CONF-9512160--Abstr.

BRAINMAP '95 WORKSHOP
FINAL REPORT

The fourth annual BrainMap Workshop was held at La Mansion del Rio Hotel in San Antonio (Dec 3-4). The conference title was "Human Brain Mapping and Modeling." This meeting was advertised in several journals and on the Research Imaging Center's WWW home page http://ric.uthscsa.edu/services/95/. A list of the attendees may be found at this web site. The web page for the meeting was expanded to include hotel information, preliminary program, application forms, and, finally, the full program with abstracts. This meeting was attended by 137 registered participants and 30 observers, from 82 institutions, representing 12 countries. Meeting support was actively solicited from numerous commercial vendors and funding agencies. The sponsors for the BrainMap '95 meeting were the U.S. Department of Energy, EJLB Foundation, National Institute of Mental Health, Advanced NMR Systems, Inc., John Wiley & Sons, Inc., Hamamatsu Photonics K.K., Biomagnetic Technologies, Inc., and Elscint, Inc. This meeting was unique in several ways. This was the first time that the presentations were almost totally scientific in nature. The meeting focused on the technical issues associated with mapping and modeling, as opposed to other scientific meetings that deal with the brain science more than technical issues. There were separate areas for software demos and commercial exhibits that could be visited between presentations. This was the first time that the BrainMap™ software was operated using internet services from the meeting site. This was a tremendous success, with many attendees using the service to check their e-mail, to upload images to test the software, and to demo their software and web pages. The BrainMap Advisory Board suggested that the format used for BrainMap '95 be adopted for future BrainMap Meetings, and that the meeting should continue as an annual event. The success of the BrainMap Meeting series demonstrates the need for such a "technical" meeting for a scientific community seeking to learn basic and advanced concepts in brain mapping and modeling.

There were no proceedings published for this meeting. A book will be published by John Wiley and Sons prior to the end of 1998. A program for the meeting and abstracts of presentations are enclosed.

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BrainMap '95
ABSTRACTS

SPATIAL NORMALIZATION AND REGISTRATION

A Modality-Independent Approach to Spatial Normalization (SN and Convex Hull)

Jack L. Lancaster, Tom Glass, Hunter Downs, and Peter Fox. Research Imaging Center, UT Health Science Center, San Antonio

The goal of spatial normalization is to adjust tomographic images of the human brain to fit a standard brain such as that detailed in the 1988 Talairach atlas. Locations within the brain can then be referenced using Talairach coordinates. A consistent method to perform spatial normalization is needed for images from different subjects and imaging modalites. To accomplish this an interactive software package, SN, was developed that assists the user in selecting key landmarks for adjusting a brain image to fit corresponding landmarks of the Talairach brain. Landmarks for both alignment and scaling that persist across subjects and modalities are discussed. An alternative approach adjusts the convex hull of a tomographic brain image to match a Talairach-brain convex hull using both affine and non-affine transformations. These transformations are then applied to the original brain image for spatial normalization. This method is currently under investigation and preliminary results with PET and MRI will be presented.

Image Registration: A Comparative Taxonomy

Roger P.Woods, M.D., Department of Neurology, Division of Brain Mapping, UCLA School of Medicine

A wide variety of techniques have been described for aligning tomographic brain images. This presentation will provide a comparative taxonomy of image registration techniques, with emphasis on automated techniques that do not depend upon explicit landmark identification. Relevant features to be discussed will include the choice of mathematical model to govern transformations (rigid-body, Talairach, affine, perspective, non-linear), the choice of cost function, and the minimization method for optimizing the cost function. Potential pitfalls in evaluating and comparing registration techniques will be reviewed, and current techniques will be compared in terms of robustness, speed, accuracy, and requirements for hardware and software.

Functional Image Registration Metrics Based on Orthogonal Subspaces

Stephen Strother, Radiology Dept., University of Minnesota

Using techniques based on principal component analysis (PCA) we present analysis procedures for removing and measuring image misregistration effects while simultaneously measuring patterns of functional activation. We have observed that the "signal" in [15O]water PET functional activation data sets exists in two distinct orthogonal vector subspaces (Strother et al.,1995, JCBFM, 15:738): an "intersubject subspace" that depends on registration and functional intersubject differences accounts for most "signal" variation, and a much smaller "intrasubject subspace" contains the subjects' common response to a task. The intersubject subspace removes image misregistration effects, and its component eigenimages and the variance of the associated eigenvectors provide metrics for quantifying the relative performance of different registration techniques. We will demonstrate that (1) different registration techniques may cause large changes in the intersubject subspace and derived registration metrics, and (2) these changes are only weakly linked to patterns of functional activation in the orthogonal intrasubject subspace.

Automated Synthesis of 3D Neuroanatomical Probability Maps for Individual Brain Regions

AC Evans, DL Collins, CJ Holmes, McConnell Brain Imaging Centre, Montreal Neurological Institute, McGill University, 3801 University St., Montreal, Canada H3A 2B4

Residual variability in brain morphology after stereotaxic transformation represents a fundamental challenge to the developing field of brain mapping. Attempts to characterize and, if necessary, correct for this variability by analysis of MRI datasets have been time-consuming and confounded by the difficulties in manual identification of homologous points in different brains. Subjective errors in defining such correspondences mask the true variability being sought. In principle, this goal requires the accurate and reproducible labelling of all voxels in any given structure for each brain within the MRI ensemble. We describe an automated procedure for 3D labelling of individual brain structures based on non-linear deformation of individual MRI volumes to match a previously-labelled target volume, followed by numerical inverse transformation of the labels to the native MRI space. Subsequent processing allows these labels to be mapped into stereotaxic space, now using a simple linear transformation, and combined to generate probability maps for the location of each pre-defined structure. The procedure is described along with validation experiments and selected examples of such maps. The general principle described is applicable to any scale and any object which can be defined within the target volume. Since the labels themselves take no part in the image-matching process, any number of labelling-schemes, representing different brain atlas formulations, can co-exist and their corresponding probability maps generated from a single determination of the mapping transformation.

Spatial Normalization: From Features to Basis Functions

Karl J Friston, The Wellcome Dept. of Cognitive Neurology, Inst. Neurology. UK

This presentation will review the development of spatial normalization techniques that are based on matching a given image with a template; starting with pattern recognition-like approaches and ending with the general and non-interactive non-linear transformations used currently. These new techniques solve simultaneously for an intensity transformation, and the spatial transformation, that jointly map one image onto another. By applying suitable constraints, and linearizing the problem, standard least sqaures solutions can be emplyed. The resulting framework is simple and potentially very useful in many forms of image registration and normalization.

Surface-Based Coordinate Systems and Two-Dimensional Warping Methods for Monkey and Human Cerebral Cortex

H.A. Drury, D.C. Van Essen, S.C. Joshi, M.I. Miller and G.E. Christensen, Washington University, St. Louis

A surface-based coordinate system offers major advantages over conventional stereotaxic coordinates for describing spatial relationships among different loci in the cerebral cortex. Two-dimensional cortical maps provide a suitable template on which such a coordinate system can be established, as we will illustrate for the macaque monkey and the human cortex. To deal with individual variability in the pattern of cortical convolutions, we use shape-based transformation algorithms that can warp one cortical map to match the shape of another. This allows all locations on a given experimental hemisphere to be associated with specific coordinates on a canonical cortical map for that species.

FUNCTIONAL-IMAGE ANALYSIS

Introduction

Karl Friston, The Wellcome Dept. of Cognitive Neurology, Inst. Neurology, UK

This introduction will frame subsequent presentations by reviewing the various univariate and multivariate approaches that have been adopted for functional image analysis and characterization. These approaches broadly divide into univariate approaches that test some hypothesis concerning functional specialization in the brain or (ii) multivariate techniques that are more concerned with functional integration.

Searching Location and Scale for Activation in PET and fMRI

Keith Worsley, McGill University

We present a theoretical P-value for assessing the significance of peaks in statistical fields searched over regions of any shape or size, which unifies previous 2 and 3 dimensional results. The theory can be used for images of Gaussian, T, chi-squared and F statistics for testing for the effects of explanatory variables in general linear models. We extend this to 4-D scale space searches over smoothing filter width as well as location. The results are used to search for activation in PET and fMRI data.

Non-Parametric Analysis of Statistic Images from Functional Mapping Experiments

Andrew Holmes, The Wellcome Dept. of Cognitive Neurology, Inst. Neurology, UK

Recent work in computationally intensive statistical methods has revived an interest in exact non-parametric and resampling based methods of inference for a wide variety of data sets. These tests present a new and flexible approach to the Multiple Comparisons Problem of assessing the significance of statistic images from designed functional mapping experiments, offering guaranteed validity with minimal assumptions at some computational expense. In this presentation an intuitive overview of the theory of randomisation and permutation tests will be given, using two examples which illustrate the power of the approach. There are three main areas of application for these methods: (1) Analysis of studies with noisy statistic images, such as single subject studies where t-statistic images have low degrees of freedom. (2) Analysis in situations where parametric theory is unavailable, or where the requisite assumptions are untenable; & (3) Validation of existing methods. These three areas will be discussed. Issues of inference, applicability and application will be considered, current work summarised, and future directions outlined.

Measuring Neural Interactions in Functional Brain Imaging Data

A. Randy McIntosh

Given the extensive connectivity of the nervous system, it is possible the role a particular brain area plays in behaviour is determined within a larger context of its interactions with other connected areas. This presentation will focus on two image analysis methods that seek to understand brain function within this context: Partial Least Squares (PLS) and network analysis using Structural Equation Modeling. PLS extracts spatial patterns of brain regions that are most related to aspects of the experimental design. The regions are then connected using neuroanatomy and the interactions between them quantified with Structural Equation Modeling. These analyses provide a more unified picture of neuroimaging data.

Experimental Design and Analysis of fMRI Data

James V. Haxby

Functional magnetic resonance imaging (fMRI) grants the investigator new freedom in experimental design by removing restrictions on repeated studies in individual subjects and increasing temporal resolution. Repeated studies afford increased sensitivity to small changes in the magnitude or extent of local activity that occur as a result of experience. Increased temporal resolution allows investigation of regional differences in the course of activity changes. Methods to analyze these effects have been implemented as part of an integrated analysis platform, the Functional Imaging Data Analysis Platform (FIDAP), and will be illustrated with experimental results from studies of implicit memory, skill learning, and working memory.

Challenges and Limitations for the Integration of Functional Imaging and Electromagnetic Recording in Studies of Cognition

G. Ron Mangun, UC Davis

Information processing in the human brain involves temporally and anatomically defined patterns of activity. One promising new approach for investigating these activity patterns is to combine electromagnetic recording (EEG and MEG) with functional neuroimaging (PET, SPECT and fMRI). When combined, these

complementary approaches can provide information about the time course and anatomical substrates of sensory, motor, and cognitive processes. Significant theoretical, methodological and physiological uncertainties and limitations make this effort a challenge that will not soon be resolved. However, many of these difficulties can be identified and new approaches are rapidly being implemented. These challenges, and approaches to their resolution will be reviewed in the context of studies of human cognition.

METANALYSIS AND MODELING

Metanalysis of Mind: BrainMap 4.0 and Envisioned Modeling Extensions

Peter T. Fox, Lawrence Parsons, and Jack L. Lancaster, Research Imaging Center, UT Health Science Center, San Antonio

BrainMap is an electronic environment for metanalysis of the human functional neuroimaging corpus: published, in press, deeper-than-published and unpublished. BrainMap facilitates understanding, metanalysis and modeling through rapid, comprehensive access to image-derived observations. BrainMap relates brain locations to specific human behaviors and to data sources. For any brain region, the mental operations (tasks) that are known to activate that area can be retrieved. For any mental operation, the brain areas known to be engaged by that operation can be viewed. For any method, journal, period of time, laboratory, or individual researcher, the body of knowledge can be retrieved. For any retrieval stream, results can be viewed (within Talairach's space) for comparison, metanalysis and modeling. BrainMap can be accessed via the WWW at http://ric.uthscsa.edu (Services). BrainMap is now being extended to include tools for modeling the brain as bounded volumes associated with specific elementary operations and as groups of volumes associated with specific tasks.

Synthetic PET: Analyzing Large-Scale Properties of Neural Networks

Michael Arbib, University of Southern California

Synthetic PET is a new computational technique for connecting neural network studies based on animal data and image studies of human brain function. Synthetic PET comparisions are taken from a computation model of interacting neural networks, for example, the monkey brain by integrating synaptic activity in each subnetwork as diffeerent simulated tasks are performed. Given a pair of tasks, comparative synaptic activity levels for each modeled neural region are then painted into the homologous regions of a three-dimensional model of the human brian corresponding to the Talairach atlas. The resulting comparison then offers predictions of relative changes of neuronal activity as obtained from PET comparisons of humans performing a similar pair of tasks.

Ensemble Neuron Recording: Detection and Mapping of Activity Patterns During Behavior

Donald J. Woodward, Bowman Gray School of Medicine, Winston-Salem, NC

A goal of behavioral neurophysiology is to clarify the distributed activity patterns within groups of neurons which provide the substrates for computation of sensory, motor, and cognitive functions. New technology for ensemble neuron recording has been created including multichannel probes, amplifiers, digital signal processors with acquisition and analysis software. Multivariate analysis and sorting analysis, canonical variate, principal components and classification trees, have been applied to associate neuronal population vectors with cognitive decision states. Organization of these complex data sets is aided by use of a relational database, and a brain atlas mapping procedure linked to a World Wide Web site for document management.

Graphically-Oriented Databases for Connectivity and Partitioning of the Macaque Cerebrum

D.C. Van Essen, H.A. Drury, W.A. Press, and B.A. Olshausen, Washington University, St. Louis

We are developing graphically-oriented databases of information about the organization and connectivity of cerebral cortex in primates. Our long-term objective is a client-server database that can accurately represent anatomical data about areal boundaries, patterns of connectivity, etc., in a variety of formats, including three-dimensional reconstructions and two-dimensional cortical maps. An exemplar of this strategy is Xanat, a database that displays information about connectivity between cerebral cortex and the pulvinar nucleus in a way that allows systematic analysis of data obtained from multiple independent experiments.

Approaches for analyzing large-scale properties of distributed brain systems: Synthetic PET and Structural Equation Modeling

Scott T Grafton M.D., University of Southern California

Accumulating results from functional imaging experiments in humans reveal activation of widely distributed brain areas during performance of even the most elementary behaviors. A fundamental question is how distributed brain areas interact as ensembles. Methods to assess regional interactions are now emerging. Two of these approaches are summarized. Synthetic PET is based on large scale neural networks defined by known anatomic connections and functional properties of neurons in each brain area. Regional neural activity is derived from the network (both inhibitory and excitatory influences). The input and output requirements of the network are then changed (reflecting a new behavioral state) and integrated activity over time is determined. Regional differences in neural activity between different behavioral states based on neural network simulations can then be used to predict results of functional imaging studies. Structural equation modeling is a method for calculating regional interactions using data derived directly from functional imaging studies. A large-scale model encompassing a distributed functional system is used to constrain the estimates of regional interactions (path analysis). Unidirectional influences of one region to another are possible. A fundamental question is what these estimates of inter-regional influences correspond to at a neuronal level. Both approaches demand a comprehensive "top down" approach to large scale modeling, incorporating anatomic, physiologic, and functional imaging data from both animal and human data sets.

NEW HORIZONS IN BIOLOGICAL DATABASES

Time and Space: Representing Gene Expression in Mouse Development

Martin Ringwald(1), Janan Eppig(1), Joel Richardson(1), Alex Smith(1), Lisa Purvis(1), Dale Begley(1), Laura Taylor(1), Duncan Davidson(2), Matthew Kaufmann(2), Jonathan Bard(2), Richard Baldock(2).
--- (1) The Jackson Laboratory, Bar Harbor, ME 04609
--- (2) MRC and University of Edinburgh, Edinburgh, Scotland

We are developing a Gene Expression Information Resource that will integrate visual information with discrete descriptive data to provide researchers with methods for querying and displaying gene expression patterns during mouse embryonic development. The main components of the Resource include: (1) The Gene Expression Database (GXD) integrating the many types of expression data and providing links to other relevant resources to place the data into the larger biological and analytical context. (2) The Anatomy database providing the standard nomenclature for queries relating gene expression to developmental anatomy. (3) The 3D Atlas: a high resolution digital representation of mouse anatomy reconstructed from serial sections of single embryos at each representative developmental stage enabling 3D graphical display and analysis of expression data. The presentation will include a short description of the underlying GXD database concepts and a description of the 3D reconstruction and labeling procedures. Image rendering methods for display and analysis of 3D expression domains will be illustrated. The challenges of the 3D approach and its applications will be discussed.

Brain Image Database and Genome Mapping Lessons

Stan Letovsky, Johns Hopkins Medical School

BRAID (Brain Image Database) is a database of brain imaging data designed to support statistical analyses of brain imaging data. It uses the Talairach space as a common frame of reference for image normalization. BRAID is implemented in Illustra, an object/relational DBMS which supports the extension of its query language with new datatypes and operators. We are adding datatypes to support a variety of 3D "image" datatypes, including boolean (ROI), integer/float, vector and tensor. Image operators allow images to be added, intersected, averaged, differentiated, and so on. The augmented query language functions as a concise scripting language for expressing image analysis methods.

BRAID is currently being applied to lesion/deficit and morphological variation data. It contains lesion/deficit data from the Cardiovascular Health Study (CHS), which used MRI to find lesions in a sample of normal individuals aged 65 and older. Statistical methods for analyzing these data using BRAID will be described. The database will also incorporate data from the Baltimore Longitudinal Study of Aging, which will image brains at yearly intervals in a sample of several thousand normal subjects over age 65. These images will be combined to produce cohort morphological averages and contrasts.

The talk will also discuss some overlooked analogies between genome mapping and brain mapping, focussing on such questions as:

- what are the objects being mapped?
- what landmarks are used to map them?
- what assumptions does mapping make about variability?
- when is mapping complete?

Federating Scientific Databases: Issues, Problems, Solutions

Dennis McLeod, Computer Science Department, University of Southern California, Los Angeles, CA 90098-0781, (mcleod@usc.edu)

Abstractly, a federated scientific database is a collection of independenly administered information repositories available to users via some information sharing network. To provide more than just the sum of the individual parts, a federation must provide tools to help users locate and integrate relevant information from multiple sources. In particular, tools are needed that help users

- identify and locate relevant information sources;
- extract desired information "units" (e.g., annotated DNA sequences, anatomical images, metabolic pathways, bibliographic records) from those sources;
- understand the content (meaning) of the information units as they are provided by the sources; and
- resolve similarities and differences among related information units from different sources.

In addition, a federation benefits from tools that facilitate coordination among the various database providers, particularly with regard to data consistency and quality. In this talk, we explore the key issues, open problems, and emerging or potential solutions involved in building and using scientific database federations. In particular, we focus on "where things were", "where things are", and "where things might be going". For concreteness, we present examples from the current USC Brain Project. We consider the key role of the "multimedia" aspect of scientific information units, which may include images, text and hypertext, structured data (e.g., tables), continuous data (e.g., curves), simulation results and "models", and program code.

Holding it all Together: Multidatabase Referential Integrity

Peter D. Karp, SRI International

The genome informatics community is becoming increasingly reliant on the creation of links among biological databases (DBs) as a foundation for DB interoperability. For example, a link might be created from a protein in one DB (such as PIR), to the gene that encodes it in another DB (such as GDB), by storing the unique identifier (id) of the gene object within an attribute of the protein object. User interfaces can then support navigation from the protein to the gene, and multiDB queries can join the protein with the gene. The unique id of the gene is serving as a foreign key. However, a variety of factors, such as changes in the underlying biology, can cause object ids to become invalid, thus producing invalid links among DBs. Invalid links are a violation of multidatabase referential integrity, and are likely to occur in BrainMap DBs as well. We propose a network protocol whereby a database administrator can provide information about changes to the identifiers of objects in their database via Internet, to allow other databases to maintain referential integrity. This problem will be illustrated in the context of EcoCyc, which is an electronic encyclopedia of the genome and the metabolic pathways of E. coli. EcoCyc encodes over 100 biochemical pathways. The talk will briefly survey other lessons learned from the EcoCyc project, such as the importance of high-fidelity representations, and the power of object-oriented knowledge-representation tools.

Developing and Exploring Scientific Databases

Victor M. Markowitz, Data Management Research and Development Group,

Information and Computing Sciences Division, Lawrence Berkeley National Laboratory

We will discuss the problems of developing and exploring scientific databases (SDBs). We will present a common approach to deal with these problems for both new and existing SDBs implemented using commercial database management systems (DBMSs). A suite of data management tools based on this approach will be briefly described with examples of applying them for (1) developing and maintaining new SDBs, such as the Genome Data Base (GDB) and the Protein Data Bank (PDB), (2) instaling object-oriented interfaces on top of existing SDBs, such as the Genome Sequence Data Base (GSDB), (3) exploring single as well as multiple SDBs, such as GDB, GSDB, and PDB. We will show how facilities for developing and exploring SDBs can support publishing and federating SDBs.

Making it all Work: No Silver Bullet

Robert J. Robbins
Fred Hutchinson Cancer Research Center
Seattle, Washington

There is now widespread recognition that a federation of scientific information resources is needed and many workers are developing tools and conceptual approaches for building a federated bioinformation infrastructure. The run-away success of the World-Wide Web shows that loosely coupled federations can be incredibly useful and provides a model for their implementation.

Although, no single solution (no silver bullet) to *all* the federation needs for bioinformation infrastructure is presently available (and none are likely soon), some general principles should still be considered:

- The history and implementation of *networking protocols* provides guidance in building robust interoperating systems that can survive weak links and local failures.
- *Componentry* will be a key success factor -- systems must be designed (like network protocols) so that components can be upgraded without necessitating compensating changes across the system.
- Support for *inter-database referential integrity* is crucial: this entails requirements that affect both the scientific providers of data and the technical providers of databases.
- We must build federated *systems* of both data resources and analytical tools. This extends the identifier problem to include version and format information to allow automatic parsing.
- The problem of *object identifiers* in a loosely coupled federation of (replicated) data resources and analytical tools contains much subtlety, with many different kinds of identity needing to be tracked. For example, do these two data objects refer to the same real-world object; are these two data objects in the same computational format; which of these two data objects that refer to the same real-world object is most current, etc.?
- We must periodically zoom out conceptually, in both time and space, to make sure that our "solutions" are not so local that they cannot scale or age well. (For example: at some point, some scientific database will decide that it needs to split or merge entire object classes, not just individual objects; when that happens, if the external identifiers of the objects are unique only within object classes, much difficulty will ensue, especially in the area of inter-database referential integrity.)
- Developing *enabling technologies* should always be the goal; we must design systems first so that they ENABLE certain things to be done, taking care all the while to avoid PREVENTING other things

from being done as much as possible. (For example: technical solutions that give authors more control over page layout for html documents should not prevent third-party formatting and should not interfere with the ability to develop check-sum based identifiers for html documents).

The best general advice for any system designer is provided by Eliel Saarinen:

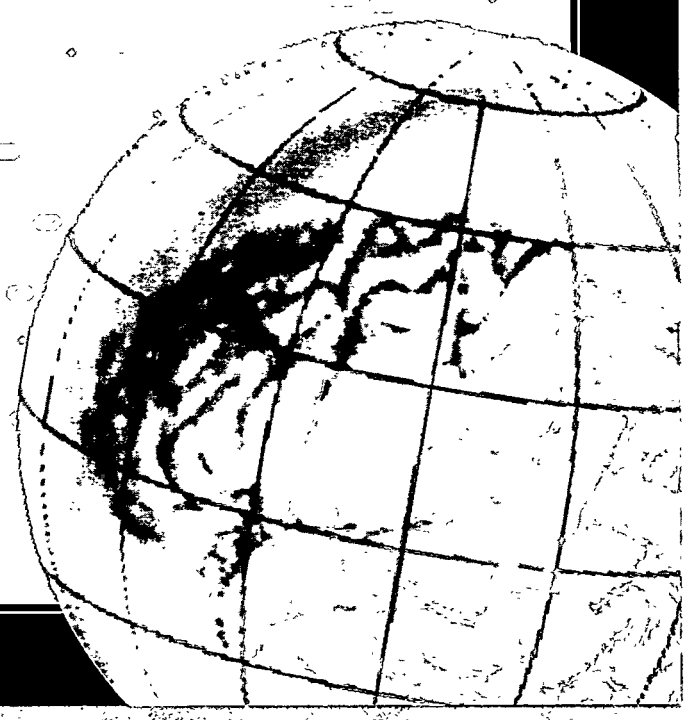
Always design a thing by considering it in its next larger context...

BRAINMAP'95

HUMAN BRAIN MAPPING & MODELING

December 3 and 4, 1995

La Mansión del Rio Hotel
San Antonio, Texas



BRAINMAP '95

HUMAN BRAIN MAPPING & MODELING

La Mansión del Rio Hotel • December 3 and 4, 1995, San Antonio, Texas

DECEMBER 3, 1995, Sunday - a.m.

SESSION I • Spatial Normalization and Registration • Iberian Ballroom

Jack Lancaster - Chair

7:30	Continental Breakfast	Veramendi Room
8:00	Welcoming Comments	Dean James Young
8:10	General Introduction	Peter Fox
8:20	A Modality-Independent Approach to Spatial Normalization (SN & Convex-Hull)	Jack Lancaster
8:50	Image Registration: A Comparative Taxonomy	Roger Woods
9:20	Functional Image Registration Metrics Based on Orthogonal Subspaces	Stephen Strother
9:50	BREAK	Veramendi Room
10:05	Automated Synthesis of 3D Neuroanatomical Probability Maps for Individual Brain Regions	Alan Evans
10:35	Spatial Normalization: From Features to Basis Functions	Karl Friston
11:05	Surface-Based Coordinate Systems and 2-D Warping Methods	Heather Drury
11:35	DISCUSSION	
12:00	LUNCH BREAK - EXHIBITS	Exhibits - Veramendi Room

DECEMBER 3, 1995, Sunday - p.m.

SESSION II • Functional-Image Analysis • Iberian Ballroom

Karl Friston - Chair

1:30	Introduction: Functional Image Analysis	Karl Friston
2:00	Searching Location and Scale for Activation in PET and fMRI	Keith Worsley
2:30	Non-Parametric Analysis of Statistic Images from Functional Mapping Experiments	Andrew Holmes
3:00	BREAK	Veramendi Room
3:15	Measuring Neural Interactions in Functional Brain Imaging Data	A. Randy McIntosh
3:45	Experimental Design and Analysis of fMRI Data	James Haxby
4:15	Challenges and Limitations for the Integration of Functional Imaging and Electromagnetic Recording in Studies of Cognition	G. Ron Mangun
4:45	DISCUSSION	

RECEPTION

6:00 - 7:30 p.m. • Exhibits • Veramendi

DECEMBER 4, 1995, Monday - a.m.

SESSION III • Metanalysis and Modeling • Iberian Ballroom

Peter Fox - Chair

7:30	Continental Breakfast	Veramendi Room
8:00	Metanalysis of Mind: BrainMap 4.0 and Envisioned Modeling Extensions	Peter Fox
8:30	Synthetic PET: Analyzing Large-Scale Properties of Neural Networks	Michael Arbib
9:00	Ensemble Neuron Recording: Detection and Mapping of Activity Patterns During Behavior	Donald Woodward
9:30	BREAK	Veramendi Room
9:45	Simulation Systems as Databases: Information GENESIzed	James Bower
10:15	Graphically-Oriented Databases for Connectivity and Partitioning	David Van Essen
10:45	Structural Equation Modeling	Scott Grafton
11:15	DISCUSSION	
12:00	LUNCH BREAK	

DECEMBER 4, 1995, Monday - p.m.

SESSION IV • New Horizons in Biological Databases • Iberian Ballroom

Robert J. Robbins - Chair

1:30	Introductory Comments	Robert J. Robbins
1:45	Time and Space: Representing Gene Expression in Mouse Development	Martin Ringwald
2:15	Brain Image Database and Genome Mapping Lessons	Stan Letovsky
2:45	Federating Scientific Databases: Issues, Solutions, Problems	Dennis McLeod
3:15	BREAK	Foyer - Iberian Ballroom
3:30	Holding it all Together: Multidatabase Referential Integrity	Peter Karp
4:00	Developing and Exploring Scientific Databases	Victor Markowitz
4:30	Making it all Work: No Silver Bullet	Robert J. Robbins
5:00	Discussion	
5:45	BrainMap '95 Concluding Remarks	Peter Fox
6:00	End	

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