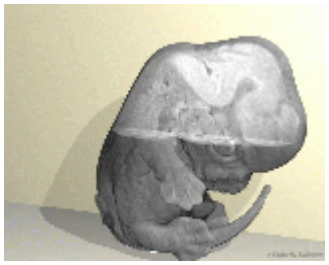

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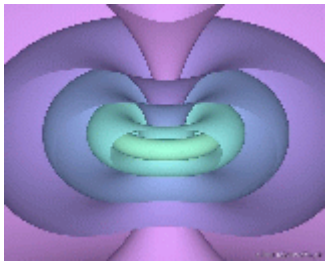
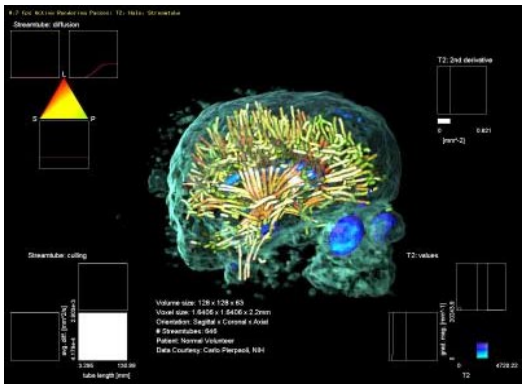
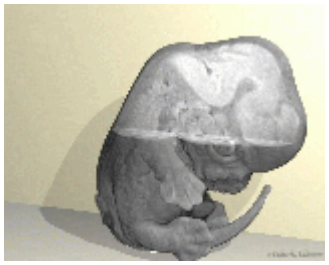




Final Projects

Fall 2003



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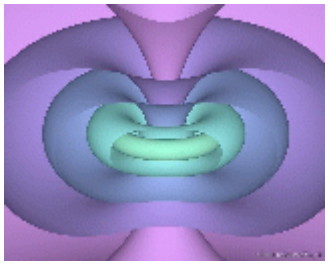

Abstracts

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NOTE: Each project has two abstracts, one per author.

Visualization of Platelets in Small Blood Vessels in a Virtual Environment

Nicholas Yang, Igor Pivkin, Peter Richardson, and David Laidlaw
Brown University, Providence RI

I. Introduction

Using the Force Coupling Method [2] to model platelets as spherical force envelopes, we visualized platelets in an interactive immersive virtual environment. Simulation of various forces were required to keep the cells within vessel boundaries and to take into account the adhesion of activated platelets to walls and other platelets. Our hope was to increase the intuition of 3D platelet data by using a 3D display, a CAVE environment. Current methods are mainly only 2D and often require multiple visualizations to correctly portray a single frame of data.

Platelets are small blood cells, usually spanning only 2 to 4 microns in diameter. They play a major role in closing ruptures in small blood vessels but can also lead to diseases such as myocardial infarction. Each cubic millimeter of blood typically has about 150,000 to 350,000 cells. Ruptures occur hundreds of times every day, and the study of platelet aggregation is important in understanding platelet activation and consequences of platelet behavior. Aggregation occurs in vascular injury, cell-cell interactions, platelet-vessel walls, and platelet-thrombus interactions [1].

Amtec Engineering, Inc. has produced a commercially available software package called TECplot, which visualizes large numbers of platelets on a standard computer monitor. As is the case with most 3D data, the visualization of 3D platelets is not easy on a 2D display.

II. Methods

This project built off of the particle-visualizer framework that was used for the current ”artery” demo in the CAVE at Brown University [3]. Support code for controlling frame rate, loading datasets, and navigating a menu structure was already in place. Our project consisted of modifying the existing code to incorporate forward and backward timestepping, as well as speed control, in an intuitive and conveniently accessible user interface.

We created a mesh, consisting of a cylindrical section of a blood vessel, and generated preprocessed simulation data for discrete timesteps. Different colors were assigned to the 3 biological states being modeled: passive, pre-active, and active. The user interface consisted of a set of headtracked stereo glasses and a 3-button wand. Using the wand, the user was able to access a menu, grab the world to navigate around, and cycle through various preset viewpoints in the scene. It also provided convenient access to timestepping and speed controls, which were essential in being able to effectively and thoroughly control and examine the animation of the data.

III. Results

To evaluate the effectiveness and success of our visualization, we invited Peter Richardson of the Engineering Department at Brown University to test our program. Richardson was able to locate and point out major features of the blood platelet data. He commented that most options available for visualizing blood flow today only allow outside views of the blood vessel, but our program allowed him to be inside, enabling him to observe each individual cell up close. Using intuitive body movements, such as ducking, looking up, and moving side to side, to observe different perspectives of the platelet data, was effective and easy to adapt to. There was a significant improvement in being able to see how and which platelets got caught, on other platelets or on the vessel walls. The visualization was clear enough that the 3 different types of platelets were easily distinguisahble. Richardson said the model was simple and straightforward, and it presented a new phenomenology that was a good way to look at platelet data with greater insight.

IV. Conclusions

By using the CAVE to visualize the flow of blood platelets, users can gain a much better intuition of the data and develop improved methods for locating and predicting critical locations in a vascular tree. Next steps would involve a more complex data model, incorporating such variables as pulsatility, volume size, and curve data. Using and implementing tools such as the one completed for this project can further help researchers and students understand 3D platelet data, and the hope is that they can develop a better sense for predicting and visualizing flow patterns.

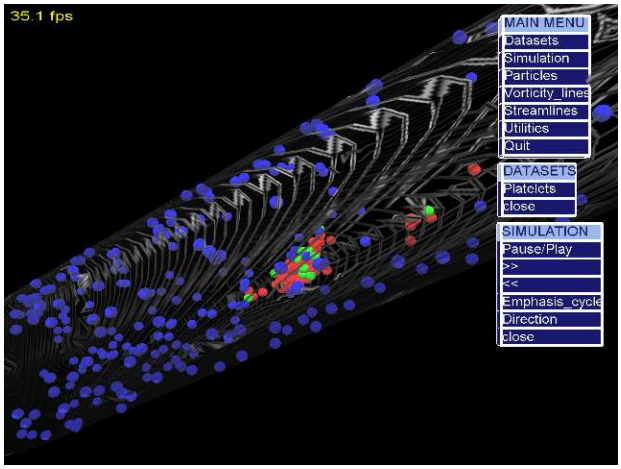

Fig. 1. An outside view of the blood vessel with an aggregate formation. Being in the CAVE allows users to observe platelets while being directly inside the blood flow.

V. References

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[3] Jason Sobel, Andrew Forsbert, David H. Laidlaw, Robert Zeleznik, Daniel Keefe, Igor Pivkin, George Karniadakis, and Peter Richardson. Particle flurries: a case study of synoptic 3d pulsatile flow visualization. *IEEE Computer Graphics and Applications*, November 2002. inpress.

Visualization of Platelets in Small Blood Vessels

I. Pivkin, N. Yang, D.H. Laidlaw, P.D. Richardson

Abstract

Platelet aggregation is important for closing the minute ruptures in small blood vessels that occur hundreds of times daily, but may also lead to arterial occlusion in the setting of atherosclerosis and trigger disease such as myocardial infarction. An interactive system was developed using immersive environment to visualize the blood platelets in the flow through small blood vessels.

Introduction

Platelets are blood cells 2 to 4 microns in diameter with a normal concentration in blood of around 150,000 to 350,000 cells per cubic millimeter. Platelet aggregation is important for closing the minute ruptures in small blood vessels that occur hundreds of times daily, but may also lead to arterial occlusion in the setting of atherosclerosis and trigger disease such as myocardial infarction. Platelet aggregation involves platelet activation due to vascular injury, cell-cell interactions, platelet-vessel walls and platelet-thrombus interactions[1].

Goals

The primary goal of the project is to visualize the three dimensional results of simulations with hundreds or thousands of platelets. We want to examine an interaction of platelets with vessel walls and other platelets, aggregate formation, its three dimensional structure and interaction of platelets with the aggregate.

Methods

The visualization tool was built using existing "artery" demo[2]. A user has an ability to move forward and backward in time. In addition, the user is able to control the visualization speed. This is important, because individual platelet interactions happen on a small time scales compared to the total simulation time. The user interface was modified to provide mentioned above. The platelets are visualized as tessellated spheres. Different colors are used to show different biological states of platelets.

Results

Our visualization tool allows user to observe the platelets in flow while being directly in the simulated blood vessel. The ability to have multiple perspectives with relative ease makes the tool more effective than Tecplot from Amtec Engineering, Inc., which was used for visualization before. It is easy to follow each platelet, its interactions with other cells, platelet aggregate or vessel walls. By controlling the speed of visualization and playing backwards, if necessary, user can study these interactions more precisely. The post-processing time of the simulation data was also reduced from 15-20 minutes, which were necessary to generate the files in Tecplot format, to only 1-2 minutes, to generate input files without significant manipulation of the data.

The visualization system was evaluated by scientific user and got a positive feedback. The user suggested adding more features to the current visualization. Among them is having easy access to variables such as time, aggregate volume, its growth rate and blood flow rate as a side panel in the CAVE. These features can be implemented in the future.

References

[1] A.C. Guyton. *Textbook of Medical Physiology.* W.B. Saunders Company, 1986.

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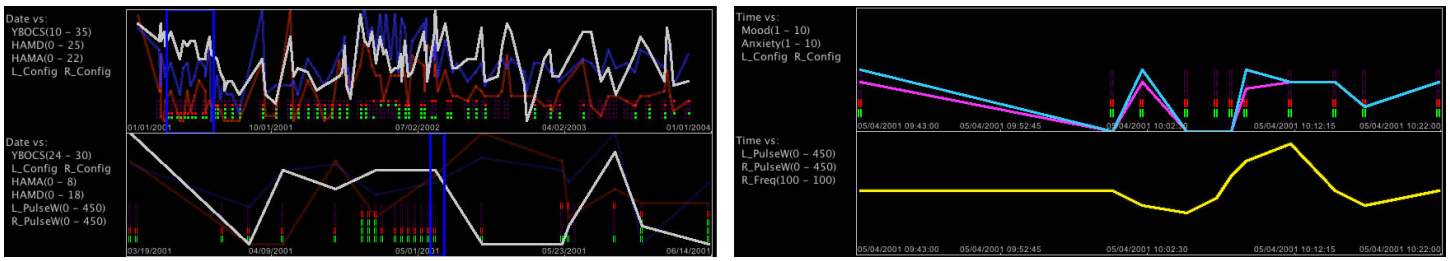
Visualizing Deep Brain Stimulation Settings in Obsessive Compulsive Disorder

David Eigen, Daniel Grollman
Brown University, Providence RI

Benjamin Greenberg, Erin Einbinder
Butler Hospital, Providence RI



Our system in use. On the left, the YBOCS measure (white) and electrode configurations (red and green boxes) are displayed at coarser scales. On the right, mood (blue), anxiety (magenta) and pulse width (yellow) are displayed for a single forty-minute adjustment session. The user selected this day using interval windows (blue) in the coarse scales.

We present a visualization system to explore data collected on Deep Brain Stimulation (DBS) for Obsessive Compulsive Disorder (OCD). DBS is a new surgical treatment starting to be applied to OCD in which electrodes are inserted into a patient's brain. After surgery, settings for the electrodes must be adjusted to find the stimulation that best reduces symptoms. Our tool is designed for interactively exploring relationships between the electrode settings and patient response. This visual exploration allows us to arrive at intuitions and tentative relationships to target with statistical analyses.

I. Background

OCD is an anxiety disorder in which the individual is overcome by fears, anxieties, thoughts or impulses. In response to these obsessions, the individual performs certain acts or rituals, often repetitively. Approximately 2% of the national population is diagnosed with OCD.

The effectiveness of DBS greatly depends on the settings of control parameters. Each electrode can be turned on or off independently. Many electrical properties can also be adjusted, such as pulse width and current. These settings change which areas of the brain are stimulated, as well as which tissue types are most affected. The problem is, which settings lead to the best results?

Complicating matters further is the fact that the effects of a certain stimulation may not appear until the patient has had hours or days with the setting. In our project, we tried to find relationships between settings and patient response for both long- and short-term data.

II. The System

Our system produces 2D visualizations from data stored in a SQL database. It can produce several types of representations, including glyphs representing which electrodes are on, line graphs and scatter plots.

The user can explore short-term data within a long-term context by viewing the data at multiple time scales. These scales are linked together by specifying interval windows in a coarse-scale visualization. The user can set the minimum and maximum values of a finer scale by changing this interval.

The user can also constrain the data by entering SQL code fragments that our system inserts into its queries. This is used, for example, to limit the data to certain electrode configurations, or to show only the so-called "pre" data — the first ratings collected in a day.

III. Results

Using our tool, we noticed that mood and anxiety, two of the acute measures, tend to be inversely related. Dr. Greenberg confirmed that this was in fact their experience. This success is important because we were able to reproduce a clinical finding without prior knowledge of the results.

We also found some adjustment sessions with links between pulse width and mood/anxiety. It is hard to tell how this affects the chronic symptoms, however, since often the settings were returned to a different value at the end of the session.

Finally, our collaborators became more convinced that they did not vary settings in a controlled enough way. There are few sessions aimed at varying only one parameter and keeping the rest constant. This makes it hard to find relationships using any method. In the future, there may be more effort to vary parameters systematically.

IV. References

[1] Greenberg, Benjamin D. et al. *Neurosurgery for intractable obsessive-compulsive disorder and depression: critical issues*, Neurosurgery Clinics of N America, 2003(14) pp. 199–212

[2] Greenberg, Benjamin D. et al. *Mechanisms and the Current State of Deep Brain Stimulation in Neuropsychiatry*, CNS Spectrums, 2003(7) pp. 522–526

Visualizing Deep Brain Stimulation Settings

David Eigen and Daniel Grollman
Brown University, Providence RI

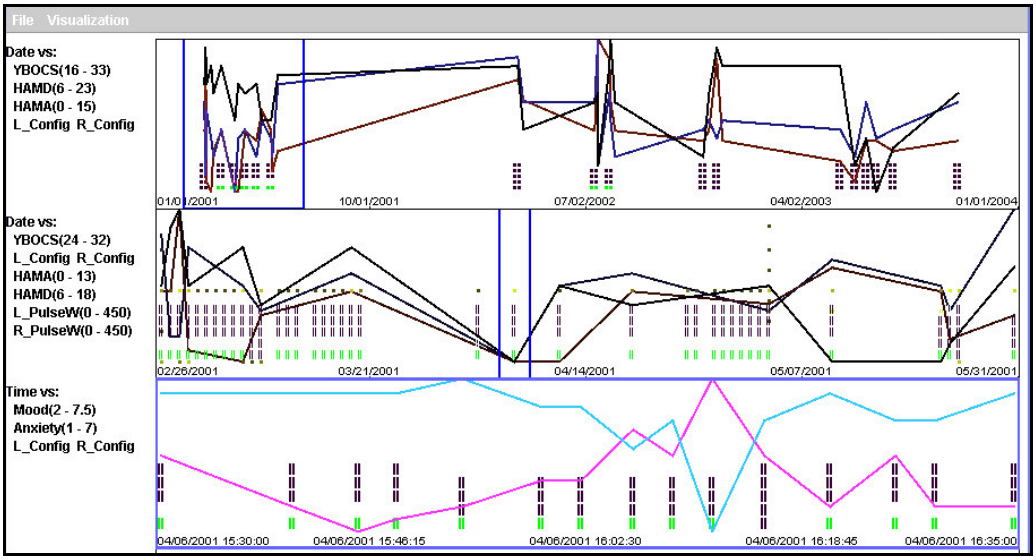


Figure 1: In this example of our visualization tool in use, the researcher has plotted the patient response (YBOCS, HAMA and HAMD) against the configuration settings and the date in the first row. In the second row, the experimenter has zoomed in on the interesting portion in the blue box in the first row, and added pulse width information to the plot. The user has further zoomed in on one day in the third row, to examine the acute response for each setting.

A new treatment for Obsessive Compulsive Disorder (OCD) involves stimulating portions of the brain with implanted electrodes. The parameter space for the settings of these electrodes is very large, and discovering relationships between settings and responses is hard. We have built a visualization tool to assist researchers in finding relationships in this high-dimensional space.

I. OBSESSIVE COMPULSIVE DISORDER

OCD is an illness characterized by recurring thoughts and actions that often lead to distress, anxiety, and the impairment of normal functioning. Around 30-50% of patients do not respond entirely, or at all, to modern behavioral or pharmacological treatment. Of those that do respond, many are unhappy with the side effects, and discontinue treatment. Severe OCD has been successfully treated by directed lesioning of the brain.

II. DEEP BRAIN STIMULATION (DBS)

Our collaborator, Dr. Greenberg, is exploring DBS as an alternative to brain lesions as a treatment for OCD. Electrodes are surgically implanted into the ventral portion of the internal capsule of the brain and the surrounding tissue is stimulated. This stimulation can vary in many parameters, such as location, frequency, and pulse width.

III. VISUALIZATION

Our visualization tool for exploring this high-dimensional parameter space consists of two parts: A Structured Query Language (SQL) database and a java program that interfaces with it. The database contains patient IDs, the electrical settings used in their implants, and the effect on their symptoms, as gathered by the researchers. Symptoms were measured by the Yale-Brown Obsessive Compulsive Scale (YBOCS), and the Hamilton Depression and Anxiety scales (HAMD and HAMA).

The Java program queries this database, and produces visualizations. In figure 1, our tool has been used to visualize the relationship between configuration settings and YBOCS, HAMA, and HAMD scores. Using the zooming capabilities of the system, the user has elected to explore more closely the interesting section at the left side of the graph.

IV. RESULTS

Feedback from our collaborators has been positive. They are excited by the prospect of being able to inspect this previously intimidating data set in an interactive way. Using this tool, and it's ability to rescale axes on the fly, and compare data at different resolutions, they hope to find interesting patterns that they can later submit to statistical analysis. In addition, they are interested in seeing if non-medical professionals can use this tool to find relationships that would back up their clinical experience.

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[1] B.D. Greenberg, M.D. Ph.D. Electrical Stimulation of the Internal Capsule for Intractable Obsessive-Compulsive Disorder. *FDA Investigational Device Exemption (IDE) G000204*

3D Immersive Visualization of Topological Defects in Nematic Liquid Crystals

Vadim Slavin, Jason Mallios, David Laidlaw, Robert Pelcovits: Brown University, Providence, RI, USA

Researchers in computational condensed matter physics deal with complex data sets consisting of 3D tensor, vector, and scalar quantities. Particularly, in the research of topological defects in nematic liquid crystal matter (LC) displaying the results of the computer simulation of molecular dynamics presents a challenge.

A conventional visualization system such as Tecplot© suffers from clutter and occlusion of objects representing data parameters and overburdens the user with the heavy volume of information necessary to convey meaningful results. Combining novel immersive and interactive visualization methods we developed a tool that attempts to provide a better way to visualize and explore LC data.

METHODS

Our visualization approach is applied to the results of molecular dynamics simulation performed at Brown [2]. This data includes order parameter tensor values for each group of molecules as well as arrangement of defects present in the LC model – all for each time step of the simulation [1].

The techniques were applied in the CAVE, a virtual reality environment[4]. This allowed application of highly interactive methods for navigating, exploring and understanding the data model presented. The same data visualization techniques were applied to a conventional desktop monitor environment with a different set of interaction tools allowed by the mouse and keyboard interface.

We chose to implement tensor data as an array of ellipsoids where the shape of each ellipsoid represents one tensor value [3]. The average orientation of molecules in each group is visualized as further scaled ellipsoids in the shape of elongated 'cigars' to represent the bidirectional vector quanitities.

The visualization of topological defects was done using thin OpenGL lines to denote the arrangement of defects based on the data fed into the visualization environment.

We implemented a set of novel interaction techniques such as navigation, dynamic selection of areas and layers to aid in detailed exploration of data. We supplemented these techniques with positional and orientational cues [Figure 1].

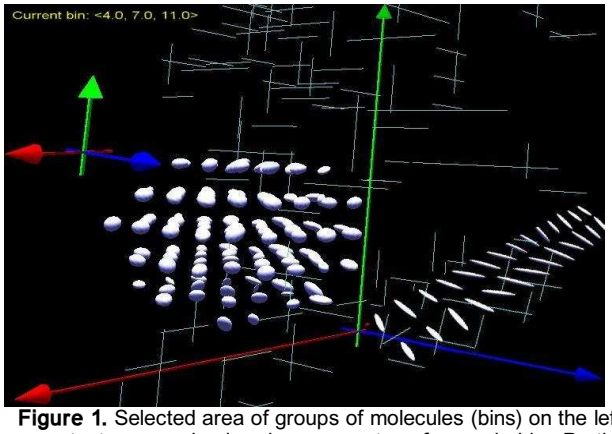

Figure 1. Selected area of groups of molecules (bins) on the left represents tensor valued order parameters for each bin. Partial layer on the right represents bidirectional vector valued average orientation of molecules within those bins. The defects are shown as OpenGL lines running along imaginary edges of the bins. In addition to the set of world coordinate axis, the miniature axis cursor follows a tracked 6 degree-of-freedom device by showing orientation of the world during navigation and displaying the coordinates (top left) of the bin it is currently in.

RESULTS

We tested our tool together with active researchers in the field of LC. Their feedback presented us with some important results.

The array of ellipsoids method allows to vary the relative size of the ellipsoids and the distance between them to increase visibility of all areas of the system and minimize occlusion. Such flexibility allowed the users to quickly pick the most comfortable settings. Particularly, the ease with which the users could vary the density of objects in their field of view was commended. The best achieved setting was reported to be where ellipsoid grid fit between the walls of the Cave. Such arrangement helped blend the real room with the virtual world and improve the perception of objects representing data.

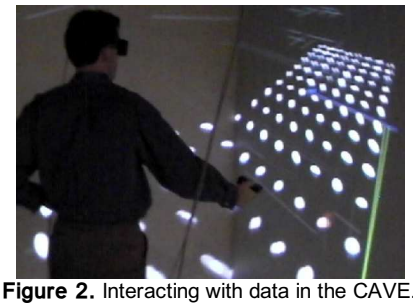

Figure 2. Interacting with data in the CAVE.

By allowing the user to physically walk through the virtual structure, all areas of the model were available for immediate inspection by either physically walking to it in the virtual space[4] or using various navigation interactors. Together with the ability to scale all ellipsoids uniformly, the relative situation of the floating objects in the virtual space minimized the occlusion and increased the user's ability to navigate and interact with the whole model or specific areas of interest.

Because the vector valued data is implicitly contained in the tensor valued dataset, users were offered to quickly toggle between the vector and tensor field views. The users found correlation between the two views seamless when switching between them. Reportedly, such interaction helped clarify the relative arrangement of molecules from one bin to the next in the context of defects.

The choice of thin OpenGL line representation of defects allowed to sacrifice the minimum amount of clarity of the model as reported by the users.

The novel methods of interaction such as selection of one layer or an arbitrary area of the system added to the explorative nature of the system allowing for greater interaction with the data. The users gave enthusiastic feedback when they were able to select a particular section or layer of the model for further inspection.

Additional depth cues such as lighting, coordinate axis, miniature coordinate axis cursor showing world orientation, as well as displaying current cursor position helped the users keep track of their orientation with respect to the model in the virtual environment.

CONCLUSIONS

As reported by the users, the system presented includes a set of features to allow for navigation, exploration and interaction with the data. This helps reduce occlusion and clutter in order to maximally use visual sense in order to understand the meaning of the visualized data.

Compared with the previous approaches[2] our methods reportedly present a better way to display the LC data and allow for structured interaction with selected parts of the system.

REFERENCES

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[3] **Laidlaw**(1998). *Visualizing diffusion tensor images of the mouse spinal cord*.
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A VE Visualization of Liquid Crystal Defects

Vadim Slavin, Jason Mallios, David Laidlaw, Robert Pelcovits
Brown University, Providence, RI

Liquid crystals (LC's) are a special phase of matter with shape, configuration and polarity [2]. Since their implementations (like LCD displays) require a strict orientation, it is necessary to isolate and correct defects within a cluster of LC molecules. Although an algorithm exists for detecting these defects, the results are difficult to confirm and isolate, especially visually. Significant success with immersive 3D virtual environments (VE's) in scientific visualization [3] convinced use to build a system for doing so comprised of a four-wall projected CAVE VE and a graphic depiction of particles and their detected defects. The system allowed scientists to step inside the grid of molecules and visually investigate the orientation of ellipsoids at defect locations.

SYSTEM

We built a 16 x 16 x 8 grid of 2,048 ellipsoids, each representing an LC molecule. Data Dr. Pelcovits obtained was parsed into the grid giving each ellipsoid an orientation defined by a major-axis vector (which way the "cigar-shaped" molecules were pointed) [1].

We first noticed that several, "tunnels," were visible while looking through the 3D grid, from within and without. This provided a valuable vantage for viewing several line-ups of ellipsoids and easily distinguishing between orientations. The main problem with former visualizations was the comparison of defects to orientation, and our system enabled this easily. A defect in LC's is generally the exception, not the rule, so there are more, "in line," ellipsoids than there are those with unique orientations. The ones that did not line up were readily spotted and confirmed (by rotating the grid in the world space). The defects themselves were depicted with lines running along the direction of defect.

In addition to mere rotation, the user is allowed to, "fly," around the grid, zoom in and out, switch to a vector-only view to confirm polarity observations, and scale the ellipsoids. A cursor allows the user to keep track of the current group of molecules of interest in, "bins," a bin being the particular world coordinate of an ellipsoid.

RESULTS

The visualization successfully allowed scientists to compare the ellipsoid orientation of an LC molecule group with the defect data. The navigation most appreciated was the scaling of the ellipsoids, which allowed them to make subtle but distinctly different visual comparisons. The main objective of an improved visualization was achieved lessening occlusion and obstruction.

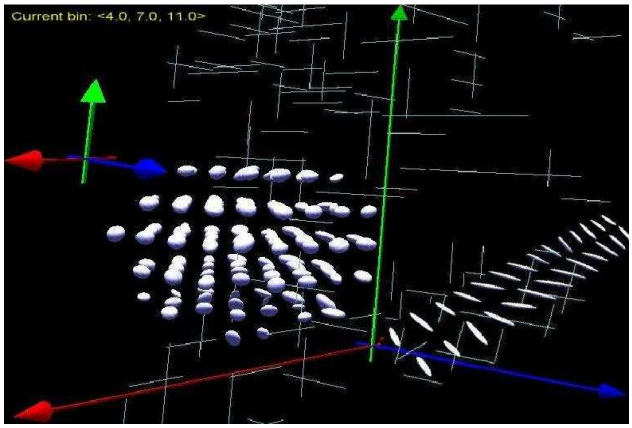

Figure 1. A screen shot of the ellipsoid grid, each white ellipsoid representing a liquid crystal particle. The world coordinate system axes are the larger arrows and the bin selection cursor is group of smaller arrows at left. The small grey lines are defects detected by the algorithm. One of the most interesting aspects of the CAVE visualization is that it allows the user to move the grid around, thus disambiguating defect lines that cross each other.

III. REFERENCES

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Visualization of Earthquake Simulation Data

Çağatay Demiralp Stephen Redihan Terry Tullis
Brown University, Providence - RI

Abstract

We present an effective tool to visualize a type of earthquake simulation data. Human and material costs of earthquakes are well known. Geologists use numerical simulations to understand the patterns in chronological behavior of earthquakes on faults, which can eventually help to predict earthquakes. These simulations result in massive, time varying data sets that are difficult to analyze. Our tool combines existing techniques, such as iso-surface extraction and color-mapping with a new, *plane-with-memory*, technique to effectively visualize spatial and temporal relations and patterns in the data. Initial feedback from geologists is encouraging and shows that the visualization tool is particularly helpful in understanding how small earthquakes grow into bigger ones.

1 Introduction

Earthquakes cost hundreds of billions of dollars and, more importantly, thousands of lives (average 10,000 deaths worldwide) each year around the globe [of The National Academies 2003]. The annualized long-term loss due to only US earthquakes is estimated 4.4 billion per year, and this figure appears to be rising rapidly [of The National Academies 2003]. Geologists study earthquake phenomena by running numerical simulations based on data collected from the field using numerical models. These simulations result in huge sets of numbers from which the mechanical behavior of faults may be understood. Analysis of such data can be time consuming and may not be very effective for further predictions. Visualization can help by integrating simulation data with useful visualization and interaction techniques augmenting geologists' ability to effectively test their hypotheses and propose new ones.

Visualization of scalar fields has been studied throughly. Color mapping, iso-contouring, volume rendering, iso-surface extraction are the few widely used techniques. Detailed discussion of these and other techniques can be found in many reference books [W. Schroeder and Lorensen 1997].

We build on previous work in applying scientific visualization to the study of earthquakes. Weber et al. visualized displacement, acceleration, and strain that were measured during an earthquake simulation experiment in a geotechnical centrifuge. The work is similar to our proposed work in visualizing an earthquake related simulation data [Weber et al. 2003]. But their simulation is of a different kind; it focuses on the moment of earthquake and its effect on the ground (buildings) whereas our model simulates the motion of the plates under the ground and the accumulated strain created on the surface by this motion. Chopra et al. introduced a volume rendering technique, which runs both in an immersive environment (CAVE) and on a desktop, to visualize large scale ground motion simulation data [Chopra et al. 2002]. The ground motion simulation data, velocity values, used in this work is similar to the data we use. But, however, in addition to velocity, we also visualize surface strain values.

2 Data

The data used in this work comes from a numerical simulation of the earthquakes occurring at the Parkfield section of the San Andreas fault plane [Tullis 1996].

The numerical simulation generates two different time varying 2D scalar data sets: One is the slip ratios on the fault plane and the other one is the strain values on the surface plane (see Figure 1). Both of these scalar fields are sampled on a hierarchical regular grid. The fault plane is the planar surface along which there is a slip during an earthquake. The slip on the fault causes changes in the strain on the surface on the earth where it is possible to make measurements in the real world. Since detection of theses changes in the strain is one of the more likely ways that the slip at depth might be detected, calculation of these changes has been done for this model. Because the rate of slip on the fault best characterizes any particular stage in the mode earthquake, the associated rate of strain at the earth's surface has been calculated [Tullis 1996].

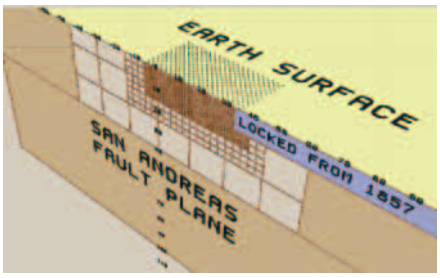

Figure 1: Shows the two types of data, which are sampled on a hierarchical grid, we use. The simulation generates slip ratio values for the fault plane (brown colored) and strain ratios for the surface plane (green) for a given time t_i.

3 Methods

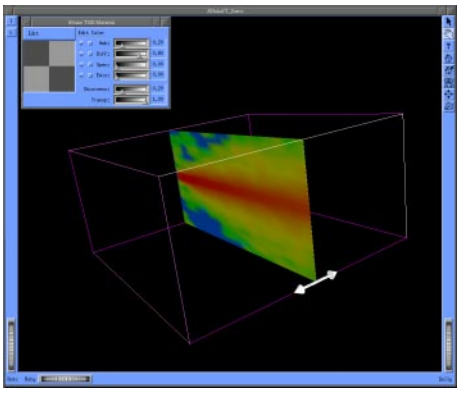

Figure 2: A screen shot from the application. Color encodes velocity values on the fault plane. Redder areas represent higher velocity values on the plane.

Visualization of the earthquake simulation data can be seen as a time-varying scalar data visualization problem. We use color mapping and iso-contouring, which are two well studied techniques, for visualizing spatial relations in the data (Color and connectedness are among the strong elements of pre-attentive segmentation). As for the temporal relations among the scalar data we use iso-surface extraction and *plane-with-memory* techniques. Iso-surface extraction is an extension of iso-contouring method to 3D domain and can

be effective for showing the temporal relations at global level. We propose *plane-with-memory* technique to visualize the local temporal relations among 2D scalar fields. It maps a function of time to the opacity value of the 2D field plane with a blurring effect. We hypothesize that the technique help to see the local temporal relations.

We have developed an interaction allowing the user to play with visualization (ie. colormaps, iso-values) and simulation parameters (ie. time) while keeping the frame-rate at an acceptable level.

We implemented the application using C++ and Open Inventor API. Open Inventor is a widely used, open source, scene-graph based graphics library.

4 Results

Initial feedback from geologists is encouraging and shows that the visualization tool is particularly helpful in understanding how small earthquakes grow into bigger ones. We are planning to conduct an anecdotal study to get more refined feedback.

5 Conclusion

In this paper, we have introduced a potentially useful tool to visualize a type of numerical earthquake simulation data.

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Visualization of Earthquake Simulation data

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Abstract

Geologists use numerical simulations to understand the patters in chronological behavior of earthquakes on faults, which can eventually help to predict earthquake occurrences. These simulations result in massive, time varying data sets that are difficult to analyze. We propose a tool to visualize a type of earthquake simulation data. This tool will help geologists understand the spatial and temporal relations and patterns of earthquakes on the fault lines that their simulation models. This visualization will be freely available.

Introduction

Our goal in this project is to develop a visualization tool to use simulation data more effectively. We have identified two paths to this goal. Firstly, the data at Parkfield is vast; it is a collection of two different time varying 2D scalar data sets. One data set being composed of the slip rations on the fault plane and the other the strain ratios of the surface plane. Secondly, for this visualization to be useful it must be available. The visualization tool integrated in the simulation method, its source code will be made available to the geological community on the web.

Methods

We define this problem as a visualization of time varying scalar data. For visualizing the scalar data we are using a combination of color mapping and iso-contouring. For visualizing the temporal relations among the scalar data iso-surface extraction and a plane with memory technique is being employed that can be effectively employed shoeing the temporal relations on a global level. The plane with memory technique maps the opacity value of the 2D-field plane to time. A hypothesis is that a geologist will obtain and intuitive grasp of earthquake phenomena more easily, then with a quantitative analysis of numerical data. Programming is written in C++ with Open Inventor API

The Visualization Tool

At startup, our visualization tool presents a user with a main window. It consists of a 3D Open Inventor examiner viewer that is used to display the experiment. On its right side several controls exist. Once the tool has read the data, the examiner viewer displays the experiment set-up. The user will then be able to see the changes propagated through a slice of earth backwards and forwards through the time of the experiment.

Results:

At this time the results of this experiment are incomplete

Future work:

The immediate future work will be to implement this tool with data collected and to study what correlations exist to verify the validity of the tool's use.

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Reducing dimensionality of flow cytometry data with manual hypercurve projections

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Christophe Benoist and Richard Park *Joslin Diabetes Research at Harvard medical school*

Constant progress in flow cytometry is now butting against our ability to visualize high-dimensionality data. We present a method of analysis inspired from the dimension-reducing techniques found in machine learning. However, in our method, the projections line are selected manually. Eventually, the data becomes amenable to direct visualization methods: 3d point clouds, 2d density plots and 1d histograms. We show that our method can handle complex datasets where previous methods would fail, and it gives more dependable measures.

Background

Flow cytometry is a common diagnostic technique used in medicine, whereby one can quickly scan a large number of living cells and individually measure a handful of properties, such as size, texture and affinity to selected antigens. With time, research has improved the range and resolution of the technique. The state of the art is now around 12 properties at once, for one million cells or so[1].

For instance, figure 1 shows a bimodal point-cloud obtained via flow cytometry during an experiment on diabetic lab mice at the Harvard Joslin Diabetes Research Center [2]. The larger cluster is red-blood cell, and the smaller cluster is white blood cells. Since diabetes is an autoimmune disease, experiments often seek to measure properties of these white cells. In particular, researchers will use flow cytometry to measure the relative population size of various kinds of white cells.

Machine learning techniques, like principal component analysis or discriminant analysis, do not handle such unlabeled, non-gaussian multimodal data very well. As a result, the analysis of flow cytometry data has traditionally relied on manual segmentation by an expert – a process called gating. However, beyond 5 and 6 dimensions, gating becomes difficult [3].

Case study

On figure 1, each light-blue ellipse is a different hand-drawn attempt at isolating the smaller cluster from the larger one. Currently, there are no principled ways to decide which one of these three is preferable. This is effectively a source of measurement error. Table 1 shows the final result of the analysis using this gating method, along with the resulting measure for each of the three ellipses, and the variance over these measurements.

We trace a line (in black) through the gap and project the points onto the line (figure 2). Notice that the two clusters are now clearly separated. Moreover, after the projection, one dimension suffices to tell the two clusters apart. Indeed, we can precisely separate the two populations at the minimum point of the histogram of figure 2 (line *b*). The two other bars, *a* and *c*, now serve to bound the error on *b*.

Now that we have isolated the population of interest, we can plot two other properties, and measure their relative frequency (figure 3). Table 1 shows the final result for each method, along with the relative error.

Results

Our preliminary result from a user study done at the Joslin Center suggests that hypercurve projections reduces the variance on the measurements by 60%. Furthermore, we suppose that hypercurve projections handle higher dimensionality counts better than gating. For instance, it should be possible to unfold mutually-occluding cluster pairs by projecting them onto U-shaped curves. Our user's initial reaction was encouraging.

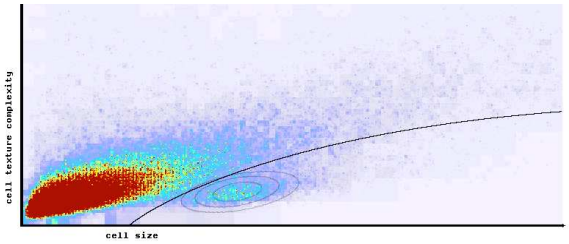

Fig. 1. A multimodal distribution obtained by flow cytometry.

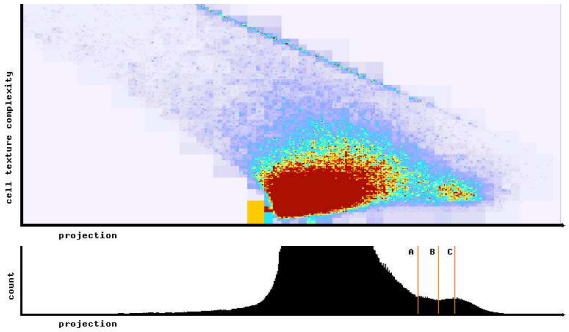

Fig. 2. Resulting distribution after projecting onto the black line in figure 1.

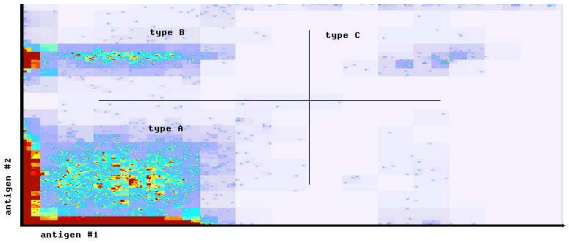

Fig. 3. Measurement of the population sizes for the target antigens.

	Type A	Type B	Type C
Gating method			
	76.1%	20.7%	3.0%
	78.2%	18.1%	3.3%
	85.7%	11.8%	1.9%
mean	78.7%	17.8%	2.96%
variance	2.50%	2.19%	0.452%
relative error	3.17%	11.8%	14.7%
Hypercurve projection method			
	80.4%	16.2%	2.5%
	79.7%	16.7%	2.7%
	83.2%	13.9%	2.3%
mean	81.09%	16.16%	2.54%
variance	1.87%	1.51%	0.219%
max relative error	2.31%	9.69%	8.81%

TABLE I

Repeatedly measuring the same value, using two analysis methods.

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Polychromatic Flow Cytometry Visualization and Analysis Utilizing Hypercurve Projections and Virtual Environment Display

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Richard Park and Christophe Benoist, M.D., Ph.D. *Joslin Diabetes Center, Harvard University, Cambridge, MA*

We present a software tool that introduces three-dimensional scatterplot representations of polychromatic flow cytometry data combined with a hypercurve projection method for facilitating the accurate and robust identification of subpopulations contained within this data. The techniques described were created to address the data analysis needs of immunology researchers investigating autoimmune diabetes onset, though we expect they can be generalized to a larger class of problems requiring multi-dimensional analysis.

I. BACKGROUND

Flow cytometry is a technique for measuring parameters of individual cells. In particular, our collaborators are interested in measuring the antigen expressiveness of pancreatic islet cells of NOD mice [1]. Traditional flow cytometry analysis involves projecting two parameters of the data onto a two-dimensional scatterplot, drawing gates on this scatterplot to limit the data in consideration, displaying two different parameters of this now gated data, and repeating the process until a conclusive answer to the specific experimental hypothesis can be constructed [2]. While this method has proven effective over the last 20 years for analysis of several-parameter data sets, recent advances in the physical techniques for performing flow cytometry have allowed up to 13 parameters per cell to be measured simultaneously [3]. This increase in the dimensionality of the data necessitates methods of visualization and analysis that provide greater access to the information contained within the data.

II. METHODS

Our software tool allows the flow cytometry analyst to arbitrarily map any of the measured parameters to any number of visual parameters specifying the scatterplot representation. In addition to the standard gating operations, we include functionality for the analyst to project multiple axes of the data onto a single hypercurve axis and to subsequently use this new data column itself to specify visual parameters as the analyst iterates over different representations. We support interactive viewing in an immersive virtual reality display, thus allowing the analyst to draw hypercurve axes in a one-to-one manner not possible with traditional desktop interfaces.

Three-dimensional scatterplot representation of flow cytometry data in an immersive viewing environment. Using a motion-tracked device, the user may input hypercurves through the data.

III. RESULTS

In a user-study conducted at the Joslin Diabetes Center, we found that our target users were able to determine cell subpopulation sizes with 60% less variance than with traditional gating. Moreover, the users have voiced their eagerness to apply our methods to their most challenging analysis problems.

IV. CONCLUSION

Preliminarily, our hypercurve projection technique has proven effective for reducing dimensionality in the analysis of polychromatic flow cytometry data. Future work will determine this technique's efficacy in immersive viewing environments and its overall accuracy.

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