WINTER WORKSHOP

http://brainmap.org/china/

BrainMap

BrainMap at a Glance

BrainMap has two online databases of published human neuroimaging experiments that report coordinates in a standard stereotaxic space (http://www.brainmap.org). They were created and developed at the Research Imaging Institute (RII) at the University of Texas Health Science Center San Antonio.

The purpose of BrainMap is to provide rapid, comprehensive access to the literature and its data in a manner that promotes the understanding of study design and results. To this end, a multi-dimensional, multi-level indexing scheme for the content and context of brain mapping studies has been developed and continues to be refined (http://brainmap.org/taxonomy/). BrainMap can also be used to perform coordinate-based meta-analyses and connectivity analyses. Papers in BrainMap are coded, revised, and entered by our coding team at the RII. Submissions are accepted from anyone, but are generally submitted by researchers interested in performing meta-analyses. There are other criteria specific to our coding structure but generally any whole-brain published or in-press functional or structural neuroimaging study in a peer-reviewed journal is eligible.

Funding

Currently, BrainMap is funded by a National Institute of Mental Health (NIMH) award to Peter T. Fox (R01-MH074457). Support for Mango software development was provided in part by the 'ICBM' grant (P01-EB01955) NIH/NIMH and the 'BrainMap' grant (R01-MH074457) NIH/NIMH. Primary support for continuing software development is being provided by the 'Mango' grant (R01-EB015314-01a1) NIH/NIBIB.

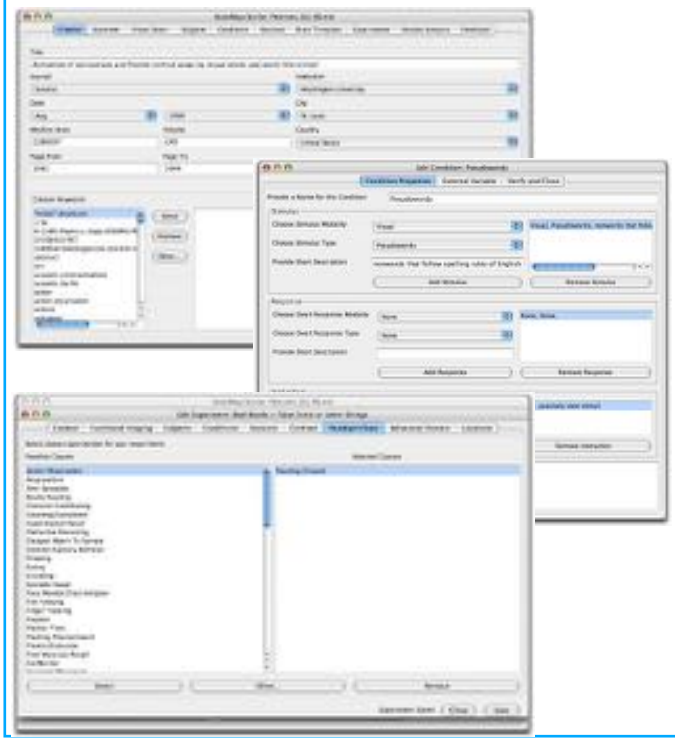
BrainMap Software

The goal of BrainMap is to develop software and tools to share neuroimaging results and enable meta-analysis of studies of human brain function and structure in healthy and diseased subjects. In support of this goal BrainMap has developed several useful programs. BrainMap's client programs are written in the Java programming language that may run under PC, Macintosh, and other systems.

1. Scribe: encode neuroimaging papers for database entry
2. Sleuth: search our databases and Talairach coordinate plotting (this application requires a username and password)
3. GingerALE: performs meta-analyses via the activation likelihood estimation (ALE) method; also converts coordinates between MNI and Talairach spaces using icbm2tal
4. Mango: provides analysis tools and a user interface to navigate image volumes. Mango is available as desktop, web, or iPad applications. In the context of the BrainMap Project, Mango may be used for viewing meta-analysis results and generating and editing ROIs for Sleuth's image-based ROI searches.

Scribe

Scribe is used to enter extracted coordinates and meta-data from published functional and structural neuroimaging studies. The Scribe (brainmap.org/scribe) and Taxonomy (brainmap.org/taxonomy) webpages include detailed information, manuals, examples, definitions, and supplementary materials to help facilitate coding. Entries are checked for errors, missing fields & overall completeness of data to ready them for submission into the BrianMap database. Submissions which include the PDF or DOI link of the article and the Scribe file, can be sent to submissions@brainmap.org. Published studies using BrainMap software or data are added to our publication page (www.brainmap.org/pubs), where a **complete citation** page is also built including the abstract and DOI/PDF link, Sleuth workspace(s) and GingerALE dataset(s).

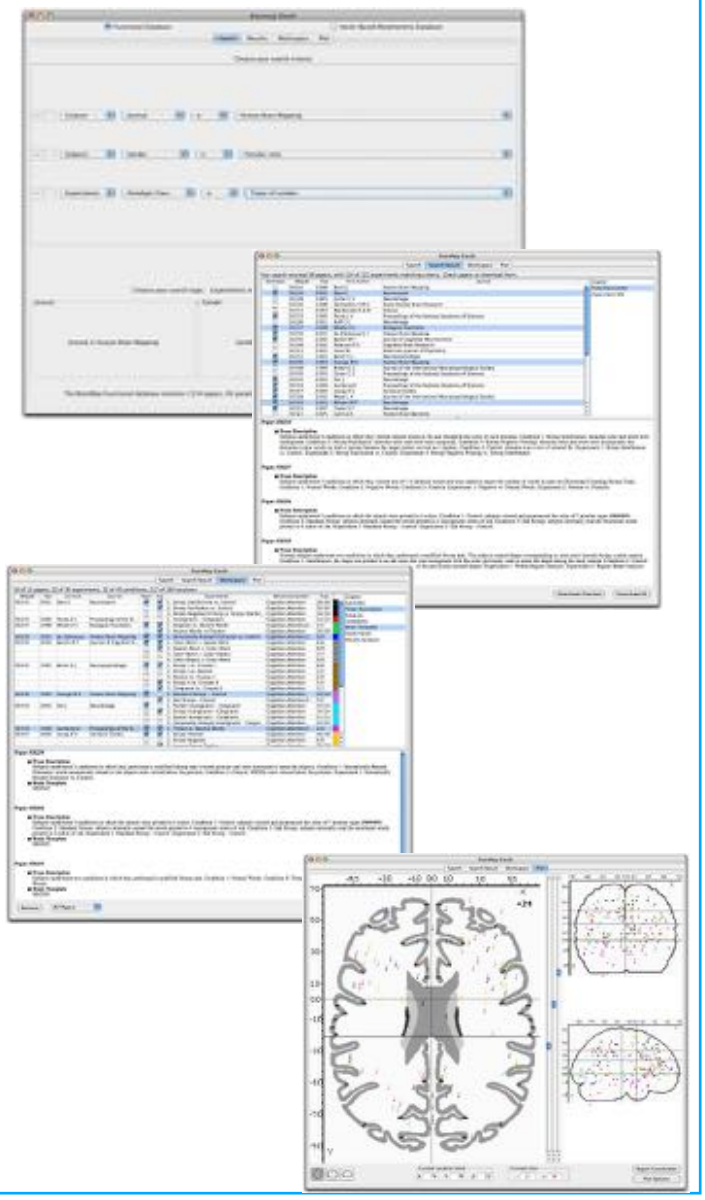


Sleuth

Sleuth is used to search for papers of interest, read their corresponding meta-data, and plot their results as coordinates on a standard glass brain in Talairach space.

Sleuth consists of four mail panels: Search, Results, Workspace, and Plot.

Learn more about Sleuth here: https://brainmap.org/sleuth.



GingerALE

GingerALE is the BrainMap application for performing meta-analyses on coordinates in Talairach or MNI space. Originally based upon activation likelihood estimate (ALE; Turkeltaub 2002), it was updated to a Random-Effects model (Eickhoff 2009), which uses one modeled activation map per experiment and allows changing the Gaussian's width and weighting by sample size. This algorithm was adjusted (Turkeltaub 2012) to limit the effect of multiple nearby coordinates within an experiment. ALE and MA maps stand for anatomical likelihood estimate and modeled anatomical maps when used with structural data from voxel-based morphometry (VBM) studies.

The input for a meta-analysis is a text file of your foci. Datasets can be exported from Sleuth or created by hand. GingerALE can also be used to convert coordinates between MNI and Talairach reference spaces using the icbm2tal transforms.

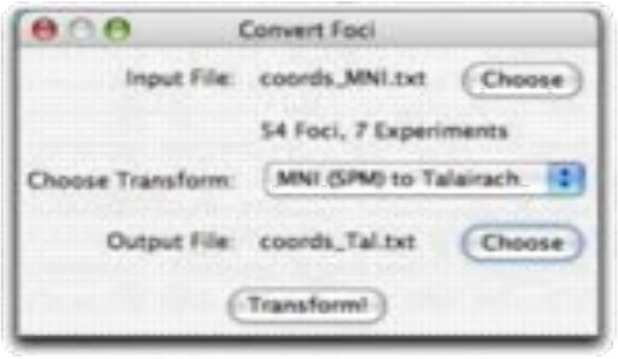
GingerALE computes the ALE values, P values and Z scores for each voxel in the brain and saves them in NIfTI (.nii) format. Thresholding methods include direct P value thresholds, Voxel-level Family-wise Error correction and Cluster-level FWE, as well as cluster-volume thresholds.

Regions above the chosen threshold are described using GingerALE's cluster analysis, which includes volume, bounds, weighted center, peak locations and anatomical labels provided by the Talairach atlas.

Talairach Daemon

The Talairach Atlas is a set of anatomical regions derived from the 1988 revision of the Talairach & Tournoux sterotaxic atlas. The labels are hierarchical, consisting of five parts associated with hemisphere, lobe, tissue type, gyrus and nuclei or Brodmann areas.

The label data can be downloaded as a 3D image, available on talairach.org. The Talairach Atlas labels can also be queried using the Talairach Daemon, a high-speed database server which accepts coordinates and returns labels. There is also a Talairach Client, which can be used either individual labels, or labels for a batch of coordinates within a spreadsheet. An interactive view is available in the Talairach Applet (talairach.org/applet/), which shows axial slices of anatomy and labels and allows for choosing locations by clicking your mouse.

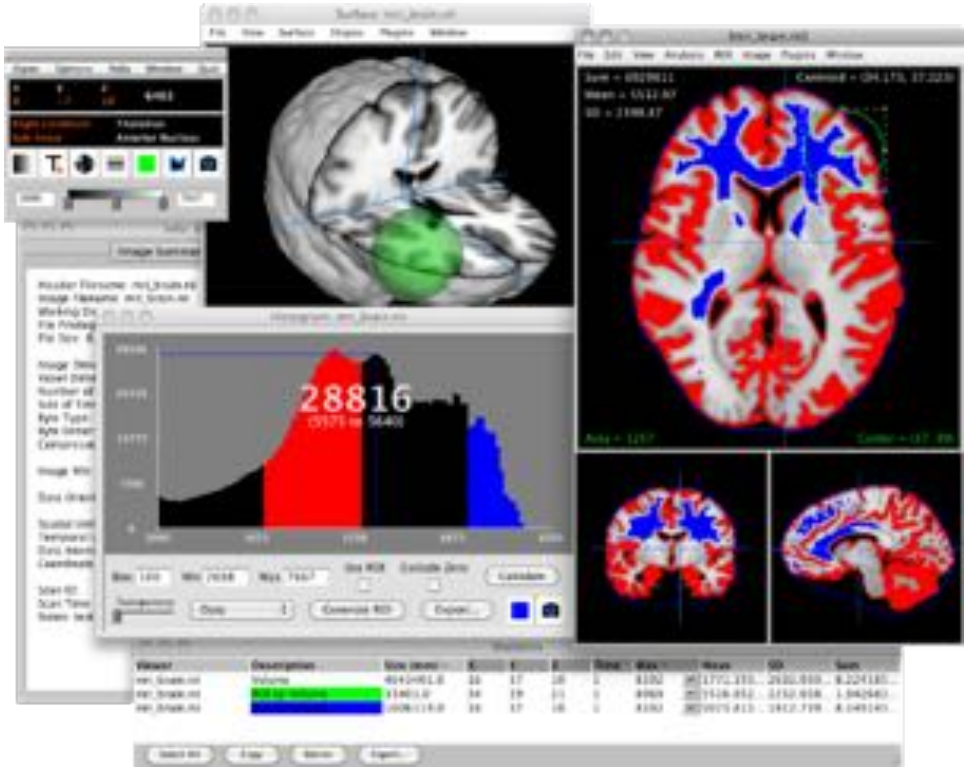


Mango

Mango (http://rii.uthscsa.edu/mango/) is a medical-image viewing application designed by J. Lancaster (PI) for use by the functional neuroimaging community. The primary programmer for Mango is Michael Martinez. Mango is a Java application, with a native-like user interface, supporting OS X, Windows, and Linux. Related applications include webMango (a Java applet), iMango (an iPad app), and Papaya (a JavaScript app). There have been over 20 formal releases since 2007. Mango is free to download and use. Community feedback from the Mango Forum since 2007 indicates that it is well accepted by basic and clinical neuroimaging researchers.

Mango supports many popular image file formats including Analyze, DICOM, NEMA-DES, MINC, and NIFTI. The surface viewer supports VTK, GIFTI, and BrainVisa formats.

Mango is readily extensible by developing plugins. Some openly distributed plugins include Behavioral Analysis and the BET and FLIRT apps developed by the FSL group. Other plugins are available using a collaboration agreement. Many of Mango's features are customizable including editors to develop new and edit existing spatial filters and color tables. The current release of Mango (June 2015) includes a scripting interface, so that scripts can be developed to automatically run a series of processing steps both from within the Mango GUI or at the command-line.



Mango has exceptional tools for analysis and ROI generation. There are many editing tools provided to modify existing ROIs along with analyses to report statistics for each ROI. Mango distinguishes ROIs using colors and supports up to 64 simultaneous ROIs. Analysis tools provide statistics for volumes, series, and ROIs. Statistics results can be exported in CSV format. An Image Calculator is provided to provide mathematical operations within and between images.

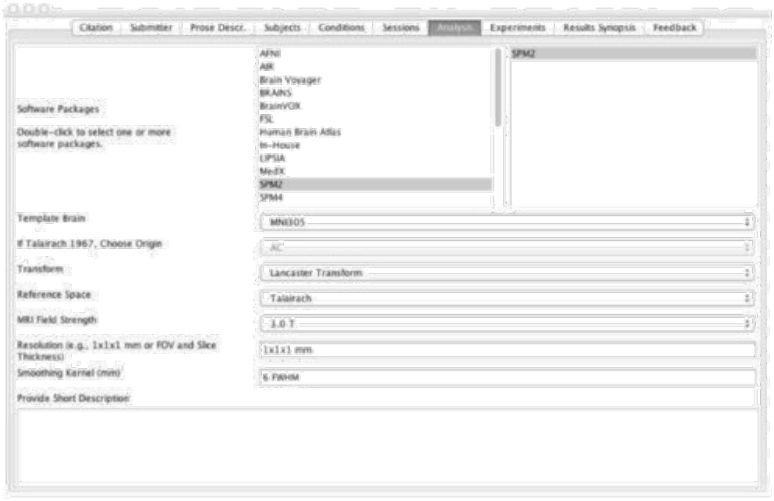
Mango's 3-D surface rendering features allow users to dynamically rotate, translate, and zoom in on surface images. Overlay colors can be painted onto the surface. Mango also supports cut-planes and settings to make surfaces and shapes transparent.

Mango is a general-purpose image viewing and analysis software application designed to supplement neuroimaging research. Mango's intuitive user interface was designed to help simplify analysis and viewing needs of many in the neuroimaging community.

What's New?

- **We are now ROI-free**
  The BrainMap database no longer accepts region of interest (ROI), volume of interest (VOI), contour or otherwise mask-based studies. This includes studies conducting scaled sub-profile (SSM) analyses or studies conducting PPI analyses, which are used to explore region-based task-specific activity.

- **New Analysis tab in Scribe**
  The Analysis tab describes the technical details of the data processing stream. From early steps, like the scanner's strength and resolution, to which software was used to align the images, and further analysis steps. The same Analysis tab is used for both functional and structural coding.



- **Sparse coding method for functional studies**
  Sparse coding is a good option for meta-analyses that will not make use of deep meta-data fields. Full coding is recommended for meta-analyses that use fields that are not included in sparse coding, like behavioral domains or parts of the conditions.

- **New BrainMap Taxonomy website**
  http://www.brainmap.org/taxonomy/

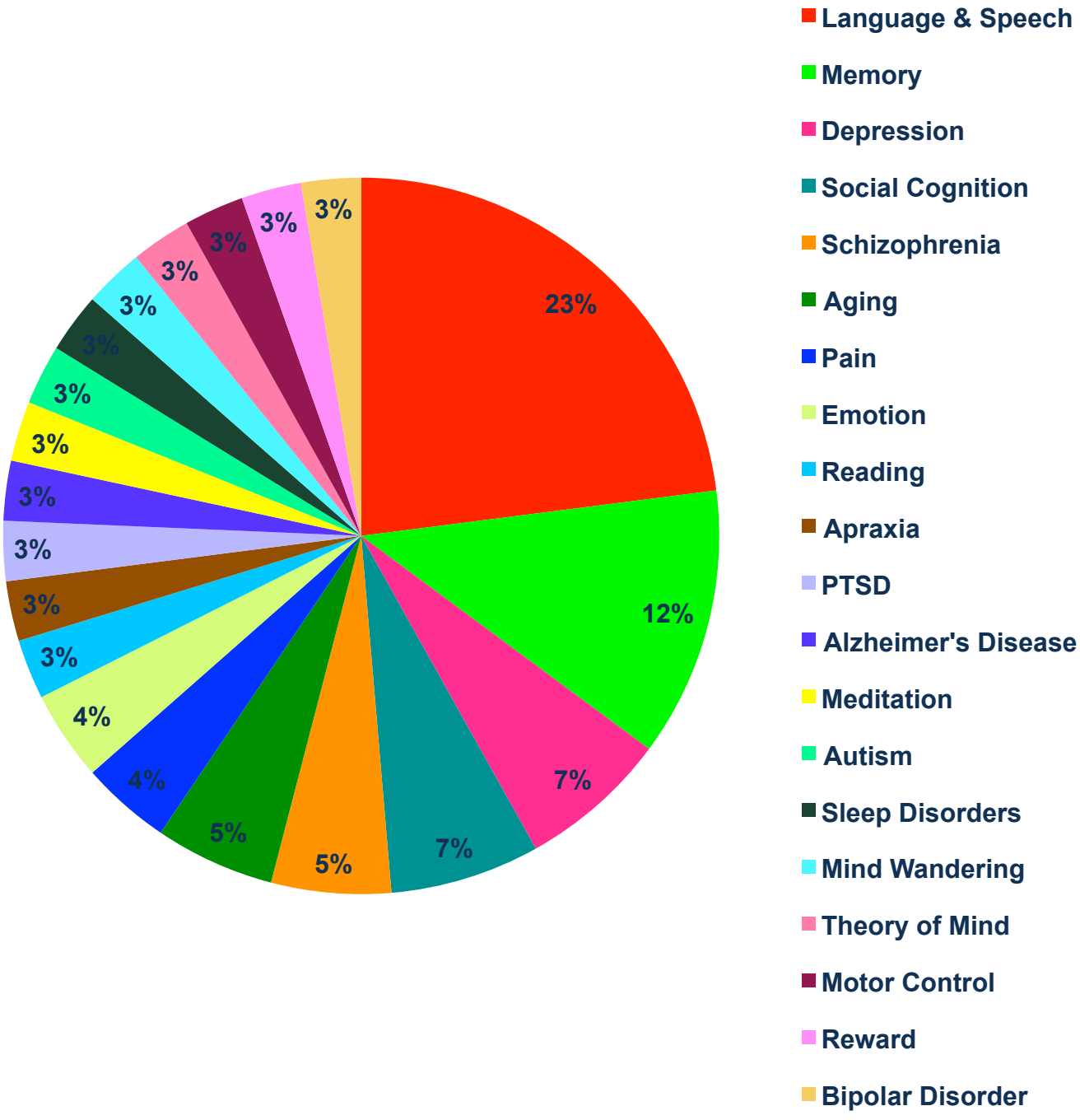
- **Updated paradigm classes and definitions can now be found online**
  http://www.brainmap.org/taxonomy/paradigms.html

- **ICD codes now being used for diagnosis of subject groups**
  http://www.brainmap.org/taxonomy/icd.html

- **Download the newest versions**
  - Scribe 3.0.10
  - Sleuth 2.4
  - GingerALE 2.3.5
  - Mango 3.7, iMango 1.3, Papaya 0.8

Publications

BrainMap has supported over 530 publications since it was created. Every year this number grows exponentially. Below we list the most published trends in 2014-2015*.



Language and Speech

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Memory

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Depression

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Aging

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Emotion

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*For a complete list of publications please visit www.brainmap.org/pubs.

Taking you back in time…

Did you know?
BrainMap has been around for almost 25 years!

The project first began in 1988, when Dr. Peter T. Fox conceived the experimental taxonomy that lead to the structure of the BrainMap database. Originally it was specifically for block-design, two condition contrasts of positron emission topography (PET) neuroimaging studies. By 1991 an Oracle relational database had been set up and the first software client applications were available. The applications were written in SuperCard for Macintosh computers, and could populate and search the database.

A series of BrainMap workshops were held, running from 1991 to 1998, to promote awareness of the project and to solicit feedback on its design from a broad cross-section of the neuroscience, psychology, image-analysis and informatics communities, including clinicians, theoreticians and experimentalists.

By 1994, the applications "Entry" and "Search&View" were re-implemented using a cross-platform interface builder named Galaxy, which expanded the platform support to include Linux with an XWindows version. At this time, BrainMap's taxonomy was expanded to include functional magnetic resonance imaging (fMRI) studies as well as additional experimental designs including event-related and mixed block/event designs. In the mid-to-late 1990s, cross-platform support was expanded to include Windows by using the recently debuted Java language. During this re-release, Entry was renamed to "Submit".

In 2004, Search&View gained meta-analysis features including activation likelihood estimation (ALE). In 2007, the meta-analysis tools were split into a stand-alone application called GingerALE, and Submit and Search&View were re-named to "Scribe" and "Sleuth", respectively. The taxonomy and database (DB) structure, as well as Scribe and Sleuth, were extended to include Voxel-Based Morphometry (VBM) anatomical studies in 2008. Currently, BrainMap's functional database has over 2,600 papers and 12,500 experiments while the anatomical database has over 850 papers and 2,800 experiments.

- **1988** — BrainMap conception
- **1991** — First Oracle database
- **1991-94** — Entry and Search&View re-implemented
- **1995-98** — Entry renamed "Submit"
- **1998** — New versions of applications released using Java
- **2004** — Search&View gained new meta-analysis features
- **2007** — Meta-analysis features became separate entity "GingerALE" while Submit and Search&View became "Scribe" and "Sleuth"
- **2008** — Taxonomy, DB, Scribe, and Sleuth now included VBM studies
- **2013-present** — Creation of Scribe training materials including manuals, videos, and tutorials and implementation of regular schema updates

BrainMap Investigators

Peter T. Fox, M.D. serves as director of the Research Imaging Institute at the University of Texas Health Science Center at San Antonio. Fox introduced the use of standardized coordinates to the field of human brain mapping in 1984, conceived the BrainMap project in 1987, first received funding in 1988 and has been project lead Principal Investigator since that time.

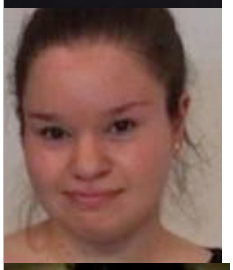
Jack Lancaster, Ph.D. is a Professor and Chief of the Biomedical Image Analysis Division (BIAD) and also the Associate Director at the Research Imaging Institute. He is an expert in spatial normalization techniques and developed the coordinate conversion algorithm, icbm2tal (Lancaster transform), to accurately compare Talairach and MNI coordinates archived in BrainMap. He also developed the Mango software and assisted in development of the BrainMap software. Currently he is a Mango Principal Investigator and a BrainMap Investigator.

Angela Laird, Ph.D. is currently an Associate Professor of Physics at Florida International University (FIU) in Miami, Florida. Dr. Laird has expertise in the development of novel neuroimaging analysis methods, with particular focus on applications in co-activation and intrinsic connectivity. Her work also focuses on developing neuroscience informatics tools and neuroimaging ontologies. Currently she is a BrainMap sub-contractor.

Simon Eickhoff, Ph.D. is currently a cognitive neuroscience professor at the Heinrich-Heine University in Düsseldorf and deputy director of the Institute of Neuroscience and Medicine in Jülich, where he leads the Brain Network Modeling group. His main research interest is the development and application of novel analysis tools and approaches for large-scale, multi-modal analysis of brain structure, function and connectivity. Currently he is a BrainMap sub-contractor.

Meet the Team

Aisling Ault, B.S is a BrainMap coder at the Research Imaging Institute. She is responsible for coding structural and functional files.



Janaye Dews, B.S. is a Research Assistant at the Research Imaging Institute. She is responsible for reviewing both structural and functional files and assists in the upkeep of the BrainMap database.

Mick Fox, B.S. is an Applications Programmer – Intermediate at the Research Imaging Institute. He is responsible for the development of Sleuth and GingerALE.

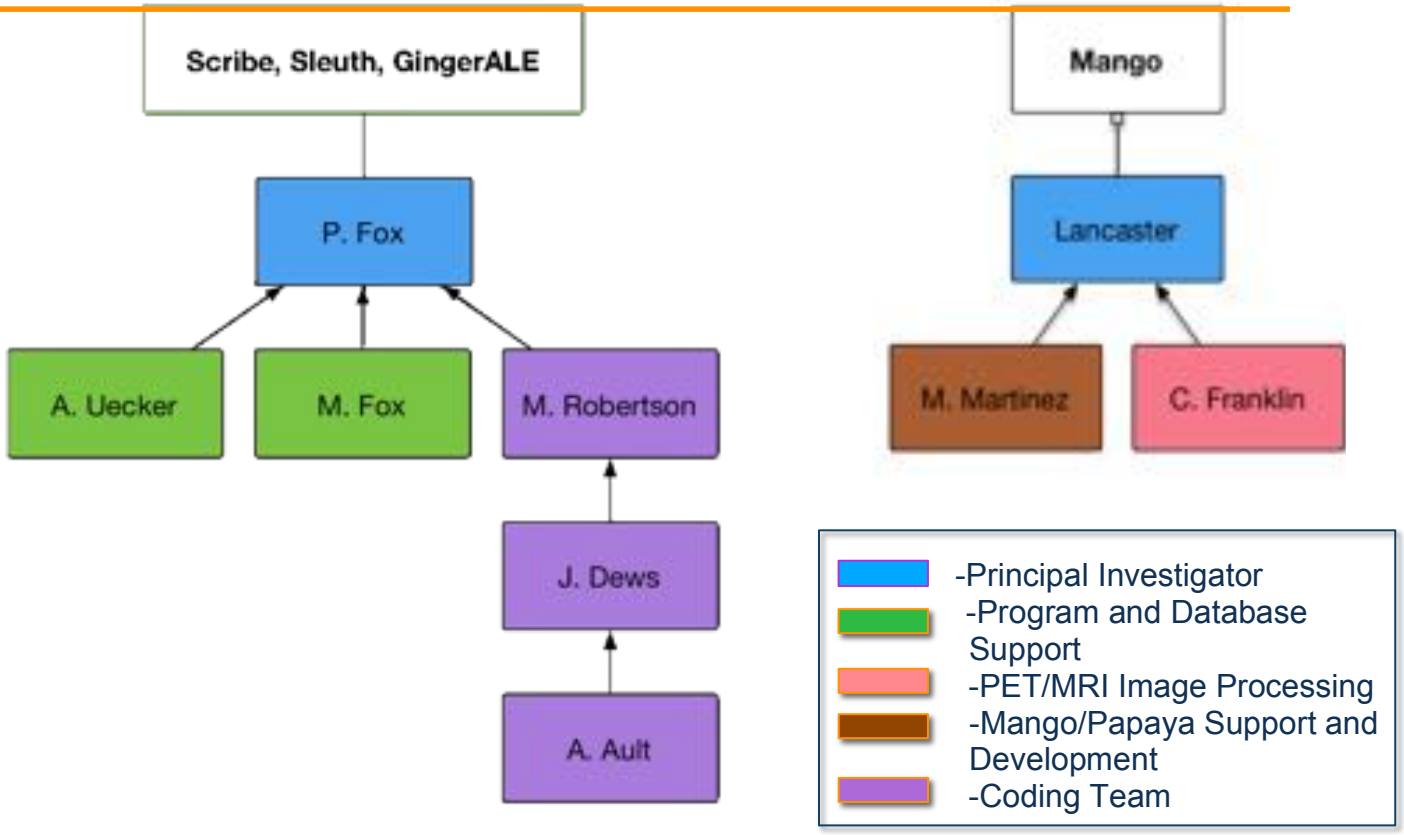
Crystal Franklin, B.S. is Statistician-Intermediate at the Research Imaging Institute. She has extensive experience in image processing of both PET and MRI data using various processing software such Mango and FSL. Her processing responsibilities include the creation of statistical parametric images, creation of standardized MRI and PET images, ICA analyses, ROI analyses, and SEM modeling.

Michael Martinez, B.A. is a software developer at the Research Imaging Institute. He is the main programmer of Mango, webMango, iMango, and Papaya.

Michaela Robertson, M.S. serves as a Research Scientist for the BrainMap project at the Research Imaging Institute. She is mainly responsible for heading up the BrainMap coding team, but also provides support as needed for various project endeavors and aids Dr. Fox with maintaining and refining the BrainMap coding scheme.

Angela Uecker, B.S. is a Senior Database Administrator at the Research Imaging Institute. She is responsible for the development of Scribe and maintenance of the Oracle database that contains all of BrainMap's meta-data and coordinate data.

Organizational Chart



Contact

To submit fully coded files for insertion into the BM database, please send a PDF or DOI link along with the Scribe file to submissions@brainmap.org. For questions about coding, please contact Janaye Dews (dews@uthscsa.edu)

Make sure to visit our forums for troubleshooting and FAQs.

- BrainMap: http://www.brainmap.org/forum
- Mango: http://rii.uthscsa.edu/mango/forum

Please email Dr. Fox (fox@uthscsa.edu) or Dr. Laird (alaird@fiu.edu) if you would like to discuss your ideas for collaboration on the development of meta-analysis tools and neuroinformatics database strategies.

For questions regarding Scribe, coding, training, or current openings, please contact Michaela Robertson (robertsonm3@uthscsa.edu)

For questions regarding Sleuth, GingerALE, or Taxonomy, please contact Mick Fox (foxm@uthscsa.edu)

For questions regarding Scribe, Database Structure, or Search Logic, please contact Angela Uecker (uecker@uthscsa.edu)

For questions with Mango, webMango, iMango, and Papaya, please contact Michael Martinez (martinezmj@uthscsa.edu)

Collaborations

The BrainMap development team welcomes collaborations. We will provide guidance and assistance in the execution of meta-analyses upon request. We encourage collaborations that develop new tools for meta-analysis or use BrainMap data to develop or validate other neuroinformatics tools and strategies.

Current Collaborators include:

- Dr. Angela Laird, Florida International University
- Dr. Simon Eickhoff, Heinrich-Heine University
- Dr. Jennifer Robinson, Auburn University
- Dr. Jessica Turner, Georgia State University
- Drs. Michael Chee & Thomas Yao, Duke-NUS Graduate Medical School
- Drs. Ed Bullmore & Nicolas Crossley, University of Cambridge
- Dr. Franco Cauda, Università degli Studi di Torino
- Dr. Kathrin Reetz, Uniklinik RWTH Aachen

Please review our Collaborative Use License Agreement
(http://www.brainmap.org/collaborations.html).

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