a guess-and-check fashion until we can replicate the data that we can measure: the 3-D geometry of points on the wings and the vorticity of the surrounding air [2]. Thus, it is imperative that we can visualize bat geometry as well as the vorticity measurements so that we can confirm that the data was captured correctly as well as make insightful guesses about simulation parameters.

Methods

In order to address this need, we have created the first visualization that displays wing geometry data in tandem with air vorticity measurements. Required to display captured data taken under a wide range of different conditions, we utilized configuration lists to enable complete compatibility with any timing or geometry. As the techniques for capturing geometry and vorticity measurements have not yet been perfected, the visualization uses simple points and planes with no optical enhancements or artistic embellishments, ensuring that no synthetic bias was added. Furthermore, in order to make sure that the location of these geometric primitives could not be mis-interpreted, we have given the user freedom to move about both in space as well as time. Another governing factor in the development of this product was the clientele: since the primary users will be biologists, not computer specialists, we have allowed all facets of the visualization to be controlled without knowledge of programming languages. Additionally, the visualization runs in both Windows and Linux environments, and does not require specialized graphics hardware. The result is that we have created the first bat flight visualization that displays the data we want to see with ease and convenience at levels conducive to everyday use.



Impact

Complete geometry and vorticity data for bat flight has not yet been obtained, and the measurement and visualization of this data is the current top priority of the Bio-Flow lab at Brown University. As this data set gradually becomes populated, researchers will use this application to visualize the measurements captured as well as to make conclusions about the potential validity of each captured run. In fact, an error in quantizing wing geometry data was already discovered with the aid of this visualization, and we expect that such contributions will continue to be made as more measurements are taken.

Scope

Measurements and analysis of bat flight will continue over the course of the next few years, and the developed visualization will be useful until a complete dataset of bat flight is captured. However, this visualization is also applicable to any bio-flow situation, and can be utilized for the study of fish, bird, or insect locomotion.

Conclusions

A bat flight visualization has been created and is the first of its kind that was designed to visualize measured geometrical and vorticity data. Intended to be convenient to use and absolutely loyal to input data, the creation of this visualization was the next important step in an ongoing initiative to understand the mechanisms of bat flight.

References

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Visualizing protein relations interactively

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Introduction

The Human Protein Reference Database is one of the results of recent efforts by the proteomics community to gather all existent knowledge about proteins and make them available to researchers around the world.

One main component of the HPRD is information about protein interactions. The HPRD offers only two ways of exploring these interactions. One is to query for a protein and retrieve all the proteins that it interacts with while the other is to look at one of the static spider-web images that illustrates the interactions between several hundreds proteins at once. The drawback is that the first method does not provide sufficient information at a time while the second one floods the researcher with information that he may not be interested in, thus occluding information that may be important.

This is why we have built a visualization system that allows a proteomics researcher to visualize HPRD data by specifying and filtering according to information that he is interested in. We have also concentrated on making the system as usable as possible by providing a powerful set of tools that the researcher can use to explore the protein space. As far as we know, this is the first system of this kind and we have already had some positive feedback from people involved in protein research.

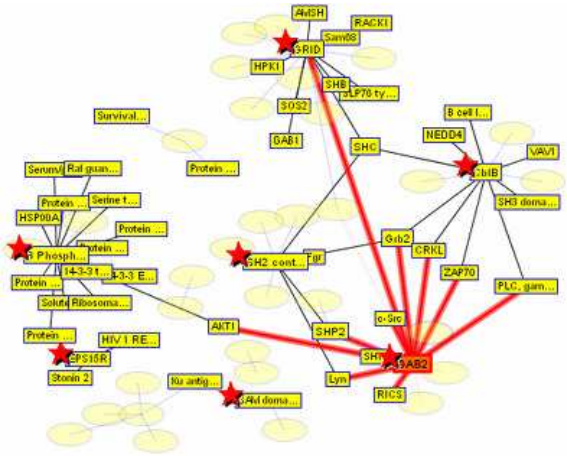

Figure 1: Visual Representation of HPRD data. Proteins marked with a star denote the initial proteins. All proteins that are not in the cytoplasm are hidden (yellow transparent ovals) and some interactions are highlighted.

Methods

We start with a list of proteins provided by the researcher as input and then parse the HPRD database, extracting context for these proteins. By context we mean important information about these particular proteins, other proteins that they interact with as well as all the interactions between these proteins.

We than create a visual graph-like representation of the proteins and the interactions between them (Figure 1).

The user can work with this visual representation in an intuitive manner: he can hover the protein to see important information about it, he can click on an interaction and have the paper discussing that interaction pop up in a separate web-browser or he can adjust the visual representation by zooming in and out, translating the image, dragging proteins to different locations, coloring various elements in the visual representation.

A major problem in this kind of representation is that the resulting image may be very dense and thus hard to explore. We have tried to overcome this issue by enabling filtering by different criteria such as location of the protein in the cell or the body, degree of connectivity etc. The researcher also has the ability to temporary hide information deemed uninteresting or highlight elements that are relevant (Figure 1).

Another aspect that we tried to address is that of analyzing data over longer periods of time. Since a researcher may work with a protein set over several days or weeks we thought that abilities such as saving and loading visual layouts are a must. We have also included some other features such as annotation of proteins or interactions so that a researcher can more easily restore his line of thought from one analysis session to another.

Results and Conclusion

We have developed the first interactive, visual tool for exploring the HPRD database. The fact that we allow the researcher to filter the database by a list of proteins of interest, and then to further refine his search with other criteria is novel and aids proteomics researchers in their work. The possibility to save and load layouts allows them to analyze protein sets over longer periods of time while a powerful set of exploration and editing tools helps them make the most of the visual representation.

We have also set the foundation for further investigation into visual analysis of relations by creating a first prototype that our proteomics collaborators can use. We hope that using this system will allow them to better define their needs and give us more insight into what makes visualizations of interactions effective.

References:

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Interactive Color Embedding-based Fiber segmentation in DTI

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ABSTRACT

We present a visualization tool which map and segments white matters of the brain in diffusion tensor magnetic resonance imaging more anatomically and interactively. DTI, a non-invasive MR technique, measures water self-diffusion rates and hereby gives an indication of the underlying tissue microstructure. Neuropsychologists are interested in understanding the white matter structure of the brain in order to study diseases such as HIV. Previous visualization techniques fail to provide users with the flexibility of free region selection in the 2D view and ability to view the characteristics and terminal points of the fiber tracks passing through a plane. Traditional segmentation methods results in a rigid clustering of the fiber bundles which may introduce confusion and error. The developed tool generates a smooth segmentation and allows verification of the fiber tracks by inspecting the regions of the brain that they pass through. The resulting tool was evaluated by neuropsychologist and feedbacks are included in this paper.

METHODS

The fiber bundles were color-coded using the perceptually uniform color space embedding based on [1] and clustered using the computed stream-tube distances [2], a measure of similarity between the whole pairs of fiber tracts. (figure 1, left) The color-embedded model is integrated into the BrainApp program [3]. We improved the unintuitive 3D box selection of the existing program to enable user to select an axis aligned plane and view the fiber coloring in a 2D view. (figure 1, right) The user can then interactively make a free selection (closed curve) on the plane (figure 2, left) to view the tractography passing through the selected region. (figure 2, right) These interactive features allows user to pick out and examine their white matter tracks of interest easily.

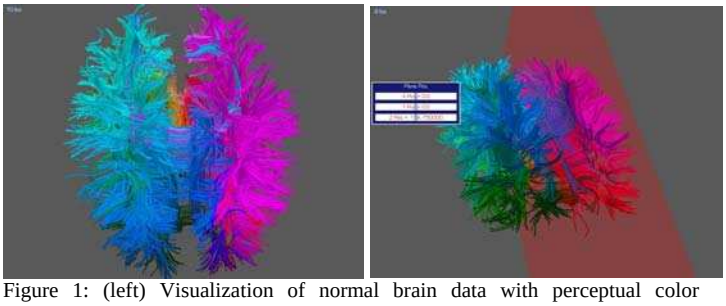

Figure 1: (left) Visualization of normal brain data with perceptual color embedding. (right) Axis aligned semi-transparent plane selected midsaggital slice of the corpus callosum.

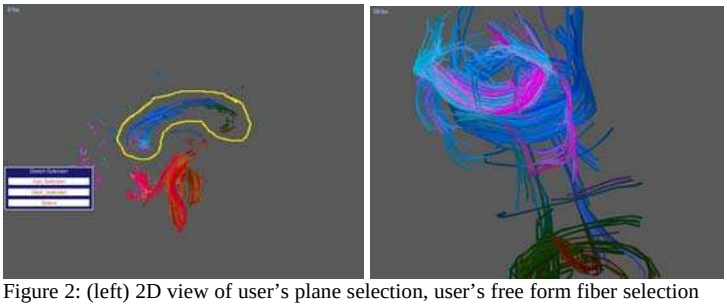

Figure 2: (left) 2D view of user's plane selection, user's free form fiber selection is shown in yellow curve. (right) Fiber tracks passing through user's fiber selection.

RESULTS

We performed informal evaluations with expert using normal and HIV positive patient datasets. The feedback we received as follows. Strong color contrast between the two hemispheres provided more contexts for 3D navigation. The color-embedding with smooth color clustering was an effective clustering method since it allowed the user to put the model together without imposing a pre-calculated rigid color fiber clusters. Anatomically meaningful fiber bundles could be easily recognized and picked out of the model despite smooth color variation. The tool allowed the expert to intuitively interact with the data model. Comparison between healthy and HIV infected patients could be performed more efficiently with the new tool.

CONCLUSIONS

We have succeeded in generating an interactive visualization tool that clearly shows anatomic brain structures. Our evaluation shows promising practical use of the tool for brain white matter fiber track analysis. This tool is continuing to be used and evaluated by neuro-psychologists studying white matter structure of the brain in order to study diseases such as HIV.

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Coloring of DT-MRI Brain Data for Interactive Segmentation

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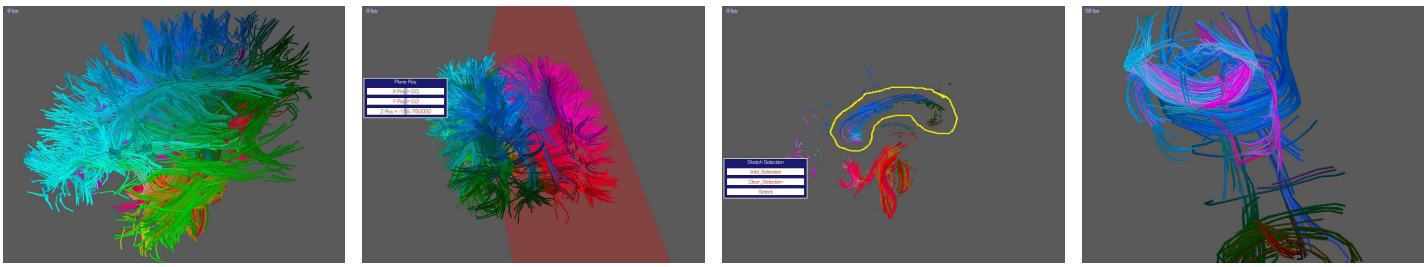

Figure 1: (Left) Brain of normal subject, color differences indicate differences between white matter tracts (shown with about $4K$ stream tubes). (Left Middle) User selects an axis align plane corresponding to the midsaggital slice of the corpus callosum, displayed with a semi-transparent red plane. (Right Middle) Selected slice is shown as 2D image , that user selects a free form region (yellow curve). (Right) All tracts passing through the region are displayed.

Understanding white matter structure of the human brain is crucial for studying diseases such as HIV. Current visualizations and analysis of diffusion tensor magnetic resonance images (DT-MRI) have focused on rendering tracts and segmentation of white matter tracts into bundles. Automatic segmentation methods impose a rigid, possibly inaccurate, model of what white matter tracts belong to which bundles. Instead, we visualize geometric disparity between white matter tracts and let the expert user of our application select regions. This approach better reflects the uncertainty in forming scientific model from the geometric information. Our system couples 3D visualization of geometric differences between tracts with a 2D sketch-based selection mechanism. Our coloring work is similar to Brun et al. [2003]. That work applies smooth coloring to DT-MRI data using a simpler distance metric.

Methods and Results

We visualize distances between white matter tracts. We use the metric and software developed by Zhang et al. [2003]. Our system consists of an interactive component and preprocessing. The preprocessing is as follows: First, stream tubes that represent white matter paths are computed from DT-MRI data. Second, we compute an adjacency matrix of distances between every pair of stream tubes in the brain. Third, using a spectral embedding method, we assign colors to every stream tube such that differences in colors correspond to the distances in the matrix. Finally these colors are converted from a perceptually uniform color space to RGB for display.

After we've assigned a coloring of stream tubes we view them in the BrainApp software, an interactive tool for visualizing DT-MRI data. The original BrainApp selection method was based on the user selecting placing cubes in 3D via menus. This method is both unintuitive and inflexible. Thus we extended the BrainApp software with a new selection interaction. The user selects axis aligned planes in 3D then views, as a 2D view, the colors of stream tubes intersecting that slice. Next the user makes a free-form closed curve. The stream tubes that pass through the this region are selected (see Fig. 1). This axis-aligned view and selection method exploits the training neuro-scientists have received viewing aligned 2D images of the brain.

We performed two informal evaluations with an expert visualizing a normal and HIV positive brain data-set. Our expert reported high anatomic specificity, he reported being able to easily pick out meaningful fiber bundles even though colors varied smoothly. He noted that the hemispheric color differences easily gave context when navigating in 3D views. He felt the subtle color variations were visually easier to process. The user felt that he was the one making the model (instead of a predefined cluster of tracts). We asked the expert how our approach fared against displaying hard segmentation where whole bundles are colored with one color versus the smooth color variation. The user felt the smooth coloring was more compatible with the uncertainty of tractography.

Conclusion

The initial evaluation shows this is promising approach. Our visualization method shows relevant anatomic structures with out imposing a segmentation. Based on user feedback in future work fractional anisotropy(FA) variation could be integrated into the stream tube distance metric which would make the tool more useful for comparing brains across many subjects.

BRUN, A., PARK, H.-J., KNUTSSON, H., AND WESTIN, C.-F. 2003. Coloring of DT-MRI fiber traces using laplacian eigenmaps. In *EUROCAST'03*, 564–572.

ZHANG, S., DEMIRALP, C., AND LAIDLAW, D. H. 2003. Visualizing diffusion tensor MR images using streamtubes and streamsurfaces. *IEEE TVCG 9*, 4 (October), 454–462.

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Visualizing the Multi-Variable Data of the Narragansett Bay Oceanography

Maribeth Rubin Kristin Boyle Warren Prell (Collaborator)

Introduction

We created a visualization tool that allows scientists to better understand the ecosystem of the Narragansett Bay. To create our tool we first developed possible prototypes. They were then evaluated through a user study that highlighted the importance of interactivity and interface in visualization design. Based on these results a more complete and effective application was developed.

Problem Statement

The Narragansett Bay ecosystem is very vulnerable and sensitive to small changes in temperature and water quality. Understanding these changes through the analysis of a large multivariable dataset is important for its preservation. Previously, scientists have only explored this dataset with simplified 2D representations that lack the ability for scientists to see interactions between the variables and the scalability necessary for both local and global phenomenon to be analyzed within the data. These issues have been addressed through our creation of a visualization tool that seeks to fill-in these gaps.

Implementation

To create this visualization tool we developed prototypes based on our critique of the original data representations and through an expansion of ideas taken from the work of Healey (1999) and Kreuseler (2000) and applied to 3D data along a path. The different prototypes included global and local views; multi-variable representations through variance in color, texture, and surface height; a horizontal surface view for detecting locations more easily; a vertical surface view for visualizing stratification in depth, and a multi-layered representation where each variable was depicted by an overlaid colored layer with texture representing the variation of the data.

Evaluation and Final Application

These prototypes were evaluated through a user study with an Estuarine Oceanography class that had previous experience performing analysis with the dataset. The prototypes were judged on their effectiveness to communicate correlations between variables at specific locations and on a more global scale, as well as on which tasks they were best suited for and how they compared to the original data representations. Participants in the study thought that the tool would be most useful when used in an interactive manner. They found correlation tasks to be easiest when the ability to switch between the color gradient and the texture was used. They also found the ability to switch from a global view to a local view to be superior in obtaining more detailed information then could be obtained through the non-scalable original 2D representations. Most participants found the use of path width as well as the specific texture pattern to be ineffective at times. They also had difficulty with the lack of labels. We reevaluated the design of the visualization based on these critiques and the overwhelming need for more interaction. A full application was developed to include a user interface that allows for better manipulation of the data through changes in the representational depictions of the different variables and scalability features. This interface also allows for comparisons over different years and locations using multiple windows.

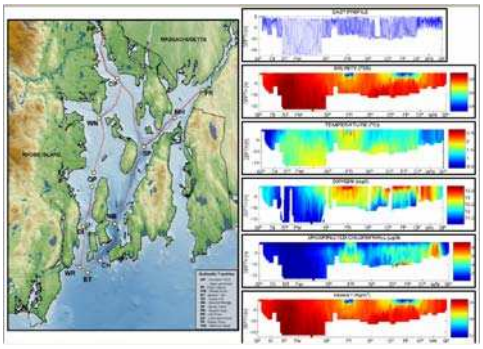

Figure 1: A map depicting the Narragansett Bay dataset and the original 2D graphical representations that were used to analyze it.

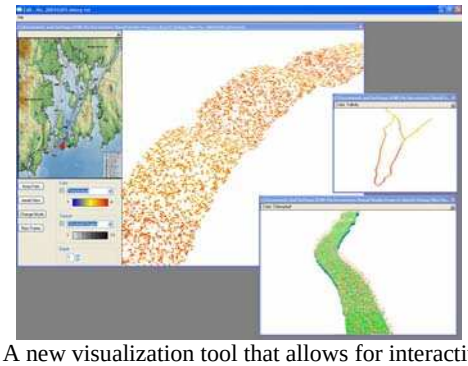

Figure 2: A new visualization tool that allows for interactive exploration of the dataset through scalability, multiple views, and an interactive user interface.

Conclusions

Our user study enforced the importance of interactivity and the need for a more interactive user interface in our final visualization design. Our finished application provides new ways to analyze and investigate the dataset as well as the ability to confirm existing scientific hypotheses about stratification, current flow effects, and water column stability within the Narragansett Bay by interactively manipulating the data through representational changes, scalability, and multiple views. This tool has been developed in the form of an application that will be accessible to scientists for everyday research use.

References

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Visualizing the Oceanography of Narragansett Bay

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Introduction

For the past ten years scientists have been collecting detailed readings from the Narragansett Bay estuarine system. The resulting data set is the largest sampling of estuarine oceanography ever collected and carries much potential for scientific discovery. With this data, research areas such as causes of low dissolved oxygen levels and effects of fresh and salt water mixing can be explored. In order to gain a complete understanding of the data set oceanographers need a way to compare the many variables. Previous attempts to analyze this data set have produced 2D graph representations of the data which fail to provide clear comparisons between variables and do not allow examination of local phenomena [1]. To fill these gaps we present a set of visualizations to assist scientists in exploring Narragansett Bay oceanography, evaluate and improve our approach through user study, and package our results into an easy to use application.

Visualization Design

To begin exploring this data set a prototype was created to display initial visualizations of the data set. To overcome the issue of global versus local examination of the data a 3D surface, based on location and depth information, was constructed along the data path allowing views of the entire bay as well as views of specific locations in the bay. Two approaches were taken to provide comparisons between variables. In one approach color, texture and surface thickness were used to represent three variables on the surface (Figure 1). Another approach used transparent textured layers to create a view of all the variables (Figure 2).

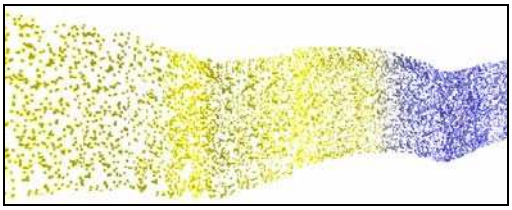

Figure 1: Surface rendered along data path. Color represents temperature and texture represents dissolved oxygen.

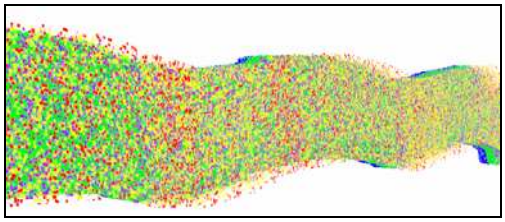

Figure 2: Transparent Layer View along data path. Each color represents the amount of a certain variable.

Evaluation

To evaluate these new approaches a user study was conducted; it consisted of 20 participants including collaborator, Professor Warren Prell, and students in the Geological Sciences Department at Brown University. The study asked users to identify correlations between variables in the original 2D graph representations and in the various new visualizations.

Users preferred the new methods when trying to compare variables along the entire data path, but preferred the original graphs to find correspondences at specific points. The importance of interaction within the new application was also highlighted; many participants felt that screenshots did not do the new methods justice. Other results included the need for clarification of texture and the addition of labels as well as the inability to gain valuable insight from surface thickness representations.

Results

As a final step user study results were applied to the visualizations and they were packaged into an intuitive and interactive 3D application (Figure 3). The surface texture variable representation was removed, texture was clarified through more fluid blending and labels were added to increase understanding of the visualizations. The resulting application allows for increased interaction with the data set and also provides multiple view capabilities.

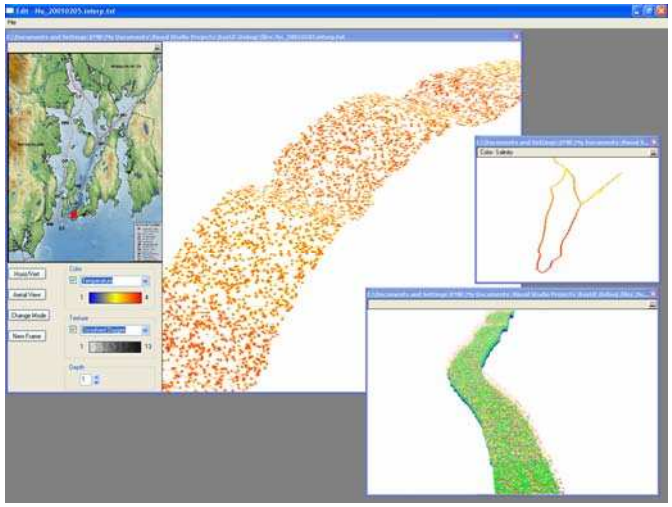

Figure3: View of the application. Multiple frames are used to allow multiple views of different data sets.

Conclusions

We have presented a series of techniques combing color and texture to visualize the Narragansett Bay data set and validated them through user study. Using the user feedback as a guide we have created an intuitive and interactive virtual environment which will allow researchers to better analyze oceanographic data sets.

References

[1] http://www.narrbay.org/d_projects/nushuttle/shuttletree.htm