Mathematics in Brain Imaging

Institute for Pure & Applied Mathematics

UNIVERSITY OF CALIFORNIA, LOS ANGELES **UCLA**

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SANTA BARBARA• SANTACRUZ

July 14, 2008

Dear Attendees:

This booklet presents a set of abstracts from the "Mathematics in Brain Imaging" Summer School held at the UCLA Institute for Pure and Applied Mathematics, from July 14 - 25 2008. As the Summer School organizers, we would like to welcome you to UCLA and thank you for participating. We expect around 240 attendees for each of the two weeks – 350 registered participants in total – all with a broad range of interests in mathematics, engineering, neuroscience and medicine.

Over forty lectures will be presented by some of the finest research groups in brain imaging. These talks, summarized in this abstract book, describe many of the mathematical techniques used in structural and functional brain imaging studies today. They highlight a diverse array of mathematical and statistical approaches: state-of-the-art algorithms for computational anatomy, and powerful new analyses of functional images of the brain. Cutting edge methods for image registration and segmentation will also be explained - indispensable steps in all brain image analyses. A special day is devoted to diffusion tensor imaging – a rapidly growing field where mathematical tools from Riemannian manifolds and differential geometry are being developed to understand fiber integrity and connectivity in the brain. We cover new directions in applied mathematics, many just beginning to be applied to tackle challenges in brain imaging. We will cover sophisticated modeling of cortical anatomy and function, statistics of anatomic variation in development and disease, creation of anatomical templates and atlases to represent populations, the modeling of functional imaging data from fMRI and PET, imaging statistics, machine learning approaches, and the new field of imaging genetics. We hope that the contents of this abstract book pique the interest of mathematicians and brain imagers alike - in short anyone interested in the mathematical developments in the field.

In a new development, we are coordinating this IPAM Summer School with the Neuroimaging Training Program (NITP) Course, chaired by Russ Poldrack, which also provides hands-on training in experimental design and practical aspects of running image analyses. NITP participants will attend some of the IPAM lectures. On the Saturday of Week 1, the UCLA Center for Computational Biology (CCB) is hosting a neuroimaging software demonstration day, chaired by Ivo Dinov, at the Neuroscience Research Building auditorium, below the UCLA Laboratory of Neuro Imaging. All Summer School registrants are very welcome and encouraged to attend this software dissemination event.

We sincerely thank all members of the UCLA Institute for Pure and Applied Mathematics for their generosity and hard work in hosting the workshop. We appreciate the vision of IPAM's outgoing Director, Mark Green, who developed the idea for the Summer School, and was extremely generous with his time in

planning the workshop, and in securing support and funding for it. We also look forward to working with IPAM's new Director, Russ Caflisch, on the Summer School.

We greatly appreciate the logistic skills and dedication of Lee Melreit, Yvette King, Edward Soong, IPAM Manager of IT Jim Kimmick, IPAM Assistant Director Stacey Beggs, and many other members of IPAM whose contributions ensure the smooth running of the workshop. We also thank Grace Liang at the Laboratory of Neuro Imaging for her work on this abstract book and Amanda Hammond for designing the cover art.

Finally, we thank all the attendees, many of whom traveled from overseas to come to the Summer School. We especially thank our invited speakers for their contributions. Their work reveals the remarkable impact mathematics is making in brain imaging today. There is no doubt that mathematical developments hold exceptional promise in taking the brain imaging field forward into new dimensions not previously imagined.

The Summer School would not have been possible without the help of several groups who supported it financially. The primary costs of financing the workshop were contributed by the Institute for Pure and Applied Mathematics, which is funded by the National Science Foundation. Additional support was provided by the UCLA Center for Computational Biology (ccb.ucla.edu; National Institutes of Health grant U54 RR021813 funded by the National Institute of Mental Health and the National Institute of Neurological Disorders and Stroke; PI: Arthur Toga, UCLA Laboratory of Neuro Imaging, Co-PI: Stott Parker, UCLA Department of Computer Science). Additional funding was provided by a neuroimaging resource grant from the National Center for Research Resources (P41 RR013642; PI: Arthur Toga).

Additional support for several of the graduate attendees was provided by the Center for Imaging Science (PI: Michael Miller) at the Johns Hopkins University, and grants from P41-RR15241, P20 MH621130 and P01 AG03991.

Organizers:

Paul M. Thompson, Laboratory of Neuro Imaging, UCLA School of Medicine

Michael I. Miller, Center for Imaging Science, Johns Hopkins University

Russell A. Poldrack, Department of Psychology and Brain Research Institute, UCLA

Thomas E. Nichols, University of Oxford and GlaxoSmithKline, UK

Keith Worsley, Department of Statistics, Brain Research Imaging Center, University of Chicago

Jonathan Taylor, Department of Statistics, Stanford University

Mark Green, Outgoing Director, UCLA Institute for Pure and Applied Mathematics

Russ Caflisch, Director, UCLA Institute for Pure and Applied Mathematics (from July 1 2008)

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Abstracts of Talks - Week II

Summer School: Mathematics in Brain Imaging

Detailed Agenda

WEEK I

Monday, July 14, 2008

Surface-Based Computational Anatomy (Chair: Paul Thompson)

8:00 - 8:50	**Check-In/Breakfast (Hosted by IPAM)**
8:50 - 9:00	**Welcome and Opening Remarks**
9:00 - 9:45	**David van Essen** (*Washington University - St. Louis School of Medicine*) "Surface-Based Computational Mapping of the Cerebral Cortex"
10:00 - 10:45	**Guido Gerig** (*University of Utah*) "Mapping Brain Changes Over Time during Development"
11:00 - 11:45	**Monica Hurdal** (*Florida State University*) "Cortical Mapping using Conformal Geometry"
12:00 - 2:00	**Lunch (on your own)**
2:00 - 2:45	**Bruce Fischl** (*Harvard Medical School*) "Automated Analysis of Cortical & Subcortical Anatomy in Brain MRI"
3:00 - 3:45	**Guillermo Sapiro** (*University of Minnesota, Twin Cities*) "Computing Sulcal Curves and the complexity of brain connectivity"
4:00 - 4:45	**Zhuowen Tu** (*University of California, Los Angeles* (*UCLA*)) "Towards Automated Whole Brain Image Segmentation"

Tuesday, July 15, 2008

Computational Anatomy of Shape (Chair: Michael Miller)

8:00 - 9:00	**Continental Breakfast**
9:00 - 9:45	**Michael Miller** (*Johns Hopkins University*) "Computational Functional Anatomy"
10:00 - 10:45	**Laurent Younes** (*Johns Hopkins University*) "Evolutions Equations in Computational Anatomy"
11:00 - 11:45	**Anqi Qiu** (*Johns Hopkins University*) "Computational Functional Anatomy"

12:00 - 2:00 **Lunch (on your own)**

2:00 - 2:45 **Sarang Joshi** (*University of Utah*)
"Brain Morphometry using Diffeomorphic Maps and Differential Geometry "

3:00 - 3:45 **Stephanie Allassonniere** (*Johns Hopkins University*)
"Generative Models and Stochastic Algorithms for Population Average Estimation and Image Analysis."

4:00 - 5:30 **Reception (Hosted by IPAM)**

Wednesday, July 16, 2008

Mathematics of Diffusion Tensor Imaging (Chair: Christophe Lenglet)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **Christophe Lenglet** (*Siemens Research Corporation*)
"Mathematical Concepts for DTI and High-Angular Resolution Diffusion Imaging"

10:00 - 10:45 **Carl-Fredrik Westin** (*Harvard University*)
"The Mathematics of DTI"

11:00 - 11:45 **Steve Smith** (*University of Oxford*)
"Tract-Based Spatial Statistics"

12:00 - 2:00 **Lunch (on your own)**

2:00 - 2:45 **Baba Vemuri** (*University of Florida*)
"Higher-Order Tensor Models for DTI Segmentation and Analysis"

3:00 - 3:45 **Lauren O'Donnell** (*Massachusetts Institute of Technology*)
"Tract-Based Morphometry: White Matter Tract Clustering and Correspondence in Populations"

4:00 - 4:45 **Ganesh Sundaramoorthi** (*Georgia Institute of Technology*)
"Tracking Fibers and Brain Connections using Finsler Geometry"

5:00 - 7:00 **Speakers' Dinner (Hosted by the Center for Computational Biology)**

Thursday, July 17, 2008

Mapping Anatomy in Population Studies (Chair: James Gee)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **John Ashburner** (*University of London*)
"Voxel-Based Morphometry and Statistical Parametric Mapping (SPM)"

10:00 - 10:45 **Christos Davatzikos** (*University of Pennsylvania*)
"Morphological appearance manifolds for computational anatomy"

11:00 - 11:45 **Steve Pieper** (*Harvard University*)
"Large-Scale Computing Frameworks for Developing Image AnalysisTools"

12:00 - 2:00 **Lunch (on your own)**

2:00 - 2:45 **Tom Goldstein** (*University of California, Los Angeles* (*UCLA*))
"Improving Image Reconstruction in MRI"

3:00 – 4:30 **Student Presentations (10 minutes each; sign up on Monday)**

Friday, July 18, 2008S

Statistics on Manifolds for Computational Anatomy and DTI (Chair: Christos Davatzikos)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **James Gee** (*University of Pennsylvania*)
"Geodesics in Deformation Morphometry and DTI"

10:00 - 10:45 **Xavier Pennec** (*Institut National de Recherche en Informatique Automatique* (*INRIA*))
"Statistical Computing on Manifolds: from Riemannian Geometry to Computational Anatomy"

11:00 - 11:45 **Natasha Lepore** (*University of California, Los Angeles* (*UCLA*))
"Group Statistics for Tensor-Based Morphometry and DTI "

11:45 **Closing Remarks**

Saturday, July 19, 2008 – CCB Demo Day in NRB Auditorium

http://cms.loni.ucla.edu/CCB_Demo_Day_2008.aspx

Week II

Monday, July 21, 2008

Morning Sessions: Advances in First-Level Modeling (Chair: Tom Nichols)

8:00 - 8:50 **Check-In/Breakfast (Hosted by IPAM)**

8:50 - 9:00 **Welcome and Opening Remarks**

9:00 - 9:45 **Martin Lindquist** (*Columbia University*)
"HRF modeling"

10:00 - 10:45 **Steve Smith** (*University of Oxford*)
"Modeling Temporal Structure"

11:00 - 11:45 **Thomas Liu** (*University of California, San Diego* (*UCSD*))
"fMRI Design Optimization"

12:00 - 2:00 **Lunch (on your own)**

Afternoon Sessions: Bayesian Methods in fMRI (Chair: Steve Smith)

2:00 - 2:45 **DuBois Bowman** (*Emory University School of Public Health*)
"Bayesian Spatial Hierarchical Modeling"

3:00 - 3:45 **Timothy Johnson** (*University of Michigan*)

"Modeling Inter-Subject Variability in Activation Locations of fMRI Data:
A Bayesian Hierarchical Spatial Modeling Approach"

4:00 - 4:45 Panel Session - ***Glover, Nichols, Poline, Poldrack, Smith, Strother, and Worsley***
"Remaining Challenges in Multi-Subject fMRI"

Tuesday, July 22, 2008

Morning Sessions: Reproducibility in fMRI (Chair: Lars Kai Hansen)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **Gary Glover** (*Stanford University*)
"Considerations in Multi-site fMRI"

10:00 - 10:45 **J.B. Poline** (*Commissariat à l'Énergie Atomique* (*CEA*))
"Reproducibility in Group Modeling"

11:00 - 11:45 **Stephen Strother** (*University of Toronto*)
"Reproducibility Across Analysis Methods"

12:00 - 2:00 **Lunch (on your own)**

Afternoon Session: Random Field Methods (Chair: J-B Poline)

2:00 - 2:45 **Jonathan Taylor** (*Stanford University*)
"Advances in RFT - Nonnegative Least Squares"

3:00 - 3:45 **Keith Worsley** (*University of Chicago*)
"The Statistical Analysis of Cortical Surface Data"

4:00 - 4:45 **Ruth Heller** (*University of Pennsylvania*)
"Advances in FDR for fMRI"

Wednesday, July 23, 2008

Morning Sessions: Improved Modelling with Multivariate Methods (Chair: Keith Worsley)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **Lars Kai Hansen** (*Technical University of Denmark*)
"Decomposition Methods for Explorative Neuroimaging"

10:00 - 10:45 **Vince Calhoun** (*University of New Mexico*)
"Group ICA"

11:00 - 11:45 **Ola Friman** (*MeVis Research GmbH, Center for Medical Image Computing*)
"Adaptive Multivariate Analysis"

12:00 - 2:00 **Lunch (on your own)**

Afternoon Sessions: Imaging Genomics (Chair: Tom Nichols)

2:00 - 2:45 **Nelson Freimer** (*University of California, Los Angeles* (*UCLA*))
"What makes a genetic association significant?"

3:00 - 3:45 **Vince Calhoun** (*University of New Mexico*)
"Combining fMRI and SNP Data with Parallel ICA"

Thursday, July 24, 2008

Morning Session: Connectivity Models (Chair: Russ Poldrack)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **Clark Glymour** (*Carnegie-Mellon University*)
"Graphical Causal Models and Inferences to Mechanisms from Brain Imaging: Possibilities and Limitations"

10:00 - 10:45 **Marta Garrido** (*University of California, Los Angeles* (*UCLA*))
"Dynamic Causal Modelling"

11:00 - 11:45 **Judea Pearl** (University of California, Los Angeles (UCLA))
"The Mathematics of Cause and Effect "

12:00 - 2:00 **Lunch (on your own)**

Afternoon Session: Meta-analysis (Chair: Jeanette Mumford)

2:00 - 2:45 **Angie Laird** (*University of Texas Health Science Center at San Antonio*)
"ALE Meta-Analysis"

3:00 - 3:45 **Lars Kai Hansen** (*Technical University of Denmark*)
"Modeling neuroimaging databases "

4:00 - 4:45 **Tor Wager** (*Columbia University*)
"Meta-analysis methods"

Friday, July 25, 2008

Morning Session: Machine Learning Methods (Chair: Walt Schneider)

8:00 - 9:00 **Continental Breakfast**

9:00 - 9:45 **Francisco Pereira** (*Princeton University*)
"Introduction to Machine Learning for fMRI Data"

10:00 - 10:45 **Stephen LaConte** (*Biomedical Imaging Technology Center* (*BITC*))
"Classification of fMRI-Based Cognitive States"

11:00 - 11:45 **Isabelle Guyon** (*Clopinet*)
"Feature Selection Methods"

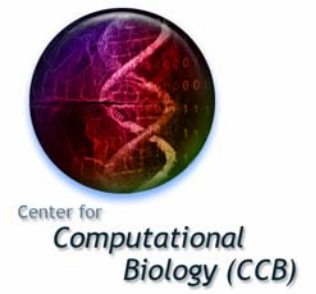
12:00 - 2:00 **Lunch (on your own)**

Afternoon Session: Advanced Topics in Machine Learning (Chair: Francisco Pereira)

2:00 - 2:45 **Nikolaus Kriegeskorte** (*National Institute of Mental Health*)
"Pattern-information fMRI and representational similarity analysis"

3:00 - 3:45 **Walt Schneider** (*University of Pittsburgh*)
"Lessons from the Pittsburgh Brain Activity Interpretation Competition"

4:00 - 4:45 **Ken Norman** (*Princeton University*)
"Testing Psychological Theories with Multivariate Pattern Analysis"



Center for Computational Biology
Demonstration Day
(Software Demonstrations and Training Event)
Saturday, July 19, 2008
Neuroscience Research Building Auditorium

8:00-9:00 AM	**Registration and Breakfast**
9:00-9:10 AM	Welcome and Meeting Outline from Arthur Toga and Paul Thompson
	9:10-10:30 AM Shape Tools
9:10-9:30 AM	Zhuowen Tu – "Automated Volume and Sulcal Parsing"
9:30-9:50 AM	Duygu Tosun – "Measures of 3-D Cortical Morphometry"
9:50-10:10 AM	Roger Woods – "Shape Tools/Libs/Viewer"
10:10-10:30 AM	Yonggang Shi – "Direct 3D Shape Mapping"
10:30-10:50 AM	**Break**
	10:50-11:50 AM DTI/HARDI
10:50-11:10 AM	Kristi Clark – "DTI Tools"
11:10-11:30 AM	Nathan Hageman – "Leviathan"
11:30-11:50 AM	Jonathan Morra – "Automated Feature Extraction Pipeline"
12:10-1:10 PM	**Lunch**
	1:30-2:50 PM Workflows & Validation
1:30-1:50 PM	Cornelius Hojatkashani & Petros Petrosyan – "Pipeline"
1:50-2:10 PM	Stott Parker – "Pipeline Intelligence Plug-in"
2:10-2:30 PM	Amanda Hammond & Cornelius Hojatkashani – "LONI Toolbench"
2:30-2:50 PM	David Shattuck – "Online Validation Resource"
	2:50-3:00 PM Discussion & Adjourn

http://cms.loni.ucla.edu/CCB_Demo_Day_2008.aspx

The mission of the Institute for Pure and Applied Mathematics (IPAM) is to make connections between a broad spectrum of mathematicians and scientists, to launch new collaborations, to better inform mathematicians and scientists about interdisciplinary problems, and to broaden the range of applications in which mathematics is used. IPAM is one of seven NSF Mathematical Sciences Institutes in the U.S. It opened its doors in 2000 with its initial five-year grant, which was renewed in 2005.

IPAM offers a variety of programs for junior and senior scholars, graduate students and undergraduate students in mathematics, engineering, and a wide range of scientific disciplines in which mathematics may be applied. Every year IPAM offers two three-month scientific programs that feature a series of workshops on a broad theme. IPAM sponsors independent five-day workshops and co-sponsors conferences on a variety of topics as well. During the summer, IPAM holds a program for undergraduates (RIPS) and for graduate students and postdocs (summer school).

Encouraging the careers of women and minority mathematicians and scientists is an important component of IPAM's mission.

More information on the Institute for Pure and Applied Mathematics can be found at http://www.ipam.ucla.edu/.

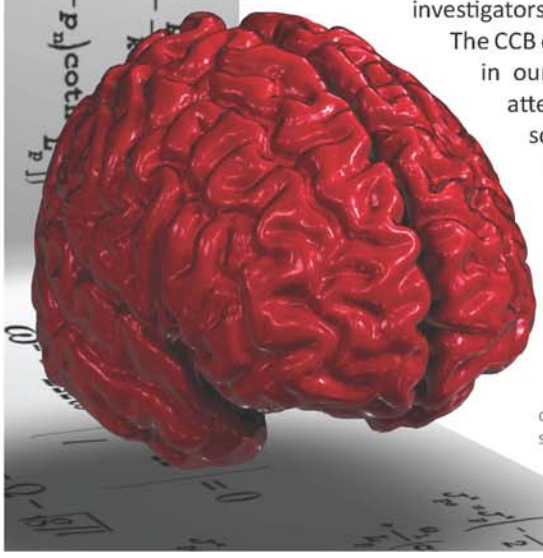
Center for Computational Biology

The mission of the CCB is to develop multi-scale, interactive, computational brain atlases. These atlases represent complex information management infrastructures that will accommodate geometric, shape, anatomical, functional, demographic, phenotypic and genomic brain data. The CCB designs, implements, and validates novel computational techniques for mathematical modeling and quantitative analysis. These methods are applied to study a wide spectrum of translational sciences such as structural and metabolic brain studies, shape-based biological trait markers, and quantitative phenotype variability in healthy and diseased populations. The CCB's outside collaborations, called Driving Biological Projects (DBPs), and investigator-initiated research projects motivate the development of new mathematical models and algorithm designs, and serve as test beds for newly developed scientific computational tools. The entire community of computational scientists can use and validate the CCB data resources and computational tools for a variety of broader applications.

THE CCB PROVIDES AN INTEGRATED MULTI-DISCIPLINARY ENVIRONMENT FOR STUDYING GENOMIC FUNCTION, BIOLOGICAL SHAPE, AND PHENOTYPIC VARIATION.

CCB Collaborations

The CCB is a collaborative research center that fosters a variety of collaborative and educational endeavors. The CCB capitalizes on the synergy of multiple scientific and computational disciplines, promotes knowledge dissemination, and seeks new investigators and opportunities for scientific studies and research collaborations. The CCB encourages fellow, graduate, and undergraduate student participation in our efforts. We also welcome utilization of our web resources and attendance in our computational biology course offerings, visiting scholar series, workshops, and seminars. The CCB strives to build a new scientific computational paradigm for future biological discovery.



Interested collaborators, fellows, students or other investigators should feel free to contact us at www.ccb.ucla.edu.

This CCB center grant U54 RR021813 is funded as a NIH Roadmap Initiative, which includes support from the National Center for Research Resources (NCRR) and the National Institute of General Medical Sciences (NIGMS). In 2004-2005 the National Institutes of Health, funded seven specialized centers for biomedical computing. These NIH National Centers are creating the backbone of a national infrastructure network, which is known as the National Program of Excellence in Biomedical Computing (NPEBC). The NIH National Centers for Biomedical Computing (www.NCBCs.org) provide datasets, software tools and web-services that researchers, clinicians and students can utilize in a variety of ways.

The Center for Imaging Science (CIS), established in 1998 by the Whiting School of Engineering at the Johns Hopkins University as part of the Whitaker Institute of Biomedical Engineering and currently the Institute for Computational Medicine, brings together an interdisciplinary group of researchers developing biomedical applications based on theoretical advances in mathematicsal statistics, signals and systems, and geometry. The principal faculty are Patrick Barta, Donald Geman, John Goutsias, Bruno Jedynak, Michael Miller, Carey Priebe, Rene Vidal, Tilak Ratnanather, and Laurent Younes who have appointments in the Departments of Biomedical Engineering, Electrical and Computer Engineering, and Applied Mathematics and Statistics. The research program at CIS is organized around several themes in Biomedical image analysis and Computer Vision including (i) representations of shape and structure in computational anatomy, (ii) computational statistics and biomarker development and (iii) image interpretation in computer vision.

To convey the flavor and purpose of the research at CIS consider the first theme. Due to the rapid development of imaging sensor technologies, investigators in the physical and biological sciences are now able to observe living systems and measure both their structural and functional behavior across many scales, from global, aggregate behavior to the microscopic scale of sub-cellular structure. Combining biomedical imaging science with computational modeling, we are now able to infer, non-invasively, the structural and functional properties of complex biological systems and neural circuits, for instance study the cohorts of neuropsychiatric illnesses including schizophrenia, depression, epilepsy, dementia of Alzheimer type, and Parkinson's.

Much of the effort at CIS is currently focused on developing systems that can interpret images of biological and evolutionary complexity such as natural scenes imaged via video cameras, or complex anatomical imagery obtained with bio-medical imaging devices across multiple spatial scales. While great advances have been made in the acquisition of image data, e.g., the development of cameras and other imaging devices, and though the semantic understanding of the shapes and other objects appearing in images is effortless for human beings, the corresponding problem in machine perception, namely automatic interpretation via computer programs, remains a major open challenge in modern science.

MBI 2008 SPEAKER ABSTRACTS

WEEK I

Monday, July 14, 2008

Surface-Based Computational Mapping of the Cerebral Cortex

- David van Essen, Washington University in St. Louis - School of Medicine

Cerebral cortex is the dominant structure of the human brain, and deciphering its many functions represents one of the grand challenges of modern neuroscience. In humans, cerebral cortex is a highly convoluted sheet whose pattern of folds varies greatly from one individual to the next. The cortex is a mosaic of many anatomically and functionally distinct areas (~100 – 200 in total), each of which is variable in size and in its relationship to cortical folds. To cope with these basic facts and to capitalize on the enormous amounts of information obtained using noninvasive structural and functional neuroimaging methods, a variety of powerful visualization and analysis tools have been developed in recent years. This lecture will discuss some of these methods and illustrate how they have been applied to the study of normal adult and developing brains and to a variety of disease conditions. These methods include (i) cortical segmentation, surface reconstruction and inflation, which greatly aid visualization of complex convolutions; (ii) surface-based registration to compensate for individual variability; (iii) surface-based morphometry as a strategy for analyzing individual variability, interhemispheric asymmetries, and disease-related folding abnormalities; and (iv) interspecies surface-based registration as a strategy for evaluating homologies and gaining insights into the evolution of primate cerebral cortex. A final topic will be the expanding role of databases and data mining in helping neuroscientists make efficient use of the flood of experimental data on the human brain in health and disease.

Mapping Brain Changes Over Time During Development

- Guido Gerig, University of Utah - Radiation Oncology, Biomedical Engineering and Computer Science

Imaging studies of early brain development get increasing attention as improved modeling of the pattern of normal development might lead to a better understanding of origin, timing and nature of morphologic differences in neurodevelopmental disorders. A main goal is the modeling of the trajectory of early brain development using structural MRI and diffusion tensor imaging (DTI) and statistical analysis of growth trajectory differences in psychiatric disorders. Studying this age group involves two major challenges, successful MRI scanning of non-sedated infants and image analysis methods designed to describe the trajectory of early growth. The talk will discuss work in progress towards longitudinal modeling of early brain growth via structural MRI and DTI but will also highlight open issues and the need for advanced image analysis concepts. Key components are the building of cross-sectional unbiased atlases per age group and its extension to spatio-temporal 4-D longitudinal atlases. A framework for population-based statistical analysis of diffusion properties of fiber tracts of interest parameterized by arc-length will be presented. Joint modeling of DTI and multi-contrast MRI reveals the importance of a statistical framework for multi-variate analysis to fully capture the pattern of early structuring of brain tissue and changes due to pathology. Preliminary results from clinical longitudinal neuroimaging studies (infants at risk for mental illness, autism study) conducted at UNC will be shown. New analytic methods show excellent potential to contribute to a better understanding of origin, timing and nature of morphologic differences in neurodevelopmental disorders.

Cortical Mapping Using Conformal Geometry

- Monica Hurdal, Florida State University – Mathematics

The locations and patterns of functional brain activity in humans are difficult to compare across subjects because of individual differences in cortical folding and the fact that functional foci are often buried within cortical sulci. While it is mathematically impossible to flatten curved surfaces in 3-space without introducing metric and areal distortion, several algorithms can minimize such distortion; consequently, metric flattening has been central in brain mapping efforts. On the other hand, while it has been known for 150 years that it is mathematically possible to flatten surfaces without any angular distortion, until the last decade there has been no algorithm for approximating these conformal flat maps. Conformal maps are particularly versatile, offering a variety of visual presentations and manipulations backed by a uniquely rich mathematical theory. Using a circle packing algorithm we obtain discrete conformal mappings which exploit this versatility. In this lecture, we present an introduction to the mathematics of conformal mappings and describe an approach based on circle packings, the first practical realization of the 150-year-old Riemann Mapping Theorem. We discuss the notion of a conformal structure on a surface, describe key features of the three geometries of constant curvature where our maps reside: the sphere, plane and hyperbolic disc, and their classical conformal automorphisms. We will also discuss conformal invariants, surface topology, cortical surface reconstruction and applications of conformal maps in neuroscientific studies.

Automated Analysis of Cortical and Subcortical Anatomy in Brain MRI

- Bruce Fischl, Harvard Medical School

In this talk I will discuss research with the goal of building models of brain anatomy. The neuroanatomical structures of interest can be broadly subdivided into two categories - cortical and non-cortical. Cortical structures (particularly the cerebral cortex) are typically highly folded, thin sheets of gray matter. Functionally, the cerebral cortex has been shown to have a "columnar" architecture. For this reason, we construct surface-based models for analysis of cortical properties. The construction of such models is a difficult task due to the high degree of folding of the cortical manifold in conjunction with the limited (~ 1 mm) resolution of current neuroimaging technologies. Once constructed, the cortical models can be deformed for morphometry, visualization and registration purposes. I will show some results of this type of analysis, including the morphometric changes that the cortex undergoes in disorders such as schizophrenia, Alzheimer's disease, and Huntington's disease, as well as healthy aging. A different set of techniques have been developed for the construction of models of subcortical structures. Here, we model the segmentation as an anisotropic nonstationary Markov Random Field. The anisotropy lets us model the local spatial relationships that exist between neuroanatomical structures (e.g. hippocampus is anterior and inferior to amygdala), while the nonstationarity facilitates the encoding of inhomogeneous properties of the tissue within a structure. This approach is based on extracting the relevant model parameters from a manually labeled training set, and has been shown to be comparable in accuracy to the manual labeling. Finally, I will discuss our ongoing efforts to link microstructural features of the brain typically only visible under a microscope, with macrostructural properties visible on standard scans. This linkage provides an objective means to assess the accuracy of various coordinate systems, and to optimize the alignment of homologous areas across subjects.

Computing Sulcal Curves and the Complexity of Brain Connectivity

- Guillermo Sapiro, University of Minnesota, Twin Cities

In this talk we will first present a geometric framework for computing sulcii curves. We will then concentrate on new techniques for computing brain matter complexity from diffusion imaging.

C. Y. Kao, M. Hofer, G. Sapiro, J. Stern, K. Rehm, and D. A. Rottenberg, A geometric method for automatic extraction of sulcal fundi,IEEE Trans. Medical Imaging 26, pp. 530-540, 2007.

G. Haro, G. Randall, and G. Sapiro, Translated Poisson mixture model for stratification learning, International Journal Computer Vision, to appear.

G. Haro, C. Lenglet, G. Sapiro, and P. Thompson, On the non-uniform complexity of brain activity, IEEE International Symposium on Biomedical Imaging, Paris, May 2008.

Towards Automated Whole Brain Image Segmentation

- Zhuowen Tu, University of California, Los Angeles (UCLA) - School of Medicine

Segmenting cortical and sub-cortical structures from 3D brain images is of significant practical importance. In this talk, we will discuss a new statistical modeling/computing framework and show its application for whole brain segmentation. The notion of using context information for solving the medical imaging problem has been increasingly realized in the field. However, how to learn an effective and efficient context model, together with the image appearance, remains mostly unknown. The current literature using Markov Random Fields (MRFs) and Conditional Random Fields (CRFs) often involves specific algorithm design, in which the modeling and computing stages are studied in isolation. Medical images observe complex patterns, contributed by many factors such as textures (homogeneous, inhomogeneous, and structured) and machine parameters. This auto-context model is about a new attempt to push the appearance and context information in a seamless way by automatically incorporating a large number of short-range and long-range features. The resulting algorithm has nearly the identical procedures in computing (testing) as in modeling (training), and thus, achieves rapid performance the holistic medical image segmentation task. We will show a variety of sub-cortical and cortical segmentation results using this model.

Tuesday, July 15, 2008

Computational Functional Anatomy

- Michael Miller, Johns Hopkins University - Center for Imaging Science

Computational Functional Anatomy is the study of structure and function in anatomical coordinates. We review some of the methods being used in CFA by our groups.

Evolution Equations in Computational Anatomy

- Laurent Younes, Johns Hopkins University

One of the main purposes in computational anatomy is the measurement and statistical study of anatomical variations in organs, notably in the brain or the heart. Over the last decade, our group has progressively developed several approaches for this problem, all related to the Riemannian geometry of groups of diffeomorphisms and the shape spaces on which these groups act. Several important shape evolutions equations that are now used routinely in applications have emerged over time. Our goal in this presentation is to provide an overview of these equations, placing them in their theoretical context, and giving examples of applications in which they can be used. We introduce the required theoretical background before discussing several classes of equations of increasingly complexity. These equations include energy minimizing evolutions deriving from Riemannian gradient descent, geodesics, parallel transport and Jacobi fields.

Computational Functional Anatomy

- Anqi Qiu, Johns Hopkins University

Emerging with advanced imaging techniques, Computational Functional Anatomy (CFA) is a new discipline in the medical imaging research to identify imaging markers associated with a specific disease and explore their relationships with clinical assessments as well as genetic and environmental factors. To achieve this, CFA mathematically models anatomical configurations and signals associated with anatomy and functions of a specific organ in anatomical coordinates in multi-modal images. We will focus on two topics in this talk: 1) tracking within-subject brain shape changes in serial images and comparing them across subjects; 2) studying signals associated with anatomy and functions of the brain in anatomical coordinates.

Statistics of Shape: Simple Statistics on Interesting Spaces

- Sarang Joshi, University of Utah - Radiation Oncology, Biomedical Engineering and Computer Science

A primary goal of Computational Anatomy is the statistical analysis of anatomical variability. A natural question that arises is how does one define the image of an “Average Anatomy”. Such an “average” must represent the intrinsic geometric anatomical variability present. Large Deformation Diffeomorphic transformations have been shown to accommodate the geometric variability but performing statistics of Diffeomorphic transformations remains a challenge. In this lecture I will further extend this notion of averaging for studying change of anatomy on average from a cross sectional study of growth. Regression analysis is a powerful tool for the study of changes in a dependent variable as a function of an independent repressor variable, and in particular it is applicable to the study of anatomical growth and shape change. When the underlying process can be modeled by parameters in a Euclidean space, classical regression techniques are applicable and have been studied extensively. However, recent work suggests that attempts

to describe anatomical shapes using flat Euclidean spaces undermines our ability to represent natural biological variability. In this lecture I will develop a method for regression analysis of general, manifold-valued data. Specifically, we extend Nadaraya-Watson kernel regression by recasting the regression problem in terms of Frechet expectation. Although this method is quite general, our driving problem is the study anatomical shape change as a function of age from random design image data. I will demonstrate our method by analyzing shape change in the brain from a random design dataset of MR images of 97 healthy adults ranging in age from 20 to 79 years. To study the small scale changes in anatomy, we use the infinite dimensional manifold of diffeomorphic transformations, with an associated metric. We regress a representative anatomical shape, as a function of age, from this population.

Generative Models and Stochastic Algorithms for Population Average Estimation and Image Analysis.

- Stephanie Allassonniere, Johns Hopkins University - Center for Imaging Science

For the last decade, we have witnessed impressive achievements and the emergence of elaborated registration theories. But the definition of a proper statistical framework for addressing the down-to-earth and fundamental problem of computing population averages in image analysis in presence of unobserved variables has not received so much attention from a more mathematical statistics perspective. This presentation will focus on two examples where statistical generative models and stochastic algorithms can lead to an estimation of such population template. We will first present a careful definition and analysis of well defined statistical generative models based on dense deformable templates for gray level images of deformable objects where the warping variables need to be considered as unobserved random variables. This coherent statistical framework addresses the problem of estimating a template image (photometry) and at the same time some geometrical variability from an image database. We carry out this estimation using two variations of the EM algorithm in a small sample setting: one of them uses a deterministic approximation of the EM, while the other is based on a stochastic formulation (SAEM), coupled with the use of MCMC methods. This approach is then generalized to a mixture of deformable template models to derive a clustering algorithm for the data. We will present some experiments done on handwritten images and 2D medical images. We applied the same methodology to the estimation of a Diffusion Tensor Image (DTI) template where experiments have been done on synthetic and real data. Finally, this approach can also be used for the estimation of Independent Component Analysis (ICA) which will be presented briefly.

Wednesday, July 16, 2008

Mathematical Concepts for DTI and High-Angular Resolution Diffusion Imaging

- Christophe Lenglet, Siemens Corporate Research, Inc.

Diffusion MRI enables us to non-invasively probe the microstructure of biological tissues. It is of the utmost importance to design powerful biomarkers for studying neurological disorders. Combined with functional MRI, it has also started to shed new light on the anatomo-functional networks of the human brain. However, the complexity of the data and the need for adequate mathematical models raise many theoretical and computational challenges. I will present a series of mathematical concepts and computational tools based on differential geometry, partial differential equations, front propagation and spherical data analysis for the processing of Diffusion Tensor Images (DTI) and High Angular Resolution Diffusion Images (HARDI). I will discuss problems such as the cerebral connectivity mapping, the segmentation of DTI/HARDI and the registration of DTI. I will show how the fusion of structural MRI and fMRI with DTI can provide exquisite insights into the architecture of the human motor and visual systems. Finally, I will describe how manifold learning techniques can help quantifying the non-uniform complexity of the cerebral white matter from HARDI.

Trends in Diffusion MRI Tractography

- Carl-Fredrik Westin, Harvard University

In this talk I will present an overview of different types of diffusion MRI tractography methods available. Tractography is a promising method for tracing and visualizing bundles of white matter fiber tracts in the brain in-vivo. A simple and effective method for tracing nerve fibers, often called stream-line tractography, uses diffusion measurements from MRI and follows the direction of the maximum diffusion along the path. Although the stream-line method is widely used, it suffers from some major disadvantages. The connectivity is restricted to a one-to-one mapping between points, not allowing the branching that real nerve fibers may undergo. It also gives the impression of being precise, not taking the uncertainty of fiber paths into account in the tracing procedure. Several alternative methods are available and actively researched. For example, stochastic methods have been proposed and have the advantage that they can model uncertainty. Methods based on heat/diffusion simulations have been proposed and have the advantage to be closely related to the data. Geometric geodesic approaches have been proposed and have the advantage to cast the problem into defining distances between locations in the brain, and thus providing a geometrically intuitive meaning of tractography. An overview of the most widely used methods will be given, and their strengths and weaknesses will be discussed.

Tract-Based Spatial Statistics

- Steve Smith, University of Oxford

Abstract not provided.

Higher-Order Tensor Models for DTI Segmentation and Analysis

- Baba Vemuri, University of Florida

In Diffusion Weighted Magnetic Resonance Image (DW-MRI) processing, a 2nd order tensor has been commonly used to approximate the diffusivity function at each lattice point of the DW-MRI data. From this tensor approximation, one can compute useful scalar quantities (e.g. anisotropy, mean diffusivity) which

have been clinically used for monitoring encephalopathy, sclerosis, ischemia and other brain disorders. It is now well known that this 2nd-order tensor approximation fails to capture complex local tissue structures, e.g. crossing fibers, and as a result the scalar quantities derived from these tensors are grossly inaccurate at such locations. In this talk, I will present a 4th order symmetric positive-definite (SPD) tensor approximation to represent the diffusivity function and present a novel technique to estimate these tensors from the DW-MRI data guaranteeing the SPD property. Several articles have been reported in literature on higher order tensor approximations of the diffusivity function but none of them guarantee the positivity of the estimates, a fundamental constraint since negative values of the diffusivity are not meaningful. In this talk, I will show an application of Hilbert's theorem on ternary quartics –- when the 4th order tensors are represented by ternary quartics -- in conjunction with the Iwasawa parameterization will guarantee an SPD 4th-order tensor approximation from the DW-MRI data. I will then present the performance of this model on several synthetic and real DWMRI data sets from excised rat and cat spinal cords.

Tract-Based Morphometry: White Matter Tract Clustering and Correspondence in Populations

- Lauren O'Donnell, Harvard University

The ability to perform statistical analysis of the brain's white matter connections (fiber tracts) has applications in neuroscience and in the study of disease. A popular approach for white matter analysis is the quantification of parameters derived from DTI tractography. We begin the presentation with an overview of white matter fiber tract anatomy as seen in streamline tractography data. Then we address two problems that must be solved to perform group analysis of DTI data within a fiber tract of interest. The tract must first be identified (segmented) in all subjects. Second, to localize group differences to a region within the tract, a common coordinate system must be generated for that tract in all subjects. Our tract-based morphometry analysis pipeline performs segmentation based on learning a model of common white matter structures in the group, followed by statistical analysis of data along fiber tracts. We explain our approach to the segmentation and coordinate system problems, and we provide pointers to related methods.

Tubular Surface Evolutions for Segmentation of Tubular Structures with Applications to Fiber Bundles From DW-MRI

- Ganesh Sundaramoorthi, Georgia Institute of Technology – Computer Science

In this paper, we provide a framework for extracting tubular structures from medical imagery. The general methodology will be applied to modeling and extracting the cingulum bundle (CB) from diffusion-weighted imagery (DW-MRI) of the brain. The CB is a tube-like structure in the brain that is of major importance to clinicians since it may be helpful in diagnosing schizophrenia. This structure consists of a collection of fibers in the brain that have locally similar diffusion patterns, but vary globally. Standard region-based segmentation techniques adapted to DW-MRI are not suitable for this application because the diffusion pattern of the CB cannot be described by a few simple global statistics. Typical active surface models extended to DW-MRI allow for arbitrary deformations that give rise to unlikely shapes, which do not respect the tubular geometry of the CB. In this work, we explicitly model the CB as a tube-like surface and construct a general class of energies defined on tube-like surfaces. Modeling the CB as a tube-like surface is a natural shape prior. Since a tube is characterized by a center-line and a radius function, the method is reduced to a curve evolution that is computationally much less costly than an arbitrary surface evolution. Our tubular model of the CB also has the advantage that computing shape statistics and functions defined on the CB are much simplified.

Thursday, July 17, 2008

Pre-processing for Voxel-Based Morphometry

- John Ashburner, University of London

This talk will describe the preprocessing steps involved in the technique of voxel-based morphometry. The procedure begins by segmenting anatomical images of a number of subjects into their different tissue classes, using a generative modeling approach. The model combines tissue classification, bias correction and nonlinear registration of pre-generated tissue probability maps. The segmentation results are used to generate approximately rigidly aligned gray and white matter images for each subject. More precise inter-subject registration is then performed by repeatedly aligning the grey and white matter images to their own mean, using a high-dimensional warping approach that preserves the one-to-one mapping among brains. Warped versions of the gray matter images are generated, which are locally scaled in order to compensate for expansion/contraction during warping. These data are spatially smoothed, prior to performing voxel-wise statistical tests within the framework of the General Linear Model.

Morphological Appearance Manifolds for Computational Anatomy

- Christos Davatzikos, University of Pennsylvania

The field of computational anatomy has developed rigorous frameworks for analyzing anatomical shape, based on diffeomorphic transformations of a template. However, differences in algorithms used for template warping, in regularization parameters, and in the template itself, as well as in other variables, lead to different representations of the same anatomy. Variations of these parameters are considered as confounding factors, since they lead to different descriptions of the same exact shape. Recently, extensions of the conventional computational anatomy framework to account for such confounding variations has shown that learning the equivalence class derived from the multitude of representations of an individual anatomy can lead to improved and more stable morphological descriptors. Herein, we follow that approach, estimating the morphological appearance manifold obtained by varying parameters of the template warping procedure. Our approach parallels work in the computer vision field, in which variations lighting, pose and other parameters leads to image appearance manifolds representing the exact same figure in different ways. The proposed framework is then used for groupwise registration and statistical analysis of biomedical images, which employs a minimum variance criterion to perform manifold walking, i.e. to traverse each individual's morphological appearance manifold until the representations of all individuals in a group come as close to each other as possible. Effectively, this process removes the aforementioned confounding effects and potentially leads to morphological representations that reflect purely underlying biological variations, instead of variations introduced by modeling assumptions and parameter settings. The nonlinearity of a morphological appearance manifold is treated via local linear approximations of the manifold via PCA.

Large-Scale Computing Frameworks for Developing Image Analysis Tools

- Steve Pieper, Harvard University

The National Alliance for Medical Image Computing (NA-MIC) has been chartered to create an open source software infrastructure to support translational biomedical imaging research. Within NA-MIC and a number of closely collaborating groups, we have assembled software to address major building blocks including file I/O, numerics, visualization, user interface, and data archiving which are collectively called the NA-MIC Kit. For all these tools we have invested heavily in interoperability and feature enhancement while in some cases we have written new tools from scratch to fill important functional blocks. In addition, we promote a software engineering methodology around the themes of open development, ongoing cross-platform testing, and coding conventions that promote maintainability and code reusability. In addition to

the core tools, we have created domain-specific workflows to address biomedical research areas from population studies of neurodegenerative diseases to robot guided prostate interventions. Addressing these clinical use cases helps refine and validate the underlying software systems. In this talk I will review the motivations, organization, and implementation of the NA-MIC Kit with particular emphasis on our efforts to build a distributed community of like-minded developers and users who share not just a common programming environment, but a common language for effective collaboration. I will review how these efforts are beginning to have a positive impact on particular research areas and how we plan to accommodate anticipated growth of the community.

Improving Image Reconstruction in MRI

- Tom Goldstein, University of California, Los Angeles (UCLA)

Many common image-processing tasks (such as denoising, deblurring etc...) involve total variation (TV) based optimization problems. One of the newest and most exciting application of TV-based imaging is the field of compressed sensing (CS), which allows high-resolution images to be constructed from small amounts of data. In this talk, we will give a brief introduction to CS and other TV regularized problems related to MRI. We will then discuss a simple and highly efficient numerical scheme for computing solutions to these problems. Finally, we will present some CS imaging results, and discuss how CS techniques can lead to faster scan times, and higher image quality.

Friday, July 18, 2008

Geodesics in Deformation Morphometry and DTI

- James Gee, University of Pennsylvania

Abstract not provided.

Statistics Computing on Manifolds: from Riemannian Geometry to Computational Anatomy

- Xavier Pennec, Institut National de Recherche en Informatique Automatique (INRIA) - Projet Epidaure

Computational anatomy aims at modeling the biological variability of the human anatomy. To reach this goal, the method is to identify anatomically representative geometric features (points, tensors, curves, surfaces, volume transformations), and to describe and compare their statistical distribution in different populations. Unfortunately, geometric features often belong to manifolds that are not vector spaces. Based on a Riemannian manifold structure, we will detail how one can develop a consistent framework for statistical computing on manifolds, starting with the notions of mean value and covariance matrix of a random element, normal law, Mahalanobis distance and test. Then, we will extend the Riemannian computing framework to PDEs for smoothing and interpolation of fields of geometric elements with the example of positive define symmetric matrices (tensors). We show that the choice of a convenient Riemannian metric allows generalizing consistently to tensor fields many important geometric data processing algorithms such as interpolation, filtering, diffusion and restoration of missing data. This framework will be exemplified with the modeling of the brain variability from a dataset of lines on the cerebral cortex. The resulting dense 3D variability map can be seen as the diagonal elements of the Green's function of the Brain accross subjects. This modeling can be extended with non-diagonal element by computing significantly correlated regions in the brain. Finally, we will discuss some of the methods that have been recently introduced to compute statistics on diffeomorphisms.

Generalized Tensor-Based Morphometry for the Analysis of Brain MRI and Diffusion Tensor Images

- Natasha Lepore, University of California, Los Angeles (UCLA)

Tensor-based morphometry (TBM) is widely used in computational anatomy as a means to understand shape variation between MR structural brain images. A 3D nonlinear registration technique is used to align all brain images to a common neuroanatomical template, and the deformation fields are analyzed statistically to identify group differences in anatomy in TBM. Differences between images are usually computed solely from the determinants of the Jacobian matrices J that are associated with the deformation fields computed by the registration procedure. The determinants give the local volume increases and reductions of the image from the registration. However, only the magnitude of the expansions or contractions is examined, while the directional components of the changes are ignored. We propose an approach which remedies this problem, by computing both shape and volume change statistics using the deformation tensors, defined as (J^T J)^1/2. Furthermore, detection power depends on several factors, and key among these is the quality of the non-linear registration, which depends both on the registration algorithm and on the common target to which all images are mapped. We designed a new fluid registration code which penalizes deviations from zero deformation tensors. To reduce dependence on the choice of individual template, we average deformation tensors from multiple registrations to individual reference images. The registration and statistics in the proposed approach can both be extended in a straightforward way to the analysis of diffusion tensor images.

WEEK II

Monday, July 21, 2008

Modeling fMRI Data with Uncertain Hemodynamic Response or Stimulus Functions

- Martin Lindquist, Columbia University

The relationship between stimuli and the BOLD response they elicit is often modeled using a linear time invariant (LTI) system, where a time series of hypothesized metabolic activity is the input and an estimated or assumed hemodynamic response function (HRF) is the impulse response function. This talk focuses on situations when the exact form of the stimulus or HRF is not known a priori. We begin by discussing a variety of linear and non-linear techniques for estimating the HRF. For each method, we introduce techniques for estimating amplitude, peak latency, and duration and for performing inference in a multi-subject fMRI setting. We then assess each technique's relative sensitivity and its propensity for mis-attributing task effects on one parameter (e.g., duration) to another (e.g., amplitude). Finally, we introduce methods for quantifying model misspecification and assessing the bias and power-loss related to the choice of model. Overall, the results show that it is surprisingly difficult to accurately recover true task-evoked changes in BOLD signal, and that there are substantial differences among models in terms of power, bias and parameter confusability. Finally, we discuss situations when the stimulus onset and duration are unknown. In these situations change point methods can be used to make inferences about activation. In this talk I will discuss methods for estimating an unknown distribution of onset times and durations using these methods.

Modeling Temporal Structure

- Steve Smith, University of Oxford

Abstract not provided.

fMRI Design Optimization

- Thomas Liu, University of California, San Diego (UCSD)

The proper design of an fMRI experiment can involve many factors that are critical to its success. In this talk, I will focus on optimizing the statistical efficiency of designs. After reviewing the framework of the general linear model, I will introduce metrics for statistical efficiency and discuss how these metrics strongly depend on the underlying assumptions that an investigator must inevitably make. I will also review methods for optimizing statistical efficiency, such as the use of m-sequences and genetic algorithms.

A Bayesian Hierarchical Framework for Spatial Modeling of fMRI Data

- DuBois Bowman, Emory University School of Public Health

Applications of functional magnetic resonance imaging (fMRI) have provided novel insights into the neuropathophysiology of major psychiatric, neurological, and substance abuse disorders and their treatments. Modern activation studies often compare localized task induced changes in brain activity between experimental groups. Complementary approaches consider the ensemble of voxels constituting an anatomically defined region of interest (ROI) or summary statistics (e.g. means) of the ROI. In this work, we present a Bayesian extension of voxel-level analyses that offers several notable benefits. Among these,

it combines whole-brain voxel-by-voxel modeling and ROI analyses within a unified framework. Secondly, the model allows for the study of inter-regional (long-range) correlations as well as intra-regional (short-range) correlations. Estimation is performed using Markov Chain Monte Carlo (MCMC) techniques implemented via Gibbs sampling. We apply our Bayesian hierarchical model to fMRI data from a study of inhibitory control in cocaine-dependent men.

Modeling Inter-Subject Variability in Activation Locations of fMRI Data: A Bayesian Hierarchical Spatial Modeling Approach

- Timothy Johnson, University of Michigan

The aim of this work is to develop a spatial semiparametric Bayesian model for multi-subject fMRI data. While there has been much work on univariate modeling of each voxel for single- and multi-subject data, and some work on spatial modeling for single-subject data, there has been virtually no work on spatial models that explicitly account for inter-subject variability in activation location. The data are fitted with a Bayesian semiparametric hierarchical spatial model. While most previous work uses Gaussian mixtures for the activation shape, at the first level we instead use Gaussian mixtures for the probability that a voxel belongs to an activated region. Spatial correlation is accounted for in the mixing weights. At the second level mixture component means are clustered about individual activation centers. At the third level individual activation centers are clustered about population centers. At the fourth level, population parameters are modeled as a Dirichlet process. Our approach incorporates the unknown number of mixture components and individual centers into the model as parameters whose posterior distributions are estimated by reversible jump Markov Chain Monte Carlo (RJMCMC) at levels two and three. A mixture of Dirichlet process priors (MDP) is used to nonparametrically model the distribution of individual centers about the population centers at level 4. We demonstrate our method with an fMRI study of resolving proactive interference.

Tuesday, July 22, 2008

Considerations in Multi-Site fMRI

- Gary Glover, Stanford University

There are many reasons for wanting to perform multi-site investigations employing MRI or fMRI, including reduced study duration with large study populations and access to a wider set of demographic characteristics. However, inter-site differences in scanner vendors and pulse sequences as well as calibration of scanners can cause difficulties when trying to combine anatomic images in multi-site studies utilizing MRI. These problems are exacerbated greatly in fMRI because of the additional need to monitor and maintain scanner stability and to carefully standardize fMRI scanning practices (e.g. subject preparation) and ancillary hardware such as response boxes and projection and auditory stimulus equipment. Uncontrolled differences in any of these aspects of study design and implementation can introduce significant inter-site variance in the data pool and render combination from multiple sites questionable. In this presentation, the use of scanner QA methods, standardization of pulse sequence parameters, inter-site and inter-subject calibration methods and the importance of controlling for scanning procedures across all sites are considered. A case study (the NIH NCRR-funded FIRST-BIRN: Functional Imaging Research in Schizophrenia Testbed Biomedical Imaging Research Network) will be discussed, including solutions that have been developed to deal with scanner upgrades and on-going data QA.

Reproducibility in Group Modeling

- J.B. Poline, Commissariat à l'Énergie Atomique (CEA)

Functional MRI is a recent and powerful tool for studying the brain functions in both normal subjects and the patients. It has therefore inspired a wealth of interesting works in statistics, signal processing, image processing and modeling. There is however a gap between the current methods used in processing those data by the neuroscience or medical community and the most advanced methods proposed in the literature. Partly, this is due to the time needed for new technique to be understood and made available with the diffusion of software, and partly because the most interesting and difficult questions in the functional imaging community are only partially addressed. In this talk, I will focus on the problems involved in analyzing the data from several subjects, in order to extract some knowledge on the parent population. The most used technique relies on a spatial normalization of the subjects' brain and on standard statistics. I will point the limitations of this and describe new techniques improving both for spatial and the brain activity models aspect of the problem. The impact of those techniques on the reliability of group analysis will be described. I will then discuss what seem to be the future challenges in functional neuroimaging with a specific emphasis on databases.

Reproducibility Across Analysis Methods

- Stephen Strother, University of Toronto

Abstract not provided.

Multiple Comparisons and Random Field Methods

- Jonathan Taylor, Stanford University – Statistics

This presentation focuses on describing the basic multiple comparison problem encountered in many different neuroimaging applications and various approaches to resolving this problem. We will describe

Random Field Theory (RFT), a technique to control Family Wise Error Rate (FWER) in some detail, comparing it to permutation methods. We will also describe some of the basic ideas of the False Discovery Rate (FDR), as yet another approach to resolve this problem.

The Statistical Analysis of Cortical Surface Data

- Keith Worsley, University of Chicago - Department of Mathematics and Statistics

This presentation emphasizes the mechanics, rather than the methods, from data to publication. I will present Matlab software (SurfStat) for the statistical analysis of univariate and multivariate surface data using linear mixed effects models (fitted by ReML) and random field theory (RFT). SurfStat is intended for cortical thickness data on triangular meshes, but it will handle any triangulated surface data; the only requirement is that the triangulation scheme must be the same for all surfaces, i.e. the data must be registered to a common surface. Inference uses RFT for T, F, Hotelling's T^2 and Roy's maximum root statistics. An attractive feature is the use of a model formula rather than a design matrix for specifying the linear model. It is fast, because everything is loaded into memory, permitting a truly interactive analysis, with no need for batch. Finally, off-the-shelf Matlab graphics are ready to publish.

Advances in FDR for fMRI

- Ruth Heller, University of Pennsylvania

The fundamental units of interests in fMRI are the spatially contiguous clusters of voxels that are activated together. The investigator may know a-priori these cluster units or an approximation to them. Since the activation may be absent from part of each cluster, we define a cluster as active if there is activation somewhere within the cluster. Testing these cluster units has a two-fold statistical advantage over testing each voxel separately: the signal to noise ratio within the unit tested may be higher, and the number of hypotheses compared is smaller. We suggest controlling the false discovery rate on clusters (FDRc), i.e. the expected proportion of clusters rejected erroneously out of all clusters rejected, or its extension to general weights (WFDRc). Once the cluster discoveries have been made, we suggest ’cleaning’ non-active voxels within the cluster discoveries. For this purpose we develop a hierarchical testing procedure that tests clusters first, then voxels within rejected clusters. Next, we address the problem of testing whether at least u out of n conditions considered activate the clusters. It offers an in-between approach to testing that non of the conditions activate the cluster (u=1) and that not all of the conditions activate the cluster (u=n). We suggest powerful test statistics that are valid under dependence between the individual condition p-values as well as under independence. We address the problem of testing many such partial conjunction hypotheses simultaneously using the FDR approach. If inference at all levels u = 1, . . . , n is of interest we suggest a procedure that controls an appropriate FDR measure, called the overall FDR, and produces an informative display of the findings. We use the above approach, replacing conditions by subjects, to produce informative group maps that offer an alternative to mixed/random effect analysis.

Wednesday, July 23, 2008

Decomposition Methods for Explorative Neuroimaging

- Lars Kai Hansen, Technical University of Denmark

Principal and independent component analysis (PCA, ICA) are widely used in neuroimaging for explorative search for activation networks. I will review a statistical framework for PCA and ICA decompositions that allows us to perform model selection and evaluate components. I will discus some generalizations of PCA and ICA with significant potential in neuroimaging, including non-negative factorization, multi-way decompositions, and convolutive mixing. Finally, I will introduce a set of Matlab based tools for explorative analysis of neuroimage data.

Group ICA of fMRI

- Vince Calhoun, University of New Mexico

Independent component analysis (ICA) is a data-driven technique which has grown in it's application to fMRI over the past 10 years. Unlike univariate methods ICA does not naturally generalize to a method suitable for drawing inferences about groups of subjects. For example, when using the general linear model, the investigator specifies the regressors of interest, and so drawing inferences about group data comes naturally, since all individuals in the group share the same regressors. In ICA, by contrast, different individuals in the group will have different time courses, and they will be sorted differently, so it is not immediately clear how to draw inferences about group data using ICA. Despite this, several ICA multi-subject analysis approaches have been proposed. The various approaches differ in terms of how the data is organized prior to the ICA analysis, what types of output are available (e.g. single subject contributions, group averages, etc), and how the statistical inference is made. In this talk we first provide an introduction to ICA and ICA of fMRI, then we provide an overview of current approaches for utilizing ICA to make group inferences and also show example of how group ICA can be utilized to make inferences from fMRI data.

Adaptive Multivariate Analysis

- Ola Friman, MeVis Research GmbH - Center for Medical Image Computing

In this presentation, linear models for optimal detection performance in single-subject confirmatory fMRI analysis will be explored. In particular, the advantage of constraining the linear models will be discussed. Furthermore, conventional mass-univariate fMRI analysis methods like the GLM will be extended to a mass-multivariate analysis via the introduction of spatial basis functions. This allows us to model variations in spatial shape of active brain regions, resulting in an adaptive spatial filtering of the data. Canonical Correlation Analysis will be presented as one possible tool for such mass-multivariate fMRI analysis.

What Makes a Genetic Association Significant?

- Nelson Freimer, University of California, Los Angeles (UCLA) - Human Genetics

Geneticists and neuroscientists often differ dramatically in their interpretation of the statistical significance of genetic association studies, and this is particularly true when fMRI phenotypes are being assessed in relation to one or a few candidate polymorphisms. This presentation will review the assumptions that underlie these differences, with particular emphasis on the concept of genome wide significance, and how this concept has been applied in genetic mapping of human diseases and other traits. Thresholds for

genome wide significance were first applied to genetic linkage studies beginning in the 1980s and are now being applied in well powered genome wide association studies (GWAS). GWAS of numerous traits are now being conducted using up to one million single nucleotide polymorphisms (SNPs) in samples of up to tens of thousands of individuals, and have already led to discovery of more than 100 novel genetic loci, for which genome wide significance has been achieved in at least two independent studies. In the era of GWAS it is challenging to design reasonably powered genetic association studies for measures, such as those obtained in fMRI, where it is typically not feasible to assess large numbers of individuals. In this presentation I will discuss one approach to this problem, which we plan to implement in the Consortium for Neuropsychiatric Phenomics at UCLA.

Combining fMRI, ERP and SNP Data with Parallel ICA: Introduction and Examples

- Vince Calhoun, University of New Mexico

Many studies are currently collecting multiple types of imaging data from the same participants. Each imaging method reports on a limited domain and typically provides both common and unique information about the problem in question. We have developed an ICA-based framework to investigate the integration of data from two modalities. This method identifies components of both modalities and connections between them through enhancing intrinsic interrelationships. We have applied this approach to link functional magnetic resonance imaging (fMRI)/event-related potential (ERP) data and also fMRI and genetic data (single nucleotide polymorphism (SNP) arrays). Results show that parallel ICA (paraICA) provides stable results and can identify the linked components with a relatively high accuracy. In our initial application of paraICA, we defined a genetic independent component as a specific SNP association, i.e., a group of SNPs with various degrees of contribution, which partially determines a specific phenotype or endophenotype. This association can be modeled as a linear combination of SNP genotypes. In our current formulation, the relationship between brain function and the genetic component is calculated as the correlation between the columns of the fMRI and the SNP mixing matrices. Thus, we have a correlation term and the maximization function based upon entropy. In this talk, we provide an overview of the use of ICA to combine or fuse multimodal data, show some simulation results and some interesting findings derived from ERP/SNP and fMRI/SNP data.

Thursday, July 24, 2008

Graphical Causal Models and Inferences to Mechanisms from Brain Imaging: Possibilities and Limitations

- Clark Glymour, Carnegie-Mellon University

Many recent studies have applied statistical techniques to imaging data to attempt to infer causal cascades and feedbacks among regions of the brain in participants performing simple cognitive or motor tasks. Statistical procedures include regression, specification of linear structural equation models, Granger causal models from time series, and other methods. In parallel, work in computer science and statistics since the 1980s has developed an abstract formalism--graphical causal models, sometimes called "causal Bayes nets"--that represents non-parametrically the constraints on probability distributions implied by causal claims imbedded in any of a wide class of statistical models and methods, including those above. The graphical causal model representations lend themselves to a number of principled, automated search methods developed in the computer science literature in the last two decades, few of which have been applied to imaging data. An understanding of the abstract formalism permits an analysis of what can and cannot be learned from fMRI and other imaging data by available methods. This talk will provide an overview of all of the above.

Dynamic Causal Modeling

- Marta Garrido, University of California, Los Angeles (UCLA)

Dynamic causal modeling (DCM) is a procedure that models interactions among cortical regions, allows one to make inferences about system parameters and investigate how these parameters are influenced by experimental factors. With DCM it is possible to access how a given experimental manipulation activates a cortical pathway rather than a cortical area. This approach uses a biological informed model that allows for inferences about the underlying mechanisms of brain function. Moreover, one can compare different mechanisms or plausible hypotheses that map onto DCMs, and disambiguate between competing theories.

The Mathematics of Cause and Effect

- Judea Pearl, University of California, Los Angeles (UCLA) - Computer Science

I will review concepts, principles, and mathematical tools that were found useful in applications involving causal relationships. The principles are based on structural-model semantics, in which functional (or counterfactual) relations represent autonomous physical processes. This semantical framework, enriched with a few ideas from logic and graph theory, gives rise to a complete, coherent, and friendly calculus of causation that unifies the graphical and counterfactual approaches to causation and resolves long-standing problems in several of the sciences. These include questions of confounding, causal effect estimation, policy analysis, legal responsibility, effect decomposition, instrumental variables, and the integration of data from diverse studies.

Meta-Analysis of Neuroimaging Data

- Tor Wager, Columbia University

Making sense of a neuroimaging literature that is growing in scope and complexity will require increasingly sophisticated tools for synthesizing findings across studies. Meta-analysis of neuroimaging studies fills a unique niche in this process: It can be used to evaluate the consistency of findings across

different laboratories and task variants, and it can be used to evaluate the specificity of findings in brain regions or networks to particular task types. This review discusses examples, implementation, and considerations when choosing meta-analytic techniques. It focuses on the multilevel kernel density analysis (MKDA) framework, which has been used in recent studies to evaluate consistency and specificity of regional activation, identify distributed functional networks from patterns of co-activation, and test hypotheses about functional cortical-subcortical pathways in healthy individuals and patients with mental disorders. Several tests of consistency and specificity are described.

Knowledge Discovery in Neuroimaging Databases

- Lars Kai Hansen, Technical University of Denmark

While neuroimaging databases have grown only at a modest pace compared to, e.g., genomic databases, several advanced analysis tools have been developed and applied for their meta-analysis. I will review a set of multivariate tools for knowledge discovery in neuroimage databases and emphasize the need for efficient machine learning tools. I will discuss new strategies for populating neuroimaging databases and means for driving neuroimaging databases beyond the functional localization paradigm.

Coordinate-Based Meta-Analysis using Activation Likelihood Estimation (ALE)

- Angie Laird, University of Texas Health Science Center at San Antonio

Functional neuroimaging studies establish function-location correlations in the human brain using imaging modalities such as functional magnetic resonance imaging (fMRI) and positron emission tomography (PET). A vast amount of research has been published in this field in the last two decades, involving a wide array of tasks and cognitive or perceptual processes. Recently, quantitative meta-analysis methods have been developed to assimilate results from across these studies, with the ultimate goal of constructing a human functional brain atlas. Activation likelihood estimation (ALE) is a popular method of performing voxel-wise, coordinate-based meta-analyses. Multiple meta-analytic strategies and applications will be presented, including a meta-analysis of the Stroop task, a well-known test of response inhibition.

Friday, July 25, 2008

Introduction to Machine Learning for fMRI Data

- Francisco Pereira, Princeton University

Over the last 5 years machine learning methods have been used with increasing frequency to analyze fMRI data in a multivariate manner. The common goal in the studies resorting to these methods is to show that there is information about a variable of interest (e.g. which stimulus is being shown to a subject or which decision the subject will make) in some subset of the data (e.g. voxels in a given location or with particular response characteristics). In this talk I'll introduce the main ideas underpinning a basic analysis of fMRI data with machine learning methods, with an emphasis on showing how the methods match particular scientific questions of interest.

Classification of fMRI-Based Cognitive States

- Stephen LaConte, Biomedical Imaging Technology Center (BITC)

Multivoxel pattern analysis uses supervised learning approaches to obtain classifiers that can take neuroimaging data and predict the sensory/behavioral conditions corresponding to the time the images were acquired. In addition to how predictive these classifiers are, their structure can provide insights about the data they model. An important goal is to know your data and understand the analysis being performed. This talk provides some general approaches, but also uses the support vector machine and linear discriminant analysis as two examples of classification methods to discuss topics such as data representation, impact of preprocessing, limitations imposed by the hemodynamic response, the relationship between class labels and the stimulus paradigm, and interpretations that can be extracted from multivariate models.

Feature Selection Methods

- Isabelle Guyon, Clopinet

Abstract not provided.

Pattern-Information fMRI and Representational Similarity Analysis

- Nikolaus Kriegeskorte, National Institute of Mental Health

A fundamental challenge for systems neuroscience is to quantitatively relate its three major branches of research: brain-activity measurement, behavioral measurement, and computational modeling. Using measured brain-activity patterns to evaluate computational network models is complicated by the need to define the correspondency between the units of the model and the channels of the brain-activity data, e.g. single-cell recordings or voxels from functional magnetic resonance imaging (fMRI). Similar correspondency problems complicate relating activity patterns between different modalities of brain-activity measurement (e.g. fMRI and invasive or scalp electrophysiology), and between subjects and species. In order to bridge these divides, we suggest abstracting from the activity patterns themselves and computing representational dissimilarity matrices, which characterize the information carried by a given representation in a brain or model. Building on a rich psychological and mathematical literature on similarity analysis, we propose a new experimental and data-analytical framework called representational similarity analysis (RSA), in which multi-channel measures of neural activity are quantitatively related to each other and to computational theory and behavior by comparing representational dissimilarity matrices. We demonstrate RSA by relating representations of visual objects as measured with fMRI in early visual

cortex and the fusiform face area to computational models spanning a wide range of complexities. The representational dissimilarity matrices are simultaneously related via second-level application of multidimensional scaling and tested using randomization and bootstrap techniques. We discuss the broad potential of RSA, including novel approaches to experimental design, and argue that these ideas, which have deep roots in psychology and neuroscience, will allow the integrated quantitative analysis of data from all three branches, thus contributing to a more unified systems neuroscience.

Lessons from the Pittsburgh Brain Activity Interpretation Competition

- Walt Schneider, University of Pittsburgh

Abstract not provided.

Testing Psychological Theories with Multivariate Pattern Analysis

- Ken Norman, Princeton University

At a high level, theories of human information processing can be viewed as collections of if-then statements: If the subject is in a particular cognitive state, this should be associated with a particular set of outcomes. To test these theories, experimenters attempt to put subjects in a particular cognitive state and then observe neural activity and behavior in that state. However, our ability (as experimenters) to control a subject's cognitive state is limited; there is almost always variability in subjects' cognitive state, above and beyond the variability that is directly driven by the experimental manipulation. In analyses that focus on comparing experimental conditions, this extra variability is treated as a source of noise and (as such)may make it harder to see the predicted effect. Multivariate pattern analysis (MVPA) gives us a way of addressing this problem: Instead of simply assuming that experimental conditions are effective in eliciting the cognitive state of interest, we can train a pattern classifier to recognize the pattern of neural activity associated with a cognitive state, and (subsequently) we can use the classifier to track fluctuations in that cognitive state over time. In paradigms where there is extensive uncontrolled variance in subjects' cognitive state, this approach gives us a much more sensitive way of testing theories of how cognitive states drive behavior. I will describe how we have used MVPA in my laboratory to test theories of how neural activation drives brain plasticity and how subjects strategically guide memory search; I will also discuss (in more general terms) how to construct appropriate experimental designs for MVPA studies. I will conclude by discussing shortcomings of current methods and some particularly challenging directions for future research.

IPAM Summer School: Mathematics and Brain Imaging – Schedule at a Glance

Monday, July 14	Tuesday, July 15	Wednesday, July 16	Thursday, July 17	Friday, July 18
8-9am: Check-In/Breakfast Welcome and Opening Remarks 9am: **D van Essen** Surface-Based Computational Mapping of the Cerebral Cortex 10am: **G Gerig** Mapping Brain Changes Over Time During Development 11am: **M Hurdal** Cortical Mapping using Conformal Geometry **12-2pm: Lunch (on your own)** 2pm: **B Fischl** Automated Analysis of Cortical & Subcortical Anatomy in Brain MRI 3pm: **G Sapiro** Computing Sulcal Curves and the complexity of brain connectivity 4pm: **Z Tu** Towards Automated Whole Brain Image Segmentation	**8-9: Continental Breakfast** 9am: **M Miller** Computational Functional Anatomy 10am: **L Younes** Evolutions Equations in Computational Anatomy 11am: **A Qiu** Computational Functional Anatomy **12-2: Lunch (on your own)** 2pm: **S Joshi** Brain Morphometry using Diffeomorphic Maps and Differential Geometry 3pm: **S Allassonniere** Generative Models and Stochastic Algorithms for Population Average Estimation and Image Analysis **4-5:30pm: Reception (Hosted by IPAM)**	**8-9: Continental Breakfast** 9am: **C Lenglet** Mathematical Concepts for DTI and High-Angular Resolution Diffusion Imaging 10am: **C Westin** The Mathematics of DTI 11am: **S Smith** Tract-Based Spatial Statistics **12-2: Lunch (on your own)** 2pm: **B Vemuri** Higher-Order Tensor Models for DTI Segmentation and Analysis 3pm: **L O'Donnell** Tract-Based Morphometry 4pm: **G Sundaramoorthi** Tracking Fibers and Brain Connections using Finsler Geometry **5:30: Speakers' Dinner (Hosted by CCB)**	**8-9: Continental Breakfast** 9am: **J Ashburner** Voxel-Based Morphometry and Statistical Parametric Mapping 10am: **C Davatzikos** Morphological Appearance Manifolds for Computational Anatomy 11am: **S Pieper** Large-Scale Computing Frameworks for Developing Image AnalysisTools **12-2: Lunch (on your own)** 2pm: **T Goldstein** Improving Image Reconstruction in MRI **3-4:30: Student Presentations (10 minutes each; sign up on Monday)**	Note: This is a half day. **8-9: Continental Breakfast** 9am: **J Gee** – Geodesics in Deformation Morphometry and DTI 10am: **X Pennec** – Statistics Computing on Manifolds: from Riemannian Geometry to Computational Anatomy 11am: **N Lepore** – Group Statistics for Tensor-Based Morphometry and DTI **11:45: Closing Remarks**
Saturday, July 19: CCB Demo Day in Neuroscience Research Building Auditorium **http://cms.loni.ucla.edu/CCB_Demo_Day_2008.aspx**				
Monday, July 21	**Tuesday, July 22**	**Wednesday, July 23**	**Thursday, July 24**	**Friday, July 25**
8-9am: Check-In/Breakfast, Welcome and Opening Remarks 9am: **M Lindquist** HRF Modeling 10am: **S Smith** Modeling Temporal Structure 11am: **T Liu** fMRI Design Optimization **12-2pm : Lunch (on your own)** 2pm: **D Bowman** Bayesian Spatial Hierarchical Modeling 3pm: **T Johnson** Modeling Inter-Subject Variability in Activation Locations of fMRI Data 4pm: Panel Session **Glover, Nichols, Poline, Poldrack, Smith, Strother, and Worsley** Remaining Challenges in Multi-Subject fMRI	**8-9: Continental Breakfast** 9am: **G Glover** Impracticalities of Multi-Site fMRI 10am: **J Poline** Reproducibility in Group Modeling 11am: **S Strother** Reproducibility Across Analysis Methods **12-2: Lunch (on your own)** 2pm: **J Taylor** Advances in RFT - Nonnegative Least Squares 3pm: **K Worsley** The Statistical Analysis of Cortical Surface Data 4pm: **R Heller** Advances in FDR for fMRI	**8-9: Continental Breakfast** 9am: **L Hansen** Decomposition Methods for Explorative Neuroimaging 10am: **V Calhoun** Group ICA of fMRI 11am: **O Friman** Adaptive Multivariate Analysis **12-2: Lunch (on your own)** 2pm: **N Freimer** What Makes a Genetic Association Significant? 3pm: **V Calhoun** Combining fMRI and SNP Data with Parallel ICA	**8-9: Continental Breakfast** 9am: **C Glymour** Graphical Causal Models and Inferences to Mechanisms from Brain Imaging 10am: **M Garrido** Dynamic Causal Modelling 11am: **J Pearl** The Mathematics of Cause and Effect **12- 2: Lunch (on your own)** 2pm: **T Wager** Meta-Analysis Methods 3pm: **L Hansen** Knowledge Discovery in Neuroimaging Databases 4pm: **A Laird** Coordinate-Based Meta-Analysis Using ALE	**8-9: Continental Breakfast** 9am: **F Pereira** Introduction to Machine Learning for fMRI Data 10am: **S LaConte** Classification of fMRI-Based Cognitive States 11am: **I Guyon** Feature Selection Methods **12- 2: Lunch (on your own)** 2pm: **N Kriegeskorte** Pattern- Information fMRI and Representational Similarity Analysis 3pm: **W Schneider** Lessons from the Pittsburgh Brain Activity Interpretation Competition 4pm: **K Norman** Testing Psychological Theories with Multivariate Pattern Analysis

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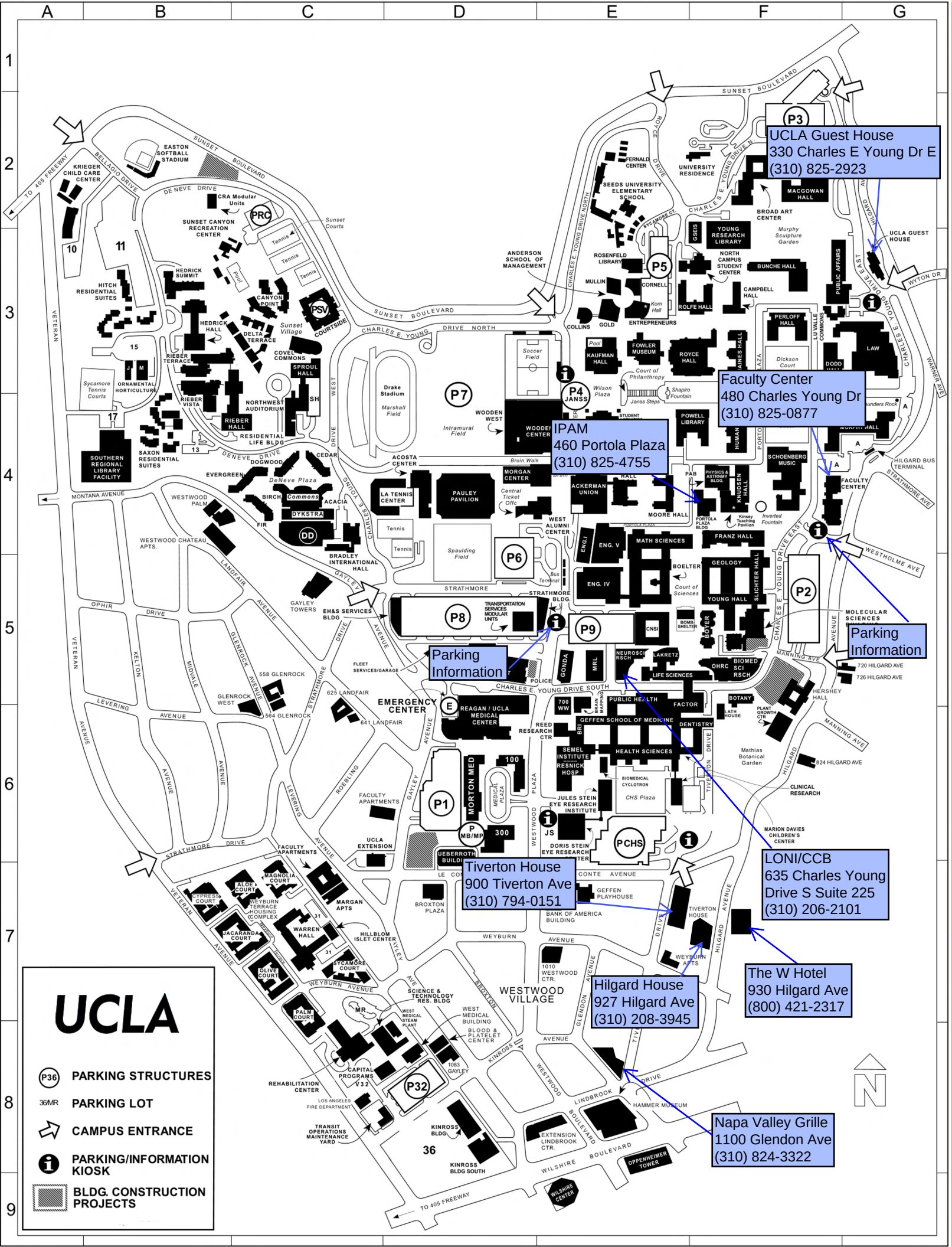
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GLENROCK AVENUE
ROEBLING AVENUE
VETERAN AVENUE
KELTON AVENUE
MIDVALE AVENUE
DENEVE DRIVE
DeNeve Plaza
Sunset Courts
Sycamore Tennis Courts
Soccer Field
Drake Stadium
Marshall Field
Intramural Field
Spaulding Field
Bruin Walk
Court of Philanthropy
Wilson Plaza
Janss Steps
Shapiro Fountain
Central Ticket Offc
Court of Sciences
Inverted Fountain
Dickson Court
Murphy Sculpture Garden
Kom Hall
Mathias Botanical Garden
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