fMRI Neuroinformatics

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Functional magnetic resonance imaging (fMRI) generates vast amounts of data. The handling, processing, and analysis of fMRI data would be inconceivable without computer-based methods. *fMRI neuroinformatics* is concerned with research, development, and operation of these methods. Reconstruction, rudimentary analysis and visualization tools are implemented in software controlling modern MRI scanners. Research in advanced methods for analysis of subtle activation patterns, realistic physiological modeling, or for integration of data from multiple subjects etc., is the basis for a lively research field and has led to the development of a large number of tools.

The standard analysis

The dominant scientific paradigm for fMRI analysis is the hypothesis-driven and voxel-based approach where consistent activation responses to a controlled behavioral brain function across multiple subjects is detected. Such an analysis requires a multi-step processing scheme where the typical steps involve: 1) spatial realignment of the individual fMRI scans for head motion correction; 2) coregistration between functional and anatomical scans; 3) spatial normalization of the subjects involved in the study, e.g., based on anatomical MRs of different subjects; 4) spatial smoothing; 5) construction of summary images ("statistical parametric maps") by estimation of the effect in each voxel with respect to a behavioral brain function; 6) statistical test on these effects with a final report on significantly activated voxels. A number of publicly available packages include functions for most of the necessary processing steps: SPM, FSL, AFNI, MEDx, BrainVoyager, VoxBo, LIPSIA, BAMM, see Table 1 for pointers. BrainVoyager is a commercial product, while SPM and VoxBo rely on Matlab (Mathworks, Natick, MA) and IDL (Research Systems, Boulder, CO), respectively. The commercial software MEDx includes a compiled version of SPM and FSL. Apart from the functions mentioned above the packages have a number of other functionalities for image processing and visualization. The description of LIPSIA exemplifies the many tools [1].

A simple count from the Brede Database (see below for this database) quantifies the dominance of the different versions of SPM (SPM99, SPM96) with only few other tools in widespread use, e.g., AIR — a dedicated image registration package, see Fig. 1. Note, however, that the count is for already published studies, — some of which are years old, thus the newest version of SPM (SPM2) does not appear on the list as well as other relatively new packages, such as FSL, that has gained significant attention.

Image processing

Motion correction, coregistration and spatial normalization, collectively referred to as image registration, rely on specialized algorithms: AIR, AFNI, INRIAlign, FLIRT in FSL and spm_realign in SPM among others implement motion correction adjusting for head motion between the scans. In this step the object, the brain, undergoes rigid body motion. Since the MR acquisition mode is also approximately constant in time, the gray level distribution of the
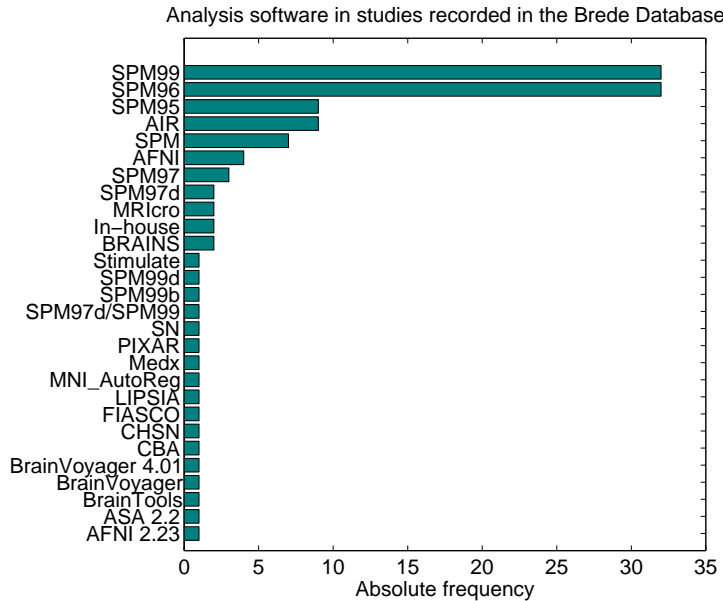
Figure 1: Popularity of analysis software. Histogram of the tools used for analysis of functional neuroimaging experiments (including fMRI and PET) as recorded in the Brede Database.

brain images are directly comparable, and a mis-registration cost-function based on gray level similarity can be used. Details distinguish the implementations, e.g., FLIRT enables apodization which suppresses the spurious modes that appear in the cost-function as parts of the brain flips in and out of the field of view of the scanner. If the activation paradigm invokes activation in large areas of the brain the signal change may be (mis-)interpreted as motion. The INRIAlign image registration program aims to correct the actual motion by using a robust cost-function, instead of the usual square error cost-function.

Co-registration of a subjects functional and anatomical MRs requires an algorithm that can match shapes across different "modalities", i.e., across different gray level representations and contrast. The most common strategy is based on the estimated mutual information based on the joint gray-level histogram of the two images. This is implemented, e.g., in FLIRT and spm_coreg in SPM2. Other approaches use different cost-functions, e.g., AIR, or brain tissue type segmentation and match the segmented regions.

Spatial ("geometric") distortions can appear in fMRI scans. Thus, a rigid body transformation may not be able to align fMRI and anatomical MR scans even within the same subject. Therefore a tool that enables warping based on a mutual information cost-function is needed, such as MRIWarp. Furthermore, SPM2 allows for modeling of movement by field inhomogeneity interactions and FUGUE/PRELUDE in FSL provides unwarping based on extra MRI data.

Spatial normalization is aimed at matching different subject anatomies by non-linear spatial alignment, so-called "warping". The warp can be based on nonlinear basis functions or free transformations regularized by, e.g., an elastic force between the voxels. Tools for this processing step include SPM, AIR and MRIWarp. In most human studies spatial normalization usually registers to a template approximately conforming to the Talairach atlas [2]. This important step allows the coordinates of activated voxel sets ("Talairach coordinates") to be compared across studies. Template volumes from the Montreal Neurological Institute (MNI) have been widely adopted, and is included in, e.g., SPM2 and FSL.

Even with careful anatomical normalization a residual intersubject variability of the activation pattern will remain. Spatial smoothing, implemented with a "Gaussian kernel" in most packages, de-focus the scans and can increase the local significance of the common (population) activation pattern.

Additional image processing steps are offered in available tools, but not necessarily performed in standard fMRI analysis: intensity correction [3]; brain extraction (BET in FSL, BSE in BrainSuite, 3dIntraCranial in AFNI, McStrip) [4]; tissue segmentation (e.g., FAST in FSL, spm_segment in SPM2). Slice

timing correction, correcting for the different acquisition times of slices in fMRI, is implemented in, e.g., SPM, FSL, LIPSIA, AFNI and in VoxBo.

Optimization of the fMRI processing pipeline is an important current research topic. The preferred approach would be a holistic optimization of the entire processing chain. However, each processing step can involve numerous interdependent parameters and algorithmic choices, hence, the methods are in practice optimized individually.

Voxel-based analysis

The aim of ordinary voxel-based analysis is to identify activated brain areas under given behavior or stimulus. The most common acquisition scheme is based on Blood Oxygenation Level Dependent (BOLD) contrast. The most common experimental setup is the so-called block design, in which fMRI scans of the behaving brain ("activation") are interleaved with scans where the brain is either resting or engaged in other reference activity ("baseline"). The task of an analysis tool is to detect the subtle differences between these scan sets.

In the simplest voxel-based analysis the time course of a voxel is modeled as two-samples — activation and baseline and the voxel is active if the no-difference null hypothesis is rejected. The BOLD signal measures activation indirectly through the so-called hemodynamic response. This response is rather sluggish and the fMRI response may be lagging by 4-6 seconds. This delay is typically compensated by a linear time-invariant system. Methods such FIR filters, discrete cosine functions and other parameterized curve forms, such as a temporally resampled version of a gamma probabil-

ity density function have been suggested and have appeared in tools. These models can be implemented within the framework of the general linear model (GLM) where activation/baseline indicators are contained in a design matrix [5]. The GLM not only allows for the modeling of activation/baseline studies but also accommodates experimental designs involving multiple states, e.g., factorial designs, and may also be used to reduce the effects of confounding signals discussed further below. GLM is implemented in a number of tools (e.g., FSL, SPM, VoxBo, LIPSIA, FMRISTAT, FIASCO), while tools such as MRVision, Stimulate and Yale implement the simpler models, see Fig. 2 for an example analysis. Even though the GLM is linear in the parameters and the data it is possible to model nonlinearities in the design variables quite simply by adding, say the squared design variables in the design matrix.

The BOLD fMRI signal is often found to vary considerably between scanning sessions and between subjects, and it has been recommended to invoke random effects models where the fMRI signal is modeled with two components: The between-scan within-session/subject variation and the between-session/subject variation. Such complex models can be simplified for balanced designs, and tools can analyze the data in two steps: In the first step the individual sessions/subjects are treated independently, in the second step the summary images of the first step are analyzed.

Tools for region based analysis

While voxel-based analysis dominates fMRI analysis, region-based analysis provides an alternative for group studies which

may be less sensitive to individual differences in anatomy. Dedicated tools available for region based analysis, e.g., MarsBaR, WFU Pick Atlas, Marina, typically provide means for creating and handling regions and extracting the relevant fMRI time series. Regions can be based on volumes labeled with respect to anatomy. Such labeled volumes include the manually segmented AAL (included in MRIcro) and ICBM Single Subject volumes. Both AAL and ICBM locate regions based on the anatomical MR of a single subject (MNI "single subject"). The ICBM atlas exists in a high resolution version as well as a probabilistic version for certain regions. An automated, consensus-based, and approximate method constructs volumes from the anatomical labels associated with Talairach coordinates available in activation foci databases [6]. The Brede Toolbox (see below) facilitates this method and probabilistic volumes are available for a large number of regions. Labeled volumes are also indirectly available through the so-called Talairach Daemon.

Modeling of confounds

Scanner hardware drift, residual head motion effects, cardiac and respiratory confounds conspire to complicate modeling of the BOLD fMRI signal. Tools that do not properly model such temporally correlated ("colored") noise can not be expected to make correct statistical inferences.

Most tools include some form of "detrending", such as extraction of low frequency signals by polynomials or other basis function sets, e.g., cosines. More elaborate schemes model these
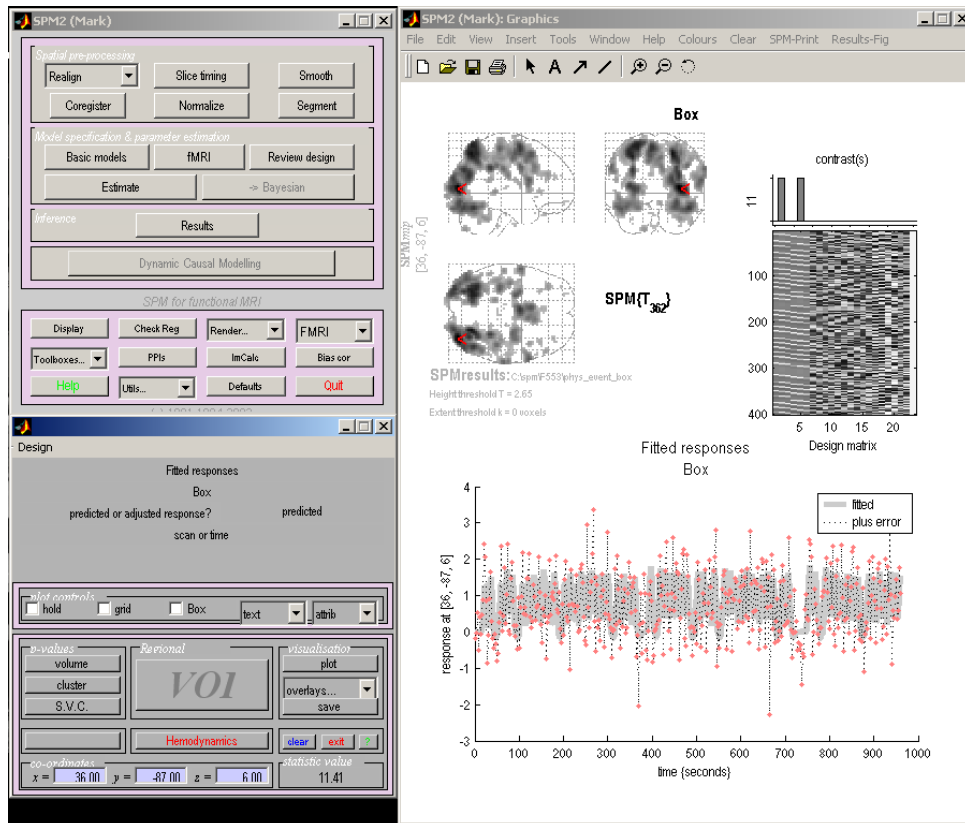
Figure 2: Screen shot of a single subject analysis performed in SPM2. The left hand side consists of two windows used as interface for design specification and analysis. The right hand side displays the activation map (as a maximum intensity projection, corrected for multiple comparisons using FDR correction ($P < 0.05$), a graphical interpretation of the design matrix and a time-series plot from a single voxel (400 samples). The time-series originates from the voxel with maximal probability of being activated in a visuo-motor experiment (vs. the baseline, which is not modeled explicitly in this analysis). The RETROICOR method is used for modeling the confounding signal from respiration and cardiac pulsation.

confounds by autoregressive processes (e.g., SPM2) as an integrated part of the analysis.

Effects of confounding signal sources for which time courses are available can be reduced by including them in the GLM design matrix. This can, e.g., be done for motion correction parameters, which can be obtained from the image registration algorithms, or for cardiac or respiratory confounds. The latter can be added after conversion, e.g., by the RETROICOR method [7]. The combined set of parameters for reduction of low frequency artifacts, head motion residuals, cardiac and respirations perform

well in modeling colored noise fMRI data [8]. GLM-based tools implicitly support this method, though the inclusion of confounds is not always seamlessly implemented in the present tools.

Multiple comparison

An fMRI study typically tests many individual hypotheses: The tests are performed in a mass-univariate setting over all voxels (or regions), and several tests can be performed for the combinations ("contrasts") of experimental states. This can result

in a massive multiple comparison problem. If the number of tests is not accounted for the statistical test will lead to an excess of significant results. Correction for the number of contrasts have been rarely made and is only limited implemented in tools. Correction for the number of tests across voxels are often performed and implemented in multiple tools (SPM, FSL, FMRISTAT) based on random field theory [9]. The so-called false discovery rate (FDR) is an alternative method for multiple comparison correction, which is implemented in SPM2, AFNI and BrainVoyager [10].

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A permutation test allows for testing statistics that have no known distribution. Under its normal operation it will not correct for multiple comparisons, but when coupled with the *maximum statistics* it becomes a versatile method both to account for multiple comparisons as well as to handle statistics of unknown distribution [11]. In this form it is implemented in AFNI, FSL, SnPM — a plug-in to SPM — and in the VoxBo program. Compared to random field theory its implementation is simple. The drawback is its assumption of exchangeability and its computation time. The multiple sources of temporal correlation in BOLD fMRI scans invalidate simple temporal sample exchangeability. This problem can be circumvented by permuting on the summary statistics of, e.g., each subject, or by permuting after wavelet transformation as implemented in BAMM. It is typically not feasible to perform all permutations and the practical implementations uses approximate permutation testing where the distribution of the maximum statistics is built from a random subset of a few thousand permutations.

Although it is considered "best practice" to correct for the number of multiple comparisons by some method it is not always done. The Brede Database records whether the P-values are a result of a procedure corrected for multiple comparison, and we have found that about a third of all reported Talairach coordinates are corrected, see Fig. 3.

Multivariate data analysis

The voxel-based (or region-based) approaches are not the only methods for supervised modeling of fMRI data: In the usual GLM approach the behavioral label encoded in the design matrix can be viewed as causes, and the estimation of the model parameters can be viewed as finding the model that predicts the fMRI data from the behavioral labels. If the process is reversed we get what has been termed "recognition models", that predict the behavioral labels from the fMRI. Linear models, artificial neural networks (ANN) and support vector machines have been applied, see, e.g., [12, 13], and the Lyngby package, implementing the ANN, supports this mode of analysis.

Explorative and diagnostic

Ordinary supervised modeling with, e.g., GLM imposes relatively strict model assumptions on the fMRI data. The SPM extension "SPMd" provides means for testing these assumptions by a multitude of diagnostic measures [14]. It is not usually reported how the different choices made during processing and analysis affect the final results. The NPAIRS framework and tool have been proposed for unbiased estimation of the generalizability of both univariate and multivariate models and for the quantification of reproducibility of the summary image [15]. The resulting performance metrics together form a complete framework for holistic optimization of fMRI processing pipelines

Unsupervised models typically make weaker assumptions and can be used for explorative investigation, or "hypothesis generation" based on fMRI data sets. Among the algorithms available in tools are: fuzzy clustering (EvIdent), singular value decomposition (MM, Lyngby), agglomerative hierarchical clustering (3dStatClust

in AFNI), K-means clustering (Lyngby) and different variations of independent component analysis (ICA) (e.g., GIFT, MELODIC in FSL, FMRLAB, BrainVoyager and Lyngby). The typical application is on preprocessed data, and ICA in particular has been shown to be able to separate signal components in different types of activations and confounds [16]. Unsupervised schemes may also be used on the residuals of a GLM analysis to explore for residual un-modeled effects [14].

Connectivity

A basic drawback of the conventional voxel or region based analysis is that the statistical inference is limited to that of a voxel or a region, hence, fail to detect global (weak) patterns or "networks" [17]. Multivariate methods, on the other hand can exploit long-range dependencies and may thus potentially detect weaker and/or more subtle effects. So-called structural equation modeling (aka path analysis) and dynamic causal modeling (DCM) are means for explicit modeling of interaction between regions, see, e.g., [18]. DCM (implemented in SPM2) is a sophisticated tool that includes hemodynamics modeling and possible temporal dependency between brain regions.

Visualization

Most tools described above include some form of visualization of the fMRI data, both in terms of the spatial and temporal dimensions. Many tools with a specific focus on visualization are available. MRIcro and mri3dX, e.g., both allow for slice-based as well as 3-D viewing.

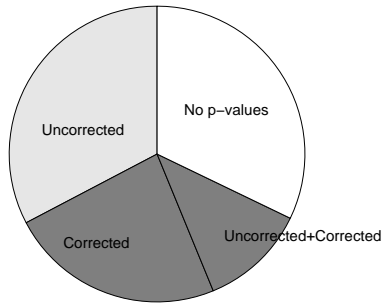Specialized visualization tools (FreeSurfer, SureFit/Caret,

Figure 3: Count on the type of *P*-values in the Brede Database.

SurfRelax, BrainVoyager, SUMA in AFNI and Anatomist in Brain-VISA) construct surface meshes of the cortices based on segmentation of anatomical scans. Thresholded fMRI result volumes can be projected onto the mesh, see the example in Fig. 4. Some tools allow for transformation of the mesh into a sphere or a plane — a so-called flatmap — with color coding according to the gyrus/sulcus pattern and projection of the functional result.

Execution environments

So-called execution environments or script-builders do not process or analyze brain data *per se*, but rather control other programs, facilitating their integration and management of the multi-step processing chain. They typically provide a graphical interface for setup of parameters and a graphical pipeline visualization where results and parameters can be routed between the programs. Current execution environments include FisWidgets, the LONI pipeline, BrainVISA and RUMBA. FisWidgets contains graphical wrappers for a number of third party tools, e.g., AIR, AFNI, FSL, and Lyngby. The LONI pipeline features a client/server model. The SPM and AFNI packages enable plug-

ins, and several tools provide facilities for controlling SPM in batch mode, e.g., spmjob and autospm2, while others enable processing via computer clusters, e.g., PSPM and VoxBo. Some of these tools are in their early stage of development.

Database issues

The fMRI Data Center (fM-RIDC) is a database with brain scans from published fMRI studies [19]. Publication of fMRI studies in the Journal of Cognitive Neuroscience requires the submission of the fMRI scans to this database. Each data set typically contains the raw fMRI data and subjects anatomical MR. Apart from rather few publicly available fMRI scans used as demonstration data for tools, the fMRIDC is the only public source of fMRI data. A simple web-interface allows for search on the bibliographic details and for request of data sets, which are delivered on CD by surface mail. fMRIDC annotates the studies against an ontology setup via Protégé (http://protege.stanford.edu/). The annotation contains information about, e.g., the experimental conditions and event timing. Data from fMRIDC has already been used in several published studies with analysis methods not anticipated in the original experimental design.

The NeuroGenerator and SumsDB are other examples of a neuroimaging databases. Neuro-Generator stores the actual imaging data in an object-oriented database management system (ODBMS). ODBMS, such as PostGreSQL, can handle special data types, enabling the storage of imaging data as volumes rather than as just a block of bytes.

Storing fMRI

The raw image data from a conventional fMRI study can easily amount to several gigabytes, and compression is desirable. Unfortunately, ordinary loss-less compression (e.g., with the *gzip* program) typically obtains relatively low compression ratios. Lossy compression is in general not feasible since the signal of interest is small part of the overall signal. A few lossless algorithms have emerged that have been aimed at fMRI compression: One such uses integer wavelet transform [20], and the SmallTime program is a compression tool specifically targeted for fMRI.

The many different file formats used for fMRI (e.g., ANA-LYZE, MINC, AFNI, DICOM, VoxBo) form a obstacle for interoperation of tools, though the ANALYZE file format has gained wide implementation across tools. The original format did not support spatial normalized volumes, (specification of origo), and storage of affine
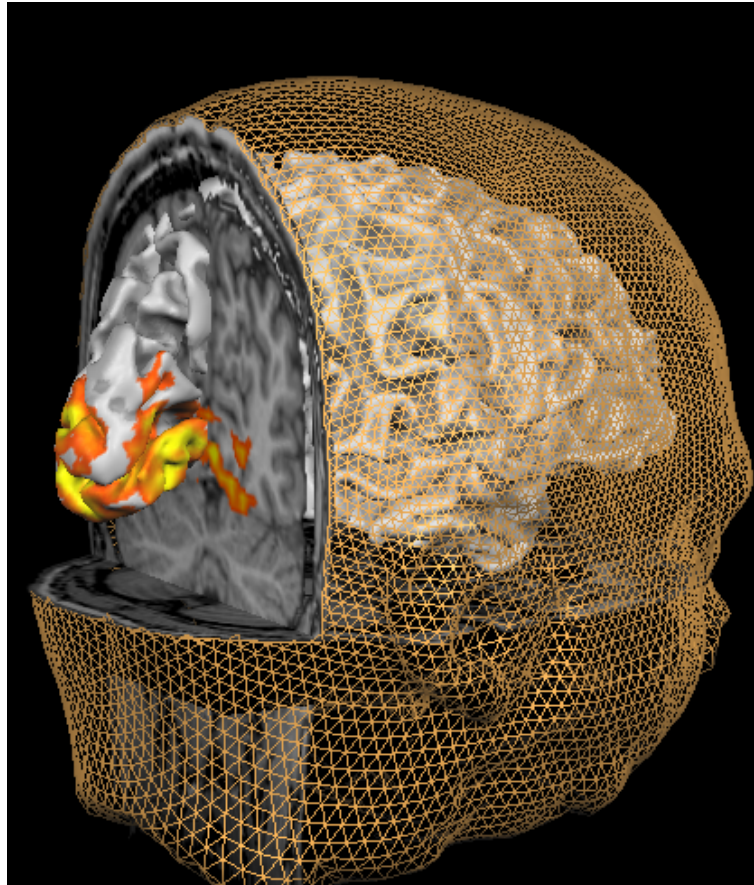
6

Figure 4: Activation from a retinotopic mapping experiment shown on a folded mesh with axial and coronal cuts in BrainVoyager.

transformation parameters. SPM extended the format by defining extra fields in the header and by augmenting the format by an additional Matlab file. The left/right orientation of the volume has been ambiguous between versions, and the Neuroimaging Informatics Technology Initiative (NIfTI) effort includes a standard left/right orientation as well as fields to include the transformation parameters while maintaining backward compatibility with ANALYZE. A number of the major packages have announced support for this format. NIfTI is not able to record all information that a typical laboratory would need, such as scanning parameters and experimental information, so laboratories will need additional information structures for storage of such information.

Bringing neuroimaging in context

The results of fMRI studies form a rapidly expanding body of knowledge which is increasingly difficult for the individual researcher to span. Text-based informatics services such as the National Institutes of Health's PubMed help to find relevant literature, but does not record the quantitative result of fMRI studies. One of the first databases that specifically targets quantitative results of fMRI and other functional neuroimaging modalities is the BrainMap database pioneered by Peter Fox and Jack Lancaster. Originally developed for PET the present version contains over 500 annotated studies with together almost 18,000 Talairach activation coordinates. An associated tool can access the central database via the Internet with queries based on, e.g., bibliographical details, behavioral domain, or specified locations in Talairach space. Furthermore, the program has also visualization options for Talairach coordinates, see Fig. 5. The Brede Database is a smaller database with a similar scope as BrainMap. The entire database is available as an XML file on the web.

Peter Fox and Jack Lancaster have also initiated meta-analytic methods for modeling of Talairach coordinates across studies — so-called functional volumes modeling (FVM) [21]. If the coordinates are confined to a spe-
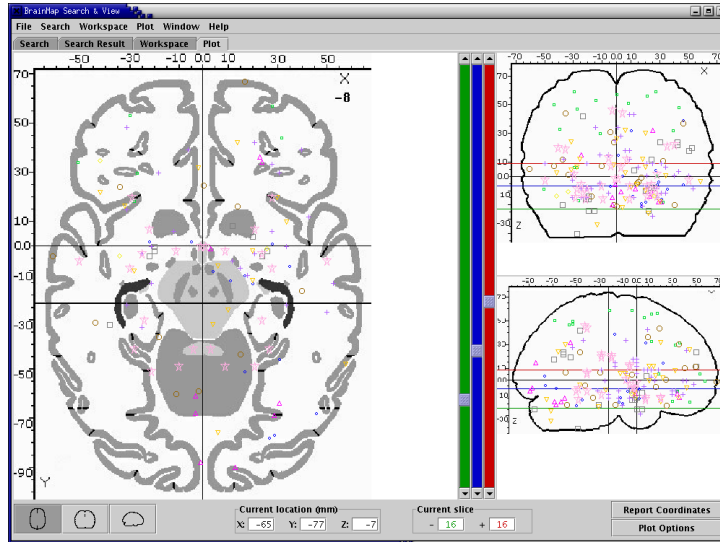
7

Figure 5: Screen shot of a graphical user interface to the BrainMap database with Talairach coordinates plotted after a search for experiments on olfaction.

cific area their distribution can be modeled with a Gaussian distribution. Spatially distributed coordinates can be modeled with more flexible models, e.g., Gaussian mixture models, and kernel density estimation has been proposed [6]. The Brede Toolbox is a Matlab-based package for FVM and implements kernel density estimates and statistical tests for sets of Talairach coordinates. Volumes can be generated by sampling the FVM distribution on a regular grid. When several sets of coordinates exist (resulting in multiple volumes) this data can be analyzed in much the same way as an ordinary fMRI data set. The Brede Toolbox has been applied on data from Brain-Map and Brede databases, e.g., for singular value decomposition, independent component analysis and maximum statistics permutation testing. The toolbox allows for query for "similar experiments" based on activation foci similarity in the Talairach space, i.e., queries beyond simple text, c.f. PubMed [22]. The Brede Toolbox furthermore contains functions for visualization of Talairach coordinates and vol-umes.

Both BrainMap and Brede provide interfaces for entry, but the task of extracting coordinates and annotating the experiments is labor-intensive and no automatic tool currently exists for this task. For meta-analysis it would thus be preferable to have access to the raw data.

The BrainMap and Brede databases facilitate a computer-based approach to placing fMRI studies in proper scientific context, and the results from a meta-analytic modeling with kernel density estimates compare well with results from an ordinary independent fMRI study [23].

Further information

fMRI neuroinformatics tools are still evolving, new methods are being described and a complete and updated list of all tools and all their functionalities for fMRI is not presented here. The list of pointers provided in Table 1 is not complete, e.g., there are numerous packages that primarily target processing and analysis of anatomical MR scans. A number of web-sites provide lists of the neuroinformatics tools and databases available: *The Neuroinformatics Portal Pilot* (http://www.neuroinf.de/) and *Internet Analysis Tools Registry*, (http://www.cma.mgh.harvard.edu/-iatr/) enable collaborative entry of information. Andrew Crabb maintains *idoimaging.com*, the Society for Neuroscience hosts a web-site: The *SfN Neuroscience Database Gateway* (http://big.sfn.org/ndg/site/), and one of the authors updates the *Bibliographies in functional neuroimaging* (http://www.imm.dtu.dk/~fn/-bib/Nielsen2001Bib/). Furthermore, SPM has a lively email list (http://www.jiscmail.ac.uk/-lists/spm.html) where new tools are often presented.

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Acknowledgment

Name	Usage	URL
AAL	Atlasing	http://www.cyceron.fr/freeware/
AFNI	General purpose	http://afni.nimh.nih.gov/afni/
AIR	Image registration	http://bishopw.loni.ucla.edu/AIR/
BAMM	General purpose	http://www-bmu.psychiatry.cam.ac.uk/software/
BrainMap	Databasing	http://www.brainmap.org
BrainSuite	Image processing	http://neuroimage.usc.edu/brainsuite/
BrainVISA	Environment	http://brainvisa.info/
BrainVoyager	General purpose	http://www.brainvoyager.com/
Brede	Databasing	http://hendrix.imm.dtu.dk/services/jerne/
EvIdent	Analysis	http://www.ibd.nrc-cnrc.gc.ca/english/info_e_evident.htm
FIASCO	General purpose	http://www.stat.cmu.edu/~fiasco/
FisWidgets	Environment	http://grommit.lrdc.pitt.edu/fiswidgets/
fMRIDC	Databasing	http://www.fmridc.org
FMRLAB	Analysis (ICA)	http://www.sccn.ucsd.edu/fmrlab/
FMRISTAT	Analysis	http://www.math.mcgill.ca/keith/fmristat/
FreeSurfer	Visualization	http://surfer.nmr.mgh.harvard.edu/
FSL	General purpose	http://www.fmrib.ox.ac.uk/fsl/
ICBM Atlas	Atlasing	http://www.loni.ucla.edu/ICBM/
INRIAlign	Image registration	http://www-sop.inria.fr/epidaure/software/INRIAlign/
GIFT	Analysis (ICA)	http://icatb.sourceforge.net/
LIPSIA	General purpose	http://granat.cns.mpg.de/Lipsia/
LONI Pipeline	Environment	http://www.loni.ucla.edu/
Lyngby	Analysis	http://hendrix.imm.dtu.dk/software/lyngby/
Marina	ROI	http://www.bion.de/Marina.htm
MarsBaR	ROI	htpp://marsbar.sourceforge.net/
McStrip	Image processing	http://www.neurovia.umn.edu/incweb/
MEDx	General purpose	http://medx.sensor.com/
MM	Analysis	http://www.madic.org/download/MMTBx/
MRI3dx	Visualization	http://www.aston.ac.uk/lhs/staff/singhkd/mri3dX/
MRIcro	Visualization, ROI	http://www.psychology.nottingham.ac.uk/staff/cr1/mricro.html
MRIWarp	Image registration	http://hendrix.imm.dtu.dk/software/mriwarp/
MRVision	Analysis	http://www.mrvision.com/
NIfTI	File format	http://nifti.nimh.nih.gov/
NPAIRS	Diagnostic	http://www.neurovia.umn.edu/incweb/
NeuroGenerator	Databasing	http://www.neurogenerator.org/
SmallTime	Compression	http://www.brainmapping.org
SnPM	Analysis	http://www.sph.umich.edu/ni-stat/SnPM/
SPM	General purpose	http://www.fil.ion.ucl.ac.uk/spm/
SPMd	Model diagnostic	http://www.sph.umich.edu/~nichols/SPMd/
Stimulate	Analysis	http://www.cmrr.umn.edu/stimulate/
SumsDB	Databasing	http://sumsdb.wustl.edu:8081/sums/index.jsp
SureFit	Visualization	http://brainvis.wustl.edu/resources/surefitnew.html/
SurfRelax	Visualization	http://www.cns.nyu.edu/~jonas/software.html
Talairach Daemon	Atlasing	http://ric.uthscsa.edu/projects/talairachdaemon.html
VoxBo	General purpose	http://www.voxbo.org/
WFU Pick Atlas	ROI	http://www.fmri.wfubmc.edu/
Yale	Analysis	http://mri.med.yale.edu/individual/pawel/fMRIpackage.html

Table 1: Tools for fMRI processing and analysis. "ROI" is dedicated region of interest (region-based) functionality.