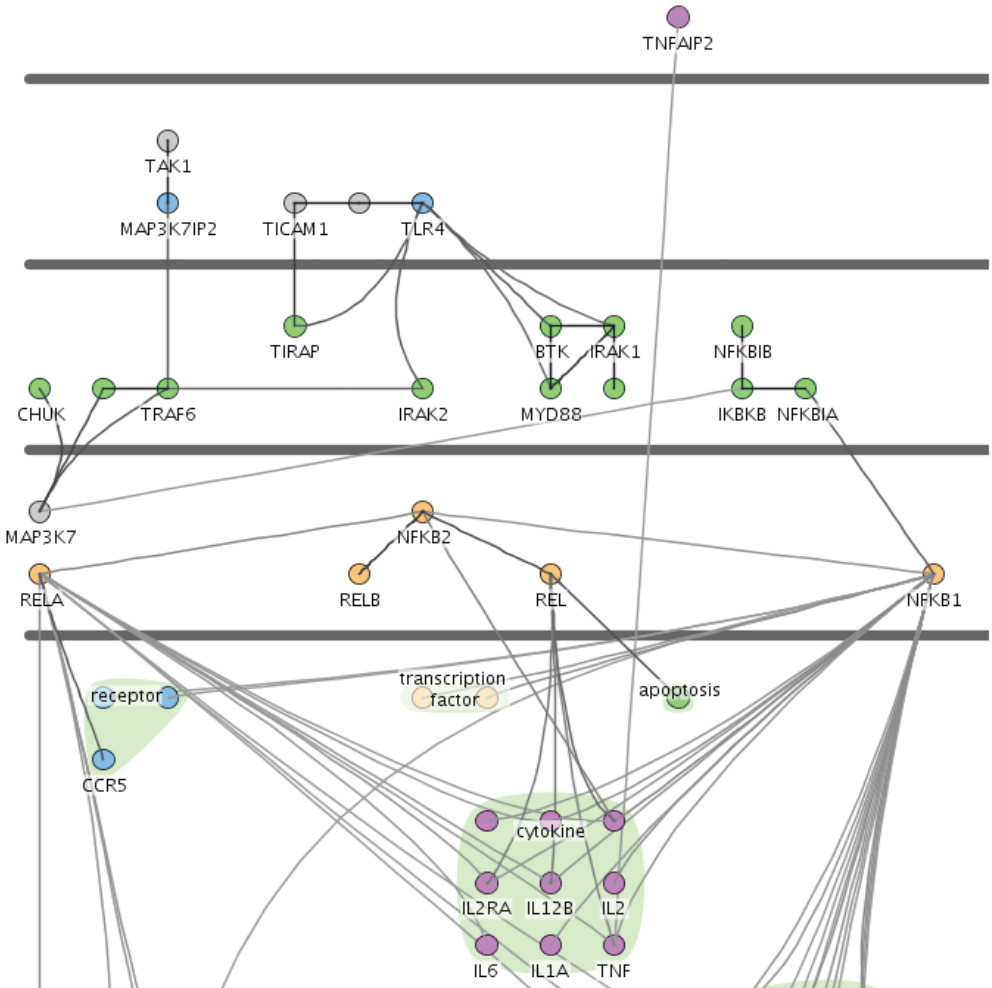


2011 VISUALIZING BIOLOGICAL DATAVIZBI

Broad Institute
Cambridge MA • USA
March 16-18, 2011



**Welcome to VIZBI 2011,
a workshop on visualizing
biological data**

www.vizbi.org

Broad Institute
Cambridge MA • USA
March 16-18, 2011

Our Sponsors:



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Wednesday 16 March 2011

Registration

» 8:30 - 9:15

Opening Remarks

» 9:15 - 9:30

Eric Lander

Keynote (Visual Complexity)

» 9:30 - 10:30

Manuel Lima

Coffee Break

10:30 - 11:00

Visualizing Single Genome Data

Session Chair: Ting Wang

» 11:00 - 11:30

Genome Browsing

Robert Kuhn

» 11:30 - 12:00 pm

Epigenomics

Bradley Bernstein

» 12:00 - 12:30 pm

Genome 2D/3D Structure

Erez Lieberman-Aiden

Fast-forward for Poster Session A

» 12:30 - 1:00 pm

Poster Session A + Lunch

» 1:00 - 3:00 pm

Visualizing Transcript Data

Session Chair: Matt Hibbs

» 3:00 - 3:30 pm

RNA

Eric Westhof

- » 3:30 - 4:00 pm
mRNA & microRNA Expression
John Quackenbush
- » 4:00 - 4:30 pm
Alternative Splicing
Yoseph Barash

Coffee Break

- » 4:30 - 5:00 pm

Keynote (Visualization Principles)

- » 5:00 - 6:00 pm
Tamara Munzner

Fast-forward for Poster Session B

- » 6:30 - 7:00 pm

Poster Session B + Dinner

- » 7:00 - 9:00 pm

Thursday, March 17, 2011

Announcements

- » 9:45 - 10:00
Organizers

Visualizing Proteins & Complexes

Session Chair: David Goodsell

- » 10:00 - 10:30
Protein Folds & Folding
John Westbrook
- » 10:30 - 11:00
Molecular Recognition and Self-Assembly
Arthur Olson
- » 11:00 - 11:30
Protein Dynamics
Gaël McGill

Coffee Break

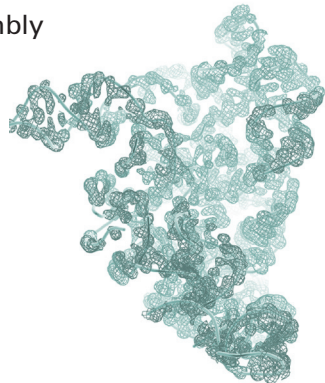
- » 11:30 - 12:00 pm

Fast-forward for Poster Session C

- » 12:00 - 12:30 pm

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Program



Poster Session C + Lunch

» 12:30 - 2:30 pm

Visualizing Cellular Systems

Session Chair: Mark Ragan

» 2:30 - 3:00 pm

Gene Regulatory Networks

Nicholas Luscombe

» 3:00 - 3:30 pm

Gene and Protein Networks

Trey Ideker

» 3:30 - 4:00 pm

Metabolic Networks

Susumu Goto

» 4:00 - 4:30 pm

Cellular Image Data

Yannis Kalaidzidis

Coffee Break

» 4:30 - 5:30 pm

Keynote (Outreach)

» 5:30 - 6:30 pm

Drew Berry

Reception + Dinner

» 6:30 - 9:00 pm

Art & Biology

Bang Wong, Tanja Gesell, Rikke Schmidt Kjærgaard and Daniel Kohn

Friday, March 18, 2011

Announcements

» 9:15 - 9:30

Organizers

Keynote (Design)

» 9:30 - 10:30

Martin Wattenberg & Fernanda Viégas

Coffee Break

» 10:30 - 11:00

Visualizing Organism Data

Session Chair: Steve Pieper

- » 11:00 - 11:30
Development
Willy Supatto
- » 11:30 - 12:00 pm
Anatomy
David Shattuck
- » 12:00 - 12:30 pm
Physiology & Function
Rob MacLeod

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Fast-forward for Poster Session D

- » 12:30 - 1:00 pm

Poster Session D + Lunch

- » 1:00 - 3:00 pm

Visualizing Population & Evolutionary Data

Session Chair: James Procter

- » 3:00 - 3:30 pm
Multiple Sequence Alignments
Des Higgins
- » 3:30 - 4:00 pm
Phylogenetics & Phylogeography
Rod Page
- » 4:00 - 4:30 pm
Metagenomics & Functional Diversity
Hervé Tettelin

Closing Remarks

- » 4:30 - 5:00 pm
Organizing Committee and
Session Chairs

Coffee Break

- » 5:00 - 5:30 pm

Poster and Fast-Forward Sessions

Poster schedule

Session A

- » Wednesday 1:00 - 3:00 pm (on view 8:30 am - 3:00 pm)
Fast-forward: 12:30 - 1:00 pm

Session B

- » Wednesday 7:00 - 9:00 pm (on view 3:00 pm - 9:00 pm)
Fast-forward: 6:30 - 7:00 pm

Session C

- » Thursday 12:00 - 2:30 pm (on view 9:15 am - 5:30 pm)
Fast-forward: 11:30 - 12:00 pm

Session D

- » Friday 1:00 - 3:00 pm (on view 9:15 am - 5:30 pm)
Fast-forward: 12:30 - 1:00 pm

Displaying your poster

Poster boards and computer displays are located in the lobby of the Broad Institute. To identify your poster board, refer to your poster number. Pins for fixing the posters are available on the actual board or at the registration desk. Please take down your poster at the end of the designated time window.

The displays are assigned to specific poster boards and are not to be moved. Additional tables are provided if you are interested in demonstrating visualizations or software on your laptop.

If you have not been assigned a poster number (e.g. due to late submission) you might still be able to put up a poster. Please ask at the registration desk for instructions. Keep in mind that space is limited and that you will not be able to participate in the fast-forward sessions.

Instructions for Fast-Forward Sessions

As a poster presenter, you have been included in one of the fast-forward sessions to give a 90 second introduction of your poster.

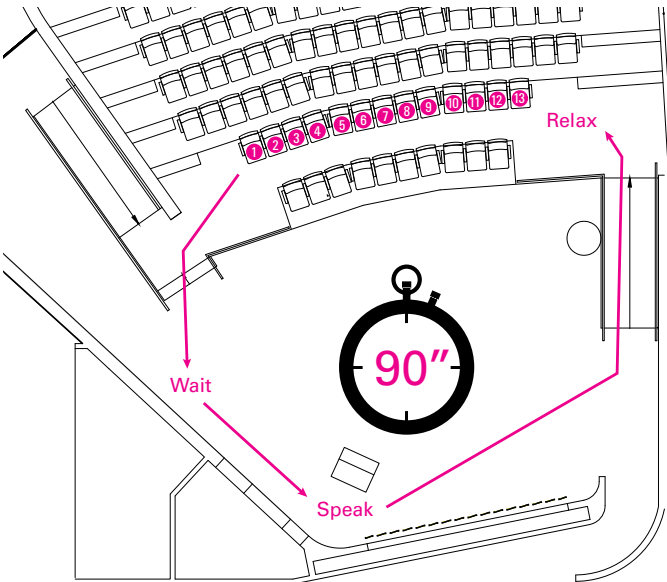
You have been assigned a seat in the auditorium according to your poster number. Please take your assigned seat just prior to the fast-forward session. This is to ensure that presenters are available on stage when it is their turn.

Your poster number determines the day and order of your fast-forward presentation. For example, if your poster number is A09, you will be the 9th person in Session A and would sit in seat 9 for that scheduled session.

Practice your pitch to make sure it is no more than 90 (ninety!) seconds. We will be strict about the time and we would hate to cut you off mid-sentence. Be creative!

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Posters



Poster Session A (Wednesday Lunch)

A01 FloTree: Peeking into the Phylogenetic Tree of Life with a Dynamic Process

Larry Kryala, Florian Block, Tanja Gesell, Hanspeter Pfister, Chia Shen

A02 Reconstructing the biogeographical and hydrological history of Central Mexico

David Kidd

A03 CBGB: An Interactive AJAX-Driven Genome Browser

Victor Chistyakov, Mick Correll, John Quackenbush

A04 Visualizing the layers of the epigenome

Kate Patterson, Susan Clark

A05 Interactive online toolbox for sequence-structure-function analysis of proteins

Annika Kreuchwig, Gunnar Kleinau, Franziska Kreuchwig, Catherine L. Worth, Gerd Krause

A06 StackedMatrix: an Application for Visualizing Biological Data as 3D Clustered Heat Maps

Georg Tremmel, Atsushi Niida, Satoru Miyano

A07 ALN2SVG: Visualizing Multiple Sequence Alignments

Saraswathi Abhiman

A08 CellVis - Interactive Exploration and Simulation of Cellular Transport Processes

Martin Falk, Thomas Ertl

A09 Visualizing Cell Biology

Janet Iwasa

A10 GenoSets: Visualization-Driven Analytical System for Comparative Microbial Genomics

Aurora Cain, Adam Price, Shatavia S. Morrison, Robert Kosara, Cynthia Gibas

A11 Novel Approaches to the Visualization of Twin and Family Studies

Oliver S. P. Davis

A12 Living Liquid: Engaging the Public with Microbial Metagenomics through Data Visualization
Jennifer A. Frazier, Joyce Ma, Isaac Liao, Kwan Liu Ma

A13 Large Scale Phenotyping in Tissue Microenvironments
Shantanu Singh, Raghu Machiraju, Thierry Pecot, Gustavo Leone

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Poster Session B (Wednesday Dinner)

Posters

B01 Supporting Research and Analysis Across the Biomedical Literature using Visual Analytics
Carsten Görg, Hannah Tipney, Karin Verspoor, William A Baumgartner Jr., K. Bretonnel Cohen, John Stasko, Lawrence Hunter

B02 SpotXplore: a Cytoscape plugin for exploration of hotspots in gene regulatory networks
Michel A. Westenberg, Jos B.T. M. Roerdink

B03 UnityMol: game engine-powered GPU-boosted molecular visualization
M. Chavent, A. Tek, Z. Lu, M. Baaden

B04 MOLEINT: Reducing Cognitive Workload through Adaptive Interaction
Megan Strait, Connor Gramazio, Jisoo Park, Sara Su, Lenore Cowen

B05 Visual Analytics of feature extraction methods applied to expression data
Kay Nieselt, Albert Pritzkau, Andreas Lehrmann

B06 Interactive Multiple Sequence Alignment and Phylogeny Reconstruction: IMAP
Elham Gharazi, Albert Y. Zomaya

B07 Human Epigenome Browser at Washington University
Xin Zhou, Mingchao Xie, Cydney Nielsen, Martin Hirst, Peggy Farnham, Robert Kuhn, Jingchun Zhu, Jim Kent, David Haussler, Joseph Costello, Ting Wang

- B08 Interactive Bioinformatics Workflows on Large Displays**
Chris North, Alex Endert, Ankit Singh, Robert Kincaid
- B09 KEGGscope Web: interactive pathway visualization on web browser**
Kozo Nishida
- B10 BioBlender, a tool to visualize biology like making movies**
*Raluca Andrei, Stefano Cianchetta, Tiziana Loni,
Maria Francesca Zini, Monica Zoppè*
- B11 Scribl: An HTML5 Canvas Based Alignment-Style Chart Library**
Chase A. Miller, Michelle M. Meyer
- B12 grabGENE - visualization of BLAST output data and selection of sequences**
Surendra Kumar, Ralf Neumann, Kamran Shalchian-Tabrizi
- B13 Savant Genome Browser**
*Marc Fiume, Eric Smith, Andrew Brook, Vanessa Williams,
Michael Brudno*

Poster Session C (Thursday Lunch)

- C01 Visualization techniques in Systems Biology**
Georgios A. Pavlopoulos, Maria Secrier, Reinhard Schneider, Jan Aerts
- C02 A virtual reality (VR) microscope for diagnostic pathology**
*Roy Ruddle, Darren Treanor, Rebecca Randell, Rhys Thomas,
Phil Quirke*
- C03 Fast tracing of microtubules in electron tomograms**
*Britta Weber, Marit Möller, Steffen Prohaska,
David Günther, Hans-Christian Hege*
- C04 Biologically-informed 3D modeling process to generate fully assembled protein complexes**
Damien Lariviere, Eric Fourmentin, Ines Winkler, Peter Friedhoff, Terence Strick
- C05 Computational Discovery of the Hallmarks of Cancer**
Daniel Gusenleitner, John Quackenbush, Aedín Culhane
- C06 Blast Atlas: Genome-scale visual exploration of protein collections**
Lawrence Buckingham, Xin-Yi Chua, James M. Hogan

C07 Cytoscape 3: Cleaner, Modular Version of Cytoscape

Keiichiro Ono

C08 Meta-analysis of gene expression and survival data using R packages SurvComp and genefu

Markus Schröder, Daniel Gusenleitner, Alexander Goesmann, Aedín Culhane, John Quackenbush, Benjamin Haibe-Kains

C09 CheS-Mapper: Chemical Space Mapping and Visualization in 3D

Martin Gütlein, Andreas Karwath, Stefan Kramer

C10 Hive Plots - A rational approach to network visualization and farewell to hairballs

M. Krzywinski, I. Birol, S. Jones, M. Marra

C11 Visualizing the next generation of sequencing data with GenomeView

Thomas Abeel, James Galagan, Yves Van de Peer

C12 Web-based visualization of large evolutionary trees

Karen Cranston, Adam Kubach, Kristopher Urie

C13 3D Spatial Mapping of Mouse Gene Expression Patterns Into Reference Embryos

S. Venkataraman, Bill Hill, Zsolt Husz, Ruben Schilling, Alexander Schliep, Lorna Richardson, Jeff Christiansen, Duncan Davidson, Richard Baldock

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Posters

Poster Session D (Friday Lunch)

D01 Modeling Geographical Impact on Metagenomes

Daniel Pick, Nao Hisakawa, Forest Rohwer

D02 Parameter visualization for biomedical image analysis

A. Johannes Pretorius, Roy A. Ruddle

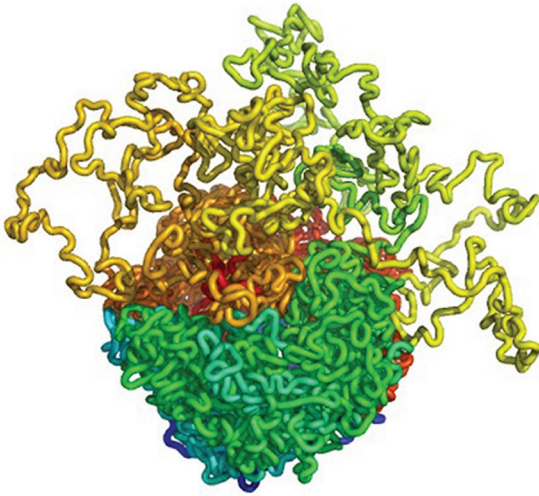
D03 Sequence Surveyor: Scalable Multiple Sequence Alignment Overview Visualization

Danielle Albers, Colin Dewey, Michael Gleicher

- D04 iHAT - interactive Hierarchical Aggregation Table**
Julian Heinrich, Corinna Vehlow, Kay Nieselt, Florian Battke, Daniel Weiskopf
- D05 Gene Finding: Visualization of the Invisible**
Alex Lomsadze, Mark Borodovsky
- D06 LineageProfiler: a map for visualizing experimental protocols**
Imtiaz Khan, Adam Fraser, Mark Bray, Victoria Griesdoorn, Paul Smith, Anne Carpenter, Rachel Errington
- D07 The Virtual Worm: A Three-Dimensional Model of the Anatomy of *Caenorhabditis elegans***
Christian A. Grove, Paul W. Sternberg
- D08 Visualizing organogenesis by high-speed selective plane illumination microscopy**
Jan Huisken
- D09 JProfileGrid: Visualizing Very Large Multiple Sequence Alignments**
Alberto I. Roca, Aaron C. Abajian, David J. Vigerust
- D10 OntologyMaps**
Jörg Bernhardt, Henry Mehlán, Julia Schüler, Michael Hecker
- D11 Discovering Relationships in Biosequences**
William Ray
- D12 TopiaryExplorer**
Megan Pirrung, Ryan Kennedy, Rob Knight
- D13 Visualizing Biological Context**
John "Scooter" Morris, Thomas Ferrin

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Posters



Tutorials (Saturday, March 19, 2011)

Tutorial schedule

- » 10:00 am - 1:00 pm
Tutorials (see below for room assignment)
- » 1:00 - 3:00 pm
Lunch (Lobby)
- » 3:00 - 6:00 pm
'Bring your own data' session (Monadnock Room, 2nd Floor)

Blender

- » Board Room (Mezzanine level)
Chris Grove & Monica Zoppè

Blender is a complete package for 3D content creation (from modelling to animation, rendering and game elaboration) developed as an open source project, which is increasingly popular for academic work. Using this tool, it is possible to visualize in an animated way any 3D subject, from atomic scale molecules to entire organisms. The workshop will introduce BioBlender and the Virtual Worm project. BioBlender is an extension of Blender developed for biomolecular visualization, and includes tools for animating (morphing) proteins, using the incorporated Game Engine, and a system of visualization studied for direct intuitive representation of physical and chemical features, via photorealistic rendering of cinema special effects. The Virtual Worm project is an attempt to construct an anatomically accurate 3D model of the nematode *Caenorhabditis elegans*, for the purpose of education, data visualization, and integration into the *C. elegans* database WormBase.org. This tutorial will focus on basic Blender operation and interface, biomolecular visualization with BioBlender, and cellular/organism anatomy applications using the Virtual Worm as an example.

Circos

- » Katahdin Room (2nd floor)
Martin Krzywinski

Circos addresses the challenge of simultaneously displaying categorical, ordinal and relationship information. One or more scales (e.g., chromosomes) are arranged circularly, with categorical (e.g. color map categorizing genes at each position) and ordinal (e.g., histogram of total conservation) data tracks arranged in concentric circles and relationships (e.g. fusion events, sequence similarity) shown as curves linking scale positions. Circos was designed in the context of genomics and displaying structural rearrangements, but is agnostic to the data type. This flexibility has made it a popular tool for generating circular data visualizations in other fields, such as computer security, politics and pop culture. Image generation is controlled using a hierarchical plain text configuration file and supports dynamic rules that adjust the output based on data values. The tutorial will focus on demonstrating how a Circos image is designed

and implemented. You will learn how to layout, order, crop and scale axes, and how to layer data tracks to create an information-rich, interpretable and attractive image. Tutorial material will be drawn from a full day course and generalized for a wide audience.

Cytoscape

- » Olympus Room (Lobby level)
Scooter Morris & Alexander Pico

Cytoscape is an open source software platform for visualizing complex-networks and integrating these with any type of attribute data. Cytoscape is arguably the most widely-used platform for visualizing and analyzing biological data in a network context. Cytoscape has been used for the visualization and analysis of cancer and other disease pathways, protein-protein interaction networks, protein similarity networks, genetic interaction data, and in a variety of other biologically relevant areas as well as domains outside of biology such as social network analysis. During this tutorial, we will be using Cytoscape to visualize and analyze biological networks. Beginning with the basics of Cytoscape: networks, attributes, and visual mappings; we will advance into how to load networks and attributes into Cytoscape from a variety of sources. We will then demonstrate and explore a variety of Cytoscape plugins for analysis and visualization. In particular, we will use the clusterMaker plugin to cluster networks and attributes; the Network Analysis plugin to explore the properties of networks; the BiNGO plugin to calculate overexpression of GO categories; and the structureViz and chemViz plugins to add structural visualization and information to the network. If time allows we will also explore the use of animations within Cytoscape.

Jalview

- » Lobby
James Procter & Geoff Barton

This tutorial will introduce you to the alignment visualization, editing, annotation and analysis functions of the widely used Jalview Desktop application. It is based on the 'Practical Jalview' guided tutorial which is being run in a number of locations around the world. During the tutorial, you will learn how to import and align sequences using Jalview's alignment services, perform and visualize protein secondary structure predictions, import annotation from public databases via the Distributed Annotation System, and visualize quantitative annotation and sequence conservation patterns on alignments and any associated 3D molecular structure data.

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Tutorials

Processing

» Monadnock Room (2nd floor)

Jer Thorp

Processing is an open source programming language and environment for people who want to create images, animations, and interactions. Initially developed to serve as a software sketchbook and to teach fundamentals of computer programming within a visual context, Processing also has evolved into a tool for generating finished professional work. Today, there are tens of thousands of students, artists, designers, researchers, and hobbyists who use Processing for learning, prototyping, and production.

VTK & ParaView

» Marcy Room (3rd floor)

Jeff Baumes & Wes Turner

This tutorial presents the fundamentals of VTK and ParaView, and describes how they can be used to construct visualization pipelines useful for biological research. VTK provides the ability to visualize and display anatomical and cellular data arising from medical imaging modalities. VTK has been used in diverse applications to view CT, MRI, PET and SPECT images, both as a collection of two dimensional slices in any of the axial, coronal, or sagittal views; or as volumetric or MIPS three dimensional displays. VTK is also suited to multidimensional data where each voxel of a volume may be composed from multiple values representing different modalities or e.g. different channels of data. In addition, VTK can look at large microscopy images, or movies of flow through a microscope stage. We will present the basics needed to write custom visualizations in VTK and how the ParaView application can view these data sources and perform large-scale visualization. In addition to visualizing geometry, images, and volumes, VTK is expanding its functionality to visualize data from 'omics fields, which includes pathways, charts, and dendrograms. We will present the current efforts in this area and how to use VTK to visualize various 'omics data.

Conference Organizers

Session Chairs

- » Nils Gehlenborg
Harvard Medical School, USA
- » David Goodsell
Scripps, USA
- » Matthew Hibbs
The Jackson Laboratory, USA
- » Chris North
Virginia Tech, USA
- » Steve Pieper
Isomics Inc., USA
- » Mark Ragan
Institute for Molecular Bioscience, Australia
- » Ting Wang
Washington University in St. Louis, USA

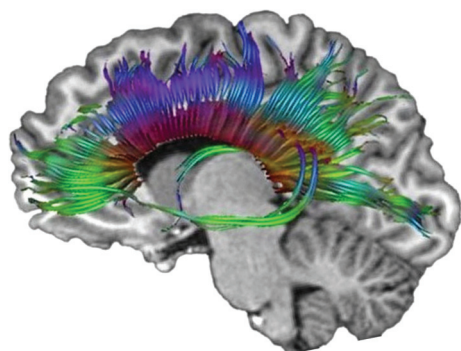
Organizers

- » Seán O'Donoghue
EMBL, Germany
- » James Procter
University of Dundee, UK
- » Lawrence Hunter
University of Colorado, Denver, USA
- » Bang Wong
Broad Institute, USA

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Tutorials

Organizers



General information

Broad Institute

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Cambridge MA 02142
617-714-7000

Wireless Internet

The Broad wireless network is an open network. There is no registration or password required to gain access. Use "Broad" wireless network.

Cab Information

- » Ambassador Brattle Taxi
617-492-1100
Accepts major credit cards
- » Cambridge Checker Cab
617-536-7000

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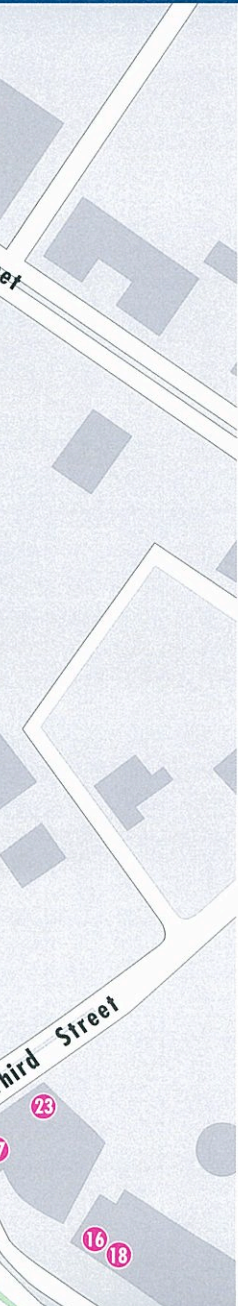
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General
Information



Cambridge Center Area Amenities





Cambridge Center Amenities

- 1 Barbershop and Hair Salon
- 2 Bank of America
- 3 Boston Marriott Cambridge
- 4 Boston Private Bank & Trust
- 5 Fidelity Investments
- 6 Instant Shoe Repair
- 7 The Kendall Hotel
- 8 MIT Coop
- 9 Residence Inn by Marriott
- 10 Quantum Book Store
- 11 U.S. Postal Office

12 Food Court

- Au Bon Pain
- Beijing Tokyo
- Damons
- Sbarro
- Teriyaki Café

Restaurants

- 13 Au Bon Pain
- 14 Black Sheep Restaurant
- 15 Character's Bar & Grill
- 16 Domino's Pizza
- 17 Dunkin' Donuts/Baskin Robbins
- 18 Florentina's Café
- 19 Kendall Market & Deli
- 20 Legal Sea Foods
- 21 MC2 American Bistro
- 22 Rebecca's Café
- 23 Zigo

24 One Kendall Square Complex

- Blue Room
- Cambridge Brewing Company
- Flat Top Johnny's Billiards & Bar
- Il Calcio Italian Cuisine
- Jasmine & the Kendall Lounge
- Tommy Doyle's Pub & Restaurant

25 Kendall Square Area

- Atasca Portuguese Cuisine
- Bright Horizons Day Care
- Emma's Pizza
- Kendall Square Cinema



ATM Machine



Bike Rack



MBTA Red Line and Bus Service



Parking



Shuttle to CambridgeSide Galleria

Service every 20 minutes
9:00 A.M. - 7:00 P.M. Mon-Sat
Noon - 7:00 P.M. Sun



Starbucks Coffee



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Notes











IMAGES: CELL NETWORK BY TAMARA MUNZNER (COVER), 3D MODEL
OF HUMAN GENOME BY EREZ LIEBERMAN-AIDEN (INSIDE PAGE),
RNA STRUCTURE BY KEVIN KEATING (INSIDE PAGE),