The CCB Cores

Computational Science
The Cores of the CCB focus on the introduction of new mathematical approaches for symbolic representation and analysis of biological data.

Computational Tools
Novel computational techniques facilitate data modeling integration and visualization.

Driving Biological Projects
Researchers study a range of neurobiological challenges from child development, to aging and dementia, to multiple sclerosis and schizophrenia.

Infrastructure & Resources
Integrates the basic mathematical techniques, computational tools and hardware resources to address driving biological problems.

Education & Training
Educational efforts are being made through the establishment of course offerings specific to computational biology, the creation of a visiting scholar series and the organization of workshops and seminars.

Dissemination
Information about our activities attracts additional collaborations and motivates scientists with similar research interests to share their findings and algorithms.

Administration & Management
Resources are utilized to their optimum levels through a forum of open exchange. CCB has established operational mechanisms, functional monitoring and evaluation protocols and regular reporting schedules.

The CCB provides an integrated environment for studying genomic function, biological structure and phenotypic variation.

CENTER FOR COMPUTATIONAL BIOLOGY

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Center for
Computational Biology (CCB)

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CCB = ∫ Genomic Function
Biological Structure
Brain Phenotype

http://www.ccb.ucla.edu

Center for Computational Biology

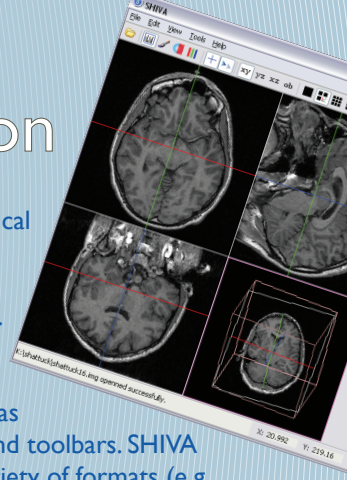
Historically, biology and neuroscience have been primarily descriptive sciences. The efforts of the Center for Computational Biology (CCB) accelerate the trends towards more quantitative science and help achieve an integrated understanding of anatomy, physiology and genetics.

The CCB involves research in mathematics, computational methods and informatics to address specific problems in neuroscience. The ultimate goal is to develop a new form of software infrastructure—the computational atlas—to manage multidimensional, multiscale and multimodal data.

The Center for Computational Biology (CCB) was established to develop, implement and test computational biology methods that are applicable across spatial scales and biological systems.

The computational sciences enable mathematical model building and quantitative analysis.

Visualization



SHIVA

The Synchronized Histological Image Viewing Architecture (SHIVA) is a Java-based image viewing environment. SHIVA provides a framework for image processing plug-ins, as well as XML-configurable menus and toolbars. SHIVA can read image files in a variety of formats (e.g., Analyze, MINC, Tiff, Bruker, CIVM) and also supports reading large image volume that cannot be fit in memory. It provides tools for label volume painting, mask volume generation, and curve delineation.

Interaction

Pipeline Processing Environment

The Pipeline features modular architecture, server/client communications via TCP, AES encrypted communications, ontology enabled data processing using OWL, runtime processing of filenames, automatic cache management, grid engine integration, file streaming, URL wrapper and data resource abstraction, comprehensive logging, process stream capturing and an integrated viewer. The friendly user interface includes consolidated messaging, node connection highlighting and multiple node operators. Runtime list processing includes bash shell script output and transparent module syntax updater framework. Documentation is available via Wiki, Doxygen, and Javadoc.

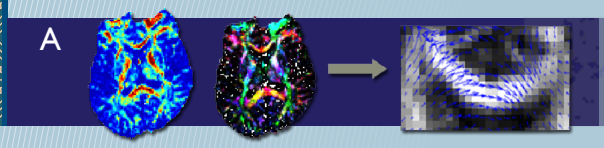
Analysis

Image Analysis Diffusion Tensor Imaging Tractography via Navier-Stokes fluid flow modeling & quantitation of white matter hyperintensitie. As seen below (figure A), the tensor field exerts a force on an artificial fluid. The flow of the fluid is damped by the viscosity, which is high in areas outside of the white matter. This flow determines a velocity vector field.

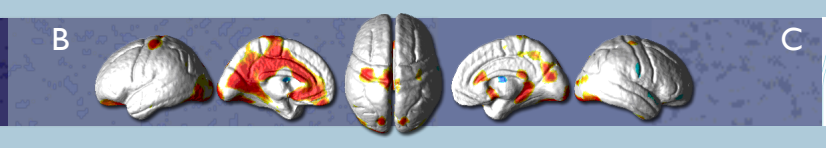
Shape Analysis Curvedness and Shape-Index measure means of individuals with Williams Syndrome and compared to healthy individuals. As seen below (figure B) regions with significant mean difference $P < 0.05$, corrected for multiple comparisons using False Discovery Rate (FDR).

Biosequence Analysis The HIV Mutation Database (figure C) is a study of mapping positive selection of recent HIV evolution. Not only is this database an order of magnitude larger than any other database in the world, it is also the first use of positive selection mapping, a powerful new tool for identifying key causes of human disease, such as pathogen drug resistance.

Graph algorithms open a new world of query capabilities for genomics data, which are poorly and incompletely modeled by the tabular structure of relational databases. Our software development of genomics graph database query systems, both in the popular Python language platform and the well-known PostgresQL database system, will open up the capabilities of graph algorithms to genomics researchers.



Viscosity Pressure Field Vector Field



Regions with significant mean difference $P < 0.05$

HIV Mutation Database