

This documentation is somewhat out-of-date. Refer to web documentation at <http://www.nmr.mgh.harvard.edu/~jbm/jip/>

Overview of jip tools

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Summary of programs

- 1) Display tool (jip-display):
 - The X11-based display tool reads either the Nifti format (.nii files) or header-less binary files accompanied by keyword-delimited ASCII header files.
- 2) Alignment tool (jip-align):
 - The alignment tool employs an interactive GUI similar to the display tool. It enables affine alignment (with a selectable set of parameters) and optional adjustment of 3-dimensional non-linear distortion fields.
- 3) Command-language scripting tool (jip)
 - This tool provides numerous commands for performing data alignment, smoothing, averaging, reordering,
- 4) General linear model for fMRI analyses (jip-glm):
 - The first-level GLM enables fMRI analyses appropriate for sensory/motor/cognitive stimuli or pharmacological stimuli.
- 5) Random-effects model (jip-rem)
 - The Worsley method (NeuroImage 2002; 15(1):1-15) is implemented for repeated measures using functional conditions produced from the 1st-level analysis.
- 6) Analysis of PET data using a GLM implementation of the simplified reference tissue model (SRTM).
 - See web site above.

Platforms

All tools use the Linux/Unix environment. The current distribution includes executables for Linux i686 (32-bit), Linux x86_64 (64-bit), Darwin for Mac OS X (universal binary), and Cygwin/X (32-bit) for Windows. The code is distributed as open source to enable creating of executables for other systems.

Citations

If you find these tools useful for your research, please provide the following in the Methods sections of your paper:

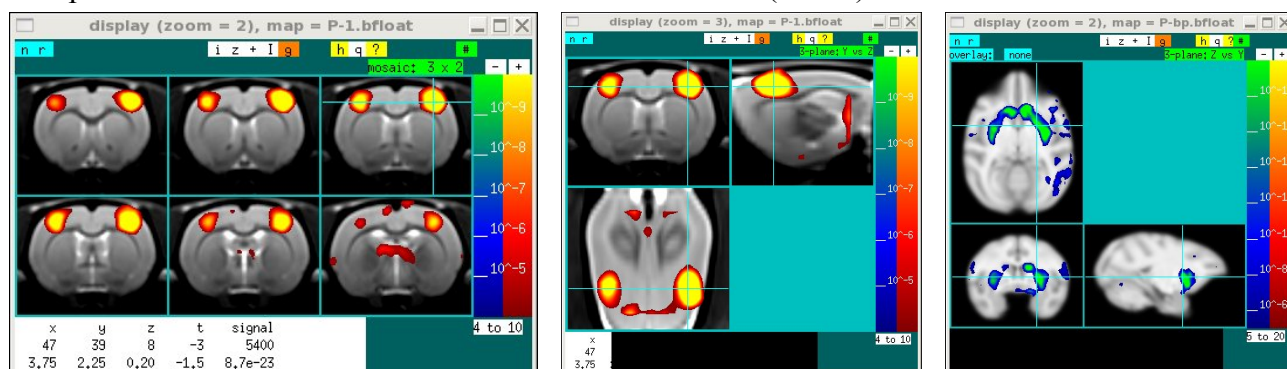
- 1) a link to the tools: www.nitrc.org/projects/jip/ ,
- 2) a citation to one of the following papers:
 - If you used the program primarily for alignment or GLM analysis of rat or mouse data:
Liu CH, Greve DN, Dai G, Marota JJA, Mandeville JB. Remifentanyl administration reveals biphasic phMRI temporal responses in rat consistent with dynamic receptor regulation. NeuroImage 2007, 34(3): 1042-1053.

- If you used the program primarily for alignment or GLM analysis of non-human primate data:
Mandeville JB, Choi JK, Jarray B, Rosen BR, Jenkin BG, Vanduffel W.
Neuropsychopharmacology 2011, In Press.

Overview of functionality

Image display tool:

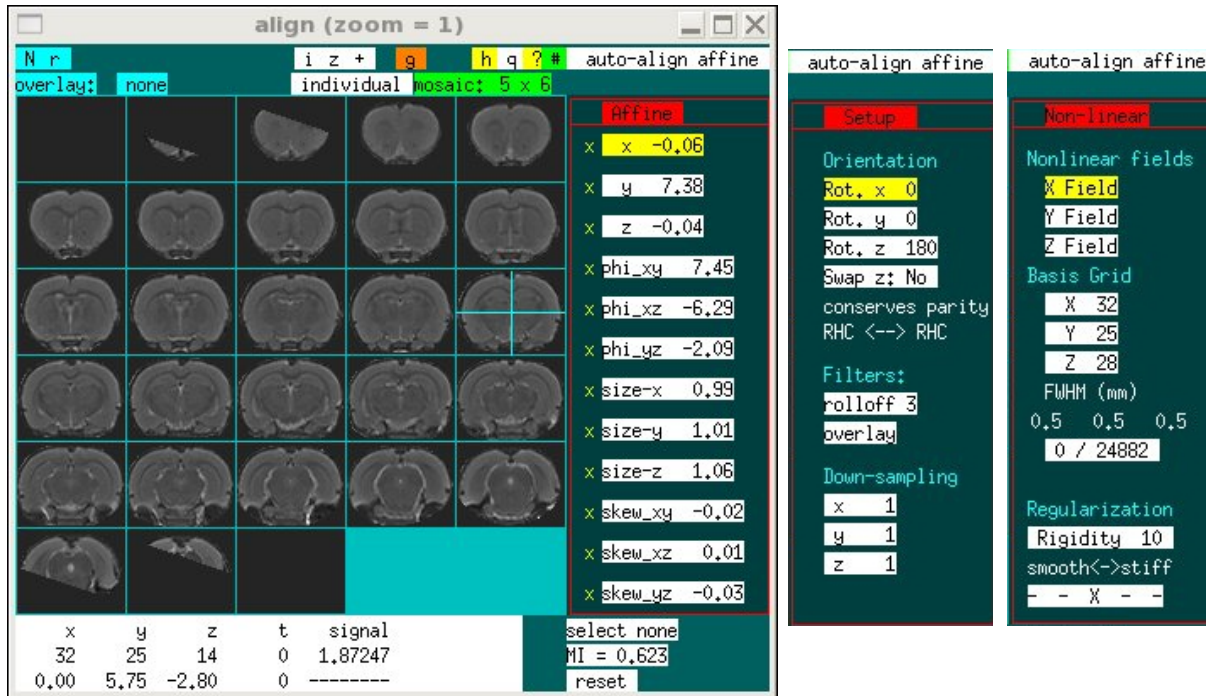
- Mosaic format:** The number of image panels can be defined at run time from the command line or entered interactively later. Slices can be displayed in a contiguous manner or selected with a mouse from a mosaic of all slices. The x/y panel arrangement can be changed as desired. Mosaics can display any of three orthogonal orientations.
- Tri-planar format:** 3 orthogonal orientations are shown. Data can be displayed in a way suitable for rodents or for primates.
- Time points & maps:** Time series can be loaded from one or more files, together with one or more color maps. Full analyses from 1st and 2nd order General Linear Model analyses can be loaded from the respective control files associated with other executables (below).



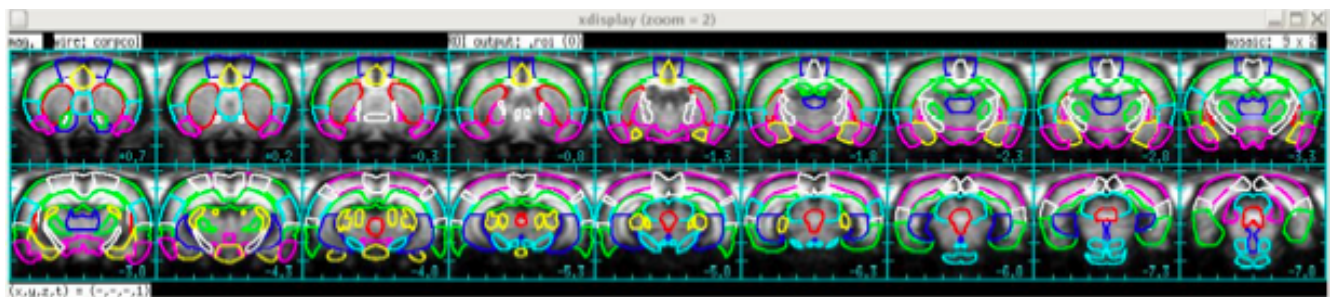
Alignment tool:

- Same display formats and conventions as image tool (above).
- Three panels for setup, affine alignment, and adjustment of non-linear distortion fields.
- Mutual information (MI) cost function, so that functional data can be aligned to anatomical data.
- Multi-resolution or single-resolution adjustment for affine registration

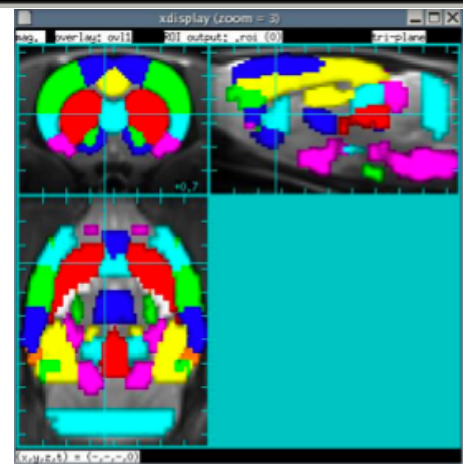
- Multi-step adjustment of variable-width cosine-squared basis functions to obtain smooth variation of distortion fields (x, y, z, or any combination); regularization of MI cost function



Wire frames and overlays

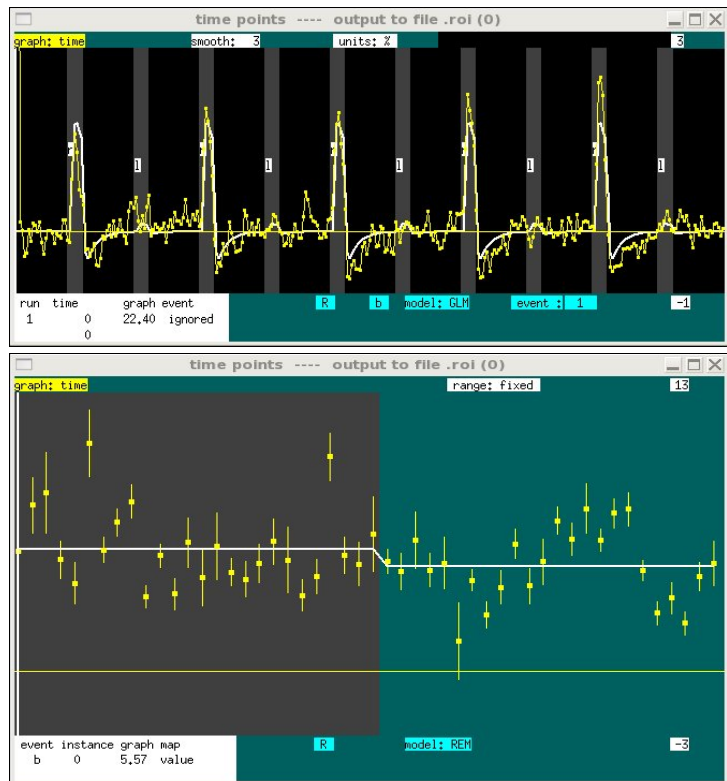


- Wire frames** are based upon voxel coordinates and not specific to image resolution. They can be used to span resolutions, to define regions-of-interest by filling closed wire frames, and to transfer regions from high-resolution digital atlases.
- Overlays** are based upon voxel indices and are specific to the image resolution. They are the basis for region-of-interest averages.
- Each can be defined interactively or loaded at run time from a predefined set.
- Region-of-interest data can be output in list format, including fits from the first or second order general linear models.



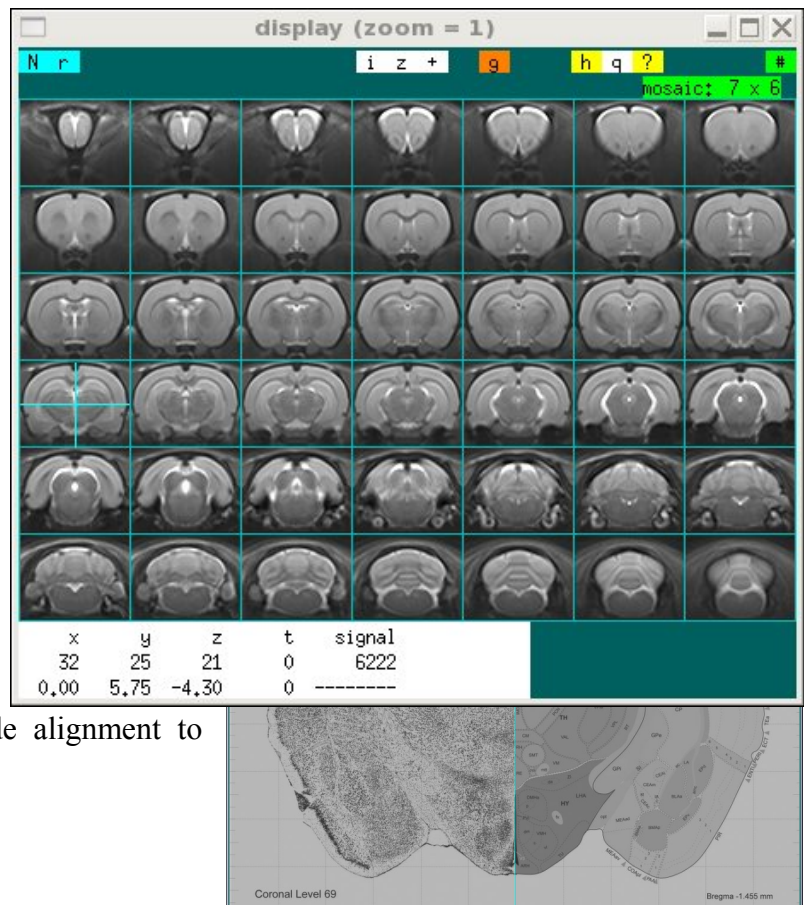
Analysis models for fMRI

- 1st-order general linear model (GLM) displays the analysis derived from the program “jip-glm”.
- Output follows the display in terms of absolute or percentage units, baseline correction, smoothing, binning, or removal of events from the GLM.
- A 2nd-order random effects model displays the analysis derived from the program “jip-rem”. Analysis uses the method of Worsely et al., NeuroImage 2002; 15(1):1-15.
- This is the “summary statistic” approach for combining subjects, sessions, or runs. Mean and error bars represent results from 1st-order GLM, and lines depict averages for 2 conditions. Alternatively, one can use the 1st order GLM for a purely fixed-effects analysis, the 2nd-order REM for a purely random-effects analysis, or the Worsely method to boost the degrees-of-freedom to provide a mixed-effects analysis.



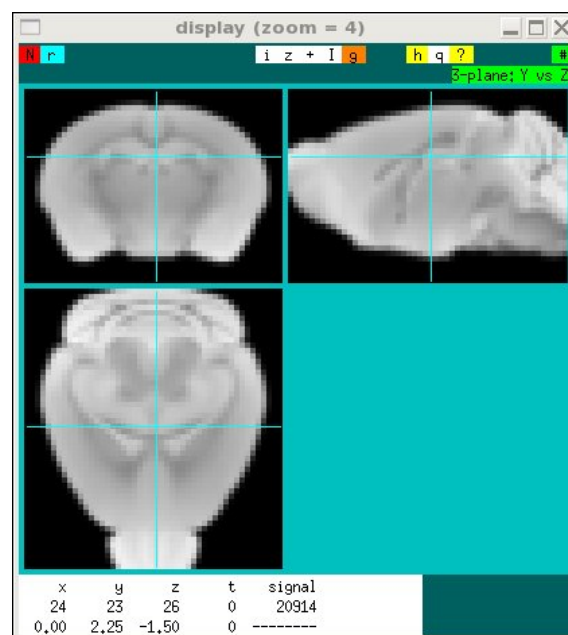
Resources: Paxinos-Watson Rat

- We collected MRI data sets (20-30 animals per set) and registered them into the coordinate space of the Paxinos-Watson rat brain atlas using a resolution of 250x250x500 microns with 42 slices.
- Three contrasts are provided: T2 (RARE), short-TE gradient-echo, and short-TE gradient-echo after injection of iron oxide contrast in order to define the regional blood volume fraction.
- Data can be down-sampled to an arbitrary resolution and number of slices to create templates for registration.
- We CANNOT DISTRIBUTE the proprietary atlas, our wire frames, or regions of interest due to copyright constraints. However, MRI data provide alignment to this space.



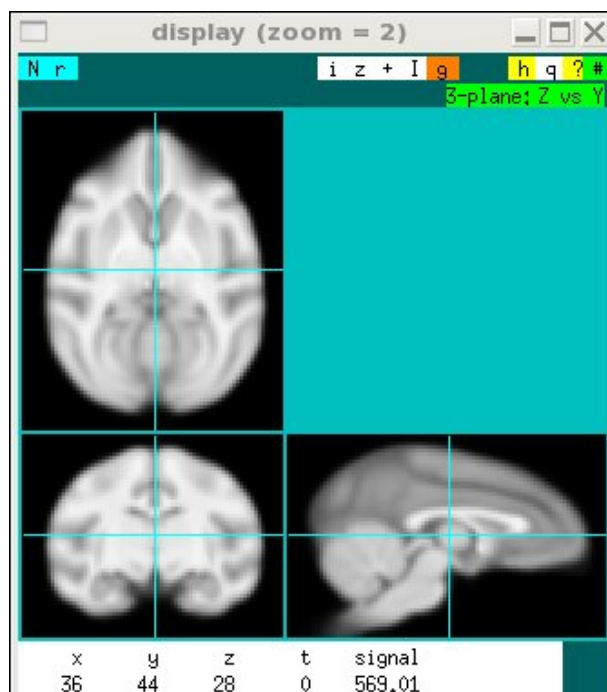
Resources: Allen/LONI Mouse

- The **Allen Mouse Brain** atlas was downloaded from mouse.brainmap.org and resampled to a resolution of 12.5 x 12.5 x 250 microns. This atlas can be used to digitally define regions of interest by tracing them as wire frames. As a basis for aligning the mouse atlas to real data, white matter and CSF were manually segmented from the atlas and used to create a “fake mouse” at arbitrary resolution. You can use this fake mouse to align your data, or you can use ...
- **LONI MDA mouse brain** aligned into the coordinate space of the Allen Mouse Brain. The LONI MDA data is not provided directly in the distribution. Instead, a transformation script is provided that you can run after downloading this data set from www.loni.ucla.edu/Atlases, or wherever the most recent version is located.
- Example transformations to place the LONI data into the Allen Mouse Brain coordinate space at an arbitrary resolution. This version shows the LONI MDA brain in the Allen space using an isotropic resolution of 250 microns. For analysis of MRI data, select a resolution and slice set that best matches the resolution and field of view for your study, and then you can access regional definitions from the Allen Mouse Brain project by transferring regions to your resolution.



Resources: Down-sampled WADRC 112RM Rhesus Monkey

- This multi-subject (112!) monkey data set is aligned to the Saleem-Logothetis stereotaxic atlas. The original atlas by McLauren et al., NeuroImage 2009; 45:52-59 can be downloaded from their web site (www.brainmap.wisc.edu/monkey.html) and then digitally resampled to create a template suitable for use as an alignment target. The image on the right has been down-sampled to 1x1x1 mm resolution. This (or another resolution) can be used as a basis for aligning fMRI or other data.



Modification since last distribution (*requested mods in red*)

jip-display

- Added the ability to display mosaics in any orientation.
- Added the option for position labels or attached to each plane (“l”).
- **Defining overlays by contiguous regions of activation now works using keyboard-“n”.**
- **The range of the colorbar scale can be input directly after clicking on the text field showing the range below the colorbar.**

jip-align

- The Jacobian determinant is output at each step of the non-linear alignment process. The minimum allowed value is hardwired to be 0.2 (i.e., compression is restrained to be less than 5-fold). As before, the registration can stumble upon Jacobian determinants less than 0 during up-scaling of the resolution of the distortion fields (e.g., basis functions) during automated alignment; use sufficient rigidity to correct this.
- If a brain mask overlay is active, it is automatically applied at the beginning of affine registration. This no longer needs to be done manually.
- The default auto-alignment choices (multi-resolution for affine, multi-step for non-linear) are now left-click.

jip

- **The interpolation used in the first distribution (hamming-weighted sinc) did not employ a sufficiently strong low-pass filter, so that ringing due to interpolation was excessive when using the “register” command. Now, the Lanczos kernel is employed to provide a good tradeoff between smoothing and ringing. This kernel is almost identical to a sinc function that has been hamming-windowed using the same cutoff length.**

jip-rem (Random effects model, or 2nd-level GLM)

- ... has been included in the distribution

Executables

- The Mac OS X Darwin executable now is a Universal Binary containing 3 architectures (thanks to Ona Wu!). The operating system should choose the correct architecture. You can also force an architecture this way: “alias jip arch -x86_64 wherever/jip”. Mac OS X executables in the Universal Binary include:
 1. ppc (Power PC chip),
 2. i386 (32-bit binary for Intel chips)
 3. x86_64 (64-bit binary for Intel chips).
- 32-bit executables for Cygwin/X for Windows have been distributed. I’m searching for a modern Windows machine to create 64-bit executables...