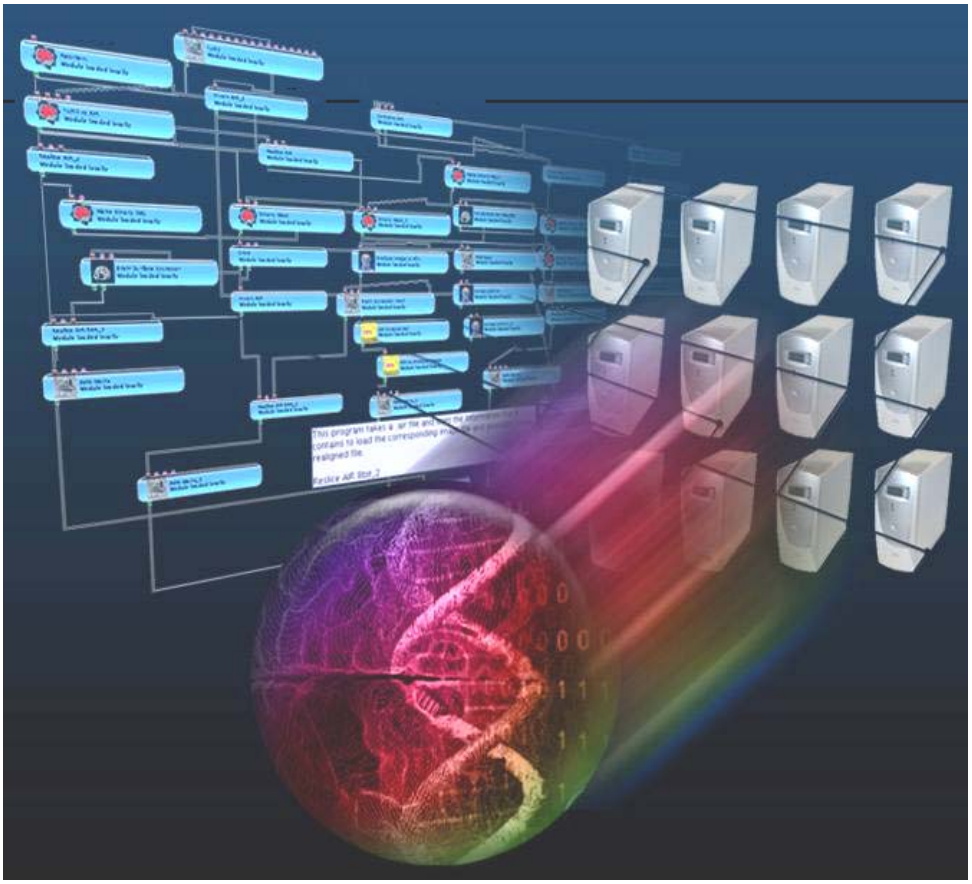
Center for Computational Biology (CCB)

2006 NCBC All-Hands Meeting



Dissemination

Time: 9:00 AM - 12:00 PM
Date: July 19, 2006
Location: Lister Hill (38A)
NIH Campus

www.loni.ucla.edu/CCB/Meetings

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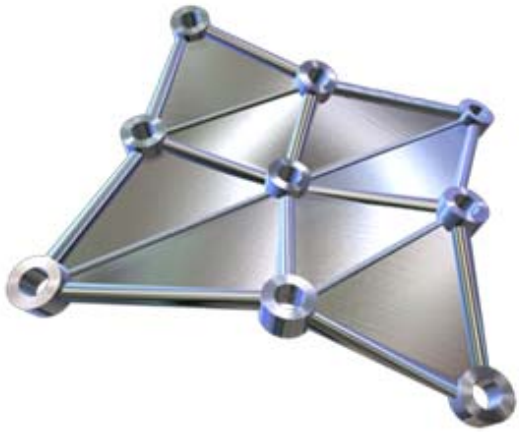

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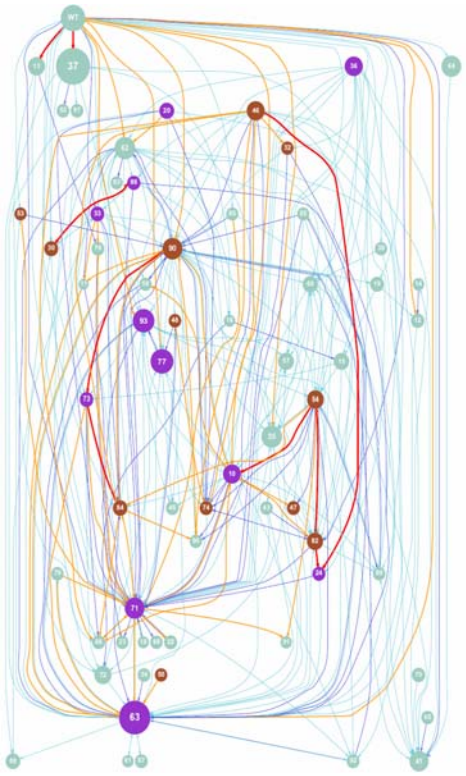
Agenda



Time	CCB Software Tool	Presenter
9:00-9:45 AM	Shape Representation	Roger Woods
9:45-10:30 AM	SHIVA and other CCB Computational Tools	David Shattuck
10:30-11:05 AM	Mapping Evolutionary Pathways of HIV-1 Drug Resistance	Chris Lee
11:05-11:15 AM	Break	
11:15-11:35 AM	Automated Shape Feature Extraction and Modeling	Duygu Tosun
11:35-11:55 AM	Volumetric Object Parcellization using Generative & Discriminative Models	Zhuowen Tu

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Description

NCBC AHM

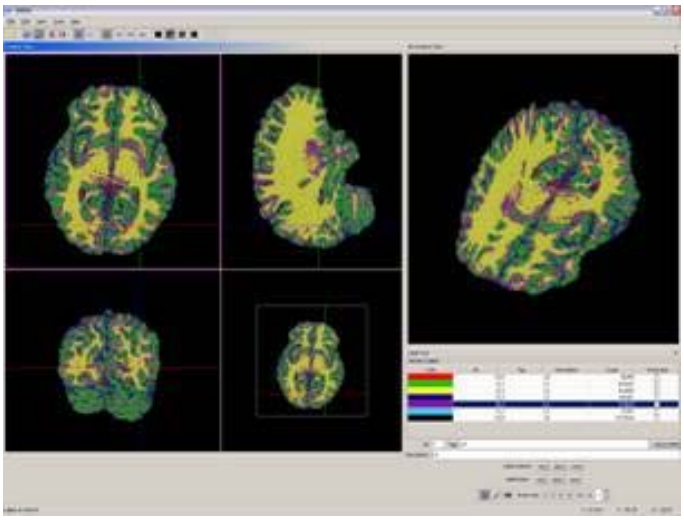
Title: Computational Tools for Modeling Analysis and Visualization of Biological Shape, Form and Size

Description: A 3-hour CCB tutorial session

Targeted Audience: NIH intramural and extramural researchers, NIH special interest groups, including the Inter-Institute Imaging Group (I3G), National Center for Biomedical Computing All Hands Meeting attendees, other government agencies and academic scientists

Hosts: CCB LSO: Dr. **John Haller** & PO: Dr. **Greg Farber**

Summary: The Center for Computational Biology (CCB) is an NCBC center established to develop, implement and test computational biology methods that are applicable across spatial scales and biological systems. The Center's objective is to help elucidate characteristics and relationships that would otherwise be impossible to detect and measure. The CCB employs an integrative approach, both in terms of the biology and the participating disciplines. The Center focuses on the brain, specifically on neuroimaging, and involves research in mathematics, computational methods and informatics. It is also involved in the development of a new form of software infrastructure – the computational atlas – to manage multidimensional data spanning many scales and modalities. This is specifically applied to the study of brain structure and function in health and disease, but has much broader applicability to both biomedical computing and computational biology.



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CCB Software Tools – May 2006

This document describes the details of all CCB Software developments that have occurred during the 2005-2006 funding period.

ShapeViewer
Description: Provides 3D interactive user interface for viewing parametric shapes commonly used in the Laboratory of Neuroimaging.
Data Input: Current version requires LONI UCF format.
Data Output: Scenes composed of multiples shape objects can be saved along with an associated view for subsequent reloading and display.
Implementation Language: Java 1.4 or higher, requires Java3D runs as application or as Applet.
Platforms tested: Macintosh, PC, Sun
Version, Date, Stage: 1.0, May 24, 2005, released
Authors: Jeff Ma, Craig Schwartz
URL: http://www.loni.ucla.edu/Software/Software_Detail.jsp?software_id=18

Pipeline Processing Environment, Pipeline
Description: A dataflow processing environment for coordinating complex and large-scale scientific analyses.
Data Input: Pipeline module
Data Output: Output of the programs that the Pipeline runs
Implementation Language: Java
Platforms tested: Linux, Windows, MacOSX
Version, Date, Stage: v3.0.0 alpha3, May 24, 2005
Authors: Current contributors:
Arthur Toga (PI)
Arash Payan (Lead)
Jagadeeswaran Rajendiran (Programmer)
Jia Wei Tam (Programmer)

Previous Contributors:
David Rex (Lead)
Jeff Ma (Programmer)
URLs: http://pipeline.loni.ucla.edu & www.loni.ucla.edu/twiki/bin/view/Pipeline/

Debabeler
Description: Neuroimaging studies often involve multiple data processing and analysis packages, each of which often use different file formats and conventions. Although "standard" file formats have been developed, no one format exists that satisfies the needs of contemporary neuroimage analyses. The LONI Debabeler acts as a data mediator between neuroimaging software packages by automatically translating data files from one format into another format. The data files are decoded and encoded using an image data plugin architecture, and the translations from one format into another are performed using an XML-based data translation automaton. The translations are visually defined and edited using the Debabeler's graphical user interface. The Debabeler

provides a flexible application and configurable automaton that can be used to develop solutions to translation problems.
Data Input: Plugins to read (decode) common imaging formats, XML, and plain text files (including almost all medical image files).
Data Output: Plugins to write (encode) common imaging formats, XML, and plain text files.
Implementation Language: Java (requires Java 1.4+)
Platforms tested: Sun Solaris, Mac OSX 1.3+, SGI IRIX, Windows NT/2000, RedHat LINUX
Version, Date, Stage: Version 2.4, May 12, 2005, Stable public release
Authors: Scott Neu and Daniel J. Valentino
URL: http://www.loni.ucla.edu/Software/Software_Detail.jsp?software_id=11

Alternative Splicing Microarray Analysis Toolkit
Description: Set of analysis tools for deconvoluting changes in splicing from simultaneous changes in gene expression from microarray datasets with multiple probes per gene. Identification of genes with alternative splicing changes between different samples; measurement of statistical significance. Clustering of samples by alternative splicing patterns.
Data Input: Tab delimited probe hybridization data tables.
Data Output: Tab delimited scoring tables
Implementation Language: Python. Uses R and Rpy packages.
Platforms tested: Linux (red hat 9, Suse Professional 10), Mac OS X (10.3)
Version, Date, Stage: 1.0, February 2005
Authors: Christopher Lee, Qi Wang
URL: http://www.bioinformatics.ucla.edu/ASAP

GeneMine
Description: GeneMine is a free sequence analysis and visualization program that makes full use of analysis servers across the Internet, to automate your sequence analysis needs and filter for meaningful results. GeneMine summarizes these results as graphical annotations on your sequence alignment, in a form that can be conveniently browsed, analyzed further, saved, and even published as web pages or presentations.
Data Input: Many: sequence (FASTA, Genbank, Swissprot, PIR, CLUSTAL, GCG), structure (PDB), sequence alignment (CLUSTAL, GCG, BLAST, LOOK), many others
Data Output: Many: sequence (FASTA, many others), Sequence alignment (CLUSTAL, GCG, LOOK), structure (PDB), structure & alignment snapshots; hypernote documents with embedded sequence and structure snapshots.
Implementation Language: C
Platforms tested: Sun, Linux, Mac OS X (10.3)
Version, Date, Stage: 3.5, April 2005
Authors: Christopher Lee, Tal Tversky, Andrew Dalke
URL: http://www.bioinformatics.ucla.edu/genemine

Python Graph Database module (Pygr)
Description: Pygr is an open source software project to develop graph database interfaces for the popular Python language, with a strong emphasis on bioinformatics applications ranging from genome-wide analysis of alternative splicing patterns, to comparative genomics queries of multi-genome alignment data.
Data Input: Many: FASTA sequence formats, BLAST databases, relational databases (e.g. MySQL), MAF multiple genome alignment format; interval alignment format; BLAST output format.

Data Output: Many: FASTA, BLAST databases, relational databases (e.g. MySQL), interval alignment format.
Implementation Language: Python
Platforms tested: Linux (redhat 9; Suse Professional 10), Mac OS X (10.3)
Version, Date, Stage: 0.1, March 2005; 0.2, May 2005; 0.3, March, 2006. This is alpha software.
Authors: Christopher Lee, Alex Alekseyenko
URL: http://www.bioinformatics.ucla.edu/

LONI Visualization Environment
Description: A multi-dimensional brain imaging viewer with *BrainMapper* functionality.
Data Input: ANALYZE, MINC, DICOM.
Data Output:
Implementation Language: Java
Platforms tested: SUN SOLARIS, PC, Mac OS X
Version, Date, Stage: Version 5.3, May, 2006
Authors: Ivo Dinov, Bae Cheol Shin
URL: http://www.loni.ucla.edu/Software

Multiphase Level Set Based Segmentation (MultiPhaseCV)
Description: MultiPhaseCV includes the implementations of active contours without edges level set based segmentation models in C++ and Matlab. These are based on the Chan-Vese version of the Mumford-Shah functional. The models implemented are:

- Two-Phase in 2D
- Two-Phase in 3D
- Four-Phase in 2D
- Four-Phase in 3D

The Matlab 2D implementations run and display the results in real time while the Matlab 3D implementations require the visualization to be done separately. The C++ implementations require results to be visualized in a Matlab based Open GL framework. Results are being compared with hand segmented volumes. The multichannel versions of each of the above models were also implemented providing a framework for future integration of Atlas information.
Data Input: 2D images and 3D volumes stored in text or binary (.img) format. The input parameters include:

- Choice of Discretization Method
- Fidelity and Length of Curve/Surface Fine-Tuning Constants
- Number of Iterations

Data Output: 2D and 3D segmentations of MRI data into white matter (WM), gray matter (GM), CSF regions. For 2D segmentation models, the segmentation results can be viewed as an image or a contour representation. For 3D segmentation models, the slice-by-slice segmentation or the surfaces of each region can be viewed. The programs also calculate the sensitivity parameters (comparison with the hand segmented data), prerecord the AVI movies and output the CPU time.
Implementation Language: C++, Matlab
Platform tested: Windows
Version, Date, Stage: 2.0, May 17, 2006, Prototype; developing
Author: Igor Yanovsky
URL: http://www.math.ucla.edu/~yanovsky/CCB/

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BLASTgres
Description: BLASTgres is a database management system designed for bioinformatics research. It provides sequence-related bioinformatics services – including sequence alignment via BLAST and query of sequence locations –- in a common framework of indexed data access.
Data Input: Standard SQL commands, and other Postgres input
Data Output: SQL query results, and other Postgres output
Implementation Languages: C, Python, and Plpgsql.
Platform tested: Linux, Mac OSX
Version, Date, Stage: February 2006
Authors: Ruey-Lung Hsiao, Dr. D Stott Parker
URL: www.blastgres.org

GObase
Description: The GeneOntology (GO) is an extremely popular new source of connections for linking biological information, but its relational implementation can make it difficult to use. GObase is a publicly-available platform for query and visualization of GO information that relies on a different implementation, using a graph datatype. It consists of a graph representation of Gene Ontology and a Java GUI called the GoTermViewer that allows interactive query and annotation of GO terms. GObase links GO with various other biological information resources, supporting scientific knowledge discovery.
Data Input: Gene Ontology relational table
Data Output: graph representation of the GO; and interactive GUI
Implementation Languages: C, Java
Platforms tested: Linux, Mac OS X
Version, Date, Stage: April 2006
Authors: Ruey-Lung Hsiao, Dr. D. Stott Parker
URL: www.GO-base.org

BioPostgres
Description: BioPostgres is a collection of compatible extensions of the Postgres database management system to support computational biology. It includes:
- PostMake – extensions for automated data derivation and materialized views
- PostGraph -- extensions for graph data management
- PostModel -- model base management system
- BLASTgres -- bioinformatics capabilities, including access to BLAST
- GO-base – extensions for the GeneOntology database

Data Input: Standard SQL commands, and other Postgres input
Data Output: SQL query results, and other Postgres output
Implementation Languages: C, R, Python, and Plpgsql.
Platforms tested: Linux, Mac OSX
Version, Date, Stage: May 2006
Authors: Ruey-Lung Hsiao, Kelvin Leung, Edwin Mach, Dr. D Stott Parker, Hung-chih Yang
URL: www.biopostgres.org

SCIRun Problem Solving and Visualization Environment
Description: SCIRun is a Problem Solving Environment (PSE), for simulation, modeling, and visualization of scientific problems.

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Data Input: Support for multiple 3D data types, structured and unstructured geometries.
Data Output: Support for multiple 3D and image file formats.
Implementation Languages: C++ and C
Platforms tested: Mac OS X, Linux, and Windows
Version, Date: Version 1.24, September 13, 2005
Authors: SCI Institute
URL: http://software.sci.utah.edu/

BioImage
Description: BioImage is a SCIRun PowerApp for processing and visualizing medical image volumes.
Data Input: Support for a variety of native data formats (e.g. DICOM, Analyze, VFF, NRRD, PICT, etc.)
Data Output: The BioImage visual interface allows users to interact with their data both in 2D "slice views" (powered by the ViewSlices module), as well as in a full 3D "volume rendering view" (powered by high-performance volume rendering modules). Users can seamlessly move between the 2D and 3D views to precisely control how different features of their data are displayed, and to gain both quantitative and qualitative insights into their data.
Implementation Languages: C++ and C
Platforms tested: Mac OS X, Linux, and Windows
Version, Date, Stage: Version 1.24, September 13, 2005
Authors: SCI Institute
URL: http://software.sci.utah.edu/

BioTensor
Description: BioTensor is a program that processes and visualizes diffusion tensor images. It can read diffusion weighted images (DWIs), perform correction for a common class of distortions in echo-planar imaging, estimate tensors from DWIs, and visualize the diffusion tensor field. BioTensor's functionality is easily extended.
Data Input: Support for a variety of native data formats (e.g. DICOM, Analyze, VFF, NRRD, PICT, etc.)
Data Output: The BioTensor application generates "diffusion tensor images" (DTIs) from DWIs. DTIs are three-dimensional fields of tensor values and produces 3D visualizations of the tensor fields using a variety of visualization techniques.
Implementation Languages: C++ and C
Platforms tested: Mac OS X, Linux, and Windows
Version, Date, Stage: Version 1.24, September 13, 2005
Authors: SCI Institute
URL: http://software.sci.utah.edu/

SHIVA (Synchronized Histological Image Viewing Architecture)
Description: Visualization tool / framework for various types of data – surfaces, curves, images. SHIVA can load, display, and process 2D and 3D image files. SHIVA provides convenient methods for users to overlay multiple datasets. For example, one can simultaneously display co-registered MRI and histology data with a set of anatomical labels that delineate structures or tissue types. SHIVA also provides tools for delineation of anatomical structures and generation of mask volumes. SHIVA uses a plug-in architecture, allowing command line tools to be easily integrated into framework.
Data Input: numerous types, including Analyze Image, MINC, MNI OBJ Surface Models, BrainSuite2 Surface Models.

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Data Output: Can output most filetypes accepted as input.
Implementation Language: Java 1.4 or higher. Use of surface views requires Java3D.
Platforms tested: Macintosh, PC Windows, PC Linux, Sun, SGI.
Version, Date, Stage: 1.0, October 16, 2005, released. Internal builds posted within CCB on a regular basis.
Authors: Heng Yuan, Allan MacKenzie-Graham, Eagle S Jones, David W Shattuck, Arthur W Toga.
URL: http://www.loni.ucla.edu/Software/Software_Detail.jsp?software_id=12

Automatic Cortical Feature Extraction and Modeling
Description: SHIVA plugins for segmenting cortical sulcal regions and representing each sulcal region as curves of sulcal fundi using 3D cortical morphometry.
Data Input: Cortical surface model either in parametric or implicit representations. Current version requires DFS triangle mesh file format as the parametric representation and signed distance function saved in ANALYZE file format as the implicit representation.
Data Output: Vertex labels identifying each connected cortical region and curves of sulcal fundi saved in OBJ curve file format.
Implementation Language: Core code in C++. Incorporated to SHIVA for visualization and interactive user interface (requires Java 3D).
Platforms tested: Linux and Sun
Version, Data, Stage: 1.0, July, 2005, released.
Authors: Duygu Tosun and Heng Yuan (SHIVA plugins)
URL: http://www.loni.ucla.edu/Software

CENTER FOR COMPUTATIONAL BIOLOGY (CCB): 2005-2006 RESEARCH HIGHLIGHTS

During the second year of funding, CCB investigators made major advances in developing new mathematical techniques, implementing robust computational algorithms and introducing new tools for bioinformatics research and translational neuroscience research. Summaries of these achievements are presented below and detailed descriptions of each are available in the complete 2005-2006 CCB Progress report. In the past year, our research was featured in dozens of national and international media outlets.

I. HIGHLIGHTS IN NEUROIMAGING APPLICATIONS: BRAIN MAPPING OF DISEASE

a. HIV/AIDS induced dementia

In October 2005, we reported a major advance in our work on dementia (Thompson PM et al., 2005). HIV/AIDS affects 40 million people worldwide, and is a major cause of dementia, but the profile of brain damage caused by HIV is unknown. Applying brain mapping algorithms we developed to detect brain changes in dementia, we reported the first maps of how HIV/AIDS damages the brain (Figure A).

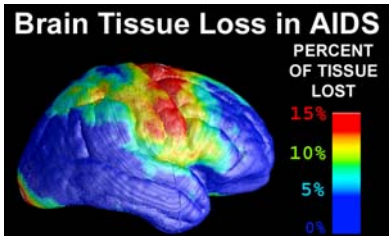


Figure A. Most Damage in brain regions controlling movement, memory and planning.

We linked these brain deficits with immune decline and cognitive impairment in patients. Our approach uses mathematics and continuum mechanics to unfold the human cortex, imaged with MRI, and aligns its features with a statistical database of information on normal cortical thickness, revealing deficits as a visual map. We discovered that HIV selectively attacks sensorimotor and caudate regions of the brain, causing 15% tissue loss in seemingly healthy patients on powerful drug regimens. The imaging research is the first to pinpoint the damage HIV inflicts on brain regions that control movement, language and judgment, explaining the early symptoms of mild cognitive/motor impairment and dementia. Press coverage of our findings (in 30 countries worldwide) noted that damage was detected before symptoms begin, offering great promise for assessing new anti-retroviral drugs in drug trials.

b. Williams Syndrome

We observe that the regional cortical complexity is consistently higher in subjects with WS compared to the ones of control. The rate of increase on sulcal complexity is more pronounced on the left cortical hemisphere and specifically in Brodmann regions 1 and 5. These results illustrate region specific shape differences, which indicate a differential impact of altered gene expression on cortical development (Figure B).

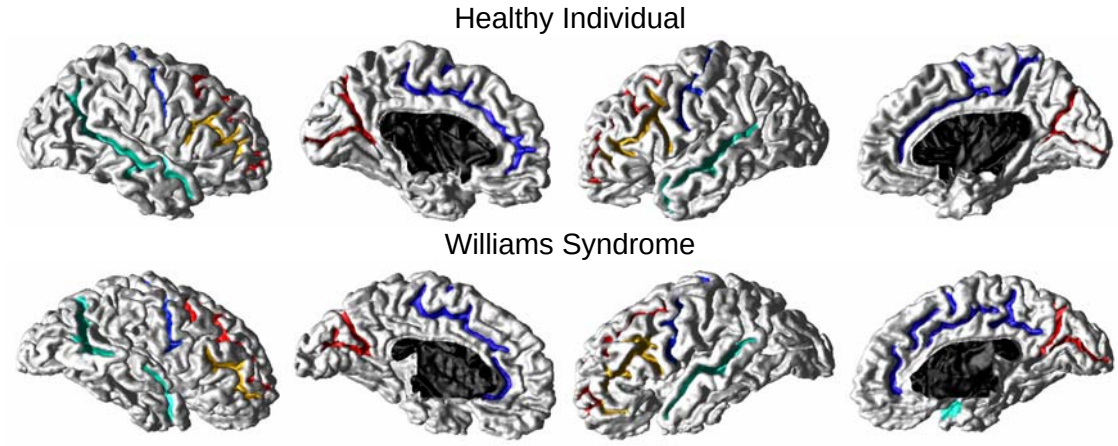


Figure B. Differences in sulcal patterns and cortical complexity between hemispheres in Normal Control and Williams Syndrome subjects.

c. Multiple Sclerosis

The two key clinical outcomes in MS are relapses and permanent disability. While gadolinium enhancing lesions on MRI are a biomarker for relapses, they are not an indicator of disability. It appears that brain atrophy, and more specifically gray matter brain atrophy, is a much better MRI correlate of disability in MS. Unfortunately, questions such as why, when and how brain atrophy in MS develops and then leads to permanent disability are poorly understood.

In 2005, we detected gray matter atrophy by MRI in mice with the MS model, experimental autoimmune encephalomyelitis (EAE). The development of atrophy on MRI in this model now demonstrate for the first time that autoimmune responses against myelin can result in gray matter atrophy. They also now provide a model in which to dissect out why, when and how gray matter atrophy occurs in this setting since mice can be studied in great pathologic detail at each stage of the disease. This model will be a major tool in understanding the pathogenesis of gray matter atrophy, which occurs secondary to autoimmune responses against myelin. Understanding events in the pathogenesis of gray matter atrophy are central to the design of therapies to stop the accumulation of gray matter atrophy, as well as permanent disability, in MS.

II. MATHEMATICS HIGHLIGHTS

a. One of our main mathematical achievements in the past 12 months, was the development and optimization of the 3D combined segmentation and registration algorithm, which is now available as a standalone tool. The fully non-rigid, morphological and multimodal registration approach has given very good results in wide range test cases of biomedical data.

b. We developed a new definition of sulcal fundi as curves that lie in the depths of sulci with maximal convolution. We used surface-based cortical morphometry analysis to introduce a method for automatic extraction of the fundal curves solely based on 3-D cortical geometry of the cortical surface. This new definition allows us to extract fundal curves not only in a stable and anatomically consistent fashion, but also without any manual initialization or prior training data set required by most of the methods.

c. An independent learning-based method for automatic detection of the cortical sulci from MRI volumes or extracted surfaces was also developed in 2005-2006. Instead of using morphometric analysis or pre-defined rules (e.g., mean curvature properties) to characterize the major sulci, this new algorithm learns a *discriminative* (classification) model by selecting and fusing features from a large pool of candidates. By extending the probabilistic boosting tree algorithm for learning the model we discover and combine rules based on manually annotated sulci traced by trained neuroanatomists. It has almost no parameters to tune and is fast due to the adoption of integral volume and 3D Haar wavelets. For a given approximately registered MRI volume, the algorithm computes the probability of how likely it is that each voxel is on a major sulcal curve. A dynamic programming method is then used to extract the curve based on the probability map. The learning aspect makes the approach flexible and it also works on extracted cortical surfaces.

III. BIOSEQUENCE ANALYSIS HIGHLIGHTS

Over the past 12 months, we have shown (experimentally) that many of the sequences of cancer-associated genes found in public databases represent tumor-specific forms that are not found in normal tissue. Specifically, our bioinformatics achievements include:

a. We have shown that protein modularity (the ease with which entire sections of a protein can be excised or inserted without affecting downstream translation) is highly associated with genes that show tissue-specific regulation of alternative splicing.

b. We have assessed the application of the Ka/Ks ratio test (which assesses the protein-coding potentials of genomic regions based on their non-synonymous to synonymous divergence rates) to alternatively spliced

exons and discovered that frequent false negatives occur. The results merit a more careful approach when applying this test in organisms which have extensive RNA alternative splicing.

c. We have developed a novel indexing algorithm for sequence interval overlaps which greatly reduces the computation time required for a whole class of comparative genomics problems.

We have generated a new dataset (addressing alternative splicing in the mouse genome) which is approximately double the size of our old dataset; by virtue of the fact that many of these alternative splicing relationships are newly-discovered, we are providing fertile ground in which other research projects can take root; in addition, we have also developed a new viewer for the Alternative Splicing Annotation Project database which is much more user-friendly.

d. We have released the open-source version of the GeneMine package (described in the progress report summary).

e. We have released three versions of the Python implementation of the Genomics Graph Database System, termed Pygr.

f. We have secured the necessary legal approvals to completely open the HIV Mutation Database to the public.

IV. HONORS AND AWARDS

a. A schizophrenia R01 application to extend the methods and approaches developed by our DBP # 4 (Tyrone Cannon) in a new study of twins concordant and discordant for bipolar disorder in Sweden was funded by the NIH on May 1, 2006.

b. CCB/LONI was nominated for the 2006 ComputerWorld Honors Award - honoring those who use information technology to benefit society (http://www.cwhonors.org/). The 18th Annual Computerworld Honors Laureates Medal Ceremony and Gala Awards Evening were held on June 5, 2006. This prestigious invitation-only event was held at the Andrew W. Mellon Auditorium in Washington, D.C. The award nomination reflects the achievements of the CCB in terms of developing and disseminating brain atlases and database infrastructure (Figure C).

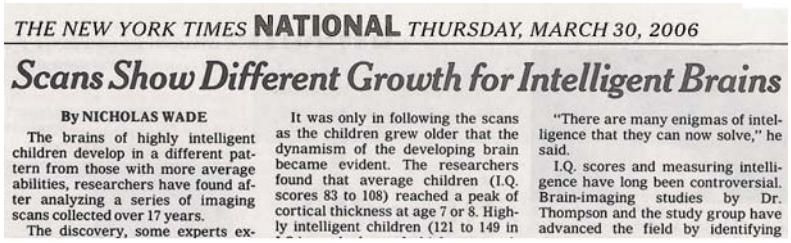
Figure C. CCB was nominated for the 2006 ComputerWorld Honors Award for its seminal work of computational brain atlases.

V. MEDIA HIGHLIGHTS

THE WASHINGTON POST SCIENCE MONDAY, MAY 1, 2006 A7

a. **NEW YORK TIMES (MARCH 30, 2006)** ***Scans Show Different Growth for Intelligent Brains***
by Nicholas Wade

The brains of highly intelligent children develop in a different pattern from those with more average abilities, researchers have found after analyzing a series of imaging scans collected over 17 years. The discovery, some experts expect, will help scientists understand intelligence in terms of the genes that foster it and the childhood experiences that can promote it (Figure D).



THE NEW YORK TIMES **NATIONAL** THURSDAY, MARCH 30, 2006

Scans Show Different Growth for Intelligent Brains

By NICHOLAS WADE

The brains of highly intelligent children develop in a different pattern from those with more average abilities, researchers have found after analyzing a series of imaging scans collected over 17 years.

The discovery, some experts ex-

It was only in following the scans as the children grew older that the dynamism of the developing brain became evident. The researchers found that average children (I.Q. scores 83 to 108) reached a peak of cortical thickness at age 7 or 8. Highly intelligent children (121 to 149 in

"There are many enigmas of intelligence that they can now solve," he said.

I.Q. scores and measuring intelligence have long been controversial. Brain-imaging studies by Dr. Thompson and the study group have advanced the field by identifying

Figure D. New York Time article featuring CCB research (03/30/06).

The finding is based on 307 children in Bethesda, Md., an affluent suburb of Washington. Starting in 1989, they were given regular brain scans using magnetic resonance imaging, a project initiated by Dr. Judith Rapoport of the National Institute of Mental Health. This set of scans has been analyzed by Philip Shaw, Dr. Jay Giedd and othersat the institute and at McGill University in Montreal. They looked at changes in the thickness of the cerebral cortex, the thin sheet of neurons that clads the outer surface of the brain and is the seat of many higher mental processes. The general pattern of maturation, they report in *Nature*, is that the cortex grows thicker as the child ages and then thins out. The cause of the changes is unknown, because the imaging process cannot see down to the level of individual neurons (Figure E, Shaw P. *et al.*, *Nature*, 440:676-9).

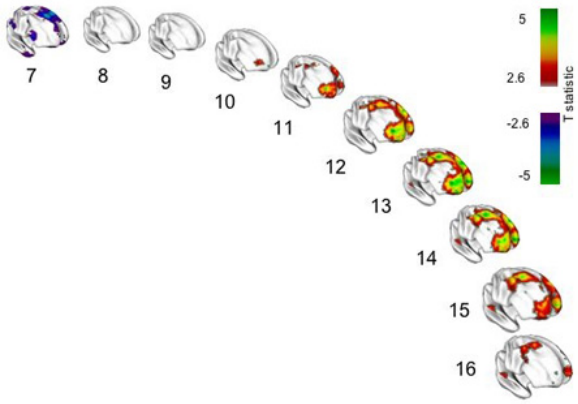
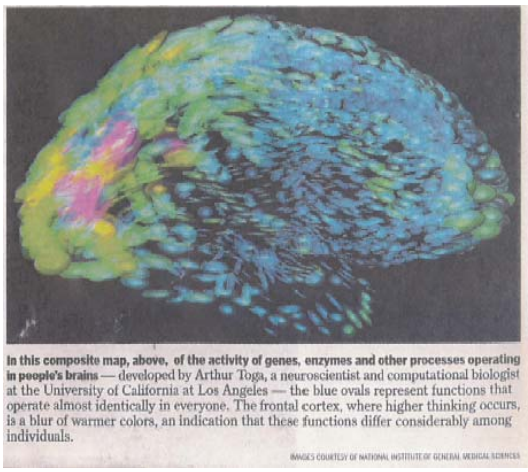


Figure E. Children with the highest IQ scores have a thinner prefrontal cortex (indicated in purple) at the earliest ages. These children then show a rapid increase in cortical thickness (indicated in red, yellow, and green), peaking at age 13.

b. **BBC News: *Scans show how HIV attacks brain* (Oct. 11, 2005)**
LA Times (Nov. 07, 2005) By Susan Brink, Times Staff Writer
NPR News: (October 11, 2005)

HIV, which attacks the body's natural defenses, also damages the brain; three dimensional medical scans have shown. The MRI images captured by a US team could show why up to 40% of people with HIV/AIDS have neurological symptoms. Compared with healthy people without the virus, the brains of the Aids patients studied were 15% thinner. Scans could be used to spot patients who might benefit from brain-protecting drugs, the authors told Proceedings of the National Academy of Sciences. HIV experts said more work was needed to check that neuroprotective drugs would be beneficial to AIDS patients and that these treatments would not be safe to take alongside the powerful anti-HIV drugs such individuals are already on.

As drugs improve, people with HIV/AIDS are living much longer. However, at least two in five living with HIV/AIDS will suffer from cognitive impairments, ranging from minor deficits to dementia, studies suggest. While researchers are aware of this, the pattern of damage the virus causes in the brain has not been well understood.



In this composite map, above, of the activity of genes, enzymes and other processes operating in people's brains — developed by Arthur Toga, a neuroscientist and computational biologist at the University of California at Los Angeles — the blue ovals represent functions that operate almost identically in everyone. The frontal cortex, where higher thinking occurs, is a blur of warmer colors, an indication that these functions differ considerably among individuals.

IMAGES COURTESY OF NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES

Figure F. Washington Post article

c. **WASHINGTON POST ARTICLE (05/01/06)**
FROM RESEARCH LABS, GLOWING COLORS AND IMAGES

In this composite map of the activity of genes, enzymes and other processes operating in people's brains – developed by Arthur Toga, a neuroscientist and computational biologist at the University of California at Los Angeles – the blue ovals represent functions that operate almost identically in everyone. The frontal cortex, where higher thinking occurs, is a blur of warmer colors, an indication that these functions differ considerably among individuals (Figure F).

Dissemination Event Evaluation - July 19, 2006

The purposes of this evaluation are to: ***Assess the computational needs*** *of biomedical researchers; Evaluate the* ***quality and functionality*** *of the spectrum of computational tools developed by CCB;* ***Improve and fine-tune the existing*** *and* ***custom design new software*** *applicable for a variety of biomedical and computational neuroscience data modeling, analysis and visualization. Please use the following 5-point scale for your ratings, adding comments at the end you think would be helpful to us.*

Overall Session Evaluation	**Very Poor**	**Below Average**	**Average**	**Above Average**	**Excellent**
Consider all materials, demos, activities, and presentations for this session. Did this session provide you with important information that may be useful for your research?	1	2	3	4	5
Comments:					
Please rank the quality of the presentations/demonstrations (e.g., organization, interactivity, consistency, etc.)	1	2	3	4	5
Comments:					
Please assess the relevance of the presented CCB Tools to your specific research.	1	2	3	4	5
Comments:					
Was there sufficient time for discussing research methods, engineering developments, hands-on demos and questions?	1	2	3	4	5
Comments:					

Modular Evaluation	**Very Poor**	**Below Average**	**Average**	**Above Average**	**Excellent**
1. **Shape Representation and *ShapeViewer*** *Roger Woods*	1	2	3	4	5
Comments:					
2. **SHIVA and other CCB Computational Tools** *David Shattuck*	1	2	3	4	5
Comments:					
3. **Mapping Evolutionary Pathways of HIV-1 Drug Resistance** *Chris Lee*	1	2	3	4	5
Comments:					
4. **Automated Shape Feature Extraction and Modeling** *Duygu Tosun*	1	2	3	4	5
Comments:					
5. **Volumetric Object Parcellization using Generative & Discriminative Models** *ZhuowenTu*	1	2	3	4	5
Comments:					

ADDITIONAL COMMENTS: _____

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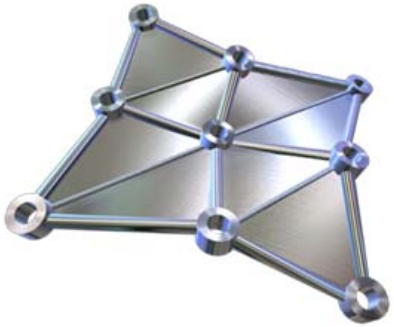
Dissemination

Center for
Computational
Biology (CCB)

Time: 9:00 AM - 12:00 PM
Date: July 19, 2006
Location: Lister Hill (38A)

Shape Representation • SHIVA and other CCB Computational Tools • Mapping Evolutionary Pathways of HIV-1 Drug Resistance • Automated Shape Feature extraction and modeling • Volumetric Object Parcellization using Generative & Discriminative Models



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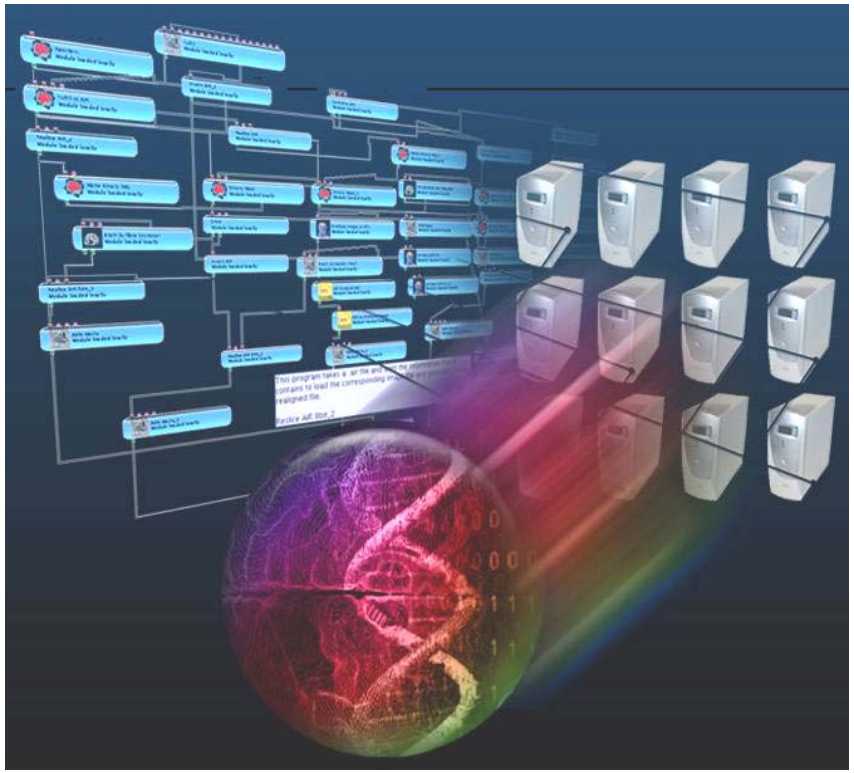
2006 NCBC All-Hands Meeting



Dissemination

Time: 9:00 AM - 12:00 PM
Date: July 19, 2006
Location: Lister Hill (38A)

ccb.ucla.edu

www.loni.ucla.edu/CCB/Meetings

Description

Title: Computational Tools for Modeling Analysis and visualization of Biological Shape, Form and Size

Description: A 3-hour CCB tutorial session

Targeted Audience: NIH intramural and extramural researchers, NIH special interest groups, including the Inter-Institute Imaging Group (I3G), National Center for Biomedical Computing All Hands Meeting attendees, other government agencies and academic scientists

Hosts: CCB LSO: Dr. **John Haller** & PO: Dr. **Greg Farber**

Summary: The Center for Computational Biology (CCB) is an NCBC center established to develop, implement and test computational biology methods that are applicable across spatial scales and biological systems. The Center's objective is to help elucidate characteristics and relationships that would otherwise be impossible to detect and measure. The CCB employs an integrative approach, both in terms of the biology and the participating disciplines. The Center focuses on the brain, specifically on neuroimaging, and involves research in mathematics, computational methods and informatics. It also is involved in the development of a new form of software infrastructure – the computational atlas – to manage multidimensional data spanning many scales and modalities. This is specifically applied to the study of brain structure and function in health and disease, but has much broader applicability to both biomedical computing and computational biology.

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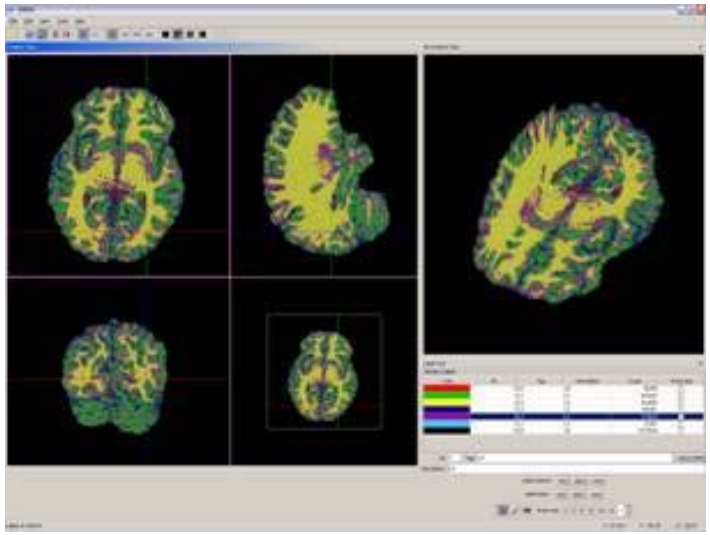
Time	CCB Software Tool	Presenter
9:00-9:45 AM	Shape Representation	Roger Woods
9:45-10:30 AM	SHIVA and other CCB Computational Tools	David Shattuck
10:30-11:05 AM	Mapping Evolutionary Pathways of HIV-1 Drug Resistance	Chris Lee
11:05-11:15 AM	Break	
11:15-11:35 AM	Automated Shape Feature extraction and modeling	Duygu Tosun
11:35-11:55 AM	Volumetric Object Parcellization using Generative & Discriminative Models	Zhuowen Tu