Interactive Color Embedding-based Corpus Callosum Segmentation and Fiber Clustering in DTI

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Consultants: David F. Tate[2, 3], Song Zhang[1]

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[2] Brown Medical School, Department of Psychiatry and Human Behavior, Centers for Behavioral and Preventive Medicine
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Abstract

We propose an inter-disciplinary project to develop a new interactive tool for color embedding-based corpus callosum segmentation. By integrating color-coding of tractography paths, our tool will allow user to interactively adjust the clustering and segmentation based on their observation of the fiber tracks. The tool will be developed and evaluated in close collaboration with neuropsychologists studying abnormal changes in the CC related to HIV disease severity.

A Specific Aims

We will develop a tool for quantifying segments in the corpus callosum (CC). The fiber bundles passing through the CC will be color-coded and clustered using the computed stream-tube distances. Using the perceptually uniform color space embedding [1], we will cluster the midsagittal CC into segments on the basis of the homogeneity of the coloring. We will then integrate the component into the brain visualization application (BrainApp) developed by Song. The improved application will allow user to visualize the termination points of the tracks passing through the CC. Also, user will be able to adjust and correct the segmentation and clustering based on their observation of the track paths and termination points. We hypothesize that the model will be used to accurately quantify anatomical features and track anatomical changes in the corpus callosum through time and within populations.

B Background and Significance

We are proposing a new way of CC segmentation with interactive accuracy correction. This would be a new application area for the perceptually uniform color space. Our proposed tool could ultimately provide a better understanding of the corpus callosum (CC), especially in HIV patients. The significance of this work can be described from two different perspectives. From an algorithmic and modeling perspective, the tool is innovative and useful for neuro-scientists. From a computational tool-building perspective, our feature detection (clustering) and user interaction is a potential extension approach.

B.1 Background: the Importance of Corpus Callosum

The CC is the largest white matter (WM) structure in the brain. About 90% of the white fiber tracts pass through the CC. Most communication between regions in different halves of the brain is carried over the CC. Understanding the trajectory of the fiber bundles passing through segments of the CC will provide us with information regarding the bundle's functions. As there is high variability in size and shape, disease and age-related changes of CC itself, new methods for describing and studying CC shape are needed to better understand and cope with these variabilities.

Researches have shown that there exists white matter abnormality in HIV patients [3, 4]. The effects of HIV on the surface area of the CC have not been previously studied. Our project would bring new insight to the HIV study.

B.2 Background: the potential of Diffusion Tensor Imaging

Diffusion tensor magnetic resonance imaging (DTI), a non-invasive MR technique, measures water self-diffusion rates and thus gives an indication of the underlying tissue microstructure [5]. DTI has great potential due to its ability to provide the information on the connectivity and coherence of the white matter fiber tracts in the human brain *in vivo*. The proposed work will realize this potential by attempting to map and cluster white matters in the CC more anatomically and interactively.

B.3 Challenge: Corpus Callosum Segmentation

In the past, various attempts have been made to subdivide and segment the corpus callosum. (see Fig. 1) In this project, we will attempt to cluster the midsagittal CC into more anatomically representative units on the basis of stream-tube distance based perceptually uniform color embedding. This particular approach was chosen because it has the potential to provide a more reasonable division of the CC.

Furthermore, current subdividing methods of the CC fail to allow users to see the characteristics and terminal points of the fiber tracks passing through it. This is a very useful function because terminal points and paths of the fiber tracks provide crucial information regarding the functions of CC.

B.4 Challenge: DTI Fiber Clustering

Recently, several approaches have been proposed to cluster the tractography paths [6, 7]. The methods generate paths that correlate well with large WM structures. It is still not clear how

reliably they can identify anatomical tracts. Our approaches allow verification of the fiber tracks by inspecting the FA-based regions of the CC that they pass through.

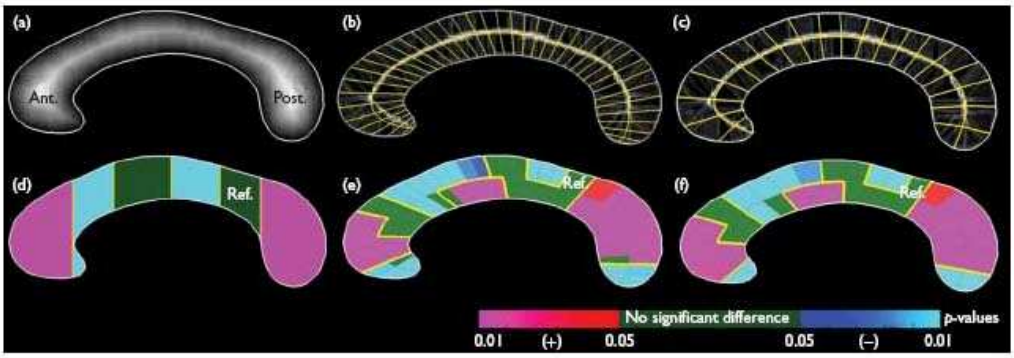

Fig. 1 Subdivisions of the CC by three different methods. (a) Distance map for construction of the medial model. (b) Boundary model-based 80 subdivisions of the CC. (c) Medial model-based 40 subdivisions of the CC. (d) Witelson's seven geometric subdivisions of the CC. (e) New CC nine divisions from boundary model-based 80 subdivisions using FA level-based clustering. (f) New CC nine divisions from medial model-based 40 subdivisions using FA level-based clustering. In (b,c), subdivisions by both methods were overlaid on the Euclidean norm of gradients in the distance map to visualize the ridge of the distance map (i.e. areas with high medialness). In (e,f), color represents differences of FA values in each subregion from those in the posterior midbody. Regions with significant differences were presented and color coded according to *p* levels. Red to magenta/blue to cyan colors mean significantly greater/less FA value regions (p=0.05 and 0.01, respectively) than the reference region (i.e. posterior midbody). The continuous yellow line marks the territories of the new nine divisions of the CC by this method, while the dotted line defines the medial or boundary model-based subdivision. Abbreviations: FA, fractional anisotropy; CC, corpus callosum; Ant, anterior; Post, posterior; Ref, reference region.

C Preliminary Studies

We demonstrate the feasibility of the proposed research with a set of preliminary studies relevant to the project. The preliminary study will also demonstrate that the collaborations that will be needed for the proposed work are in place.

C.1 3D Exploratory Visualization

Zhang et al. have developed a visual representation model, BrainApp, introducing streamtube and streamsurface representation [8]. (See Fig. 2) In the model, streamtubes represent where diffusion is fastest along a path and follow this direction of fastest diffusion. These streamtube paths tend to follow coherent WM structures. Streamsurfaces represent regions where diffusion is fastest within a 2D planar surface; they are locally perpendicular to the slowest direction of diffusion.

C.2 DTI Fiber Clustering

Zhang et al. developed a model for the unsurpervised clustering of tractography paths and an automated matching of the resulting clusters across two brains [2]. (see Fig. 3) The application provides a possible approach to identify relevant features automatically.

D Methods

D.1 Color Embedded division of CC and clustering of tractography paths

We will compute a color embedding based on the perceptually uniform color space. The coloring will be assigned based on the stream-tube distance, a measure of similarity along the whole fiber tract. The CC will be clustered into segments based on the embedded color map. The fiber paths will be color coded based on the color map of their corresponding passing points on the CC.

D.2 Interactive CC segmentation and fiber tracks clustering

We will then combine and visualize the developed models using Song's streamtube and streamsurface model [8] in BrainApp. The midsagittal CC will be represented as a flat surface in the space. The CC area will be colored according to the resulting segmentation from step 1. Also, the clustered fiber tracks that pass through the CC will be shown as colored streamtubes lying on the 3D space. We will then implement interactive component allowing the user to adjust the segmentation and coloring of the CC and fiber tracks after viewing their actual fiber paths. Hence, the tool would provide more accurate and functionally meaningful segmentation of the CC.

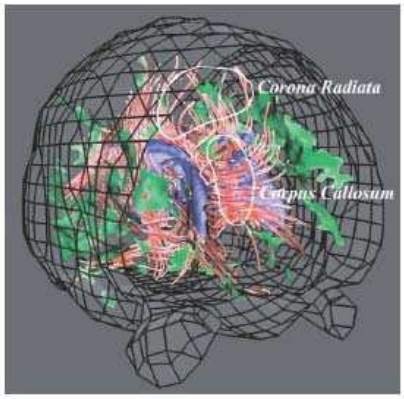

Fig. 2. Visualization of a human brain using our method. Geometric models include the red streamtubes, the green streamsurfaces, the blue ventricle surface, and the wireframe skull surface. Large neural structures such as the corpus callosum and the corona radiata are represented by the red streamtubes in this view.

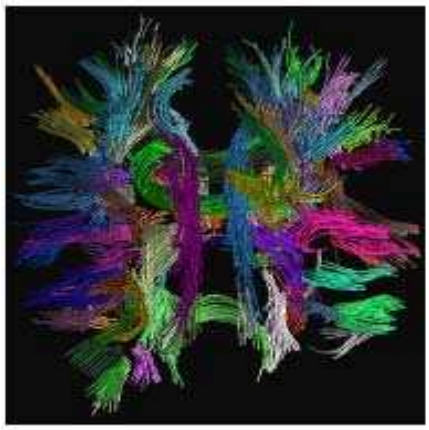

Figure 3 Top view of the path clusters. Paths within the same cluster share the same color.

E Application Area: HIV

The Human Immunodeficiency Virus remains a dire health problem worldwide. HIV is an aggressive disease that affects multiple organ systems and body compartments, including the central nervous system (CNS).

Studies by Prof. Tate have demonstrated abnormal changes in the CC are related to HIV disease severity and progression. Better approaches to understanding the evolution of HIV-related CC disturbance are clearly needed. Our tool would provide a potentially better CC segmentation and fiber clustering to assist in the HIV study in CC.

F Verification

We would verify our work with the following hypothesis:

- The perceptually uniform color embedding is an effective method for CC segmentation. We will compare the resulting segmentation with existing segmentation method - FA based segmentation. The effectiveness of the method will be verified by neuropsychologists.
- Severe abnormality in CC exists in HIV patients.
- Information about terminal points of the fiber tracks passing through the CC is crucial to CC functions and segmentation.

G Timeline

Week 1-2	Review basic implementation and usage of BrainApp. Implement perceptually uniform color embedding for the CC based on stream-tube distance.
Week 3	Continue work on prototypes. Generate 2D CC segmentation and 3D fiber clustering results and verify with Tate.
Week 4	Integrate the prototypes into BrainApp. Add interactive component: CC segment and fiber cluster coloring adjustment. Show Tate the 3D colored stream tube passing through the 2D segmented midsagittal CC area.
Week 5	Test the application on a collection of normal and HIV-positive subjects. Incorporate user feedback. Generate static visualization of frontal CC clusters over fixed group of normal and HIV-positive subjects. Compare and verify the results with traditional CC segmentation method [9].
Week 6	Identify a normal and an HIV-positive subject which very clearly demonstrate the white matter difference and fiber track change to use in a demo. Prepare Final Report and presentation.

Literature Cited

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David F. Tate
Assistant Professor (Research)
Department of Psychiatry and Behavioral Medicine
Brown University

Education

Brigham Young University , BS/BA, 12/1994, Psych/Anthro
Brigham Young University , Ph.D., 12/2003, Clinical Psychology
Brown Medical School Training Consortium,
Internship,2002-2003,Neuropsychology
Brown Medical School-Immunology,
Fellowship,2003-2005,Neuropsychology/Immunology

Positions

- *2003 – 2005* T32 National Institutes of Health Research Fellow, Immunology, Miriam Hospital, Brown Medical School, Providence, RI
- *2005* Brigham and Women's Hospital/Harvard Medical School Visiting Fellow, Center for Neuroimaging, Brigham and Women's Hospital, Boston, MA
- *July 2005 – Current* Assistant Professor, Department of Psychiatry and Behavioral Medicine, Brown Medical School, Providence, RI

Honors

- *2005 – 2010* Mentored Patient-Oriented Career Development Award (K23), National Institutes of Mental Health
- *2003 – 2005* T32-National Research Award, National Institutes of Health

Selected Publications

Paul RH, Brickman AM, Navia B, Hinkin C, Malloy PF, Jefferson AL, Cohen RA, **Tate DF**, & Flanigan TP (2005). Apathy is associated with volume of the nucleus accumbens in patients infected with HIV.
J Neuropsychiatry Clin Neurosci. 17(2):167-71.

Hopkins RO, **Tate DF**, & Bigler ED. (2005). Anoxia versus traumatic brain injury: The amount of tissue loss not etiology, alters cognitive and emotional functioning. Neuropsychology, 19 (2), 233-242.

Rice SA, Bigler ED, Cleavinger HB, **Tate DF**, Sayer J, McMahon W, Ozonoff S, Lu J, Lainhart JE. (2005). Macrocephaly, corpus callosum morphology, and autism. Journal of Child Neurology. 20(1):34-41.

Paul R, Flanigan TP, Tashima K, Cohen R, Lawrence J, Alt E, **Tate D**, Ritchie C, Hinkin C (2005). Apathy correlates with cognitive function but not CD4 status in patients with human immunodeficiency virus. Journal of Neuropsychiatry and Clinical Neuroscience, 17(1):114-8.

Research Support

Functional Neuroimaging of HIV,CFAR ,2004-2006
Neurocognitive consequences of HIV in Southern India,NIMH, 2004—2006

Song Zhang

Position title: Ph.D. student

EDUCATION

- **Brown University**, Providence, RI
  Ph.D. in Computer Science, expected graduation: 2006
  M.Sc. in Computer Science, May 2000

- **Nankai University**, China
  B.Sc. in Computer Science, May 1996

RECENT PUBLICATIONS

- Song Zhang, Mark E. Bastin, David H. Laidlaw, Saurabh Sinha, Paul A. Armitage and Thomas S. Deisboeck. Visualization and Analysis of White Matter Structural Asymmetry in Diffusion Tensor MR Imaging Data. Magnetic Resonance in Medicine, 51(1):140-147, 2004.
- Song Zhang, Çağatay Demiralp and David H. Laidlaw. Visualizing diffusion tensor MR images using streamtubes and streamsurfaces. IEEE Transactions on Visualization and Computer Graphics, 9:454-462, 2003.
- Andreas Wenger, Daniel Keefe, Song Zhang, and David H. Laidlaw. Interactive rendering of multivalued volume data with layered complementary volumes. Submitted to IEEE Transactions on Visualization and Computer Graphics, August 2003; under review.
- Song Zhang, Çağatay Demiralp, Daniel Keefe, Marco DaSilva, Benjamin D. Greenberg, Peter J. Basser, Carlo Pierpaoli, E. A. Chiocca, T. S. Deisboeck, and David H. Laidlaw. An immersive virtual environment for DT-MRI volume visualization applications: a case study. Proceedings of IEEE Visualization 2001, pages 437-440, October 2001.
- Marco DaSilva, Song Zhang, Çağatay Demiralp, and David H. Laidlaw. Visualizing the differences between diffusion tensor volume images. Proceedings ISMRM Workshop in Diffusion MRI: Biophysical Issues, pages 237-238, March 2001.
- Marco DaSilva, Song Zhang, Çağatay Demiralp, and David H. Laidlaw. Visualizing diffusion tensor volume differences. Visualization '01, Work in Progress Proceedings, pages 16-17, October 2001.
- Song Zhang, Çağatay Demiralp, Marco DaSilva, Daniel Keefe, David H. Laidlaw, Benjamin D. Greenberg, Peter J. Basser, Carlo Pierpaoli, E.A. Chiocca, and T. S. Diesboeck. Toward application of virtual reality to visualization of DT-MRI volumes. Proceedings MICCAI, October 2001.
- Song Zhang and David H. Laidlaw. Elucidating neural structure in diffusion tensor MRI volumes using streamtubes and streamsurfaces. In Proc. 9th International Society of MR in Medicine, April 2001.

PROFESSIONAL EXPERIENCE

- **Research Assistant**, Brown University Computer Science Department (August 1998 – present)
- **Teaching Assistant**, Brown University Computer Science Department (January 2001 – May 2001), Computer Networks
- **Internship**, Microsoft (Summer 2001), Automatic Arrangement of the map texts

Subject: RE: sketch of proposal that we'll be talking about tomorrow.
From: "Tate, David" <DTate1@Lifespan.org>
Date: Wed, 28 Sep 2005 09:57:02 -0400
To: 'Peter Sibley ' <pgs@cs.brown.edu>
CC: "'wzhou@cs.brown.edu '" <wzhou@cs.brown.edu>

Dear Peter and Wenjin,

I am writing this email to express my interest and support of your proposed project entitled "Corpus Callosum Segmentation and ROI Segmentation for Brainapp." This is an exciting proposal and I look forward to working closely with you throughout the duration of this six week project.

In my role as a consultant, I will be available to answer questions regarding neuroanatomy, neuroimaging, and/or user interface issues. I will also meet with you regularly to discuss your progress and discuss the dissemination of scientific information that will result from the development of this visualization application.

I am excited about this project and look forward to working with the the toward the successful completion of this project. This application will be useful in future studies aimed at understanding the processes of normal aging and a multitude of additional clinical syndromes impacting brain anatomy and function. Please, feel free to contact me via email (dtate1@lifespan.org) or by phone (401.323.9238) if I can be of any assistance in this project.

Sincerely,

David F. Tate, Ph.D.
Assistant Professor (Research)
Department of Psychiatry and Behavioral Medicine
Brown Medical School

Subject: letter of intent to consult your project
From: Song Zhang <sz@cs.brown.edu>
Date: Mon, 3 Oct 2005 12:42:38 -0400 (EDT)
To: Peter Sibley <pgs@cs.brown.edu>, Wenjin Zhou <wzhou@cs.brown.edu>

Dear Peter and Wenjin:

I am happy to participate as a consultant on your project "Corpus Callosum Segmentation and ROI Segmentation for Brainapp". I will provide consultation regarding the Brainapp specifics and DWI/DTI technology in general. I will be paid one Cappuccino per meeting during the course of the project. My envolvement will entail on demand meetings beginning in the implementation phase of the project.

The segmentation of CC tracts in the brain will make advances in neuro-tracts identification and registration.

Song Zhang

Visualizing Topological Defects in Smectic Liquid Crystals

Jean Tsong (PI)
Mark Moseley (Co-PI)
Computer Science Department

David Laidlaw (Collaborator)
Computer Science Department

Bob Pelcovits (Collaborator)
Physics Department

Brown University

Abstract

Liquid crystals can be characterized by their unique phases of matter. One such phase, the smectic phase, can have topological defects that affect the quality of a liquid crystal substance. Due to current visualization techniques being unable to track such faulty behavior, we propose to develop a visualization that clearly shows the defects in the smectic phase.

I. Introduction

We propose a new interdisciplinary endeavor between the computer science and physics departments at Brown. Utilizing the latest results in liquid crystal simulations, our goal is to create a visualization system that helps scientists gain a more lucid understanding of the toplogical defects of the smectic phase, a common phase in liquid crystals.

What is the smectic phase? Liquid crystal (LC) molecules, or mesogens, come in two types, lyotropic and thermotropic. The simulation model that we will work with focuses on the thermotropic mesogens which form ordered phases according to variations in temperature. If a disordered, isotropic liquid is cooled, the mesogens enter the nematic mesophase. Once in the nematic mesophase, the rod-shaped molecules are oriented along the same director (the average direction of alignment) and have short-ranged positional order. Upon further cooling, we get the smectic phase (see Figure 1). At this point, the still oriented molecules now form a stack of two-dimensional layers. If the molecular center-of-mass positions are random in each layer, the mesogens are in the smectic A phase. Or, if each molecule is surrounded by six neighbors in a roughly hexagonal configuration, we have the smectic B phase.

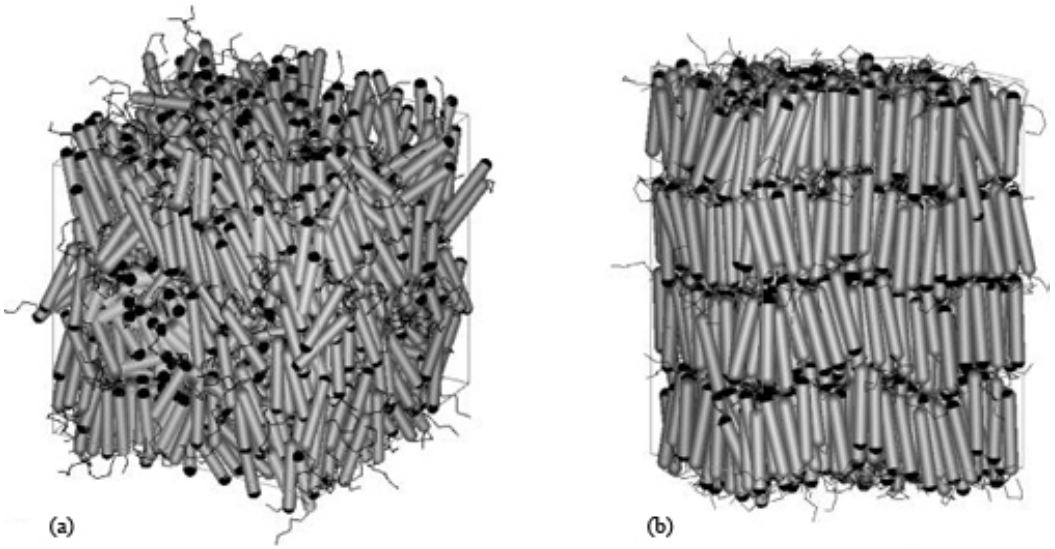

Figure 1: Depictions of (a) the nematic phase and (b) the smectic-A phase, from simulation snapshots [1].

II. Problem Statement

This project is driven by a requirement for being a capable investigator of liquid crystals: we refer to the citation, "Thirty years ago, in the preface to the first edition of *The Physics of Liquid Crystals*, P G de Gennes has written that '…the study of liquid crystals is complicated because it involves several different scientific disciplines…and also a certain sense of vision in three-dimensional space in order to visualize complex molecular arrangements" [2]. Thus, the ability to visualize in 3D is highly valued in studying LCs at a molecular level. By developing a way of visualizing the behavior of the smectic phase, we aim to provide this much needed vision in readily seeing topological defects.

The LC research group led by physics professor Pelcovits has developed a molecular dynamics simulation system using the Gay-Berne phenomenological model [3]. The primary goal here is to effectively visualize the data generated from this simulation which tracks 64K+ liquid crystal molecules as they evolve over time.

III. Research Plan

The simulation system can be described as a 3D set of molecules. For each box or area in the set, an average tensor value keeps track of the information about the group of molecules inside. The tensor is a traceless 3x3 matrix that stores the order of that group and the eigenvector of the largest eigenvalue in the matrix. This vector is the director, the preferred direction of alignment for the molecules. Therefore, the data we are parsing comes in the form of a 2^{nd} order 3D tensor field.

Processing data. We will be using the data interpretation method developed by Slavin et al. for processing nematic phase data [4]. The techniques applied to diffusion tensor MRI do not work well for liquid crystals, because they only have to deal with positive eigenvalues. The method by Slavin, however, defines a new tensor that allows for negative eigenvalues and can recover the trace from the tensors in the simulation system. For sampling data, we will use a cubic B-Spline as a sampling kernel or point spread function [4]. This effectively converts the simulation data into a sampled version of a continuous 2^{nd} order diffusion tensor field, allowing us the flexibility to work back and forth from the discrete to the continuous. Also as a result, the visual clutter of thousands of molecules will also be reduced.

Developing layer algorithm. The first part of our methodology incorporates the Slavin et al. work as a way of maintaining standard data interpretation between the nematic and smectic visualizations. Once past the data processing step, we will be dealing with a new set of challenges unique to the smectic phase. As the molecules are separated into layers based on their mass densities, we will build a system to identify which molecule belongs to what layer accordingly. Difficulty lies in the fact that the molecules are not necessarily in perfectly segregated layers. Layers of molecules can merge at certain points, which would be recorded in the simulation data. This challenge represents our very impetus for developing an effective visualization, as such merged layers are the topological defects that concern scientists when trying to analyze the smectic phase.

Generating layer geometry. Upon separating the molecular data into layers, we will use the following approach to define the surface for each smectic layer: we will use the molecular orientation to help establish the continuity of the layers. If we consider the molecules as pancakes (or square polygons, see Figure 2) oriented normal to the local director field in the smectic phase, we can then use the orthonormal vectors that span the pancake to generate a continuous surface, similar to how streamsurfaces are constructed in the nematic phase visualization [5,6]. The major and medium eigenvctors of the molecules, i.e. the directors, would lie in a plane tangent to the generated surface.

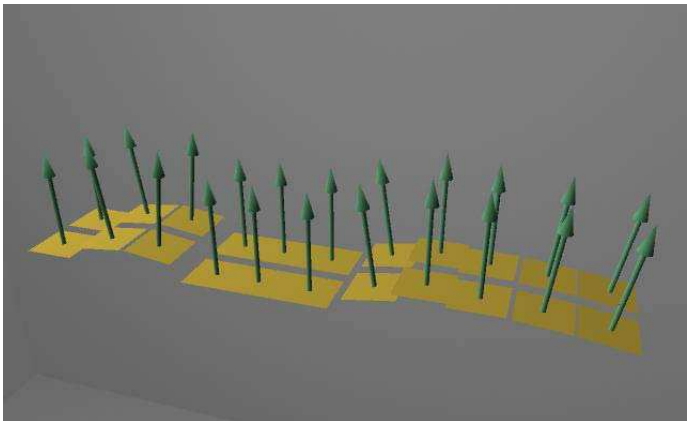

Figure 2: A streamsurfaces approach. We would connect the pancakes normal to their corresponding vectors, thus expanding the layer's surface.

Display. The generated surfaces, i.e. the smectic layers, will be displayed in AVS. We will use a color scheme on the surfaces to provide information on the varying orientation of the molecules on each layer. Users would then be able to see where the topological defects are from the geometry and also study the directors for any relevant relationships between molecules and the defect area.

Validation. For checking the basic accuracy of our algorithms, Pelcovits will provide us with two sets of data to interpret and visualize. One set will include an actual smectic phase simulation as determined by his group; the other will not. In this manner, we will test our visualization's ability to computationally discern between the two.

IV. Significance

While best known for their use in displays, liquid crystals are taking bigger roles in other areas in science and technology, including optical imaging, erasable optical disks, and light modulators for color electronic imaging. In addition to the overall contribution of expediting LC research, our visualization would have immediate impact in current smectic phase studies in physics and chemistry, because we would be providing the power of perception, easing the difficult task of mentally trying to envision LC molecular behavior from numerical data.

With regards to the field of scientific visualization, this project will be a significant contribution in two ways. First, we will be implementing a novel application for streamsurfaces, further establishing it as an effective technique in visualizing tensor fields. Second, our layer separating algorithm embraces the interesting concept of creating a visualization that highlights errors, rather than hiding or smoothing them. Such error visualization may prove to be useful in other areas of science, where focusing on the errors or strange behavior of the substance under investigation is vital.

V. Related Work

Prior related work reflects the need for visualizing liquid crystal behavior, but there are currently no established techniques for displaying topological defects in the smectic phase.

One approach taken towards displaying the orientational order of LC molecules involves fluorescence confocal polarizing microscopy (FCPM) [2]. The FCPM technique uses LC properties to orient fluorescent dye molecules of anisometric shape which are added in small amounts to the LC. The density of dye is uniform throughout, with the exception of areas near topological defects. Using polarized light furthers the contrast of the dye in the final image. We note that this technique uses actual liquid crystal molecules to derive the visualization, unlike our input simulation data.

Another approach is the aforementioned work by Slavin et al. on visualizing topological defects in the nematic phase based on time-evolving data computed by the same molecular dynamics computational model that we will use [4]. Due to the key geometric difference between the nematic and smectic phases—the latter has layers—the techniques in visualizing nematic LC data cannot be applied to the smectic. However, we can learn from their results in experimenting with two styles of visualization [5]. The first style used cigar-shaped ellipsoids to describe the location and orientation of the LC molecules. The second and more successful style used streamtubes and streamsurfaces to display information surrounding each topological defect.

VI. Timeline and Milestones

Weeks 1-2: Familiarizing ourselves with AVS, the visualization system used by Slavin. We will study Slavin's code to see if there are any modules that we can reuse, particularly the data parsing and sampling code. Milestone: Building algorithms for finding layers and generating surface geometry.

Weeks 3-4: Implementing the algorithms in AVS and refining them as necessary and testing robustness of our code. Milestone: Readying work for evaluation.

Week 5: Validating and evaluating end product through Pelcovits. Milestone: Determining effectiveness of visualization.

Week 6: Writing final abstract, preparing final presentation and demo on AVS.

VII. References

[1] J.S. van Duijneveldt, A. Gilvillegas, G. Jackson, and Michael P. Allen. Simulation study of the phase behavior of a primitive model for thermotropic liquid crystals: Rodlike molecules with terminal dipoles and flexible tails. J. Chem. Phys., 112:9092-9104, 2000

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[6] S. Zhang, C. Demirlap, and D. Laidlaw, "Visualizing Diffusion Tensor MR Images Using Streamtubes and Streamsurfaces", IEEE Transactions on Visualization and Computer Graphics, vol. 9, no. 4, pp. 454-462, Oct 2003.

Statement of Support from David Laidlaw, Collaborator

From: David Laidlaw <dhl@cs.brown.edu>
To: Jean Tsong <jtsong@cs.brown.edu>
Subject: Re: cs237 collaborator support

Hi Jean -

I would be happy to be a collaborator on your project. I will provide help in understanding the existing process for studying nematic liquid crystals and in migrating our approach for looking at diffusion tensor data to this new problem area. I will also provide my expertise in signaling theory, which is a key step in going from discrete simulation data to a continuous representation.

Sincerely,

-David Laidlaw

Statement of Support from Robert Pelcovits, Collaborator

From: Bob Pelcovits <pelcovits@physics.brown.edu>
To: jtsong@cs.brown.edu
Subject: RE: collaborator support, cs237

Jean,

Here's a statement of support:

I have met with Jean Tsong regarding my suggestion that we collaborate on visualizing data from large-scale numerical simulations of smectic liquid crystals. Jean impressed me with her strong interest in the project and excellent questions about my work. I look forward to collaborating with Jean on this project if her proposal is approved.

Bob Pelcovits

Particle Image Velocimetry Visualization in Aeromechanics of Bat Flight

Mykhaylo Kostandov (PI)
Radu Jianu (Co-PI)

David H. Laidlaw
Department of Computer Science
Brown University

Sharon Swartz
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Abstract

We propose working on a visualization method for studying aeromechanical aspects of bat wing kinematics with focus on flow vectors and vorticity in cross-section planes, as well as motion and forces on the wing. Visualization is based on data obtained with particle image velocimetry (PIV) combined with motion capture data.

Introduction

The study of bat flight is one of the areas in biomechanics and evolutionary biology that has recently emerged due to a variety of characteristics that make bats, and bat wing mechanics in particular, an exceptional subject of research. The only flying mammals, bats (*Chiroptera*) are extremely maneuverable and fly with energy efficient aerodynamics. Flexible wing frame construction, extensible membrane with varying stiffness, and distributed shear sensors are among the features that are unique to bats and make unsteady flight patterns possible.

Most animal flight models in the past used a simple convention for wing movement, approximating wing surfaces as rigid planes. However, bat wing construction and unsteady patterns mentioned above render this approach insufficient, and new techniques need to be considered for correct analysis of the wingbeat mechanics of a bat. In [1], Rayner et al. supported this opinion by defining a relationship between wingbeat kinematics in a bird and the geometry of flight path, pointing out that the traditional approaches don't apply to study of intermittent flight. The new models of complex flight, such as bat flight, may then lead not only to significant new discoveries in the biological evolution of flight, but will also provide data, models, and methods useful for a plethora of engineering applications, especially concerning the design and implementation of flight vehicles with increased maneuverability and in-flight sensing.

Some of the key elements, which are important in studying the above-mentioned characteristics of bat flight, include the forces on the wing, as well as velocity and vorticity fields around the wing (especially in the tip regions). Visualization of these elements, combined with a mesh representation of the wing, is the main goal of our proposed work.

Related Work

Professor Sharon Swartz's team at the Department of Ecology and Evolutionary Biology has been studying bat flight mechanics for several years, and the group's interdisciplinary collaboration with researchers across a variety of disciplines, including computer science, engineering, and applied mathematics, led to development of several data collection, analysis, and visualization methods, described in [2-5]. Preliminary work on wing curvature based on motion capture data from the group's experiments was done by Hueso [6], who concentrated on visualizing pathlines and streamlines in representing vortices. Most of recent work, including the latter, however, focused mainly on flow simulations around the wings and not the underlying wing structures themselves, which did not give the answer to the questions about biological meaning of bat mechanics.

Experimental Setup

The experimental method that the study is based on is particle image velocimetry (PIV), which provides instantaneous velocity vector measurements in a cross-section of the flow. Previous studies of bird flight [7,8], which used PIV to establish a new model of distinct gait patterns in the wakes behind birds, showed that the method is very efficient in determining power, forces, and vorticities, and describing wake structures in general.

In the experimental setup (Figure 1), the bat flies through a fog of micron-sized particles and triggers a beam break sensor, which activates the laser sheet plane. Then, PIV cameras capture imagery from the plane to obtain a signature footprint of the flow in the wake behind the bat. It

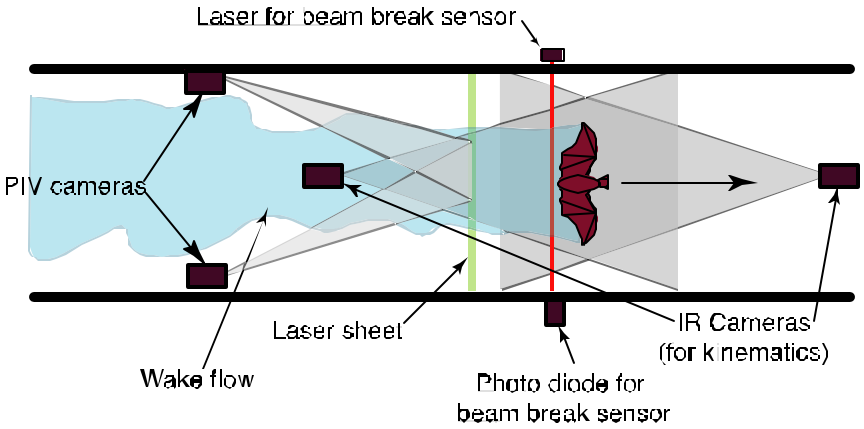

Figure 1. PIV experimental setup.

should be noted that the two cameras are used to obtain two coordinates directly, and the third coordinate for each particle is computed based on positions of the cameras. From two-image sequences at different time points, then, the wake velocities will be calculated. In addition, two IR cameras are set up to capture the positions of markers attached to the wing joints in order to obtain corresponding 3D geometry data.

Proposed Methods

In our work, we would like to concentrate on bat wings and provide automated tools for visualization and analysis of motion and forces in bat-centered and global coordinate systems with simultaneous integration of flow vector and vorticity data in cutting planes.

The first step will include parsing the digitized data from the experiment and being able to display a single slice of motion-capture data at a predefined position along the bat's flight path. Once that is completed, interactive controls for the slice position will be provided, so a user can control the spatial slicing.

At the same time, we will work on displaying PIV slice data and associated velocity vectors in the wake. It should be pointed out that PIV sampling plane is stationary (see Figure 1), so the original data may only be used to display temporal changes in the wake structure at the laser sheet location.

Knowing the time elapsed between the bat passing through the laser sheet plane and the appropriate PIV slices of the wake, as well as airflow velocity vectors at contour points of the slices, we may then estimate the evolution of the wake behind the sheet. As a result, spatial slicing of the wake flow at a given time will be implemented. Combining the spatial slices from motion-captured data and PIV will help establish the connection between the wing form dynamics and the wake evolution.

Displaying and interactively controlling both types of data, complemented with providing necessary information such as velocity fields, vorticity, and force vectors, in the same visualization package, will be the final result of the work outlined above.

Project Novelty and Significance

Immediate Impact

This project proposes several novel methods and techniques that may enhance understanding of biological and evolutionary factors behind bat flight mechanics, as well as provide new visualization methods for data obtained with particle image velocimetry.

Unlike the traditional approach, in which wing movements were approximated with rigid oscillating planes, we emphasize internal wing structure, which is a realistic way to analyze complex mechanics associated with bat wing movement.

One of the important techniques that will be developed in the course of the work is determining the evolution of the wake in the bat flight path based on PIV slices, which are stationary by definition. We will also set up a new method of using PIV to establish a relationship between wake structures and wing dynamics, and combine PIV flow data with 3D motion capture data.

Understanding the connection between wing structure and wake flow behind the bat will provide insight into the characteristics of wing beat dynamics and the strategies that bats utilize in unsteady flight patterns.

An important contribution to the field of visualization is establishing PIV data, combined with motion data from IR cameras, will be used to produce kinematic visualization of flight, focusing on wing motion, and tools that will allow interactive slicing of wing motion data and display of appropriate force and flow vectors at different time points will be implemented.

Broader Impact

The results of this work have a potential to help understand the connection between wing structure features and bat flight behavior, which is a crucial task that can help gain insight into evolution of flight mechanisms and biological world in general. It will also provide new techniques for three-dimensional geometry modeling and flow analysis based on particle image velocimetry.

Aside from fields directly affected by the project, namely biology and visualization, the results of this work will potentially have significant influence on other disciplines, especially engineering. As the mechanics of unsteady flight are better studied and understood, the design and implementation of complex flight vehicles that will mimic such flight behavior may be possible. Such vehicles would feature changing wing geometry and integrated flight sensing, characteristic of bats, which will lead to enhanced maneuverability (e.g. in enclosed small spaces), lower acoustic signatures, and energy-efficient cruising and gliding.

Another long-term goal includes integration of visualization and computational tools such as the airflow analysis tool, NεκTαρ, which will be of direct importance to the field of scientific visualization, especially in fluid flow applications and large multi-dimensional time-varying dataset simulations.

Project Timeline

Week 1: Parse the data and work on displaying motion-capture information at predefined slice locations. Program the basic interface and framework for displaying data points.

Week 2: Work on displaying PIV data at different points in time. Display the associated velocity vectors.

Weeks 3-4: Estimate wake evolution based on elapsed time and velocity field. Work on combining temporal and spatial slicing for both motion-captured and PIV data.

Week 5: Program force and vorticity calculations and simultaneous visualization with wing and flow geometry slices.

Week 6: Work on adjusting the visualization and fix interfacing issues. Run the evaluation with Prof. Swartz.

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Sharon Miriam Swartz

Professional Preparation

1977-1981	B.A.	Oberlin College. Biology and Sociology/Anthropology, with High Honors
1982-1985	M.S.	The University of Chicago. Evolutionary Biology
1985-1988	Ph.D.	The University of Chicago. Evolutionary Biology

Appointments

1996-present	Associate Professor, Brown University, Department of Ecology and Evolutionary Biology Adjunct Associate Professor, Division of Engineering
February – July, 1996	Parental Leave
1990-1996	Assistant Professor, Brown University, Department of Ecology and Evolutionary Biology Adjunct Assistant Professor, Division of Engineering
April – August, 1993	Parental Leave
1987-1990	Assistant Professor, Northwestern University Medical School, Department of Cell Biology & Anatomy; & Northwestern University College of Arts and Sciences, Department of Anthropology

David H. Laidlaw

Professional Preparation

1983 Sc.B. in Computer Science, Brown U., Prov., RI, *Topology and Mechanics.* Also completed requirements for
an A.B. in Mathematics.
1985 Sc.M. in Computer Science, Brown U., Prov., RI, *Rendering Parametric Surfaces.*
1992 M.S. in Computer Science, Caltech, Pasadena, CA, *Material Classification of Magnetic Resonance Volume*
Data.
1995 Ph.D. in Computer Science, Caltech, Pasadena, CA, *Geometric Model Extraction from Magnetic Resonance*
Volume Data.

Appointments

2003-present Associate Professor, Computer Science
Department, Brown University
2000-2003 Stephen Robert Assistant Professor, Computer Science
Department, Brown University
1998-2000 Assistant Professor, Computer Science Department, Brown
University
1996-1998 Senior Research Fellow, Division of Biology, Caltech
1989-1996 Postdoctoral Research Fellow/Research Assistant, Computer Science, Caltech
1989-1993 Consultant Stardent/Advanced Visual Systems
1986-1989 Software Engineer, Stellar Computer
1983-1985 Research Assistant, Computer Science, Brown University
1984 Consultant, Basel Institute for Immunology, Switzerland

Kenneth Breuer

Professional Preparation

Bachelor of Science (Sc.B)	Engineering (Concentrating in Fluids and Thermal Sciences) *Brown University*, 1978-1982
Masters of Science (M.S)	Dept. of Aeronautics and Astronautics, *Massachusetts Institute of Technology*, 1982-1984.
Doctorate (Ph.D.)	Department of Aeronautics and Astronautics, *Massachusetts Institute of Technology*, 1984-1988
Postdoctoral Fellow	Division of Applied Mathematics, *Brown University* 1988-1990.

Appointments

Associate Professor	Division of Engineering, *Brown University*, 1999-present
Principal Research Scientist,	Department of Aeronautics and Astronautics, *Massachusetts Institute of Technology*, 1998-1999
Associate Professor,	Department of Aeronautics and Astronautics, *Massachusetts Institute of Technology*, 1996-1998
Assistant Professor,	Department of Aeronautics and Astronautics, *Massachusetts Institute of Technology*, 1990-1996

BROWN

DIVISION OF BIOLOGY AND MEDICINE

October 15, 2005

Dear Mr. Kostandov,

I am writing to document my enthusiastic support for your project concerning visualization of bat flight and experimental fluid dynamics. I understand that you will be developing visualizations based on the kinematics of wing motion that will facilitate analysis of complex and time-varying data by biologists and engineers. We will be happy to supply you with measurements of bat wing motion and documentation of fluid flow in the wake of the bats, and to provide ongoing scientific consultation. We look forward to working with you on the exciting, promising project.

Sincerely,

Sharon Swartz, Ph.D.
Division of Biology and Medicine
Division of Engineering
Brown University

Brown University Box G Providence, RI 02912

From: David Laidlaw <dhl@cs.brown.edu>
To: Mykhaylo Kostandov <mk@cs.brown.edu>

Hi Misha -

I will be happy to collaborate with you, Sharon, and Kenny on developing visualization tools for exploring kinematic and PIV data for flying bats.

Cheers,

-David

From: Kenny Breuer <kbreuer@brown.edu>
To: Mykhaylo Kostandov <mk@cs.brown.edu>

Thanks -

I am happy to support your efforts in this way

Kenny

Prof Kenny Breuer
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Recently, effort ha been ma to gather all information regar protein an centrali it in large databa to make it a to re aro the world One of the pro i the H Protein Reference Databa (HPRD) A q look on the HPRD web gi an idea abo the magnit of thi pro 2 protein and 33 protein interaction It i no do that thi proliferation of information will greatly benefit re b it al create problem related to the limited capacity of h to proce large amo of data

Altho thi pro pro some basic tools that are intended to allow users to operate with this database, we found that the researcher's needs are far from being met Lookup and protein information retrie is no doubt important but gaining an o of the e relations between proteins, e if only locally, can ha a great impact on the researcher's reasoning process

This is why we will try to build a powerful visuali tool that will represent the protein interactions and allow for quick, intuitive information retrieval along with efficient reasoning methods We will aim towards making this tool as useful as possible for proteomics researchers by maintaining a tight collaboration with Professor Arthur R Salomon in the Brown Medical department We believe that an adequate visual tool would greatly benefit proteomics researchers and would significantly speed the process of understanding cellular processes

1 V b a m

New visuali techniques for representing relations and large networks are needed in the conte of rapid data proliferation and increasing global connectivity in almost all domains Effective visuali of networks and relations can have dramatic impacts on science, security, management and many other areas

Network visuali has been intensively investigated by the graph drawing community in the last years Many graph drawing algorithms have been devised leaving the impression that there is not much more to be done in this direction However, network visuali is not widely used outside of the computer area and has not yet reached its full potential

The graph community was primarily concerned with producing "good" **s** visual representations of graphs It is our believe that graph should start moving into a different direction The use of state of the art technology such as caves or fishtanks, adding more interactivity to graph visuali binding visuali to the underlying data instead of just considering the graph abstract data type are issues we consider worth investigating Cutting it short we want to move from graph **d** to network and relation **v** .

Our project is meant to make a couple of steps towards this goal. We want to build our protein interaction visuali tool starting from the needs of proteomics researchers. Our hypothesis is

that by learning what Arthur R. Salomon's needs are and what specific tasks he wants to perform on his data, we will find out what kind of features a network visuali tool should include.
We are optimistic that the new visuali methodologies we will develop to solve this particular problem may be successfully used to represent other types of relations within the molecular field and beyond.

1 C b

Aside from the scientific and visuali benefits of this project there is also an indirect contribution that comes with a successful collaboration. We think that this project will serve as an e of the benefits that can be obtained if researchers take the time to engage into interdisciplinary projects.
Computers are after all tools that are meant to solve problems and computer science should be regarded as the science of solving the problems of others using a computer. Researchers from other fields should be encouraged to turn to computer for help and the success of such collaborative projects is probably the best way to do it.

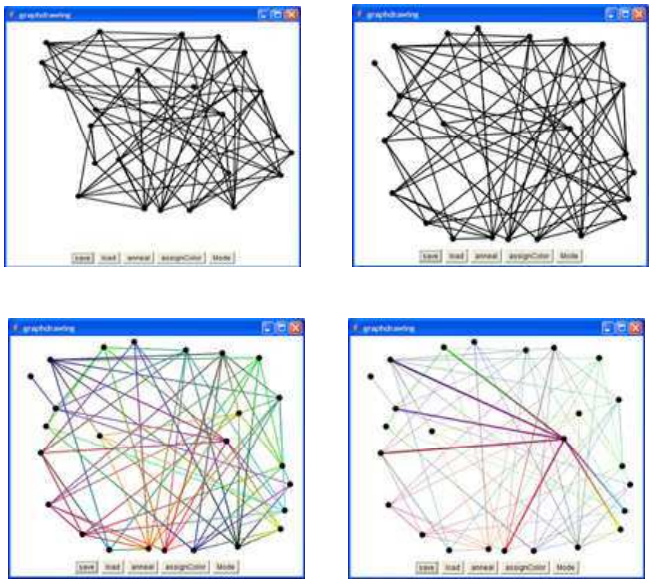
2 M

1 G As

There are several ways to draw relations. The most common is using a graph or tree structure where the nodes represent entities or concepts and an edge between two nodes indicates a relation.
Many graph algorithms have been devised in the last years. Some of them generate a static layout for a graph while some use a more dynamic approach in order to deal with very large graphs.
We will choose one of the e algorithms to build and test our system. We will build our system to be independent of the algorithm that generates the initial graph We want to do that in order to create a fle system and because we want to have an easy way to test more algorithms if the 6 weeks time frame will allow us.
Our system's design will evolve incrementally, building several prototypes and validating them with the help of dr. Salomon. By working with many intermediate versions, dr. Salomon will be able to better define his needs and pin what features he finds useful or wishes to be added. This methodology also reduces the risk of failure and ensures that by the end of the si weeks dr. Salomon will have a better tool to visuali protein interactions than he has now.

2 P w

Within about a week we managed to create a first prototype that helped us refine some of our ideas and give us a better view of what needs to be done. It also gives us reason to believe that our project can be successfully fitted into si



The first image represents a graph generated by the algorithm in [The drawing depicts a high degree random graph similar to those on the HPRD website. In the second image you can see how we could improve the representation by manually dragging and moving nodes to better positions. We than assigned colors to nodes and drew edges with changing colors from one node to another. We thought that this would enable the user to better understand which edges belong to which nodes and reduce the negative impact of crossing edges. Finally we added some features for loading and saving the graph and its layout as well as giving the possibility to select a node and highlight all his edges while shading the rest of the graph.

2 R D

Once bound to the actual HPRD database, the prototype we already have will be used as the basis for a first session of testing with Arthur R. Salomon. We think that offering him a prototype to test is the best way to help him refine his e and come up with a first set of features that he considers useful. Our visuali e will also recommend some features and discuss their opportunity with him. We plan to have at least two more such sessions within the si allocated to the project. This process of refinement should give us more control over the process of development and minimi the risk of failure.

Some of the directions we are considering are: finding ways to update a graph while preserving the mental map of the user and highlighting the changes, possibility of posing visual queries and obtaining visual results (such as: is there a connection, even indirect, between two selected proteins), allowing the user to place markers or annotations on the graph or color edges and nodes.

One of our main preoccupations will be to enhance the capacity of a person to become familiar with an image and create a mental map. This is why saving and loading layouts, placing markers, and highlighting changes are crucial for us.

Still, while these are the some of the features we consider including at the moment one of the purposes of this project is to establish, through the collaboration with a visuali user, what some of the most useful tools are when it comes to working with network data.

If there is enough time we would like to implement another version of graph algorithm to test another hypothesis: the features we will integrate will lessen the impact of the graph

algorithm that produces the initial layout.

3 Va

Our validation method is one of the things that make our proposal novel. Unlike other protein visuali systems in particular and network visuali systems in general we will not measure our success by the speed of the drawing algorithm or the number of edge crossings in the representation. We will prove successful if our system enhances and speeds up dr. Salomon's research. By employing an incremental approach with multiple validation stages we want to lessen the risk of getting a useless tool and making sure that we meet as many of dr. Salomon's needs as possible.

3 R W

The idea of visuali protein interaction itself is not novel nor is the approach of using a graph representation. There were several attempts to represent various kinds of protein interaction as graphs: [However, neither of them concentrated on building a system starting from the needs of the researcher, thus having more theoretical value than actual utility. [does nothing more than drawing a graph using a force directed method [2 and providing some basic interaction such as rotating the graph, zooming. [1 proposes an interesting application called Inter that can rapidly generate graph representations of protein interaction. Although the graph are of high quality and the algorithm is very fast the authors concentrate mostly on scalability and speed rather than on research usability, being very close to graph methodology in this respect. Another application is [11 which generates a huge indistinguishable graph that has no real use. Some of the projects involved in the creation of protein databases have constructed some visualization capabilities of their own. This is the case of HPRD or DIP (Database of Interacting Proteins) which both provided some sort of visualization. HPRD allows only for a static visualization while DIP is a more evolved one being closer to what we want to develop, but still fairly simplistic. We want to do better than all this systems by focusing less on the graph algorithm and more on the usability aspect of our end product.

4 R P

Week 1 – Coupling our prototype to the HPRD database and tuning it.
Week 2 – First validation session with Dr. Salomon. Implementation of the identified features.
Week 3 uc1– Implementation of identified features.
Week 4 – Second validation session with Dr. Salomon. Implementation of the revised features.
Week 5 – Implementation of the revised features and final meeting with Dr. Salomon.
Week 6 – Final revisions, documentation writing and presentation.

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	B. J 2 Computer Science and Engineering "Politehnica" University of Timisoara, Romania
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P ***n***	C++, Java, C Prolog, ML, Scheme, PHP, ORACLE, MYS
Ma ***P***	• *Mars* – for the 2003/2004 *L* Software Engineering Competition (C • *Pascal* – Compiler Techniques Coursework Project 2003 (C++ implementation) • *We* – Bachelor's Thesis (Java implementation)
P	**Co Pa** • *Area Vis of We Data* with Adrian Rusu, Vishal Anand and Keith Hansen. Proc. 5th International Conference on Internet Computing – IC 04, CSREA Press 2004, ISBN 1- pp. 83-8
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	• Team Award at the Loose Software Engineering Contest, Timisoara, Romania, 2004

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Dear Radu Jianu,

I would be happy to collaborate with you on the visualization of signaling pathways based on our proteomic data. I feel that you could make a significant contribution to this important field. Our goal would be to develop an algorithm for displaying the interactions between our data set and freely available datasets such as the Human Protein Reference Database. I look forward to working with you on this.

Sincerely,

Dr. Arthur Salomon
Brown University
Department of Molecular Biology, Cell Biology, and Biochemistry

Visualizing the Oceanography of Narragansett Bay

Kristin Boyle (PI)
Computer Science

Maribeth Rubin (Co-PI)
Visual Arts

Professor Warren Prell (Collaborator)
Geological Sciences

Abstract: We propose to take oceanographic data collected from Narragansett Bay and produce new and innovative visualizations to aid in oceanographic research of the Narragansett Bay and estuaries in general. To best achieve this goal several methods of visualization will be applied, and tested through a user study before a visualization application accessible to researchers is produced.

1. Introduction

Visualization has long attempted to provide methods of representing data in order to aid in the advancement of science. In this project we attempt to continue in that tradition by taking an exciting new dataset representing the oceanography of the Narragansett Bay and attempting to visualize the data in new ways. The data set varies in both time and space and has multiple variables represented at each point. In order to gain a complete understanding of the dataset oceanographers need to compare these variables. A suitable setting to do this does not currently exist; it will be our goal to produce an environment to aid researchers is analyzing this data. It is a challenging dataset, but one which, if utilized to its full extent, may provide exciting new insights into the ecosystem of Narragansett Bay and perhaps more importantly estuaries in general.

2. Problem Statement

In April of 1998, the Narragansett Laboratory of the National Marine Fisheries Service established an ecological monitoring program for Narragansett Bay. Once every month a heavily instrumented oceanic sampler is towed on a circular transect through the Narragansett Bay (*Figure 1*). The instruments move through the water column at varying depths recording data including time, position, depth, temperature, salinity, chlorophyll fluorescence and dissolved oxygen concentration. Currently this wealth of data is being used as a baseline for assessing changes in the structure and functioning of the Narragansett Bay ecosystem. In other words, the data is used primarily to identify major changes in the ecosystem which may cause adverse reactions.

Throughout the course of this program there have been approximately 60 cruises around the bay (typically one every month). During each cruise a reading is taken about every second and each cruise takes around 7 to 8 hours. All told the resulting dataset for one cruise consists of approximately 30,000 samples.

Figure 1: Path of data in Narragansett Bay

Figure 2: Current Visualization of this data

Over the course of the seven years during which this data has been collected, surprisingly little work has been done to examine the data for use in expanding our knowledge of the ecosystem of the bay and estuaries in general. In *Figure 2* you see an example of the type of visualizations which have been done up to this point with the gathered data. Although these charts do provide some information, they fail to bring much insight into the overall ecosystem of the bay. First, notice the condensed nature of the data

in these visualizations. A large transect of the bay was traversed, yet the data being displayed is condensed to a very small window. This method proves beneficial in getting an overall view of the bay but focusing in on more detailed areas in the bay would be more useful than these current visualizations. It also would be more useful to see a geographically based portrayal of the bay, instead of a linear representation. Another area where these visualizations fail is in the ability to look at the interactions between variables. For example one might want to study the density gradient in comparison to dissolved oxygen levels in the bay. Using the current views this becomes difficult. What is needed is a way to look at several variables in the same visualization, thus allowing the interactions between variables to be clearly evident.

It is important to note that a study of this kind has never before been attempted in an estuary. Although much smaller scale work has been done in the Chesapeake Bay [1], a data set so vast has never been available.

3. Research Plan

Our research will be conducted in three distinct phases. First we plan to create three different visualizations of an area of the bay. Next, we will conduct a user study of experts in the field to determine the most useful methods. Finally we will produce an application which can be used by researches studying the data.

3.1 Initial Visualizations

First, we will produce a visualization which produces a three dimensional vertical surface determined by the depth and geographic location of each sample point (Figure 3). The width of the surface will serve to represent one variable, the color gradients on the surface will represent another variable and yet another variable will be displayed in the texture of the surface.

Similarly, our second method will construct a surface but using a horizontal surface as its basis. Although this method is essentially the same as that mentioned above in terms of implementation it has the potential to produce differing overall understanding of the full data set.

Third we will visualize all variables at once using a multilayered color and texture approach (Figure 4). Each variable will be represented in a horizontal layer where the density of color represents the amount value of that variable. The end result will be a view of the layers put together, producing a surface where color and texture serve to represent all variables at once. This method will allow variable layers to be swapped to give focus to particular variables of interest.

The implementation of these visualizations will be done using the G3D graphics library.

Figure 3: vertical surface mockup

Figure 4: color and texture mockup

3.2 User Study

The Geological Sciences department at Brown has expressed great interest in collaborating with us on this research. As a result we have been given the opportunity to get the opinion of many people who have worked with, and are familiar with the Narragansett Bay data set. Among the researchers examining the data is Professor Warren Prell, an expert in Estuarine Oceanography. Professor Prell is currently teaching an Oceanography class which is utilizing this specific data set in a series of assignments. We have already set up a time to present our three initial visualizations to this class in mid-November. We plan to survey students about their overall understanding of the visualizations we present and also to gather opinions as to what they find the most useful in understanding such a large data set. More specifically we will present four different visualizations, three of which will be our new visualizations and the other of which will be the original visualizations used for this data. We will then ask participants to score each visualization for a set of criteria, and examine a set of tasks. Tasks will include analysis of stratification, correlation between variables and location of data points. In addition to surveying students we will also be presenting our initial visualizations to a set of Geological Sciences researchers working with Professor Prell on this project. These will be the very people that we hope will use our finished product and therefore they are ideal subjects on which to conduct a user study.

3.3 Produce Visualization Application

Upon completion of our user study we will determine which visualization method or methods should be refined and brought through to completion. We will produce an interactive application which, given a tour of the bay, will produce visualizations in an environment ideal for use by researchers. The packaging of our methods into this form will allow researchers to use this program on their personal computers and with this access they will have the opportunity to use the visualizations to there full advantage.

4. Scientific Contributions

Much can be learned by visualizing the oceanographic data which has been gathered by the Narragansett Bay program. The knowledge to be gained goes beyond the bay itself and could produce worthwhile information to aid in the understanding of estuary

ecosystems in general.

The first focus area of this research will be in assessing how the distribution of hypoxia, low dissolved oxygen, evolves throughout the bay. A focus will be on evaluating the stability of the water columns in the bay. This stability can be calculated from the density gradients of the water. The analysis of how water column stability relates to the evolution of low dissolved oxygen levels both spatially and through the seasons will be studied. Increased knowledge of dissolved oxygen activity in estuaries is vital. Oceanographers have long studied this area because of the direct effect that dissolved oxygen levels have on the wildlife and vegetation in the water. When levels of dissolved oxygen drop too low many species are either killed or forced to leave there environment. Such events have major effects on the ecosystem of the body of water in question as well as to the rest of the earth's ecosystem. Increased knowledge about the factors contributing to dangerously low dissolved oxygen levels could allow prevention of such occurrences and help to stabilize the ecosystems of estuaries in general.

Another area of study will focus on how mixing of fresh and salt waters occurs in the Bay. Though some general information is known about the water mixing in estuaries this data set provides a unique way to look at different areas of the bay in terms of multiple variables in order to detect patterns which could provide an increased understanding of the water flow in the bay and estuaries in general.

5. Related Work in Scientific Visualization

Much work has been done in the area of representing spatio-temporal datasets. These techniques have often been applied specifically to geographic datasets, presenting tools for visualizing properties of spatial and temporal periodicity in geographic data[5]. This particular work focuses however only on the temporal-spatial aspects and does not succeed in also tying in the multivariable visualizations which this project will attempt.

Similarly, work has been ongoing in working with multivariable data sets. The breadth and depth of this work is highlighted in 30 Years of Multidimensional Multivariate Visualization, a paper presented by Wonk. The development of multivariable techniques as seen here and in other, more recent, papers cited present some very interesting methods but seems to reiterate the difficulties of such visualizations. The challenge comes in making the visualization understandable without to much additional analysis.

Our methods will propose to attack this problem using 3D surfaces containing texture and color in order to allow representation of many variables at one. Our techniques will be unique in the way they will allow the user to move spatially through a data set and also in its unique approach to representing data through transparent colored layers. Our work will also contribute by analyzing different approaches to visualizing this type of data and discovering what type of visualization appeals to users perceptually while also relaying significant amounts of data.

6. Timeline

Weeks 1-2: Produce initial visualizations on a confined subset of the dataset

Weeks 3-4: Conduct user studies and analyze results

Weeks 5-6: Refine methods and package into application for researchers. Prepare paper and presentation on our findings.

References

[1] Farang, Adam and Hamann Bernd. *Visualization of Water Quality Data for the Chesapeake Bay*. Seventh IEEE Visualization 1996 (VIS '96) p.417.

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[3] Jimmenez etal. *Visualizing Spatial and Temporal Variability in Coastal Observatories*. IEEE Visualization 2003.

[4] Li, Xia. *New Methods of Multivariable Spatiotemporal Data: PCP-Time-Cube and Multivariable-Time-Cube.* 2005.

[5] Edsall, Robert et al. *Tools for visualizing properties of spatial and temporal periodicity in geographic data*. Computers & Geosciences 26 (2000) p 109-118. Pergamon.

Curriculum Vitae for Kristin Boyle

Personal

Name: Kristin Boyle
E-mail: kboyle@cs.brown.edu

Education

Bachelor of Arts: Mathematics, 2004. Stonehill College, North Easton MA

Related Skills and Experience

Programming Languages: C, C++, Java
Experience working in Graphics programming using OpenGL and G3D graphics libraries

June 2005- Present: Consultant Programmer ITA Software, Cambridge MA.

August 2005: SIGGRAPH Poster Session Participant, Plausible Physics in Augmented Images

Curriculum Vitae for Maribeth Rubin

Personal

Name: Maribeth Rubin
E-mail: Maribeth_Rubin@brown.edu

Education

Bachelor of Arts: Interactive Digital Media, May 2007, Brown University

Related Skills and Experience

Experiences in Cognitive Science studying human visual perception and developing user studies and also in the Visual Arts and design

Relevant Classes: Perception, Illusion, and the Visual Arts, Perception Psychology, 3D Shape Perception, and Visualizing Vision

Note of Collaborative Support

Subject: Re: Visualization of Narragansett Bay Oceanography
From: Warren Prell <Warren_Prell@brown.edu>
Date: Mon, 3 Oct 2005 07:14:59-0400
To: Kristin Boyle <kboyle@cs.brown.edu>

Kristin,

This email is to confirm that I welcome collaboration with you and Maribeth on the visualization of Narragansett Bay oceanographic data. Your initial ideas look promising and I look forward to working with you and possibly coordinating some of your work with my estuarine oceanography class.

Thanks for your interest in visualizing this interesting data set.

WLP

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