Multimodal Volume Visualization of Geophysical Data for Archaeological Analysis

PI: Andrew Loomis
Brown University
Computer Science

Co-PI : Tyler Parker
Brown University
Computer Science

Collaborator: Margaret Watters
Brown University
Institute of Archaeology and the Ancient World

October 12, 2010

Abstract

We propose an interdisciplinary research project to investigate the use of multimodal volume visualization techniques in the integration of multiple geophysical datasets in an archaeological context. These techniques will be evaluated on their ability to enhance subsurface anomalies and classify archaeological features.

Introduction

Archaeologists use noninvasive geophysical surveys to measure the different physical properties of a site and to identify buried features. In many cases, the more geophysical surveys an archaeologist has at his or her disposal, the greater the insight the archaeologist has into the composition and structure of the subsurface [3, 6, 9]. Recently, there has been significant work in creating integrated visual representations of the data collected from these surveys (e.g. [6, 9]). These representations are intended to aid in the detection of subsurface anomalies, which may indicate the presence of archaeological features.

The work of Kvamme [6] took data from several different sources and integrated them into a single image representation. This was accomplished by a variety of techniques including mapping different measures to different color channels and the use of mathematical functions to produce a single scalar value from multiple inputs. A limitation of this work is that inherently three-dimensional datasets such as Ground Penetrating Radar (GPR) and Electrical Imaging were only viewed in a two-dimensional space. Watters [9] explored techniques for visualizing multiple three-dimensional archaeological datasets using Amira, a software package developed for medical imaging. This work presented each volume as a separate visual representation in the same space. This research project will focus on treating these volumetric datasets as a single multivalued volume. It is our hypothesis that integrating these datasets during the visualization stage will produce a better representation of subsurface anomalies and underlying features.

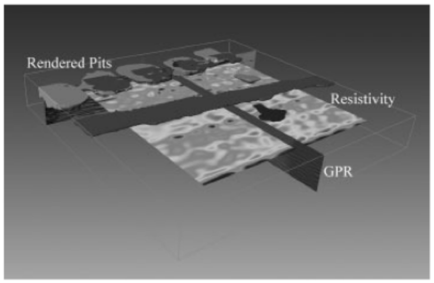


Figure 1: A screen-shot of Amira visualizing three different types of archaeological data [9].

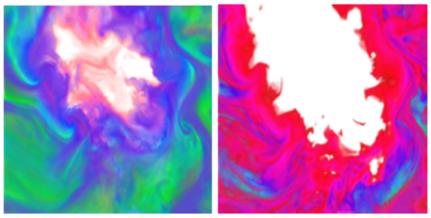


Figure 2: An example of a multimodal volume rendering of a meteorological dataset. On the left color is mapped to temperature and humidity is mapped to opacity. On the right the mappings are reversed [4].

From a visualization perspective this problem is one of multimodal or multivariate volume visualization. Multimodal visualization integrates data collected from multiple sources into a single representation. Work in this area has been explored by a number of different researchers in a number of different contexts, for example [10, 1, 8, 7]. The work by Cai [2] sets up a nice framework to explore several different approaches to volume visualization in this area. It describes three different techniques that are primarily distinguished by the points in the rendering pipeline at which the data is integrated. For instance, the volumes can either be rendered separately and composited together at the end, or the volumes could be rendered together using the components of each voxel as axes of a multidimensional transfer function. This second type of integration, is the type that we believe will be the most useful in presenting the archaeological data. A detailed treatment of multidimensional transfer functions with applications to medical imagery and meteorology can be found in [5] and [4]. As these works point out, selection of the transfer function is one of the most important tasks in volume visualization, and it becomes much more difficult as the dimensionality of the transfer function increases. Archaeological data, in particular GPR, is very different from previously studied medical and meteorological data. Each voxel of a GPR dataset contains the amplitude value of the reflected radar wave. It is not the voxel values themselves that determine the structure of subsurface but the shape of the reflected waves. We believe that this presents a nontrivial problem for volume visualization of these datasets and presents a particular challenge in selecting appropriate transfer functions.

Research Goals

There are two distinct goals of this research proposal. The first goal is the use of multimodal volume visualization techniques to integrate multiple geophysical measures into a single representation. The second goal is to test the hypothesis that these visualizations are more effective at representing known subsurface anomalies and archaeological features than the current techniques using Amira software.

Significance

The results of this research project are important in several different ways. First, effective visualizations that integrate multiple geophysical measures can lead to the extraction of new information for archaeological analysis. This analysis is crucial in determining the nature of archaeological features at a particular site prior to excavation. Second, multimodal and multivalued volume visualization is an active area of research with applications to fields such as medical imaging and meteorology. This work has the potential to not only validate the effectiveness of previously established visualization techniques in the field of archaeology, but also to investigate new methods in multimodal visualization with applications to the aforementioned fields.

Methods

The archaeological site that we will be investigating is the Catholme Ceremonial Complex. It is a collection of ritual monuments located at the convergence of the Trent, Tame, and Mease rivers in England [9]. We will be using data that was obtained from two geophysical surveys, GPR and Electrical Imaging. Both of these measures are collected in slices on a regular grid and then extensively processed to remove noise and artifacts. See Watters [9] for a more detailed description of the data collection and processing pipeline. Once processed the slices can be assembled into two three-dimensional raster volumes. Each voxel of those volumes contains a single scalar value representing the measurement taken by each geophysical survey at that point. These volumes are then georegistered so that the voxels in one volume correspond to voxels in the other.

As previously discussed in the introduction, there are many different techniques to integrate data for multimodal volume visualizations. We will be focusing on techniques that integrate these datasets prior to rendering. We will take two distinct approaches. The first will build directly on the work of Kvamme [6] by using several simple mathematical functions to produce a single scalar value from multiple inputs. This technique has obvious advantages in its simplicity, however It is unclear whether this simplification will be effective in capturing all of the necessary archaeological information. The second approach will treat the volume as multivalued. We will build off of some of the more advanced volume visualization methods described in [4, 5], which take advantage of multidimensional transfer functions. All of this software be efficiently implemented on state of the art graphics hardware using the Cuda architecture.

Each of the above techniques will be compared and evaluated against current visualization methods using Amira software. A simple user study will be conducted using a class of archaeology students. The study will evaluate each visualization on two measures: the number of identifiable archaeological features present in each visualization and the speed it takes to identify those features. An advantage of using the Catholme Ceremonial Complex is that it has been extensively studied and most of the archaeological features have already been identified. That allows us to not only compare the fidelity of our visualizations against other visualizations, but also against the known locations of archaeological features.

Work Plan

Week 1: Obtain the data and convert it to manageable/non-proprietary formats. This may include some preprocessing and registration.

Week 2: Develop software for a basic volume renderer that will provide the framework for multimodal visualizations. The core rendering algorithm by be a ray marching technique, which can be efficiently implements on modern graphics hardware.

Week 3-4: Implement and explore various techniques for multimodal volume visualizations.

Week 5: Evaluate the effectiveness of these visualizations through several simple measures such as the number of identifiable archaeological features and the speed it takes to identify these features.

Week 6: Prepare final presentation and results.

References

[1] R. Bürger and H. Hauser. Visualization of Multi-variate Scientific Data. *Eurographics 2007 STAR*, pages 117–134, 2007.

[2] W. Cai and G. Sakas. Data Intermixing and Multi-volume Rendering. In *Computer Graphics Forum*, volume 18, pages 359–368. Wiley Online Library, 1999.

[3] R.B. Clay. Complimentary Geophysical Survey Techniques: why two ways are always better than one. *Southeastern Archaeology*, pages 31–43, 2001.

[4] J. Kniss, C. Hansen, M. Grenier, and T. Robinson. Volume Rendering Multivariate Data to Visualize Meteorological Aimulations: A Case Study. In *Proceedings of the Symposium on Data Visualisation 2002*, page 189. Eurographics Association, 2002.

[5] J. Kniss, G. Kindlmann, and C. Hansen. Multidimensional Transfer Functions for Interactive Volume Rendering. *IEEE Transactions on Visualization and Computer Graphics*, pages 270–285, 2002.

[6] K.L. Kvamme. Integrating Multidimensional Geophysical Data. *Archaeological Prospection*, 13(1):57–72, 2006.

[7] F. Röbler, E. Tejada, T. Fangmeier, T. Ertl, and M. Knauff. GPU-based Multi-volume Rendering for the Visualization of Functional Brain Images. In *Proceedings of SimVis*, pages 305–318, 2006.

[8] H. Tang, J.L. Dillenseger, X.D. Bao, and L.M. Luo. A Multi-Volume Visualization Framework for Spatial Aligned Volumes after 3D/3D Image Registration. *icise*, pages 3571–3574, 2009.

[9] M.S. Watters. Geovisualization: An Example from the Catholme Ceremonial Complex. *Archaeological Prospection*, 13(4):282–290, 2006.

[10] A. Wenger, D.F. Keefe, S. Zhang, and D.H. Laidlaw. Interactive Volume Rendering of Thin Thread Structures within Multivalued Scientific Datasets. *IEEE Transactions on Visualization and Computer Graphics*, pages 664–672, 2004.

Andrew C. Loomis

23 Thomas Olney Cmn.
Providence, RI 02904
andy.loomis@gmail.com

Education

Brown University, Providence RI Class of 2009
Bachelor of Science – Applied Mathematics/Computer Science
Brown University, Providence RI Class of 2013
Master of Science – Computer Science

Computer Skills

Software: After Effects, CVS, Eclipse, Matlab, Maya, Microsoft Office, Photoshop
Programming: C, C++, Java

Experience

Brown University, Providence RI October 2009 - present
Graphics Systems Programmer
Center for Computation and Visualization
Work done in High Performance Computing and Visualization.
I'm currently developing software for the markerless tracking of bone motion from x-ray video sequences. This work is part of the XROMM project and is funded by the Keck Foundation.

Brown University, Providence RI June 2008 – present
Adviser Project
Development of a portable C++ library to efficiently display high resolution terrain and image data in a virtual reality environment. This project is funded by a geological research grant from NASA.

TYLER PARKER

bryan_parker@brown.edu | Brown University, 69 Brown Street, Box 4704, Providence, RI 02912 | (845) 901-1051

objective

Brown University Senior going into Masters Program **seeking internship** that will put to challenging use my skills, work experience and education in Computer Science thus far.

experience

HBO 6/2010 - 8/2010

Web Technologies Intern

Led an intern team for designing iPad app concepts, developed workflow templates and networking tools, researched and developed internal Wiki upgrade

Evolving Media Network 6/2009 - 8/2009

Web Development Intern

Created and updated Ruby on Rails and WordPress sites for clients, server setup and maintenance.

Nokia 6/2008 - 8/2008

Web Analytics and Programming Intern

Using Java and PHP, created software solutions for the Digital Marketing Team, analyzing user data for the launch of Ovi. Compiled and updated the weekly Digital Marketing Key Performance Indicator report.

education

Brown University 9/2007 - Present

Class of 2011, Bachelor of Science in Computer Science

Relevant Coursework

Interdisciplinary Scientific Visualization, Interactive Computer Graphics, Software Dev.

research

HCI and Graphics (Ongoing)

Advisor: Andy van Dam, Brown University.

Developing and rapid prototyping innovative tools and interfaces for large multi-touch surfaces, primarily Microsoft Surface

Scientific Visualization of Human Task Reaching (Ongoing)

Advisors: David Laidlaw and Joo-Hyun Song, Brown University.

Developing novel visualization tools for a Cognitive Science research project that aims to create a model for Human Task Reaching.

projects

Prospect and Meeting site (independent group project).

Web designer and coder for a popular Brown University dating site titled 'Prospect and Meeting', implemented in Ruby on Rails.

Event Management Software (group project).

Software Engineering, Brown University.

Designed and coded the front end client for a web Application that allows students to filter events, save them, and display them on a map.

Comedy-Thriller Movie Script

Currently being represented by Mike Esola, William Morris Agency.

skills

Programming Languages: C/C++, Java, Python, Matlab
Web Languages: Ruby on Rails, PHP, HTML, AJAX, CSS, MYSQL
Graphics Applications: Maya, Blender, Flash, Photoshop, After Effects, Premiere Pro
Operating Systems: Linux, Windows, some OSX

interests

Acting and singing in musical theatre, 3d Animation, listening to remixes and mashups

MARGARET S. WATTERS

Meg_watters@hotmail.com Margaret_Watters@brown.edu

EDUCATION

2007 **PH.D. IN ARCHAEOLOGY**, Institute of Archaeology and Antiquity, University of Birmingham, UK.
PhD Dissertation: *New Methods for Advanced Archaeo-Geophysical Data Visualization*.

1998 **M.A. IN ARCHAEOLOGY**, Boston University, Boston, MA.
M.A. Thesis: *Greek Colonial and Indigenous Interaction at Empuries, Spain: Ground Penetrating Radar (GPR) through Advanced Analytical Methods*.

1990 **B.A. IN STUDIES IN ANTIQUITY**, Trinity College, Hartford, CT.

EMPLOYMENT & AFFILIATIONS

2010 ADJUNCT FACULTY. Institute of Archaeology and the Ancient World, Brown University, *Archaeo-geophysical Survey and Visualization*. (Autumn 2010)

2010 ADJUNCT FACULTY. Frederic W. Olin College of Engineering: Department of Arts, Humanities and Social Sciences, *Introduction to Archaeology*. (Spring 2010)

2007- present HONORARY RESEARCH FELLOW IN ARCHAEOLOGICAL VISUALIZATION, Institute of Archaeology and Antiquity, University of Birmingham, UK.
STAFF, IBM Visual and Spatial Technology Centre, University of Birmingham, UK.

2007-2008 GEOPHYSICAL SURVEY AND GIS DIRECTOR, Time Team America, PBS television program, aired 2009.

2006-2010 FREELANCE GEOPHYSICAL SURVEY CONSULTANT

2000-2002 APPLICATIONS SPECIALIST, GEOPHYSICAL SURVEY SYSTEMS, INC.
Training Manager, responsible for writing equipment and software instruction manuals, conducted geophysical research and field work, worked in marketing and sales.

1998-2000 ARCHAEOGEOPHYSICIST, IMAC, Minneapolis, MN
Developed geophysical survey department within a Cultural Resource Management company, which included sales, field survey and reporting.

TEACHING

2010 ADJUNCT FACULTY. Joukowsky Institute of Archaeology and the Ancient World, Brown University, RI. Autumn 2010.

2010 ADJUNCT FACULTY. Fredrick W. Olin College of Engineering, Department of Arts, Humanities, and Social Sciences, Needham, MA. Spring 2010.

2008 INSTRUCTOR. Archaeology and Geophysics short course at Discovery World, Pier WI. (July 2008).

2002-2008 INSTRUCTOR. Geomatics and Practical Archaeology MA Module and undergraduate lectures, Institute of Archaeology and Antiquity, "Geophysical Theory and Method." University of Birmingham, UK.

2006 INSTRUCTOR. Geophysics for landscape archaeology, XV International Summer School in Archaeology. As part of the *Culture 2000 Project, European Landscapes: past, present and future*. (July 2006).

1999-2002 INSTRUCTOR. "Recent Archeological Prospection Advances for Non-destructive Investigations" National Park Service Archaeological Geophysics Workshop. United States Department of the Interior.

2001-2002 INSTRUCTOR: "Interpreting Archeological Ground Penetrating Radar Data: A Users Workshop," University of Arkansas, Fayetteville, AR (November 2001) and University of Georgia, Athens, GA (March 2002) Sponsored by National Center for Preservation Technology and Training and the USDA-Forest Service, Southern Region.

- WORKSHOP ON GEOPHYSICAL APPLICATIONS IN ARCHAEOLOGY: Bowdoin College, Brunswick, ME.

1999 INSTRUCTOR. American Academy in Rome, Geophysical Investigations in Archaeology Seminar, June 10-11.

ARCHAEOLOGICAL EXPERIENCE

2010 Project Leader, Ancient Water Management of the Stabiae Research Project, Restoring the Ancient Stabiae, Italy.

2007-2008 Geophysical Survey Coordinator: The Avkat / Euchaita Project, Turkey. Princeton University, University of Birmingham, UK.

2006-2009 Remote Sensing and Geophysical Survey Coordinator: Restoring the Ancient Stabiae, Italy.

2006 Geophysical Survey Coordinator: Three Tier Survey for San Giovanni in Laterano, Rome. Newcastle University, University of Birmingham, UK, British School Rome, Vatican Museums, and Institute of Technologies Applied to Cultural Heritage ITABC-CNR (Rome, Italy).

- Geophysical Survey Consultant: The Büyük Menderes Nehri Research Project. University of Birmingham, UK.

2003-2005 Geophysical Survey Coordinator: Where the Rivers Meet, Aggregates Extraction Study, English Heritage, Staffordshire, UK.

12 October 2010

To whom it may concern:

This letter is in support of the scientific visualization project on geophysical anomaly extraction for archaeological research being undertaken by Andrew Loomis. Certain types of geophysical data are 2.5 to 3 dimensional in nature, yet are regularly considered as flat, 2 dimensional data. Resulting plan maps from surveys are laboriously analyzed by hand, using only the experience and visual recognition for the identification of a variety of anomaly types within the data.

Andrew's proposed project to consider the analysis of these data types through 3 dimensional visualization techniques for a more automated anomaly extraction protocol is an important step in the consideration of landscape-scale geophysical surveys in archaeology.

Sincerely,

Margaret S. Watters
Adjunct Lecturer in Archaeology
Joukowsky Institute for Archaeology and the Ancient World
Brown University

Representing Choice Reaching Tasks through the Visual Metaphor of Force Attraction

Bryan Tyler Parker[1], Samuel Birch[2] and Joo-Hyun Song[3]

[1] PI; Department of Computer Science, Brown University, Providence, RI 02912 USA
[2] Collaborator, Brown University, Providence, RI 02912 USA
[3] Consultant, Department of Cognitive Science, Brown University, Providence, RI 02912 USA

Abstract

We propose an interdisciplinary research project to develop and investigate the effectiveness of methods for the visualization of user reach trajectories, with the goal of revealing hidden cognitive states in the choice reaching tasks and to develop a model for user reaching trajectories. We do this through a multiview visualization tool, one free allows free manipulation and viewing of 3D user tracking data, the complementary view showing the 2D projection of this data alongside 2D eye tracking data. Both views allow portray the temporal nature of the data, as well as uses a novel force visualization that displays the influence of distractor targets on the use reaching.

1. Research Goals

The first goal is to create a static visualization technique for 3D user hand movement data that effectively visualizes temporal information. The second goal is to create a multi-view technique of visualizing the correlation between 3D user hand movement and 2D eye-tracking data. The third goal is to develop a novel technique for the visualization of the influence of “attractor targets” on user reach trajectories that uses the visual metaphor of force attraction. The final goal is to evaluate the effectiveness of these techniques.

2. Background

Perceptual and cognitive processes have largely been deduced based on studies involving discrete responses.. However, discrete responses are not enough, and there are likely to be more internal processes at work that are not represented by past studies. Recent studies measuring continuous hand movements during target choice reaching tasks reveal the temporal evolution of hidden internal events. For example, a curved user reach trajectory can represent attention to the task at hand. New research exploring the user reach trajectory itself, not just the end result, provides new opportunities to integrate information across different disciplines such as perception, cognition and action, which have usually been studied in isolation.

Joo-Hyun Song’s research attempts [1] to create a model of continuous hand movements during selection of a target when presented with distracter targets. However, understanding of the data collected has been hindered by ineffective visualization techniques.

3. Methods

Song’s experimental trials involve a user selecting a specified target on a screen, with other distracter targets on screen. The users hand motion is captured in 3d, and their eye gaze on the screen is tracked in 2D. Visualization of these various components has been limited to 2D plots.

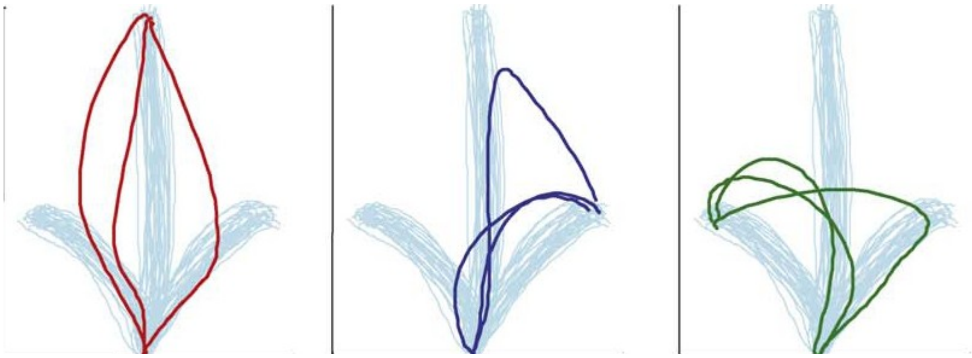


Figure 1: Original 2D plot of user tracking data

However, these visualizations have been somewhat unsuccessful in revealing a potential model for user reach trajectories during choice making due to their limitability. For instance, these graphs do not display time, just the full path. New visualizations are needed to improve the ability to interpret the data.

For the 3D hand movement data, a visualization that allows for recognition of temporal information will be created. This will take the form of a trajectory that has points along it that represent discrete time units. Given a still 3D model of the trajectory, temporal information would be readily evident: points bunched together on the trajectory indicate the user slowing down or stopping while reaching; points spaced far apart indicate fast movement. An option of having multiple user trials of the same task visible at the same time would allow for visual pattern recognition, and will likely have a visual style similar to [4]. An option to 'playback' the motion data in real time (like an interactive animation) will also be included. We hypothesize this will allow the user to be able to gain a better understanding of their data as opposed to using solely a 2D projection.

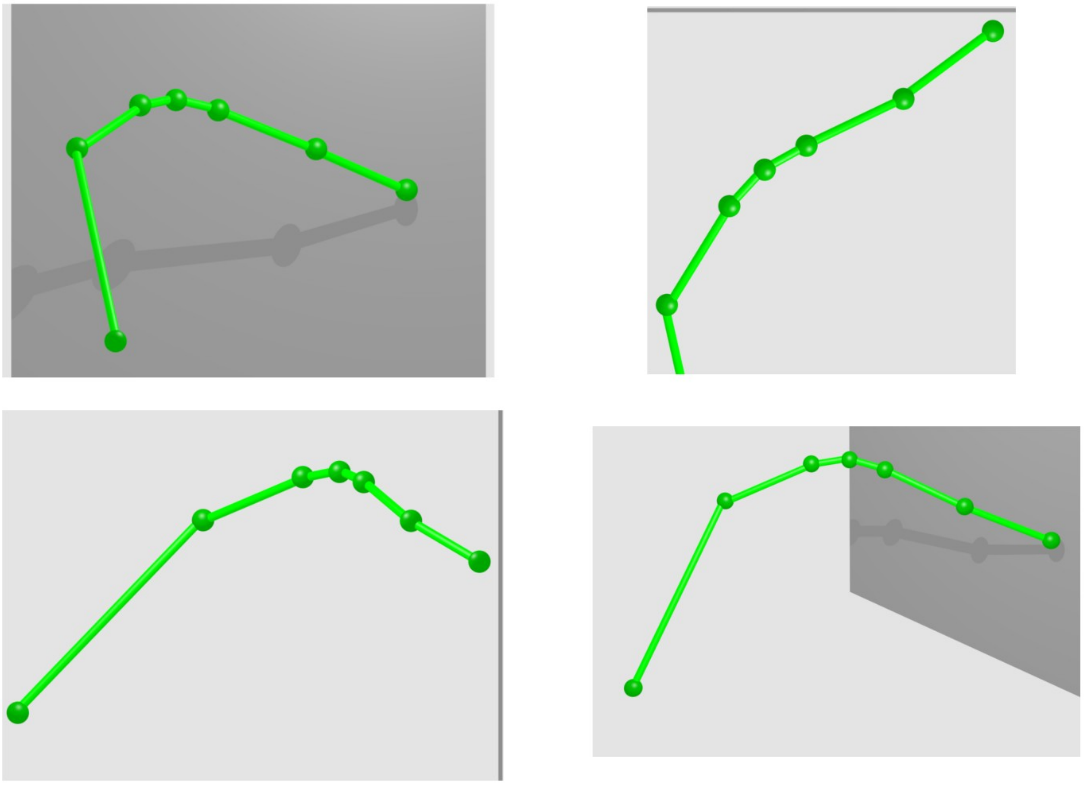


Figure 2: Proposed 3D visualization of user tracking data (front view, top view, side view, perspective view). Time unit points are represented by the spheres along the path.

This 3D hand movement data will also have to be related to the 2D eye-tracking data. For this, a multi-view solution will be implemented. A 2D window will contain trajectories of the eye-tracking data, with discrete time units much like those used in the 3D visualization. Alongside the eye-tracking trajectories, the 2D projection of the 3D data will also be displayed. This will allow for the analyzer of the data to see how the hand movement follows the eye-movement, as well as related the 3D movement data to the 2D plane of the target screen.

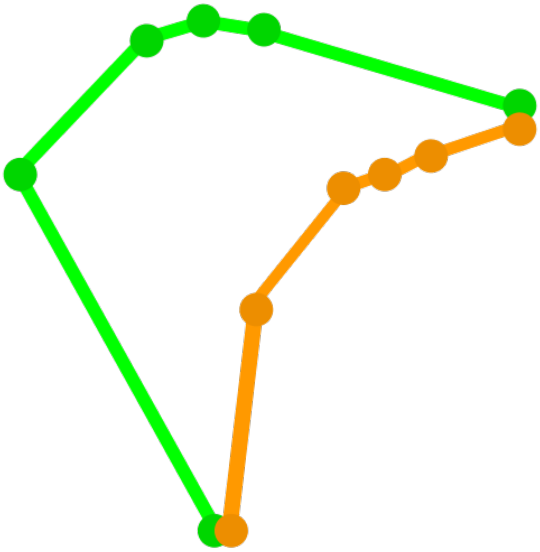


Figure 3: 3D user reach data projected onto plane with 2D look data. Green is user reach data, orange is user look.

In addition, a novel technique for the visualization of the ‘distracter targets’’ influence on a task reaching trajectory will be developed. By knowing the 2D location of the different distracter targets, as well as the motion data, one can use an equation similar to the one of gravitational force to enumerate the distracter target’s influence on the user. Visualizing this imaginary force can lead to real understanding.

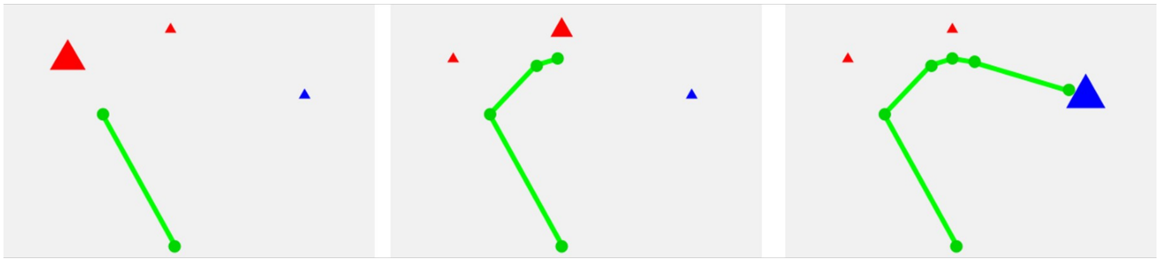


Figure 4: Target scale is used to visualize force attraction over a user reach movement.

These techniques will be evaluated both individually and together as a multiview tool with the current 2D graph visualization already in place. A user study involving experts in the field of cognitive science will be used to evaluate the different methods' effectiveness. This evaluation will likely take the form of a Likert Scale. The results of this study will determine the success of the multiview technique and its methods. If a decent model of human reaching trajectories is created with the use of these techniques, where with the current 2D graphs this was proving difficult and they were yet to be able to create such a model, then the new techniques would be considered effective.

4. Impact

The combination of the techniques developed through this project will could directly benefit the cognitive science community, for if successful will aid in the model of human target reach trajectories, which would lead to insight on the perception, cognition, and action behind target selection. This in turn could impact the HCI community in developing interfaces.

The static visualization of 3D data technique could be applicable to any disciplines that analyze motion data, such as flocking behavior exhibited in birds or fish. Most motion can be relatively defined as the summation of attraction/repulsion influences; therefore the novel force visualization technique is also applicable to a wide range of disciplines.

6. Timeline

Week 1: Obtain the data and develop software to import it and roughly display it temporally.

Week 2-3: Implement technique to effectively display the 3D data temporarily, as well as view multiple user trials simultaneously.

Week 3: Implement multi-view capability for the viewing of 2D eye-tracking data and visualizing the correlation between it and the 3D hand movement data.

Week 4: Implement "attractor target" influence visualization.

Week 5: Evaluate the effectiveness of these methods.

Week 6: Prepare final presentation and results.

7. Facilities

Windows machines in the CIT as well as personal machines will be used to develop and deploy the software. Software will be developed with Cinder. No other facilities will be required.

8. References

[1] Joo-Hyun Song and Ken Nakayama. Hidden cognitive states revealed in choice reaching tasks. *Trends in Cognitive Sciences,* 13(8):360-366, 2009.

[2] Roberts, J.C. State of the Art: Coordinated Multiple Views in Exploratory Visualization. *Coordinated and Multiple Views in Exploratory Visualization,* 67-71 July 2007

[3] Räihä, Kari-Jouko and Aula, Anne and Majaranta, Päivi and Rantala, Harri and Koivunen, Kimmo. Static Visualization of Temporal Eye-Tracking Data. *Human-Computer Interaction - INTERACT 2005,* 3585: 946-949

[4] Harald Piringer and Robert Kosara and Helwig Hauser. Interactive Focus+Context Visualization with Linked 2D/3D Scatterplots. *Coordinated and Multiple Views in Exploratory Visualization* 49-60 2004

[5] http://www.toyfoo.com/pedestrian_levitation/index.html

[6] Cignoni, P.,Montani, C. and Scopigno, R..Magicsphere: an insight tool for 3D data visualization. *Computer Graphics Forum*, 13(3):317-328, 1994

[7] Pingali, Gopal and Opalach, Agata and Jean, Yves and Carlbom, Ingrid. Visualization of sports using motion trajectories: providing insights into performance, style, and strategy. *VIS '01: Proceedings of the conference on Visualization '01,* 75-82, 2001

TYLER PARKER

bryan_parker@brown.edu | Brown University, 69 Brown Street, Box 4704, Providence, RI 02912 | (845) 901-1051

objective

Brown University Senior going into Masters Program **seeking internship** that will put to challenging use my skills, work experience and education in Computer Science thus far.

experience

HBO 6/2010 - 8/2010

Web Technologies Intern

Led an intern team for designing iPad app concepts, developed workflow templates and networking tools, researched and developed internal Wiki upgrade

Evolving Media Network 6/2009 - 8/2009

Web Development Intern

Created and updated Ruby on Rails and WordPress sites for clients, server setup and maintenance.

Nokia 6/2008 - 8/2008

Web Analytics and Programming Intern

Using Java and PHP, created software solutions for the Digital Marketing Team, analyzing user data for the launch of Ovi. Compiled and updated the weekly Digital Marketing Key Performance Indicator report.

education

Brown University 9/2007 - Present

Class of 2011, Bachelor of Science in Computer Science

Relevant Coursework

Interdisciplinary Scientific Visualization, Interactive Computer Graphics, Software Dev.

research

HCI and Graphics (Ongoing)

Advisor: Andy van Dam, Brown University.

Developing and rapid prototyping innovative tools and interfaces for large multi-touch surfaces, primarily Microsoft Surface

Scientific Visualization of Human Task Reaching (Ongoing)

Advisors: David Laidlaw and Joo-Hyun Song, Brown University.

Developing novel visualization tools for a Cognitive Science research project that aims to create a model for Human Task Reaching.

projects

Prospect and Meeting site (independent group project).

Web designer and coder for a popular Brown University dating site titled ‘Prospect and Meeting’, implemented in Ruby on Rails.

Event Management Software (group project).

Software Engineering, Brown University.

Designed and coded the front end client for a web Application that allows students to filter events, save them, and display them on a map.

Comedy-Thriller Movie Script

Currently being represented by Mike Esola, William Morris Agency.

skills

Programming Languages: C/C++, Java, Python, Matlab
Web Languages: Ruby on Rails, PHP, HTML, AJAX, CSS, MYSQL
Graphics Applications: Maya, Blender, Flash, Photoshop, After Effects, Premiere Pro
Operating Systems: Linux, Windows, some OSX

interests

Acting and singing in musical theatre, 3d Animation, listening to remixes and mashups

Samuel M. Birch

sbirch@cs.brown.edu
312-772-4724

Education

Brown University, Providence, Rhode Island
- B.Sc. in Computer Science, expected May 2014.
- M.S. in Computer Science, expected May 2014.

Boston University, Boston, Massachusetts
- No degree (completed as part of high-school coursework), 2008-2010.

Boston University Academy, Boston, Massachusetts
- Summa Cum Laude, and with Highest Honors on Senior's thesis, 2010.

Research Experience

- Boston University, Boston, Massachusetts
  - 1/09-5/10
  - Member of the HyNeSs Laboratory

Employment

- The MITRE Corporation 5/2010-8/2010

Publications

M. Kloetzer, S. Itani, S. Birch, C. Belta. "On the Need for Communication in Distributed Implementations of LTL Motion Specifications," ICRA 2010.

C. Belta, Y. Chen, A. Stefanescu, S. Birch. "A Hierarchical Approach to Automatic Deployment of Robotic Teams with Communication Constraints," IROS 2010.

S. Birch. "Two Novel Methods for Precise Image Thresholding" (Senior Thesis). 2nd Place, Southern New England Regionals, Junior Sciences and Humanities Symposium (JSHS). Presented at the National JSHS.

Awards

- AFCEA Fellowship, 2010.
- AFCEA Barrett Award, 2010.
- Xerox Award for Technology, 2009.

Statistical Assessment of Individual Peak Quantitation in Mass Spectrometric Data

PI: Justin A. DeBrabant[1]
co-PI: Steven Gomez[1]
Collaborators: Arthur Salomon[2,3,4], Kebing Yu[2]

[1] Brown University, Department of Computer Science, Providence RI, USA
[2] Brown University, Department of Chemistry, Providence RI, USA
[3] Brown University, Department of Molecular Biology, Cell Biology, and Biochemistry, Providence RI, USA
[4] Brown University, Center for Genomics and Proteomics, Providence RI, USA

Efficient analysis of large mass-spectrometric data sets has become essential in the field of MS-based proteomics. There are multiple methods for both collecting the data and quantitating it in a way such that the underlying protein structure can be determined with a high level of confidence. Although much work has been done on the quantitation process itself, to our knowledge there is no available metric to compare the relative qualities of different peak quantitations. We propose the development of such a metric, as well as a complimentary visualization tool that will allow quick and efficient quality comparisons among a group of peak quantitations. This work will allow researchers to not only collect the best possible data, but will also allow them to understand the possible error in the data they've collected in way comparable across experiments.

1. SPECIFIC AIMS

There are several goals of this project. First we will develop a metric that will quantify the quality of an individual peak quantitation for mass spectrometric data. This metric will then be implemented in a visualization framework that will allow researchers to easily identify the quality of their data as well as better compare that data across multiple experiments. Within the visualization component will be the ability to filter and rank data based on their individual quality scores as well as simultaneously view data across several experiments.

Once the visualization component is developed, it will be implemented within the framework of the High Throughput Autonomous Proteomic Pipeline (HTAPP). HTAPP, developed by researchers at Brown University, is in an instance of a proteomic pipeline that completely automates the data collection, filtering and analysis as well as the transfer of data between all the distinct components [13]. Specifically, the proposed tool will be adjacent the "Quantitation" and "Relational Database Exploration Tool" components within the framework of the pipeline, with input coming from the quantitation component and output going to the exploration component.

Finally, after implementation within the proteomics pipeline is complete, we will conduct a small user study to evaluate the relative effectiveness of our metric and corresponding visualization component in the comparison of experimental results. As a basis for comparison, we will use the Xcalibur application as it is currently the state-of-the-art in data collection and analysis of MS data [1].

2. BACKGROUND AND RELATED WORK

In recent years, proteomics has emerged as a technique for better understanding the metabolic pathways of the cell, to which proteins are essential. A large part of proteomics research is based around the technique of mass spectrometry (MS), a tool for measuring the molecular mass of molecules in a sample. In proteomics, peptides in a sample are identified by comparing the mass given from the mass spectrometer to known peptide masses, usually from a peptide database such as PeptideDepot [13]. By inducing different environmental conditions and measuring cellular response as a function of protein production, researchers can better understand intracellular functions.

Unfortunately, this process is inherently noisy, and there are several phases in the data acquisition and analysis pipeline that require quantitation of this noisy data, most notably to compare to known peptide masses. The efficient use and analysis of this data has been a continued challenge in the field of MS-based proteomics, as only a fraction of proteins in a sample can be identified, and even a smaller fraction of the identified proteins can be reliably quantified.

Much effort has been invested in the filtering and analysis phases of the pipeline and there are several techniques that can efficiently automate post-acquisition tasks such as peptide quantitation and protein identification [3,4,5,6,7]. Also there has been work in confidence scores of the protein identification phase, i.e. how good of a match is a given spectrogram to a known protein [8, 9, 10]. However, there is no technique to efficiently compare the individual peak quantitations produced by the pipeline. Basically, what this means is that there are methods measure how a given peak quantitation fits to a known protein, but no way to measure the quality of the given peak to begin with. The assumption here is that proteomic researcher has already intuitively categorized peaks as "good" or "bad" and is only using "good" peaks. This manual processing contrasts sharply with the automated nature of all other aspects of the proteomics pipeline, and will become all but impossible as the amount of proteomics data continues to grow.

Also lacking in the field of proteomics is a way to efficiently visualize changes over time and across different runs of the experiment with different conditions. This is the key to proteomics, i.e. given an outside stimulus what is the intracellular response as measured by protein synthesis, so it is surprising that no tool to effectively view these changes is currently available. The present software allows the visualization of an individual peak, with the ability to click through related peaks from other experiments [1]. This method has clear limitations on the ability to understand how the peaks are changing given a change in stimuli, which is the ultimate goal of the experiments.

This work proposes to define a set of variables that will accurately summarize the quality of MS peak data and allow meaningful inter-experiment comparisons. In conjunction with this metric, we will develop a visualization tool that will allow efficient comparison of the individual peaks and their associated quality score across a wide range of experiments. Also available will be the ability to filter results being visualized by the proposed quality score, i.e. only view results above a certain threshold.

3. IMPACT

Already proteomics has emerged as our best method to both understand and subsequently model complex biological systems [11]. With many researcher turning to proteomics as the successor of genomics and the possible future of clinical research, the impact of the above contributions to proteomics are potentially profound. By better modeling and understanding cellular functions, scientists will be able to better understand how and why these functions sometimes break down, e.g. in cancer or autoimmune diseases. However, the difficulty of analyzing the mass of data available is only getting more challenging as the data grows, so better computational methods are needed. To this end, we propose this project.

On its own, the quality metric represents a huge step in the more efficient comparison of peak quantitations, as current methods are are limited to manually labeling peaks “good” or “bad” based on expert user knowledge. With an explosion in the amount of proteomic data being produced in recent years, this manual process will only become less feasible. Using the quality metric to assess the peak quantitations would save the researches time and provide more consistent results by automating the filtering process. It would also give researchers a better understanding of the quality of the results they were viewing, which is important in many contexts.

The proposed quality metric, implemented within the framework of the proposed visualization, will greatly aid researchers in their quest to understand the different cellular responses to varying stimuli. The current software, Xcalibur [1], allows only the viewing of the data one experiment and one time point at a time, from which it is extremely difficult for researchers to effectively deduce cellular changes across varying stimuli. Again, as the amount of data available continues to grow, this will only become more difficult.

Overall, the more formal evaluation of peak quality will reduce the bottleneck in the automated proteomics pipeline currently caused by manual peak quality assessment. Also, a visualization of multiple results together with their quality score will simultaneously allow researchers to better understand their results as well as increase the confidence of their assessment, both of which are essential to the advancement of proteomics research.

4. METHODS

This project can be broken down into 4 distinct phases, each depending on the previous one. A description of each phase follows.

4.1 Phase 1: Data Collection

The first phase of the project will be the reformatting of the MS data from a proprietary binary file format into a relational database. The raw binary file produced by the instrument can only be read by the application, Xcalibur [1] , that is provided by the instrument manufacturer. This software provides the quantitation of the data, but without access to the underlying data there is no way to quantify the quality of the quantitation. As such, we propose to create a layer in the pipeline that will take the binary data being produced by the mass spectrometer, translate it into text, and store it in a relational database. This way, the quantitation software can continue to use the binary file, while our quality metric will be able to access the data from a relational database. To make this possible, we have obtained an API from the manufacturer for extracting the binary data into text.

4.2 Phase 2: Metric Implementation

The next phase of the project will be the calculation of the quantitation quality metric. This metric will rely on the characteristics of the underlying data acquisition component. We plan to take into account several error-inducing factors such as signal-to-noise ratio and continuity of the peak shape in order to estimate the selected ion chromatogram quality. We will then measure variance in the experimental results by applying a Gaussian curve to the individual peaks and aggregating variance from the curve.

4.3 Phase 3: Visualization Component

The final phase will be the implementation of the visual component and its integration into the HTAPP. The most important characteristic of the visual component will be the simultaneous visualization of peaks from replications and variances from the same experiment. In this context, a replication is when the same sample is run through the MS multiple times in order to increase the confidence of the results. The other type is when the sample is changed some minute way and run through the MS, looking for changes from the control run. For each experiment, there will be multiple condition runs, each with 2-5 replications. For each run, the individual peaks will have an associated quality score. The visualization will give the ability to view repetitious runs and their associated quality score in a 3 dimensional grid where each replication occupies a unique plane in x-y grid parallel to the planes for the other replications. The quality score will be indicated by a color scheme on the graphs. A similar view will be available for each of the different conditions, with each condition graph representing an aggregate score from each of its replications and colored to represent the aggregate of the quality metrics of these aggregations. The key to this visualization will be the side by side comparison across both replications and experiments with varying conditions, thus visualizing, with confidence, intracellular response to a given stimuli.

4.4 Phase 4: Evaluation

The final phase will be the evaluation of the quality metric and the visualization component of the project using a small user study. To evaluate the quality metric we will have expert users from the Salomon Lab at Brown University manually label peaks as “good” or “bad”. We will then decide on a threshold that will separate the “good” and “bad” peaks and apply our quality metric and label and the peaks below the threshold “bad” and all those above as “good”. Then, we will compare the intersection of the two sets to determine how accurately our metric models expert user intuition. Also, we will simulate a random labeling of peaks as “good” or “bad” with some expected distribution mirroring the threshold in our algorithm (e.g. 70% good, 30% bad); this will ensure that both our algorithm and the expert user intuition are better than the random case. For the evaluation of the visualization component, we will use the Xcalibur [1] system as a basis for comparison, as it is widely used to compare and analyze MS data. We will develop a list of tasks and measure the relative efficiency (time, accuracy, ...) of which they are completed.

5. TIMELINE

Week 1: Transfer of raw binary data files to a relational database
Week 2: Study of the possible underlying parameters that would best describe the quality of the quantitation
Week 3: Quality metric for peak quantitations
Week 4: Begin phase 3, implementation of the visual component
Week 5: Finish visual component and insert into HTAPP
Week 6: User study of quality metric and visualization component

6. REFERENCES

[1] Xcalibur. http://thermoscientific.com

[2] M. Bantscheff, et al. (2007). ‘Quantitative mass spectrometry in proteomics: a critical review’. Analytical and Bioanalytical Chemistry 389(4):1017-1031-1031.

[3] J. Cox & M. Mann (2008). ‘MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification’. Nature biotechnology 26(12): 1367-1372.

[4] Craig, R., and Beavis, R. C. (2003). ‘A method for reducing the time required to match protein sequences with tandem mass spectra’. Rapid Commun. Mass Spectrum. 17(20):2310-6

[5] Craig, R., and Beavis, R. C. (2004). ‘TANDEM: matching proteins with tandem mass spectra’. Bioinformatics. 2004 Jun 12;20(9):1466-7. Epub 2004 Feb 19.

[6] J. K. Eng, et al. (1994). ‘An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database’. Journal of the American Society for Mass Spectrometry 5(11): 976-989.

[7] J. K. Eng, Bernd Fischer, Jonas Grossmann, Michael J. MacCoss (2008). ‘A Fast SEQUEST Cross Correlation Algorithm’. Journal of Protemics 7 (10), 4598-4602

[8] David Fenyö and, Ronald C. Beavis (2003). ‘A Method for Assessing the Statistical Significance of Mass Spectrometry-Based Protein Identifications Using General Scoring Schemes’. Analytical Chemistry 2003 75 (4), 768-774

[9] Martinez Lundgren and Han Wright (2009). ‘Protein identification using Sorcerer 2 and SEQUEST’. Curr Protocol Bioinformatics.13(13.3).

[10] L. C. McHugh & J. W. Arthur (2010). ‘Harvest: an open-source tool for the validation and improvement of peptide identification metrics and fragmentation exploration’. BMC bioinformatics 11(1): 448+.

[11] S. Patterson and R. Aebersold (2003). ‘Proteomics: the first decade and beyond’. Nature Genetics (33):311-323.

[12] K. Yu, et al. (2009). ‘Integrated platform for manual and high-throughput statistical validation of tandem mass spectra’. Proteomics 9(11):3115-3125.

[13] K Yu, et al. (2009). ‘PeptideDepot: flexible relational database for visual analysis of quantitative proteomic data and integration of existing protein information’. Proteomics 9(23):5350-8.

Dear Justin,

I would like to confirm our enthusiastic support for your project to create a quality metric for quantitative analysis in proteomics and an associated facility to visualize both this metric and the underlying data. The ability to effectively perform visual analysis on replicate experiments and different time points of biological stimulation will be invaluable in the biological understanding of the quantitative data. To our knowledge a quality metric has not been developed to this point, severely reducing both the quality of proteomics data analysis and leading to inefficient and inherently biased manual validation of spectral quality. We are also excited about your preliminary effort to liberate the quantitative data from the shackles of the proprietary binary file. We feel that this step will not only facilitate the proposed project but will also lead to a flood of new tools which can more efficiently access proteomic data. Please let us know any way that we can help you to be successful in your proposed work.

Sincerely,
Arthur Salomon
Assistant Professor
MCB Department
Brown University

Justin A. DeBrabant

Department of Computer Science, Brown University

81 Hudson St, FL 1
Providence, RI
Phone: (954) 253-4050
Email: debrabant@cs.brown.edu

Profile

Computer science PhD student at Brown University researching database systems. Advised by Ugur Cetintemel and a member of the Brown Database Group.

Experience

RA, Brown University; Providence, RI -- 06/2010 - present

Researching query sequence optimization.

RA, Florida State University; Tallahassee, FL -- 08/2008 - 05/2010

Working on several projects within the Database Group, including an Honors Thesis.

TA, Florida State University; Tallahassee, FL -- 08/2008 - 05/2010

Teach several weekly recitations for both majors/non-majors intro to c++ course.

Editor-in-Cheif, Florida State Undergraduate Research Journal -- 06/2009 - 05/2010

Manage every aspect of the journal publication including a staff of 10 assistant editors and over 30 peer-reviewers.

Education

Brown University, PhD in Computer Science, 08/2010-present

- Adviser: Ugur Cetintemel

Florida State University, B.S. in Computer Science, 06/2006-05/2010

- Graduated Magna Cum Laude
- Adviser: Feifei Li
- Florida State Honors Program
- Member of Student Council on Undergraduate Research and Creativity
- Honors/Awards:
    - Recipient of 2009 Undergraduate Research and Creativity Award
    - Selected as one of FSU's 2009 Star Students

Skills

Proficient with experience in the following languages:

- C/C++, Perl, Java (including Swing and JSP), and SQL

Experience with the following technologies:

- Database Systems (MySql, Oracle, TRIO, and PostgreSQL)

Steven R. Gomez

Contact Information

Department of Computer Science
Brown University
Box 1910
Providence, RI 02912 USA

office: CIT 423
cell: (802) 272-4941
e-mail: steveg@cs.brown.edu
www.cs.brown.edu/∼steveg

Research Interests

Scientific visualization, visual computing and analytics, human-computer interaction, computer graphics, vision

Education

Brown University, Providence, Rhode Island USA

Second-year graduate student in doctoral program in Computer Science

- Courses completed: Computer Graphics, Computer Vision, Computational Photography, Distributed and Parallel Computing, Networking and Distributed Systems

Dartmouth College, Hanover, New Hampshire USA

B.A. *magna cum laude*, Computer Science, June 2007

Industry

M2S, Inc., Lebanon, NH – *Software Engineer* – 2008–09
Development for several tools, including virtual stent grafts for Preview aortic aneurysm visualization software.

Awards

Brown University Graduate Fellowship – 2009–10
Rufus Choate Scholar (top 5% of class) – 2006–07
John G. Kemeny Undergraduate Computing Prize – First Place, 2006, for *BlitzChat*
Dartmouth Presidential Research Scholar – 2005–06
Class of 1928 Endowed Scholarship – 2003–07

Publications

Steven R. Gomez, Radu Jianu, and David H. Laidlaw. A Fiducial-Based Tangible User Interface for White Matter Tractography. In Proceedings of *ISVC*, 2010.

Steven R. Gomez. Interacting with Live Preview Frames: In-Picture Cues for a Digital Camera Interface. In Proceedings of *ACM UIST* (Poster), 2010.

Keller, R., Hunt, M., Jones, S., Morrison, D., Wolin, A., and Gomez, S. 2007. Blues for Gary: Design Abstractions for a Jazz Improvisation Assistant. *Electron. Notes Theor. Comput. Sci.* 193 (Nov. 2007), 47-60.

Technical Skills

Languages: Java, MATLAB, C, C++, Scheme, Perl, Tcl/tk, PHP, SQL, X/HTML, LaTeX
Applications: Eclipse, Netbeans, Xcode, Apache, CVS, Subversion, MS Office, Adobe CS
Operating Systems: Mac OS X, Linux, Windows 98/2000/XP

HOW USERS PERCEIVE AND INTERPRET EMBELLISHED DATA ON GRAPHS?

PI: Diem Tran Co-PI: Justin Debrabant
Consultant: Caroline Ziemkiewicz

Department of Computer Science, Brown University, Fall 2010

Abstract

Graphical data embellishment is reported as one of the top unsolved problem in visualization. Though several studies have been conducted to understand the problem, its solution is still in dispute due to opposite findings from the studies. We create a new model to predict human cognition in reading quantitative data displayed in graphs, in order to explain various outcomes of previous studies as well as suggesting a unified approach in drawing graphs, benefitting a considerable portion of the visualization community. A timeline of 6 week research includes a preliminary study to collect data for model design, a three-week period of developing as well as evaluate the model and one last week to write final report.

1 INTRODUCTION

According to Chen [1], the problem of embellishing graphs is among top unsolved problems in the visualization field. This problem involves directly the understanding of how users perceive data from different kinds of visualization techniques, hence affects design of information visualization systems. It is further related to evaluation of effects that visualization tools have on users. Overall, whether or not and how to make graphs become appealing and easier to retrieve for people is an open problem to the field of visualization.

In this proposal, we use ACT-R, a widely used cognitive architecture to model human cognition on graphical data embellishment to understand more about how people read, interpret and memorize information presented on different kinds of graphs. Our model will be compared with real results obtained from user experiment to evaluate the validity of predictions we made.

2 RELATED WORK

Several works have been done to model cognitive tasks in general. ACT-R [2] is a cognitive architecture to explore how human cognition works. It is used to physically model the process that occurs inside human's mind. Scientists can use it to replicate cognition when users perform different tasks, and test the validity of replication by comparing its results with results obtain from real users. GOMS [3] is also a similar architecture to ACT-R in terms of modeling human cognition through decomposing the cognitive process into procedural steps which can be imitated and performed by computers. Lohse implemented a GOMS-based model to understand graphical retrieval of human in general [4]. However, no complex model has been built to understand human cognition in perceiving different kinds of enhancement in presenting data graphically.

On the other hand, there are empirical evidences of how graph embellishments affects capability to memorize data. Nevertheless, results are very controversial as they are opposite to the ones found in earlier studies. Recent results yield favor for enhancement of displaying data [5, 6] in various ways, from using picture [7] to applying emotional tones of the data [8] to make users remember them more accurately. However, there has been a long-established trend of keeping graphs as plain and simple as possible [9, 10]. There are also neutral results in which non of the two, enhanced of minimalist approach in graphing is effective [11, 12]. All of these outcomes show a shift in treating data embellishments from opposition to approval. Nevertheless, there is no universal approach to identify the problem, as the key to it lies behind human cognition in perceiving data. To unify and explain all results, we need a general model to describe how a user retrieve data in a procedural way.

3 CONTRIBUTION & SIGNIFICANCE

3.1 Contribution

In this project, we create a new model using ACT-R with the aim of predict what a user typically does when reading graphs. By modeling this cognitive process, we are able to have more insight in how graph embellishments affect users' memory. In particular, we can understand how specific portions of data display in a graph are retrieved, interpreted, analyzed and synthesized. Following this cognitive procedure, we are able to explain why there are controversial results in previous studies, and provide guidelines for future graph drawings as well as design of visualization systems.

3.2 Significance

If successful, the model will contribute significant resources to help solve a renown problem of visualization. It will help graph drawers in designing more appealing and effective graphs, transmitting data more persuasively in ways that drawers want readers to perceive. Furthermore, scientists interested in how displayed data affect users' perception can based on our model to design more effective techniques to display data. It also open paths for future development of models to predict human cognition in other complex data display techniques.

4 APPROACH

4.1 Hypothesis

Following Bateman's results [5], we predict that data embellishment affect human perception in a positive way. We are going to verify the following 3 hypotheses during the project, through a user study and our model:

- **Hypothesis 1:** Users are able to identify more striking features of embellished graphs than the ones of non-embellished graphs. Striking features are regions contain data that users find eye-catching.
- **Hypothesis 2:** Embellished graphs increase user memorability but decrease interpretation speed, relatively to non-embellished graphs.
- **Hypothesis 3:** Human cognition in reading embellished graphs can be decomposed into procedural knowledge, and simulated by computers.

4.2 User study

We run a controlled study to collect user data in reading, interpreting and memorizing data in graphs. In the study, a user is allowed to view a graph for a certain amount of time. The length of this time will be determined by a one-day pilot study, in which we ask 10 users to look at a graph and say out loud what they are seeing. The amount of time from the beginning until they mention enough data presented on the graph will be calculated. Based on this number, we will estimate the length for viewing a graph in the real study.

4.2.1 Participants

The number of anticipated users are 60, 30 of which will be used to collect data and build the model, while the remaining 30 are used to evaluate the newly built predictions. Call for participants will be posted in CIT building, and if necessary, other buildings of Brown University. A user will work on a small software written to display graphs and collect data simultaneously.

4.2.2 Method

We select a set of 20 graphs, half embellished and half non-embellished, from Nigel Holmes' book, Designer's Guide to Creating Charts and Diagrams, to be embedded in our software. Graphs are chosen to be pairwise similar in terms of type. For example, there will be 1 embellished and 1 non-embellished graph that are both pie chart. Collected data of 2 graphs in a pair will be compared against each other to verify the first two hypotheses. A user views all graphs in the set one by one. A typical view section for a single graph is as follow:

- A user views a graph for a short amount of time, whose length has been determined in the pilot study. During this period, a user clicks on a point or selects a region which he finds striking. As the time expires, for each click and selection the user made, he will be asked to elaborate more about reasons for his choice. This is a sample question: " why did you select this region? What is the content of it?".
- After viewing and answering questions for all 20 graphs, we ask recall prompts to measure accuracy and subjective reports on mechanism users use to read and interpret graphs. Below is a sketch of the question form, which will be repeated until no more graph is recalled. For each recalled graph, question 2 and 3 are asked 3 times for 3 different data on the graph. If the user does not understand the question, we will elaborate more or give example if needed.

Table 1: Questions for a recalled graph

Number	Description
1	What graph can you remember?
2	What specific data do you remember ?
3	What makes you remember that data?
4	What is the trend of the graph?

4.2.3 Measurements

The following factors will be measured in the study. Measurements are inter-related and will be used to add constraints to our model.

Table 2: Questions for a recalled graph

Factor	Method
Striking features of a graph	Users' clicks and selections during graph viewing period
Users' choice justification	Elaboration on clicks and selections
Short term memory	Accuracy rates of answers to question 2 and 3 in Table 1.
Cognition mechanism	Question 4 in Table 1

4.2.4 Data Analysis

We are add constraints to our model to make better predictions using data collected in the study. Different measurements contribute different constraints of the model:

- *Users' selection and elaboration:* By plotting user clicks and selections, we can find the common pattern of reading specific areas on graphs. This helps us determine striking features on a graph. Order of clicks and selection and elaboration are used to prioritize those striking features, based on reasons users provide when making a selection. We verify hypothesis 1 using this result.
- *Accuracy rates of recalled data:* These numbers are used to generate probability in memorizing and recall short term memory of the model. Hypothesis 2 are verified by analyzing this data.
- *Cognition mechanism:* This is used to justify relevance striking features priority and other constraints.

4.3 Model

4.3.1 Initial sketch

We build a cognitive model using ACT-R [2] architecture, a tool to model procedural knowledge that human process. We decompose the graph perception process into discrete steps and use model to make predictions on what a user might do when he is reading a graph. The initial sketch of the model is as follow:

```
Repeat {
        Find the most unexplored striking feature of the graph.
        Look at the newly found feature.
        Memorizing information on that specific area with constraints added.
} Until there is no unexplored area of the graph.
```

4.3.2 Evaluation

The newly built model will go through the same study as a real user does and same numerical data will be collected. Those data will then be compared with data from the remaining 30 users. Statistical tests such as ANOVA or t-tests will be run to validate them. Based on difference between data from real users and from the model, we are able to verify hypothesis 3.

5 TIMELINE

Week 1-2: Preliminary user study. We conduct a user study to grasp initial understanding of how a person read different kinds of graphs. In the study, questionnaires and interviews are used to collect data. A one day pilot study will also be run to estimate and adjusting factors needed for the real study.

Week 3-5: Developing and evaluating the model. Based on results obtained from the user study, we will create the model to predict user's cognition process. We aim to use ACT-R. Small experiments may be conducted to verify and refine the model. Evaluation is carried out by comparing results produced by the model and real data from the study.

Week 6: Analysis of results and report writing. Using statistical testing units, we validate our results and write final report.

References

[1] C. Chen, "Top 10 unsolved information visualization problems," *IEEE Comput. Graph. Appl.*, vol. 25, no. 4, pp. 12–16, 2005.

[2] J. R. Anderson, M. Matessa, and C. Lebiere, "Act-r: a theory of higher level cognition and its relation to visual attention," *Hum.-Comput. Interact.*, vol. 12, no. 4, pp. 439–462, 1997.

[3] B. E. John and D. E. Kieras, "The goms family of analysis techniques: Tools for design and evaluation," tech. rep., Pittsburgh, PA, USA, 1994.

[4] G. L. Lohse, "A cognitive model for understanding graphical perception," *Hum.-Comput. Interact.*, vol. 8, no. 4, pp. 353–388, 1993.

[5] S. Bateman, R. L. Mandryk, C. Gutwin, A. Genest, D. McDine, and C. Brooks, "Useful junk?: the effects of visual embellishment on comprehension and memorability of charts," in *CHI '10: Proceedings of the 28th international conference on Human factors in computing systems*, (New York, NY, USA), pp. 2573–2582, ACM, 2010.

[6] N. Holmes, "Designer's guide to creating charts and diagrams," 1984.

[7] W. Hockley, "The picture superiority effect in associative recognition," *Memory and Cognition 36*, pp. 1351–1359, 2009.

[8] M. Mather and K. Nesmith, "Arousal-enhanced location memory for pictures," *Journal of Memory and Language 58*, pp. 449–464, 2008.

[9] E. R. Tufte, *The visual display of quantitative information*. Cheshire, CT, USA: Graphics Press, 1986.

[10] W. S. Cleveland, *The elements of graphing data*. Belmont, CA, USA: Wadsworth Publ. Co., 1985.

[11] J. Kulla-Mader, "Graphs via ink: Understanding how the amount of non-data-ink in a graph affects perception and learning," 2007.

[12] A. Blasio and A. Bisantz, "A comparison of the effects of data-ink ratio on performance with dynamic displays in a monitoring task," *International Journal of Industrial Ergonomics 30*, pp. 89–101, 2002.

Resumé

Diem Thi-Hong Tran

Last updated: Aug 30th, 2010.

Email: diemtran@cs.brown.edu diem_tran@brown.edu, tthdiem@apcs.vn

RESEARCH INTEREST

I am interested in developing interactive techniques/ new user interfaces to help users interact with computers more easily.

EDUCATION

2010: Master Student at Computer Science at Brown University, RI, US.

- My current advisor is Professor Andy Van Dam.

2006 – 2010: BSc. in Computer Science. Expected Graduation: 8/2010.

- Advanced Program in Computer Science, Ho Chi Minh City University of Sciences (Formerly University of Natural Sciences), National University, Ho Chi Minh City in association with Portland State University, Oregon, USA. (*http://www.apcs.hcmuns.edu.vn/en/*)
- Cumulative GPA (until the 3rd year): 3.84/4.
- Major GPA (until the 3rd year): 3.98/4.
- Rank in class: 1/38.
- Rank in faculty: 1/550.

2003 – 2006: High School Diploma.

- *Le Hong Phong High School for The Gifted, Ho Chi Minh City, Vietnam.*
- Graduation Scores: 54/60. Type: Excellent.

CURRENT PROJECTS

September 2010 – present: Garibaldi 2.0

- I participate in designing and implementing ideas for Garibaldi, a system for viewing large artworks on wall and tabletop displays.

PAST PROJECT

May 2010 – August 2010: Automatic Tab Ordering (working title).

- *Instructor:* MSc. Son Do-Lenh – Swiss Federal Institute of Technology Lausanne (EPFL), Switzerland.
- *Teammate:* Nguyen Ngoc Dan Vy (06CTT, HCMUS), Nguyen Van Khoa (06CTT, HCMUS).
- *Research topic:* We are concerning of usage and techniques to support tabbed browsing in softwares such as web browsers (Firefox, IE, Safari, etc) and text editors in which users have to deal with a large amount of opened tabs.

- Undergraduate Thesis: This is a part of our project. We deployed a field study to get an overview of current conditions in tabbed browsing among knowledge workers in SeLab, HCMUS. Based on collected results, we develop two interaction techniques to help a user access his favourite tabs as well as find his tabs of interest in a fastest way.
- *Undergraduate thesis grades:* **9.7/10.**

October 2009 – May 2010: Software Capstone Project – Advising System.

- *Instructor:* MSc. Lam Quang Vu – HCMUS, Vietnam.
- *Advisor:* Dr. Tran Minh Triet – HCMUS, Vietnam.
- *Teammate:* Nguyen Ngoc Dan Vy (06CTT, HCMUS), Nguyen Van Khoa (06CTT, HCMUS).
- *Description:* A project of developing an advising service for credit-based education system: based on input courses and grades of students, the system generates recommendation on which courses to take toward a degree. It also manages the curricula and plans students make, helps them to keep track of their study and provides a communication channel between students and advisors in Faculty of Information Technology, HCMUS.
- This project is developed through a spiral software engineering model, with a prototype created first and upgraded gradually. Technology used: .NET, Ajax, SQL.

July 2009 – May 2010: Usage patterns of large displays and multiple displays.

- *Instructor:* MSc. Son Do-Lenh – Swiss Federal Institute of Technology Lausanne (EPFL), Switzerland.
- *Research topic:* We concerned of usage patterns, interaction techniques, user interfaces when working with a large display and/or multiple displays. We conducted a study to collect trends in using two setups and provide guidelines for future research or technique development.
- We developed a logging program to record data on users' screen, and then an extracting & visualizing program to analyze data. Design guidelines will be brought out based on analyzing results.

March 2008 - June 2008: SC203 - Scientific Method course project.

- *Instructor:* Prof. Vu Duong – Eurocontrol, France.
- *Advisor:* MSc. Van Chi Nam – HCMUS, Vietnam.

- *Publication:* Thoughts of youths about human values. *06CTT Proceeding – SC203*. 2008. (Vietnamese).
- *Descriptions:* From various beliefs about the origin of human beings, our ancestors developed a system of morals and ethics. Through a survey of more than 100 participants from age 18-25, we'd like to depict the current state of how they think about the system as well as how the system affects their daily lives.

July 2008: CS305 - Social, Ethical and Legal Issues course project.

- *Instructor:* Prof. Cynthia Brown – Portland State University, USA.
- *Project:* Negative effects of social networks on Vietnamese teenagers.
- *Descriptions:* Based on news and trends among Vietnamese teenagers which are widely found on the Internet, I wrote a report on how teenagers used Internet, particularly Yahoo!360, as a mean of communication and present their personalities. I especially focused on the negative sides of their presentations, which caused a lot of severe consequences.

AWARDS

- APCS Scholarship for three first rank students – School year 2007-2008 and 2008-2009.
- University Scholarship for excellent students - School year 2006-2007, 2007-2008 and 2008-2009.

10/11/2010

Dr. Laidlaw,

I am writing to express my support for Diem Tran's research project and my willingness to collaborate further with her on this work. I believe Diem's plan to study the role of embellishments in visualization reading and recall through user experimentation and cognitive modeling is novel and interesting. Her proposed plan of research seems well thought-out and I believe it should be executable within the time period given. I will be happy to lend my support to Diem in the planning and execution of her research project in any way I may be of assistance.

Regards,

Caroline Ziemkiewicz

An evaluation of mechanistic and covariation-based explanations for promoting confidence in uncertainty visualizations

Gideon Goldin
PI; Cognitive, Linguistic & Psychological Sciences, Brown University

Steve Gomez
Collaborator, Computer Science, Brown University

Elizabeth Bird
Consultant, Rhode Island Hospital

Steven Sloman
Consultant, Cognitive, Linguistic & Psychological Sciences, Brown University

Abstract

How to best represent uncertainty remains an unsolved problem in visualization research. Providing explanations for uncertainty, rather than uncertainty information itself, can have positive effects on user's trust levels, but the nature of these contributions is not well understood. We compare mechanistic and covariation-based explanations and see how they affect confidence in a given probabilistic assessment.

Specific Aims

We hypothesize that mechanism-based explanations will promote more confidence in uncertain probabilistic assessments than covariation-based ones within medical diagnosis. A mechanism in this context is broadly defined as that which links a cause to an effect via the transfer of force or causal power. Getting sneezed on causes you to get sick. The mechanism here is infection since germs are transferred from one person to another. A co-variation account, on the other hand, describes a causal system by way of appealing to the manner in which certain variables co-occur. For example, it may most often be the case that when someone sneezes on you, you get sick. Starting from the empirically justified assumption that people construe the world (i.e., perform categorization) in terms of mechanism, and not (just) covariation (Ahn & Kalish, 2000), we predict that probabilistic uncertainty which relies on the same type of mechanistic, explanatory representation that people use will lead users to infer that the system has a similar understanding of that uncertainty, ultimately leading to more trust in the system's computations. Though some work has addressed the issue of which types of explanations to provide in certain Decision-Support Systems (DSSs), none so far has empirically tested mechanistic versus covariation-based accounts.

We will run a study for the purpose of comparing these types of explanations. A series of user-cases will be presented to people as simulated diagnoses. The explanations for these cases will not rely on sophisticated medical knowledge *a priori*. This way, we will broaden our subject pool to non-physicians, such that we may run our study online during our 6-week project. Subjects will be given the likelihood of a disease given a set of symptoms with either no explanation, a covariation-based explanation, or a mechanistic based explanation (with or without a causal diagram). If the results from these preliminary data support our hypothesis, measures will be taken to attempt a replication with medical residents in a clinical environment, though not likely within our 6-week time-frame.

Given that people will trust mechanistic explanations more than covariation-based explanations, the implications for medical diagnosis and the myriad related fields are vast. First, visualizations of uncertainty may be more intelligently augmented with explanations, which will lead to higher adoption rates of DSSs. In turn, this will lead to safer medical practices, as diagnoses in general should benefit from more normative decision-making approaches (e.g., Bayesian inference rather than intuition). Apart from clinical impact, scientific significance will be cross-disciplinary as potential benefactors reside in computer science (e.g., human-computer interaction, visualization, AI), psychology (e.g., probability & decision-making), and even education (e.g., medical school, self-diagnosis). Finally, this work will serve as an exploratory basis for studying the interpretation of causal diagrams, which could result in strong contributions to fields in visualization and visual analytics.

The results of our project will be a mechanism-driven visualization technique. This lends itself well to being implemented in clinical settings and analysis sectors, as it is inexpensive and would be simply a matter of coupling graphical (and/or verbal) elements to otherwise textual and numeric data. Scoping beyond our 6-week work plan, this work has the potential to be integrated into a general framework for visualizing explanations of uncertainty. The ultimate goal of such a framework would be intelligent, automatic generation of visualizations, including a system for producing effective causal diagrams as a function of the task and user. Since automatic presentation tools are beyond our 6-week scope, we must focus our attention to investigating only a coarse, yet scientific evaluation of the contributions of mechanistic explanations.

Background & Related Work

Despite progress in artificial intelligence, psychology, and even human-factors, physicians are slow to adopt DSSs (Egea & Gonzalez, 2010). There are numerous hypotheses for why this is the case; some based on models of technology acceptance such as TAM (Davis, Bagozzi & Warshaw, 1989). One large factor is trust in information sources, and we propose that a central cause of low-trust is poor explanation.

Most of the work addressing explanations in computer science resides in the expert-system literature. Tintarev and Masthoff (2007) provide a recent review on the state of explanations in these AI systems, but seem to focus on covariation information. Cunningham, Doyle, and Loughrey (2003) come closer by comparing case-based and rule-based explanations. The two methods are even tested empirically in medical diagnosis (Doyle, Cunningham, & Walsh, 2006). Though the case-based approach is in-essence a covariation approach, the rule-based approaches often used are not explicitly mechanistic, but rather comprised of a causal retracing of the system rules.

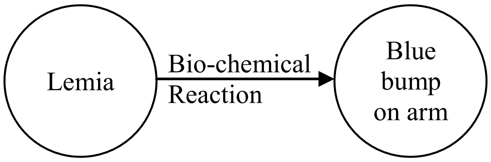
However, the notion of mechanistic-causality has been addressed in AI (Roth-Berghofer and Cassens (2005); Lacave and Díez (2003); Sørmo, Cassens and Aamodt (2005)). Our proposed work fills in the gap by providing an empirical study to verify the actual usefulness of mechanistic explanations, with and without supporting causal diagrams.

Research Design & Methods

In order to test our hypothesis that mechanism-based explanatory information promotes use of DSSs more so than covariation-based approaches, we will run a study that consists of hypothetical scenarios tested in four conditions (*no explanation*, *covariation-based explanation, mechanistic explanation, mechanistic explanation with a causal diagram*). We will systematically vary the probabilities used so as to prevent potential interpretation effects arising from probability judgment interactions. Subject will indicate to some degree their confidence in the presented uncertainty. Consider an example:

Imagine you are a doctor and have been presented with a patient, Amy, who has a strange blue bump on her arm. Amy may have a rare condition known as Visius. In the past, Visius has been associated with this type of bump. Visius may cause this type of bump. You have been given a computer which purportedly can make predictions about diagnoses. You ask it for predictions about whether or not Amy has Visius, and it suggests that:

(1) The probability that Amy has Visius is 80%.
(2) The probability that Amy has Visius is 80% because of the past 100 people that have had bumps like this one, it has been shown that around 80 of them also had Visius.
(3) The probability that Amy has Visius is 80% because Visius can cause particular bio-chemical reactions which result bumps like this one about 80% of the time.
(4) The probability that Amy has Visius is 80% because Visius can cause particular bio-chemical reactions which result bumps like this one about 80% of the time.



How confident are you in this diagnosis?

In each scenario, a novel symptom set and disease will be introduced, and the mechanistic explanation will be relatively vacuous in nature, stating things like, "a bio-chemical reaction occured," which will presumably be necessary for any of our disease-symptom pairs.

A one-way ANOVA will be run [Explanation (*no explanation vs. covariation-based explanation vs. mechanism-based explanation* vs. *mechanism-based explanation with causal diagram*]. We predict that the two mechanistic explanations will result in more confidence than both the covariation-based explanation, and the lack of explanation condition. We also predict the diagrammatic condition will be more trustworthy than the diagram-less one. All tasks in the study will be run on the web, using Mechanical Turk to recruit and pay participants.

Work Plan

Week 1: A meeting will be held with the consultants to design and validate a comprehensive set of experimental stimuli for the purposes of testing online. A private web site will be made available for disseminating project progress, with initial study details put online.
Week 2: A pilot-study will be run. Feedback and results from this pilot will be used to refine the task (modifying scenarios, etc.) in a second group meeting. Discussion will be put online.
Week 3-4: During these weeks, the study will be put online, and run over the internet using Mechanical Turk to recruit and pay subjects. The study itself will be programmed in a modified version of LimeSurvey.

Week 4-5: Data collection will be completed after week 4. Week 5 will entail an analysis of the data, and a meeting to discuss the findings. Results and discussion will be made available online. Any final tasks or modifications will be agreed upon during this meeting.

Week 6: If more data must be collected, it will be done and analyzed in the first half of week 6 (the experimental setup will already be in place). Finally, a write-up of the project and its results will be completed and put on the private web site.

References

Ahn, W., & Kalish, C. (2000). The role of covariation vs. mechanism information in causal attribution. In R. Wilson & F. Keil, *Cognition and explanation* (Vol. 54). MIT Press.

Cunningham, P., Doyle, D., & Loughrey, J. (2003). An evaluation of the usefulness of case-based explanation. *Case-Based Reasoning Research and Development*, (Ml), 1065–1065.

Davis, F.D., Bagozzi, R.P., & Warshaw, P.R. (1989). User acceptance of computer-technology: A comparison of two theoretical-models. *Management Science* 35(8), 982–1003.

Doyle, D., Cunningham, P., & Walsh, P. (2006). An evaluation of the usefulness of explanation in a case-based reasoning system for decision support in Bronchiolitis treatment. *Computational Intelligence*, *22*(3-4), 269–281.

Egea, J.M.O., & Gonzalez, M.V.R., (2010). Explaining physicians' acceptance of EHCR systems: An extension of TAM with trust and risk factors. *Computers in Human Behavior*, In Press.

Lacave, C., & Díez, F. J. (2003). A review of explanation methods for Bayesian networks. *The Knowledge Engineering Review*, *17*(02), 107-127.

Roth-Berghofer, T., & Cassens, J. (2005). Mapping goals and kinds of explanations to the knowledge containers of case-based reasoning systems. *Case-Based Reasoning Research and Development*, *3620*, 451–464.

Sørmo, F., Cassens, J., & Aamodt, A. (2005). Explanation in Case-Based Reasoning–Perspectives and Goals. *Artificial Intelligence Review*, *24*(2), 109-143.

GIDEON GOLDIN

Box 1978, Cognitive, Linguistic & Psychological Sciences,
Brown University, Providence, RI 02906
(321) 720-5377 Gideon_Goldin@Brown.edu

EDUCATION

Doctor of Philosophy in Cognitive Science, Fall 2008 – Present
Department of Cognitive & Linguistic Sciences, Brown University
Providence, Rhode Island

Bachelor of Science in Computer Software Engineering, Spring 2008
College of Computer Information Science and Engineering, University of Florida, Gainesville, Florida
Minor: Linguistics, Spring 2008

RELEVANT COURSEWORK

Independent Study in Human-Computer Interaction and Visualization
Professor Katherine Spoehr
Department of Cognitive & Linguistic Sciences, Brown University

Cognition, Human-Computer Interaction, and Visual Analysis
Professor David Laidlaw
Department of Computer Science, Brown University

Human-Computer Interaction
Professor Benjamin Lok
College of Computer Information Science and Engineering, University of Florida

Aesthetic Computing
Professor Paul Fishwick
College of Computer Information Science and Engineering, University of Florida

RESEARCH EXPERIENCE

Research Assistant, Fall 2010-present
Sloman laboratory, Brown University

- Automated system for conducting online experiments.
- Researched effects of deliberation on consumer goods evaluation

Graduate Researcher, Fall 2008-present
Sloman Laboratory, Brown University

OCD Research, Butler Hospital

- Designed, conducted, and analyzed an experiment assessing the probability judgments of risk of healthy and obsessive-compulsive people.

Undergraduate Researcher, June 2007 - August 2007
Linguistics Laboratory, University of Florida
Psycholinguistics Group

- Migrated an ERP study for usage in an eye-tracking environment.

Undergraduate Researcher, September 2006 - December 2006
High-Performance Computing & Simulation Research Laboratory, University of Florida
Unified Parallel C Group

- Programmed small-scale simulation applications in Unified Parallel C.

SKILLS

Computer Languages: Java, Perl, LISP, C, XHTML, JavaScript, JQuery, CSS, ActionScript, MATLAB, PHP
Software Packages: MATLAB, Net beans, Eclipse, SPSS, Adobe CS

ACHEIVEMENTS AND HONORS

Research Award, Brown Institute for Brain Sciences, Brown University (2009-2010)
University Fellowship, Brown University (2008-2009)
Dean's List: Fall 2004, Spring 2006, Spring 2007
Florida Academic Scholar

CONTACT INFORMATION

Steven R. Gomez
Department of Computer Science — office: CIT 423
Brown University — cell: (802) 272-4941
Box 1910 — e-mail: steveg@cs.brown.edu
Providence, RI 02912 USA — www.cs.brown.edu/∼steveg

RESEARCH INTERESTS

Scientific visualization, visual computing and analytics, human-computer interaction, computer graphics, vision

EDUCATION

Brown University, Providence, Rhode Island USA

Second-year graduate student in doctoral program in Computer Science

- Courses completed: Computer Graphics, Computer Vision, Computational Photography, Distributed and Parallel Computing, Networking and Distributed Systems

Dartmouth College, Hanover, New Hampshire USA

B.A. magna cum laude, Computer Science, June 2007

INDUSTRY

M2S, Inc., Lebanon, NH – Software Engineer – 2008–09

Development for several tools, including virtual stent grafts for Preview aortic aneurysm visualization software.

AWARDS

Brown University Graduate Fellowship – 2009–10
Rufus Choate Scholar (top 5% of class) – 2006–07
John G. Kemeny Undergraduate Computing Prize – First Place, 2006, for BlitzChat
Dartmouth Presidential Research Scholar – 2005–06
Class of 1928 Endowed Scholarship – 2003–07

PUBLICATIONS

Steven R. Gomez, Radu Jianu, and David H. Laidlaw. A Fiducial-Based Tangible User Interface for White Matter Tractography. In Proceedings of ISVC, 2010.

Steven R. Gomez. Interacting with Live Preview Frames: In-Picture Cues for a Digital Camera Interface. In Proceedings of ACM UIST (Poster), 2010.

Keller, R., Hunt, M., Jones, S., Morrison, D., Wolin, A., and Gomez, S. 2007. Blues for Gary: Design Abstractions for a Jazz Improvisation Assistant. Electron. Notes Theor. Comput. Sci. 193 (Nov. 2007), 47-60.

TECHNICAL SKILLS

Languages: Java, MATLAB, C, C++, Scheme, Perl, Tcl/tk, PHP, SQL, X/HTML, LATEX
Applications: Eclipse, Netbeans, Xcode, Apache, CVS, Subversion, MS Office, Adobe CS
Operating Systems: Mac OS X, Linux, Windows 98/2000/XP

Letter of Support from Elizabeth Bird

from Elizabeth Bird <embird@brown.edu>
to Gideon Goldin <gideongoldin@gmail.com>
date Thu, Sep 23, 2010 at 7:12 AM
subject Re: Visualizing Risk in the Medical Domain

HI Gideon,
Yes, I am interested. Lets plan on talking tomorrow or Monday. Tomorrow I could talk in the evening; Monday in the afternoon. Let me know if either of those work.
Lizzie

Letter of Support from Steven Sloman

from Sloman, Steven <steven_sloman@brown.edu>
to Gideon Goldin <gideongoldin@gmail.com>
date Tue, Sep 14, 2010 at 5:41 PM
subject Re: Meet up?

How's Friday around 3?

s

Visualization of Hyperspectral Images Through Interactive Non-linear Sections

PI: Ryan P. Cabeen[1]
Co-PI: Andrew C. Loomis[2]
Collaborator: Jeffrey Nettles[3]

[1]Department of Computer Science, Brown University, `rpc@cs.brown.edu`
[2]Department of Computer Science, Brown University, `andrew_loomis@brown.edu`
[3]Department of Geological Sciences, Brown University, `Jeffrey_Nettles@brown.edu`

October 12, 2010

Abstract

The proposed study develops a method for visualization of hyperspectral images where a user interactively creates a curve in spatial coordinates, defining a non-linear section through an image, reducing the spatial dimension and resulting in several types of visualizations of the spectra along the curve. The effectiveness will be investigated with expert users, and integration with existing tools will be explored.

1 Overview

In the proposed study, we intend to develop and evaluate a visualization method for understanding hyperspectral image data through interactive spatial dimension reduction. The research will result in an implementation of the method for use with remote sensing data. The efficacy of the method will be evaluated with expert users, and the integration of the tool with existing remote sensing data analysis environments will be explored.

In the fields that use hyperspectral imaging, there has been both an increase in the number of images being taken, as well as their spatial and spectral resolution, producing a need for new visualization techniques. Unlike traditional photography, where there are sensors for bands in red, green, and blue bands, remote sensing systems sample a broad spectrum on a two-dimensional grid with as many as hundreds of bands. This type of imaging can give insight into the fine structure of the subject; however, intepreting the shape of the spectra is a highly specialized skill that requires knowledge both of the physics of the imaging process and the subject's composition. Furthermore, the broad spectrum being recorded at each pixel is difficult to render as an image that can be intepreted by the human visual system, given the high dimensionality. The combination of increases in data volume and resolution has produced a need for not a single visualization method but an array, to which the proposed study will contribute.

The proposed study investigates the use of a spatial reduction method that uses interaction to benefit from the expertise of the user. The user will graphically specify a simple curve in the two-dimensional spatial coordinates. At each point along this curve, the spectra are sampled. The result can then be rendered as an image that represents the spectra along the curve. Unlike spectral reduction techniques, the spectra along the curve are presented in full, which might be advantageous when the user is accustomed to interpreting the data based on fine details. Through the course of this study, the implementation, advantages and limitations of this method will be investigated from both the perspective of a tool maker and an expert user.

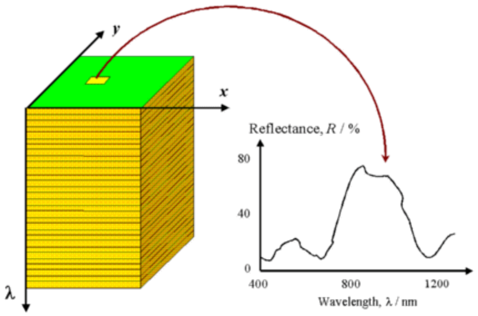


Figure 1: Point sample of a spectrum in a hyperspectral image

2 Aims

There are several goals of the proposed study including the development of the visualization method, application to remote sensing data, evaluation by expert users, integration into existing research environments, and broader distribution.

The proposed visualization method fills a niche in the array of visualization techniques by providing a spatial data reduction technique that is not available in the traditional remote sensing image analysis environment. Purely spatial data reduction techniques might be advantageous because they allow the user to understand specific characteristics of the spectra. One potential benefit for this is the ability to trace features in the image that are not linear, which is often the case in natural scenes. This non-linear section can be rendered in an image, where one dimension is length along the curve, another is wavelength and the intensity is data value of the image at that path length and band. Another possible rendering is as a 3D plot where the height is the data value at a certain path length and band. Part of the development stage will be to evaluate the curve representation, path parameterization and interpolation schemes. Additionally, it is not necessarily the case that the regions of interest are already quantified, and they may change with further visualization. Thus, interaction and real-time rendering are chosen to be a focus to the method.

In the initial stage, the graphical and algorithmic design of the tool will be developed, where the aim is to create a full featured tool that allows the user to access real-world image data, interact and render in real time, and save and load intermediate measurements for later analysis.

If the initial stage is successful, the strengths and limitations will be investigated. Real-world remote sensing images will be tested with the application to understand the performance with images of high spatial and spectral resolution. Then, a group of several expert geologists will evaluate the tool with respect to scientific problems that are part of their work. The aim is to compare similar parts of traditional image analysis workflows with the developed tool and gain a qualitative understanding of how they affect inferences.

Finally, with the success of all of these parts, the application of the tool to existing image analysis environment will be investigated. Several tools offer a framework for third-party tool integration, and the utility of such an integration will be evaluated.

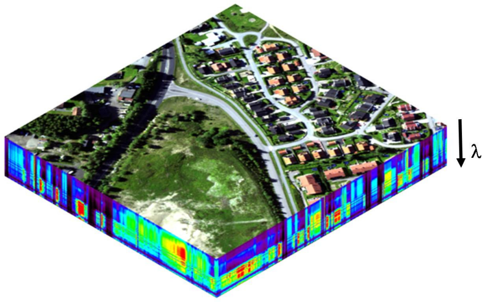


Figure 2: Image cube rendering of a hyperspectral image

3 Significance

This project has numerous applications in the scientific community including minerology, physics and agriculture. In particular, there are a large number of data sets whose value has yet to be exhausted. The missions collecting hyperspectral data include the terrestrial Airborne Visible/Infrared Imaging Spectrometer (AVIRIS), the Moon Minerology Mapper (M^3), the Lunar Observatoire pour la Minralogie, l'Eau, les Glaces, et l'Activit (OMEGA) and the Mars Thermal Emmission Spectrometer (TES). These projects focus on minerological and environmental analysis, which can potentially benefit from visualization methods that allow for better interactions with natural landmarks. In particular, the M^3 dataset will be used for testing and evaluation with our collaborators from the geological sciences.

Outside of remote sensing, this method can be applied to any data with a planar domain that maps to data with a dimension of prohibitive size. For example, spatial maps of consumer preferences, political trends or environmental factors can generate high dimensional data that can be explored through the proposed method.

4 Related Work

Existing visualization methods mostly revolve around data reduction in the spectral or spatial domain. In the spectral domain, there are a number of methods for reducing the dimension of the data to three or fewer, to enable a color rendering on a standard display. Methods for spectral reduction include priciple component analysis, independent component analysis, band ratios and support vector machines, among many others[5, 11]. Methods for spatial data reduction include point sampling, image cube rendering, planar slicing, and neighborhood statistics. Point sampling measures the spectrum at a single pixel, plotting the data in a typical graph, which is illustrated in Fig. 1. It is also common to compute statistics of the spectra in a region of interest in the image, such as a rectangle, ellipse or simple polygon[7]. Image cube rendering[10] is a type of planar slicing that samples the spectra along line segments that are parallel to the coordinate axes then renders those samples as the faces of a cube, which can be seen in Fig. 2. The proposed method can be thought of as a generalization of this type of slicing to an arbitrary curve in spatial coordinates. In addition to data dimension reduction, there have also been attempts to understand the variety of possible visualizations in review[3] and to create experimental environments[1, 12, 6].

These methods are implemented in a variety of tools, which are part of a larger environment that includes many processing steps to calibrate, register and organize the image data. Currently, these tools do not offer visualization tool similar to the proposed method. Some common packages include ENVI[7], ERDAS[2], Opticks[8] and SpecTIR[4]. The ENVI package includes a plugin framework, enabling third-party developers to integrate new tools into the workspace. This may offer a way to smoothly incorporate the propsed tool into the analysis chain.

5 Research Plan

The schedule of the proposed work is to take place over the course of six weeks, with the following landmarks:

Week 1: Meeting with collaborators to obtain M^3 data. Development tools and external tools chosen. Preliminary graphical user interface designed and implemented.

Week 2: Curve representation and interaction designed and programmed. Image interpolation scheme chosen and programmed.

Week 3: Image rendering and color mapping programmed. Loading and saving of curve and image data implemented.

Week 4: Components integrated into application. Tool tested with real data and need for optimization assessed.

Week 5: Meeting with collaborators to evaluate the tool through several case studies chosen to illustrate strengths and weaknesses. Integration with ENVI assessed.

Week 6: Tool and evaluation written up, presented, and disseminated.

References

[1] Shangshu Cai. *Hyperspectral image visualization using double and multiple layers*. PhD thesis, Mississippi State, MS, USA, 2008. Adviser-Moorhead, Robert J. and Adviser-Du, Qian.

[2] ERDAS Inc. Erdas, inc. – the earth to business company. `http://www.erdas.com`, September 2010.

[3] Gupta MR Jacobson, NP. Design goals and solutions for display of hyperspectral images. *Geoscience and Remote Sensing, IEEE Transactions on*, 43(11):2684–2692, 2005.

[4] SpecTIR LLC. Spectir: End to end hyperspectral solutions. `http://www.spectir.com`, September 2010.

[5] Brian S. Penn. Using self-organizing maps to visualize high-dimensional data. *Comput. Geosci.*, 31(5):531–544, 2005.

[6] Vito Roberto and Massimiliano Hofer. Theia: open environment for multispectral image analysis. In *AVI '08: Proceedings of the working conference on Advanced visual interfaces*, pages 462–465, New York, NY, USA, 2008. ACM.

[7] ITT Visual Information Solutions. Envi software - image process and analysis solutions, September 2010.

[8] Kip Streithorst. Opticks. `http://opticks.org/confluence/display/opticks`, September 2010.

[9] James M. Torson. Interactive image cube visualization and analysis. In *VVS '89: Proceedings of the 1989 Chapel Hill workshop on Volume visualization*, pages 33–38, New York, NY, USA, 1989. ACM.

[10] Fuan Tsai, Chun-Kai Chang, Jian-Yeo Rau, Tang-Huang Lin, and Gin-Ron Liu. 3d computation of gray level co-occurrence in hyperspectral image cubes. In *EMMCVPR'07: Proceedings of the 6th international conference on Energy minimization methods in computer vision and pattern recognition*, pages 429–440, Berlin, Heidelberg, 2007. Springer-Verlag.

[11] Thomas Villmann, Erzsébet Merényi, and Barbara Hammer. Neural maps in remote sensing image analysis. *Neural Netw.*, 16(3-4):389–403, 2003.

[12] Jianting Zhang, Le Gruenwald, and Michael Gertz. Vdm-rs: A visual data mining system for exploring and classifying remotely sensed images. *Comput. Geosci.*, 35(9):1827–1836, 2009.

Ryan Payne Cabeen

CONTACT

Email: cabeen@gmail.com

EDUCATION

Brown University, Providence, Rhode Island

Ph.D. Pre-candidate, Computer Science, 2010 - Current

California Institute of Technology, Pasadena, California

B.S., Engineering and Applied Science, 2001 - 2005

PROFESSIONAL EXPERIENCE

University of California, Los Angeles, Laboratory of Neuro Imaging

Programmer Analyst II **June, 2006 - June, 2010**

Developed libraries and applications for structural analysis of brain imaging data in a grid computing environment. Responsibilities included research, design, implementation, testing, documentation and support of algorithms and software

Service Machines Inc., Los Angeles, California

Software Engineer **October, 2005 - May, 2006**

Developed a real-time machine vision library and applications for industrial automation. Responsibilities included software design and implementation

Caltech Vision Laboratory, Pasadena, California

Research Assistant **October, 2004 - May, 2005**

Assisted with collection of behavioral fly data and development of supporting software

PUBLICATIONS

SH Joshi, RP Cabeen, AA Joshi, RP Woods; KL Narr, AW Toga. Diffeomorphic Sulcal Shape Analysis for Cortical Surface Registration. IEEE Conference on Computer Vision and Pattern Recongition (CVPR) 2010, 475-482

SH Joshi, RP Cabeen, B Sun, AA Joshi, BH Gutman, A Zamanyan, S Chakrapani, ID Dinov, RP Woods, AW Toga. Cortical Sulcal Atlas Construction Using a Diffeomorphic Mapping Approach. Medical Image Computing and Computer-Assisted Intervention (MICCAI) 2010. T. Jiang, N. Navab, J. Pluim and M. Viergever, Springer Berlin / Heidelberg. 6361: 357-366

OR Phillips, KH Nuechterlein, KA Clark, RF Asarnow, RP Cabeen, RP Woods, AW Toga, KL Narr. Mapping disturbances in cortico-cortico connectivity in schizophrenia patients and their biological relatives. 16th Annual Meeting of the Organization for Human Brain Mapping (OHBM) 2010, Barcelona, Spain

SKILLS

- Languages: Java, Python, C, C++, Bash
- Operating Systems: Linux and Unix variants, Mac OS X, Windows XP
- Software: vim, bash, svn, cvs, ant, Eclipse, $\LaTeX\,2_\varepsilon$, MATLAB, Sun Grid Engine, AIR, LONI Pipeline, FreeSurfer, MNI Brain Imaging Tools, BrainSuite, BrainVisa, ENVI

Andrew C. Loomis

23 Thomas Olney Cmn.
Providence, RI 02904
andy.loomis@gmail.com

Education

Brown University, Providence RI Class of 2009
Bachelor of Science – Applied Mathematics/Computer Science
Brown University, Providence RI Class of 2013
Master of Science – Computer Science

Computer Skills

Software: After Effects, CVS, Eclipse, Matlab, Maya, Microsoft Office, Photoshop
Programming: C, C++, Java

Experience

Brown University, Providence RI October 2009 - present
Graphics Systems Programmer
Center for Computation and Visualization
Work done in High Performance Computing and Visualization.
I'm currently developing software for the markerless tracking of bone motion from x-ray video sequences. This work is part of the XROMM project and is funded by the Keck Foundation.

Brown University, Providence RI June 2008 – present
Adviser Project
Development of a portable C++ library to efficiently display high resolution terrain and image data in a virtual reality environment. This project is funded by a geological research grant from NASA.

Visualizing Relative Gene Expression Between Many Populations

S. Birch, Tyler Parker

***Abstract*—A new approach for comparing the gene expression profiles of dozens of populations employing parallel coordinates is proposed. The objective in mind is twofold: one, that it aids in identifying anomalies in the data; two, that the visualization be suitable for publication and easy to interpret. These objectives are acheived through novel coordinate semantics and visual optimization techniques for clarity. The technique will be quantitatively evaluated by cross-validation with known results found from other techniques and qualitatively for ease of use and pattern-finding ability.**

I. BACKGROUND & SIGNIFICANCE

The space of a population's gene expression profiles (with n populations and m genes) can be seen as a set of m points in $\mathbb{R}^n$, where each point is positioned on each population axis at the expression rate of its corresponding gene (so as to effectively represent a feature vector of expressivity in the space), such as shown in Figure 2. To explore the relationships between different populations each pair of coordinates is examined for a total of $\binom{n}{2}$[1] comparisons. For the case of $n = 2$ these comparisons are trivially visualized on a scatterplot, as in Figure 1. These graphs are interpreted by looking at the distance of the points from $y = x$, indicating the degree that genes are expressed differently in the two populations (where a point perfectly on the line is expressed equally in both populations), and their absolute position on both axes, indicating the magnitude of expression. Further dimensions can be added by extending the plot to three dimensions or by encoding extra dimensions in color or size. For large numbers of populations, however, the problem becomes much more difficult to visualize as the pairwise comparisons scale $\mathcal{O}(n^2)$[2]. Nevertheless, these comparisons are critical to understanding how gene expression varies across condition and person.

Current approaches focus on either an analytic approach, such as clustering or by visualizing standard scatterplots after applying dimensionality reduction techniques to the data [1], [2], [3]. Popular techniques for dimensionality reduction include principal component analysis, multidimensional scaling and singular value decomposition [4], [1], [5]; the first is shown in Figure 3. A problem is that dimensional reduction functions by choosing data to throw away. Slonim notes: "recall that data-reduction and visualization tools are projecting many thousands of dimensions into two or three may prevent frustration if the reduced data fail to capture the expected aspects of a data set" [4]. Clustering suffers from the same problem, but in addition, by definition its goal is to find patterns in the data rather than anomalies.

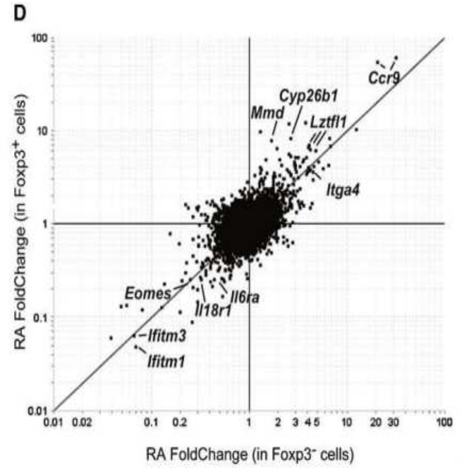


Figure 1. Gene expression in two populations ($Foxp^-$ versus $Foxp^+$) on a log-log scale. Genes on $y = x$ are expressed with the same magnitude. Figure 2d in [6].

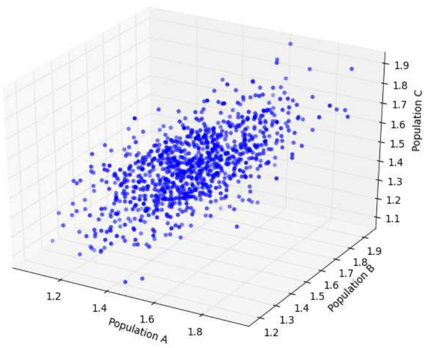


Figure 2. Plot of (random) genes in three populations' expression magnitude space. Note that the scale is arbitrary.

II. SPECIFIC AIMS

This proposal hypothesizes that visualizing the high-dimensional space with parallel coordinates will allow for effective analysis of larger numbers of populations. This approach will present all the data at once, eliminating the choice of data to omit and the potential dangers associated with that choice. The primary goal is therefore clarity and

---

sbirch@cs.brown.edu
Bryan_Parker@brown.edu

[1] i.e. n choose 2, the number of unique pairs selectable from n axes. Given by $\frac{n!}{2!(n-2)!}$.

[2] $\binom{n}{2} = \frac{n!}{2!(n-2)!} = \frac{1}{2}(n-1)(n-2) = \frac{1}{2}n^2 - \frac{3}{2}n + 1 = \mathcal{O}(n^2)$

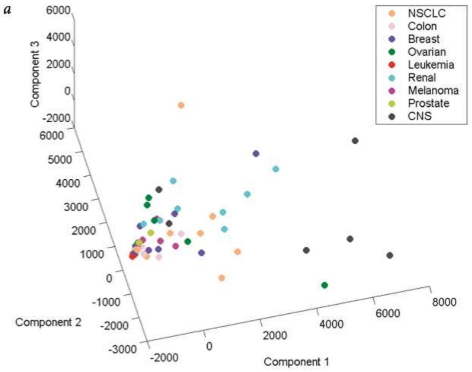


Figure 3. Three dimensional PCA plot of the gene expression profiles of various cancer types. Figure 2a in [4].

organization of the massive amount of data to be represented. This appears to be unprecedented in the literature. The proposed visualization contructs one axis for each pair of populations and the distance metric is plotted for each gene. The distance metric encodes how far the gene is from being equally expressed in both populations. Given M_A and M_B, magnitudes of expression in populations A and B respectively, it is given by:

$$\delta(M_A, M_B) = \left\| proj_E \begin{pmatrix} M_A \\ M_B \end{pmatrix} - \begin{pmatrix} M_A \\ M_B \end{pmatrix} \right\|_2 \qquad (1)$$

Where E is the line $A = B$. A geometric interpretation on the $A - B$ plane is given in Figure 4.

These axes are arranged in parallel and ordered to maximize the clarity of the resulting graph. Dimension reordering has been studied in the context of reducing clutter in [7]. Whether the order is more important to preserve the locality of populations (in order to make population-wide trends apparent), interpretability (e.g. to order the axes from most to least regular) or to minimize clutter is a novel question we hope to address. Finally, additional clarity may be lent by "bundling" genes together to reduce the space used by similar genes. [8] has implemented "visual clustering" using bundling techniques by curving the lines between axes (see an example in Figure 5). This serves to make anomalies more apparent, but also to show natural patterns in the data.

Should time permit, interactivity will be explored as an aid to finding anomalies. These have been explored in the context of general parallel coordinate plots in [9], [10].

A. Benefits

The most significant benefit of parallel coordinates is that it scales to an many of dimensions while still being interpretable in two dimensions (which also allows for publication). It's unclear how many dimensions will be practical; certainly more than current techniques allow (while showing all the data, $3-5$), and theoretically as many as needed, though limited by the interpretability of the result. $15-20$ is a likely maximum range (resulting in $105-190$ axes). The cost of the ability to plot highly dimensional data is that interpretation is often more difficult as direct comparison is only explicitly shown between

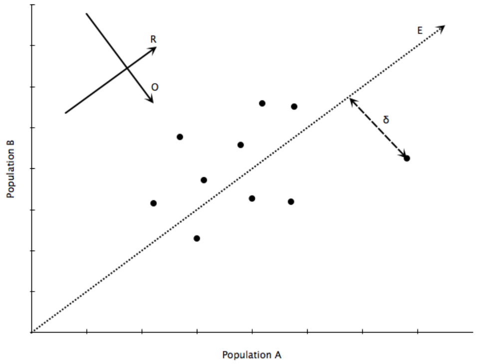


Figure 4. Geometric interpretation of the distance metric on the projected plane. Note the basis formed by R and O.

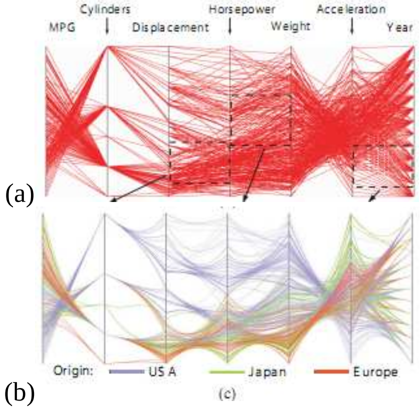


Figure 5. Before (a) and after (b) "visual clustering," as presented in [8].

adjacent axes. This problem is resolved here by using $\binom{n}{2}$ axes, allowing for the direct comparisons to be shown on the axis itself. The cost of this is that all the magnitude information in the R coordinate is lost. Because the goal is to look at relative expression however, the absolute magnitude isn't relevant (it is also possible to encode it in another dimension, such as color)[3].

This scheme in fact is generalizable to comparing any number of populations on a single axis, but the number of axes scales $\binom{n}{k}$, where k is the number of populations to compare on each axis. Comparisons between 3 or 4 populations per axis will be experimented with in week 2, but their ultimate value is limited by the $\mathcal{O}(n^k)$ growth. The extension is simply to project onto the $e_0 = e_1 ... = e_d$ line (where e_d is the basis vector for dimension d) and likewise extend the population magnitude vector in equation 1. Note that for the case of $d = 0$ (adjusting the second instance of the magnitude vector $\begin{pmatrix} M_A \\ M_B \end{pmatrix}$ to some constant baseline) this results in a parallel coordinates plot of the absolute magnitudes of gene expression for each population as has been explored in the literature [11]. This work can be seen as a mathematical generalization of the absolute plot.

---

[3] Note how this differs from the data omitted in clustering or dimensionality reduction, however: this is an a priori choice about the meaning of the visualization rather than an a posteriori selection of data to represent.

B. Evaluation

The result of the proposal will be evaluated quantitatively and qualitatively at the completion of the timespan. Experts in bioinformatics will qualitatively asses the software for ease of use with regard to finding anomalies in the data. Quantitatively, the method will be cross-validated using known anomalies froma combination of other techniques.

III. FACILITIES

Currently availible hardware (personal laptops, Brown Computer Science department Linux machines) should be suffecient for the prosposed work.

IV. TIMELINE & METHODS

Week 1

Acquire data. Set up environment, choose technology platform.

Week 2:

Initial visualization prototypes: parallel coordinates alone and with relative axes (without optimizations). Evaluate feasibility and clarity of graphs.

Week 3:

Optimize visualization with regard to dimension reordering. Find a balance between visual clutter, locality of populations, and interpretability.

Week 4:

Optimize visualization with regard to bundling and clustering.

Week 5:

Interactivity, user tests, evaluation.

Week 6

Write up and disseminate results.

REFERENCES

[1] G. Sherlock, "Analysis of large-scale gene expression data," *Current Opinion in Immunology*, vol. 12, no. 2, pp. 201–205, 2000.

[2] D. Jiang, C. Tang, and A. Zhang, "Cluster analysis for gene expression data: A survey," *Knowledge and Data Engineering, IEEE Transactions on*, vol. 16, no. 11, pp. 1370–1386, 2004.

[3] R. Sharan, A. Maron-Katz, and R. Shamir, "CLICK and EXPANDER: a system for clustering and visualizing gene expression data," *Bioinformatics*, vol. 19, no. 14, p. 1787, 2003.

[4] D. Slonim, "From patterns to pathways: gene expression data analysis comes of age," *Nature Genetics*, vol. 32, pp. 502–508, 2002.

[5] L. Wouters, H. Gohlmann, L. Bijnens, S. Kass, G. Molenberghs, and P. Lewi, "Graphical exploration of gene expression data: a comparative study of three multivariate methods," *Biometrics*, vol. 59, no. 4, pp. 1131–1139, 2003.

[6] J. Hill, J. Hall, C. Sun, Q. Cai, N. Ghyselinck, P. Chambon, Y. Belkaid, D. Mathis, and C. Benoist, "Retinoic acid enhances Foxp3 induction indirectly by relieving inhibition from CD4+ CD44hi Cells," *Immunity*, vol. 29, no. 5, pp. 758–770, 2008.

[7] W. Peng, M. Ward, and E. Rundensteiner, "Clutter reduction in multidimensional data visualization using dimension reordering," in *Information Visualization, 2004. INFOVIS 2004. IEEE Symposium on*. IEEE, 2005, pp. 89–96.

[8] H. Zhou, X. Yuan, H. Qu, W. Cui, and B. Chen, "Visual clustering in parallel coordinates," in *Computer Graphics Forum*, vol. 27, no. 3. John Wiley & Sons, 2008, pp. 1047–1054.

[9] H. Siirtola and K. Raiha, "Interacting with parallel coordinates," *Interacting with Computers*, vol. 18, no. 6, pp. 1278–1309, 2006.

[10] J. Johansson, P. Ljung, M. Jern, and M. Cooper, "Revealing structure within clustered parallel coordinates displays," 2005.

[11] O. Rubel, G. Weber, S. Keranen, C. Fowlkes, C. Hendriks, L. Simirenko, N. Shah, M. Eisen, M. Biggin, H. Hagen *et al.*, "PointCloudXplore: Visual analysis of 3D gene expression data using physical views and parallel coordinates," in *Data Visualization*. Citeseer, 2006, pp. 203–210.

Samuel M. Birch

sbirch@cs.brown.edu
312-772-4724

Education

Brown University, Providence, Rhode Island
B.Sc. in Computer Science, expected May 2014.
M.S. in Computer Science, expected May 2014.
Boston University, Boston, Massachusetts
No degree (completed as part of high-school coursework), 2008-2010.
Boston University Academy, Boston, Massachusetts
Summa Cum Laude, and with Highest Honors on Senior's thesis, 2010.

Research Experience

Boston University, Boston, Massachusetts
1/09-5/10
Member of the HyNeSs Laboratory

Employment

The MITRE Corporation 5/2010-8/2010

Publications

M. Kloetzer, S. Itani, S. Birch, C. Belta. "On the Need for Communication in Distributed Implementations of LTL Motion Specifications," ICRA 2010.

C. Belta, Y. Chen, A. Stefanescu, S. Birch. "A Hierarchical Approach to Automatic Deployment of Robotic Teams with Communication Constraints," IROS 2010.

S. Birch. "Two Novel Methods for Precise Image Thresholding" (Senior Thesis). 2nd Place, Southern New England Regionals, Junior Sciences and Humanities Symposium (JSHS). Presented at the National JSHS.

Awards

AFCEA Fellowship, 2010.
AFCEA Barrett Award, 2010.
Xerox Award for Technology, 2009.

TYLER PARKER

bryan_parker@brown.edu | Brown University, 69 Brown Street, Box 4704, Providence, RI 02912 | (845) 901-1051

objective

Brown University Senior going into Masters Program **seeking internship** that will put to challenging use my skills, work experience and education in Computer Science thus far.

experience

HBO 6/2010 - 8/2010

Web Technologies Intern

Led an intern team for designing iPad app concepts, developed workflow templates and networking tools, researched and developed internal Wiki upgrade

Evolving Media Network 6/2009 - 8/2009

Web Development Intern

Created and updated Ruby on Rails and WordPress sites for clients, server setup and maintenance.

Nokia 6/2008 - 8/2008

Web Analytics and Programming Intern

Using Java and PHP, created software solutions for the Digital Marketing Team, analyzing user data for the launch of Ovi. Compiled and updated the weekly Digital Marketing Key Performance Indicator report.

education

Brown University 9/2007 - Present

Class of 2011, Bachelor of Science in Computer Science

Relevant Coursework

Interdisciplinary Scientific Visualization, Interactive Computer Graphics, Software Dev.

research

HCI and Graphics (Ongoing)

Advisor: Andy van Dam, Brown University.

Developing and rapid prototyping innovative tools and interfaces for large multi-touch surfaces, primarily Microsoft Surface

Scientific Visualization of Human Task Reaching (Ongoing)

Advisors: David Laidlaw and Joo-Hyun Song, Brown University.

Developing novel visualization tools for a Cognitive Science research project that aims to create a model for Human Task Reaching.

projects

Prospect and Meeting site (independent group project).

Web designer and coder for a popular Brown University dating site titled ‘Prospect and Meeting’, implemented in Ruby on Rails.

Event Management Software (group project).

Software Engineering, Brown University.

Designed and coded the front end client for a web Application that allows students to filter events, save them, and display them on a map.

Comedy-Thriller Movie Script

Currently being represented by Mike Esola, William Morris Agency.

skills

Programming Languages: C/C++, Java, Python, Matlab
Web Languages: Ruby on Rails, PHP, HTML, AJAX, CSS, MYSQL
Graphics Applications: Maya, Blender, Flash, Photoshop, After Effects, Premiere Pro
Operating Systems: Linux, Windows, some OSX

interests

Acting and singing in musical theatre, 3d Animation, listening to remixes and mashups

Interactive Maps for Functional Brain Connectivity Queries

PI: Steven R. Gomez* Co-PI: Ryan Cabeen† Collaborator: Jeff (Chi-Tat) Law‡

October 12, 2010

Abstract

We propose to build an exploratory map environment that visualizes neural connectivity queries in the human brain and integrates these queries with analytics tools that track user hypotheses and evidence regarding functional connections. This work will help brain researchers more effectively target neuronal relationships for further connectivity experimentation. We will conduct a preliminary evaluation of our proposed tool with neuroscientists studying brain connectivity, and analyze design choices for dense circuit visualizations in this domain.

---

*Department of Computer Science, Brown University, `steveg@cs.brown.edu`

†Department of Computer Science, Brown University, `rpc@cs.brown.edu`

‡Schnitzer Lab (Depts. of Biology and Applied Physics), Stanford University, `lawjeffw@gmail.com`

1 Research Aims

The goal of this research is the development and evaluation of a visualization method for combining structural neural connectivity maps – given by tractography or other imaging – and functional connectivity networks (i.e. measured signal projections between cells) into a single visual representation. Our method is valuable because displaying a structural map provides an anatomical landmark or coordinate system for understanding functional connectivity. This may be critical in forming hypotheses about spatial/structural relationships in functional connectivity. For instance, a user could quickly identify parts of the brain that operate in isolation with few projections in and out of these regions – a finding that may be important in neurobiological, cognitive, and medical research communities. We hypothesize that our combined approach will enable expert users to generate more total and significant insights about the brain circuit than when using current tools.

2 Background and Significance

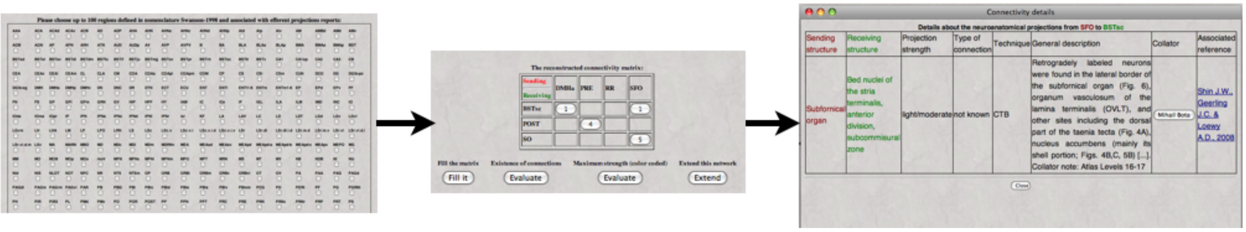
Researchers in neural circuitry are concerned with understanding connections between spatially distributed and functionally differentiated parts of the brain. Insight from these connections may give way to new medical treatments and diagnostic techniques for neurological disorders. While scientists have access to a growing collection of experimental connectivity data collated and disseminated on the web, the scale and complexity of these data make it difficult to gain insight from individual, textual queries – the standard interface to database access in current tools [4, 5] like the Brain Architecture Management System (BAMS) shown in Figure 1. Our work proposes a visualization tool for neural connections that communicates many connections as a 2D map with anatomical landmarks, allowing the user to filter connections of interest and quickly retrieve details about these connections.

Circuit Analysis Recent work in neural circuit analysis has called for improved representations of these networks and their integration into analytics tools for brain scientists. Bullmore and Sporns [6] give a broad overview of graph theory relevant to brain circuit analysis that provides a computational formulation for studying experimental connectivity data. The motivation for analyses like this is described in the survey by Bohland et al. [3], which outlines a research agenda for studying brain connectivity and the tool-building to facilitate that research. An application of such tools for the neural network of *C. elegans* is demonstrated at Wormweb.org [2], which shows a lightweight graph visualization of cell connections and allows the user to walk through this graph interactively. The motivation and data for this work comes from a study [7] investigating a hypothesis about evolution toward "wiring optimization" in the neuron circuit. For our purposes, this work demonstrates the kind of *hypothesis-exploration-validation* environment we want to support for domain scientists studying human brain circuitry.

There are many visualization tools that try to expose structure in biological systems for analysis by domain scientists. For instance, Jianu et al. presented proteomic data and interaction networks in an interactive graph framework [10]. Tools for interacting with brain data – the domain of the proposed project – have used multiple linked views of DTI models, spanning more concrete/anatomical representations (e.g. streamtubes) and abstract ones (e.g. dendrograms) [8].

Information Visualization The project will consider current methods in information visualization, including embeddings of higher dimensional data into map representations, graph drawing techniques and interaction. Jianu et al. have created 2D visualizations of structural brain connectivity (DTI streamtubes) and disseminated them using the familiar interface of the Google Maps API [9]. We will explore embedding functional connectivity (i.e. projections) into maps like these in creating a tool for 'full network' connectivity, as described by Bullmore and Sporns [6], for brain researchers.

We also must take care in building interaction methods on network abstractions. With graphs at the scale of the human brain, representing individual axons will be a "data deluge" and may hide interesting or insightful patterns in the connection data. Ham and Perer [15] examine filtering methods for user navigation of details in dense graphs that may be useful in our tool. Users should also be able to interact with and



The reconstructed connectivity matrix:

Sending / Receiving	DMBa	PRE	RR	SFO
BSTsc	1			1
POST		4		
SO				5

Details about the neuroanatomical projections from SFO to BSTsc

Sending structure	Receiving structure	Projection strength	Type of connection	Technique	General description	Collator	Associated reference
Subfornical organ	Bed nuclei of the stria terminalis, anterior division, subcommisural zone	light/moderate	not known	CTB	Retrogradely labeled neurons were found in the lateral border of the subfornical organ (Fig. 6), organum vasculosum of the lamina terminalis (OVLT), and other sites including the dorsal part of the taenia tecta (Fig. 4A), nucleus accumbens (mainly its shell portion; Figs. 4B,C, 5B) [...]. Collator note: Atlas Levels 16-17	Mihail Bota	Shin J.W., Geerling J.C. & Loewy A.D., 2008

Figure 1: Querying neural projections in BAMS [4] requires the user to select in/out cell types from an incidence matrix of checkboxes, returning existing database entries in an HTML table. Selecting individual results from this table loads another webpage with more details about the connection. This workflow, which we hope to simplify with a visual map tool, is illustrated above.

rearrange graph layouts to investigate topological hypotheses; recent work in this kind of subgraph interaction and manipulation is explored by McGuffin and Jurisica [11].

3 Contributions

We propose a map-style environment that allows the user to explore, and filter/query (by selecting cell types with standard UI tools, like a pull-down menu) neural connections by anatomical coordinates and function. Our contributions are as follows:

1. A novel visualization tool for multiple neural connection display over a 2D anatomical map. A module for tracking hypotheses and evidence from queries will be integrated in the environment to facilitate scientific workflow using the tool.
2. A preliminary evaluation using a "think aloud" protocol with neuroscientists at Stanford (over Skype or with a screencast tool) to assess the effectiveness of our tool. We will develop a rubric for an insight-based methodology [13, 12, 14] to quantify user performance during a session with our tool.

The proposed project is *significant* because it will release a major bottleneck in access to collated brain circuit data by allowing visual, multi-connection analysis supported by sense-making analytics features. The *impact* of this work is high because our tool will be evaluated and integrated by the research team of Drs. Jeff Law and Mark Schnitzer at Stanford University. We will extend this evaluation to brain researchers at Brown if time permits. Furthermore, the proposal establishes an interdisciplinary collaboration between computer science and biology labs at these institutions, and may lead to further deployment of computational tools to scientific domains, which is healthy for each discipline.

4 Plan

4.1 Milestones

We will deliver the following:

- **Week 1:** BAMS circuit data (rat) cleaned and written into easily accessible format. Platform for map drawing (see Available Tools below) explored and decided upon.
- **Weeks 2–4:** Graph drawing for connections over map with anatomical landmarks. Filtering and interaction in the graph tool. Hypotheses-tracking and query storage (Week 4).
- **Week 5:** User evaluation (our tool and BAMS) using screencast or Skype with the Stanford lab. Analysis of findings and plan for iterative improvements for the tool/extensions for the research.

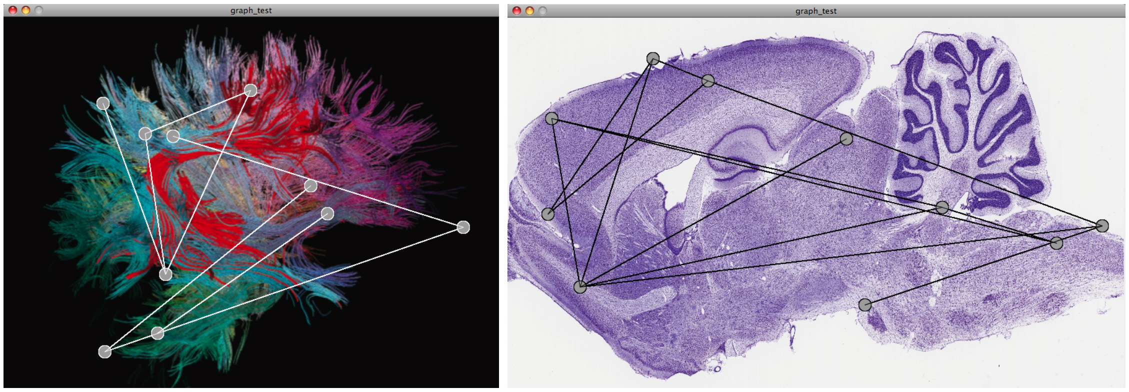


Figure 2: Examples compositing a connectivity graph over anatomical brain maps (left–human tractography map; right–rat histology map.) Query and analysis modules are not sketched here, but will be included in a panel to the left of the main image window, with widgets for text input and list selection.

- **Week 6:** Final report and tool dissemination.

Our aim is to continue after the semester with a quantitative evaluation that demonstrates the usefulness of our tools, and prepare a submission for IEEE InfoVis 2011 (deadline: late March) describing our results.

4.2 Available Tools

Several environments are available for prototyping graph visualizations, including Processing (see the example applets we made with Processing in Figure 2), Prefuse, and Protovis – all of which can be integrated with non-toolkit code (Java or Javascript). Jianu's visualization framework [10] has been used to render both graph visualizations (proteomics data) and 3D tractography models. Some initial brain atlas data is available at BrainMaps.org [1], which also provides a Javascript API for building visualizations from their images of model organism histology. Finally, the Google Maps API is available as a general tool to create and distribute 2D map visualizations with basic interactions.

4.3 Contingency Plan

Atlas integration A large challenge in this work is retrieving and integrating brain atlas data (from BrainMaps.org and other sources) that allows us to draw the functional connectivity network with appropriate anatomical coordinates. If this becomes too difficult to complete in our timeframe, we will either 1) manually position a subset of the brain connections into the correct coordinates, or 2) generate random locations for all data (that illustrates how the tool will work at scale, even if biologically inaccurate for the prototype), or 3) both.

Analysis support The analysis support module we propose will be an interface for noting hypotheses and aggregating queries as evidence that supports or disconfirms them. We see this as a feature that could become complex and rich (e.g. being able to lasso groups of nodes, or sketch notes in the image pane) or minimal (e.g. saving queries/screenshots to a directory). This flexibility will allow us to trim or upscale our work on this feature based on the available time. Since we focus on this in Week 4, we will have encountered the most challenging parts of this project already and can make that contingency assessment with confidence.

4.4 Facilities and Resources

The Linux workstations provided by the Computer Science Department at Brown will be used to develop and deploy our software; workstations in the Schnitzer Lab will be sufficient for evaluating our tool.

References

[1] Brainmaps.org. http://brainmaps.org/index.php.

[2] Wormweb. http://wormweb.org/.

[3] Jason W. Bohland, Caizhi Wu, et al. A proposal for a coordinated effort for the determination of brainwide neuroanatomical connectivity in model organisms at a mesoscopic scale. *PLoS Comput Biol*, 5(3):e1000334, 03 2009.

[4] M. Bota, H.-W Dong, and L.W. Swanson. Brain Architecture Management System. *Neuroinformatics*, 3(1):15–48, 2005.

[5] M. Bota and L.W. Swanson. Online workbenches for neural network connections. *Journal of Comparative Neurology*, 500(5):807–814, 2007.

[6] Ed Bullmore and Olaf Sporns. Complex brain networks: graph theoretical analysis of structural and functional systems. *Nature Reviews Neuroscience*, 10(3):186–198, 2009.

[7] Beth L. Chen, David H. Hall, and Dmitri B. Chklovskii. Wiring optimization can relate neuronal structure and function. *Proceedings of the National Academy of Sciences*, 103(12):4723–4728, March 2006.

[8] R. Jianu, C. Demiralp, and D.H. Laidlaw. Exploring 3D DTI Fiber Tracts with Linked 2D Representations. *IEEE Transactions on Visualization and Computer Graphics*, 15(6), 2009.

[9] Radu Jianu, Cagatay Demiralp, and David H. Laidlaw. Exploring brain connectivity with two-dimensional neural maps. *IEEE TVCG*, 2010. In Review.

[10] Radu Jianu, Kebing Yu, Vinh Nguyen, Lulu Cao, Arthur Salomon, and David H. Laidlaw. Visual integration of quantitative proteomic data, pathways and protein interactions. *IEEE Trans. on Visualization and Computer Graphics*, September 2009.

[11] Michael J. McGuffin and Igor Jurisica. Interaction techniques for selecting and manipulating subgraphs in network visualizations. *IEEE Transactions on Visualization and Computer Graphics*, 15:937–944, 2009.

[12] Chris North. Toward measuring visualization insight. *IEEE Comput. Graph. Appl.*, 26(3):6–9, 2006.

[13] Trevor M. O'Brien, Anna M. Ritz, Benjamin J. Raphael, and David H. Laidlaw. Gremlin: An interactive visualization model for analyzing genomic rearrangements. In *Proceedings of IEEE InfoVis'10*, Salt Lake City, UT, USA, 2010.

[14] Purvi Saraiya, Chris North, and Karen Duca. An insight-based methodology for evaluating bioinformatics visualizations. *IEEE Transactions on Visualization and Computer Graphics*, 11(4):443–456, 2005.

[15] Frank van Ham and Adam Perer. Search, Show Context, Expand on Demand: Supporting Large Graph Exploration with Degree-of-Interest. *IEEE Transactions on Visualization and Computer Graphics*, 15:953–960, 2009.

Steven Gomez <steveg.07@gmail.com>

brain circuit database visualization

Chi-Tat (Jeff) Law <lawjeffw@gmail.com> **Mon, Oct 11, 2010 at 1:12 PM**
To: Steven Gomez <steveg@cs.brown.edu>

Yes. I'm very interested in your project. I've been really busy these 2 weeks but please keep me update, and please shoot me emails when you've questions. I'll be responding faster than I did before from now on (things has been a bit crazy in the past few weeks.

Below is my email of support, would it help?

To whom it may concern,

I would like to express my support for Steven Gomez's proposed work on brain circuit visualization. This tool will allow us to view projections between cell types visually, and if successful, will allow us to query available circuit data more easily than using current web-based tools.

Sincerely,

Chi-Tat (Jeff) Law
Oct 11, 2010

[Quoted text hidden]

Steven R. Gomez

Contact Information

Department of Computer Science
Brown University
Box 1910
Providence, RI 02912 USA

office: CIT 423
cell: (802) 272-4941
e-mail: steveg@cs.brown.edu
www.cs.brown.edu/~steveg

Research Interests

Scientific visualization, visual computing and analytics, human-computer interaction, computer graphics, vision

Education

Brown University, Providence, Rhode Island USA

Second-year graduate student in doctoral program in Computer Science

- Courses completed: Computer Graphics, Computer Vision, Computational Photography, Distributed and Parallel Computing, Networking and Distributed Systems

Dartmouth College, Hanover, New Hampshire USA

B.A. *magna cum laude*, Computer Science, June 2007

Industry

M2S, Inc., Lebanon, NH – *Software Engineer* – 2008–09
Development for several tools, including virtual stent grafts for Preview aortic aneurysm visualization software.

Awards

Brown University Graduate Fellowship – 2009–10
Rufus Choate Scholar (top 5% of class) – 2006–07
John G. Kemeny Undergraduate Computing Prize – First Place, 2006, for *BlitzChat*
Dartmouth Presidential Research Scholar – 2005–06
Class of 1928 Endowed Scholarship – 2003–07

Publications

Steven R. Gomez, Radu Jianu, and David H. Laidlaw. A Fiducial-Based Tangible User Interface for White Matter Tractography. In Proceedings of *ISVC*, 2010.

Steven R. Gomez. Interacting with Live Preview Frames: In-Picture Cues for a Digital Camera Interface. In Proceedings of *ACM UIST* (Poster), 2010.

Keller, R., Hunt, M., Jones, S., Morrison, D., Wolin, A., and Gomez, S. 2007. Blues for Gary: Design Abstractions for a Jazz Improvisation Assistant. *Electron. Notes Theor. Comput. Sci.* 193 (Nov. 2007), 47-60.

Technical Skills

Languages: Java, MATLAB, C, C++, Scheme, Perl, Tcl/tk, PHP, SQL, X/HTML, LaTeX
Applications: Eclipse, Netbeans, Xcode, Apache, CVS, Subversion, MS Office, Adobe CS
Operating Systems: Mac OS X, Linux, Windows 98/2000/XP

Ryan Payne Cabeen

Contact

Email: cabeen@gmail.com

Education

Brown University, Providence, Rhode Island

Ph.D. Pre-candidate, Computer Science, 2010 - Current

California Institute of Technology, Pasadena, California

B.S., Engineering and Applied Science, 2001 - 2005

Professional Experience

University of California, Los Angeles, Laboratory of Neuro Imaging
Programmer Analyst II **June, 2006 - June, 2010**
Developed libraries and applications for structural analysis of brain imaging data in a grid computing environment. Responsibilities included research, design, implementation, testing, documentation and support of algorithms and software

Service Machines Inc., Los Angeles, California
Software Engineer **October, 2005 - May, 2006**
Developed a real-time machine vision library and applications for industrial automation. Responsibilities included software design and implementation

Caltech Vision Laboratory, Pasadena, California
Research Assistant **October, 2004 - May, 2005**
Assisted with collection of behavioral fly data and development of supporting software

Publications

SH Joshi, RP Cabeen, AA Joshi, RP Woods; KL Narr, AW Toga. Diffeomorphic Sulcal Shape Analysis for Cortical Surface Registration. IEEE Conference on Computer Vision and Pattern Recongition (CVPR) 2010, 475-482

SH Joshi, RP Cabeen, B Sun, AA Joshi, BH Gutman, A Zamanyan, S Chakrapani, ID Dinov, RP Woods, AW Toga. Cortical Sulcal Atlas Construction Using a Diffeomorphic Mapping Approach. Medical Image Computing and Computer-Assisted Intervention (MICCAI) 2010. T. Jiang, N. Navab, J. Pluim and M. Viergever, Springer Berlin / Heidelberg. 6361: 357-366

OR Phillips, KH Nuechterlein, KA Clark, RF Asarnow, RP Cabeen, RP Woods, AW Toga, KL Narr. Mapping disturbances in cortico-cortico connectivity in schizophrenia patients and their biological relatives. 16th Annual Meeting of the Organization for Human Brain Mapping (OHBM) 2010, Barcelona, Spain

Skills

- Languages: Java, Python, C, C++, Bash
- Operating Systems: Linux and Unix variants, Mac OS X, Windows XP
- Software: vim, bash, svn, cvs, ant, Eclipse, LaTeX 2$_{\varepsilon}$, MATLAB, Sun Grid Engine, AIR, LONI Pipeline, FreeSurfer, MNI Brain Imaging Tools, BrainSuite, BrainVisa, ENVI

Curriculum Vitae: Chi-Tat (Jeff) Law

Department of Biological Sciences, Stanford University
Rm W080 Clark Center, 318 Campus Dr W, Stanford, CA 94305
Office Phone: (650) 725-4097
Email: lawj@stanford.edu

PROFESSIONAL PREPARATION:

B.Eng. 2003	Department of Electrical Engineering, Hong Kong University of Science and Technology, Hong Kong, China
2008	Computational Neuroscience: Vision Course, Cold Spring Harbor Laboratory, New York, USA
Ph.D. 2009	Department of Neuroscience, University of Pennsylvania, Pennsylvania, USA

APPOINTMENTS:

2010-	Postdoctoral researcher, Department of Biological Sciences, Stanford University, California, USA

TEACHING EXPERIENCE:

2006	Teaching Assistant - Cellular Neurobiology, University of Pennsylvania

AWARDS AND FELLOWSHIPS:

2000-2003	Dean's List
2000-2001	Chiap Hua Cheng's Foundation Scholarship
2000-2001	Hong Kong & Kowloon Electrical Appliances Merchants Association Scholarship
2000-2001, 2001-2002	MTR Tertiary Scholarship
2002-2003	HKTIIT Scholarship
2010	Saul Winegrad Award for Outstanding Dissertation

INVITED PRESENTATIONS:

2008	The Swartz Initiative in Theoretical Neuroscience at Yale Seminar Series: *Mechanisms of learning a visual discrimination task.*

PROFESSIONAL MEMBERSHIPS:

2000-2003	Institute of Electrical and Electronics Engineers
2003-now	Society for Neuroscience

PUBLICATIONS

Jha SK, Jones BE, Coleman T, Steinmetz N, Law CT, Griffin G, Hawk J, Dabbish N, Kalatsky VA, Frank MG. Sleep-dependent plasticity requires cortical activity. J Neurosci. 2005 Oct 5;25(40):9266-74.

Eckhoff, P., Holmes, P., Law, C., Connolly, P.M. & Gold, J.I. On diffusion processes with variable drift rates as models for decision making during learning. *New Journal of Physics* **10** (2008).

Law, C.T. & Gold, J.I. Neural correlates of perceptual learning in a sensory-motor, but not a sensory, cortical area. *Nat Neurosci* **11**, 505-513 (2008).

Gold, J.I., Law, C.T., Connolly, P., & Bennur, S. The relative influences of priors and sensory evidence on an oculomotor decision variable during perceptual learning. *J Neurophysiol **100**, 2653-2668 (2008).*

Law, C.T., & Gold J.I. A reinforcement learning rule can account for both the associative and perceptual learning on a visual discrimination task. *Nat Neurosci* 12(5), 655-63 (2009).

Law, C.T., & Gold J.I. Shared mechanisms of perceptual learning and decision making. Topics in Cognitive Science 2009 Aug 10 [Epub ahead of print]

Gold JI, Law CT, Connolly P, Bennur S. Relationships between the threshold and slope of psychometric and neurometric functions during perceptual learning: implications for neuronal pooling. *J Neurophysiol*. 2010 Jan; **103**(1):140-54

CONFERENCE ABSTRACTS

B.E. Jones, J. Law, G. Griffin, T. Coleman, S. Jha, M.G. Frank. Sleep dependent plasticity requires cortical activity. Program No. 77.3. San Diego, CA: Society for Neuroscience, 2004.

C. Law, J.I. Gold. Physiological correlates of perceptual learning in monkeys areas MT and LIP. Program No. 621.15. Washington, DC: Society for Neuroscience, 2005.

P. M. Connolly, C. Law, J. Gold. Behavioral and neural correlates of response bias on multiple timescales in monkeys learning a visual discrimination task. Program No. 161.1. Atlanta, GA: Society for Neuroscience, 2006.

C. Law, J. I. Gold. Effects of stimulus specificity on behavior and neural activity in areas MT and LIP of monkeys learning a visual discrimination task. Program No. 161.2. Atlanta, GA: Society for Neuroscience, 2006.

P. Eckhoff, P. Connolly, C. Law, J. I. Gold, P. Holmes. Variable drift rate models for monkeys learning a perceptual decision. Program No. 161.3. Atlanta, GA: Society for Neuroscience, 2006.

C. Law, P., Eckhoff, P. Holmes, J.I. Gold. A variable drift rate model of decision making fit to behavior and neural activity during learning. *Society for Neuroscience Conference, Program No. 636.8*. San Diego, CA: Society for Neuroscience, 2007.

C. Law, P., J.I. Gold. A simple reinforcement learning rule can account for improvements in sensory readout with perceptual learning. *Society for Neuroscience Conference, Program No. 812.7*. Washington, DC: Society for Neuroscience, 2008.

C. Law, P., J.I. Gold. Changes in the temporal dynamics of evidence accumulation during learning on a visual motion discrimination task. *Society for Neuroscience Conference,* *Program No. 263.18*. Chicago, DC: Society for Neuroscience, 2009.

GRADUATE ADVISOR:

Prof. Joshua Gold, Department of Neuroscience, University of Pennsylvania,
Philadelphia, PA 19104
Phone: (215) 746-0028
Email: jigold@mail.med.upenn.edu

POSTDOCTORAL ADVISOR:

Prof. Mark Schnitzer, Department of Biological Sciences and Applied Physics, Stanford
University, CA 94305
Phone: (650) 704-6209
Email: mschnitz@stanford.edu