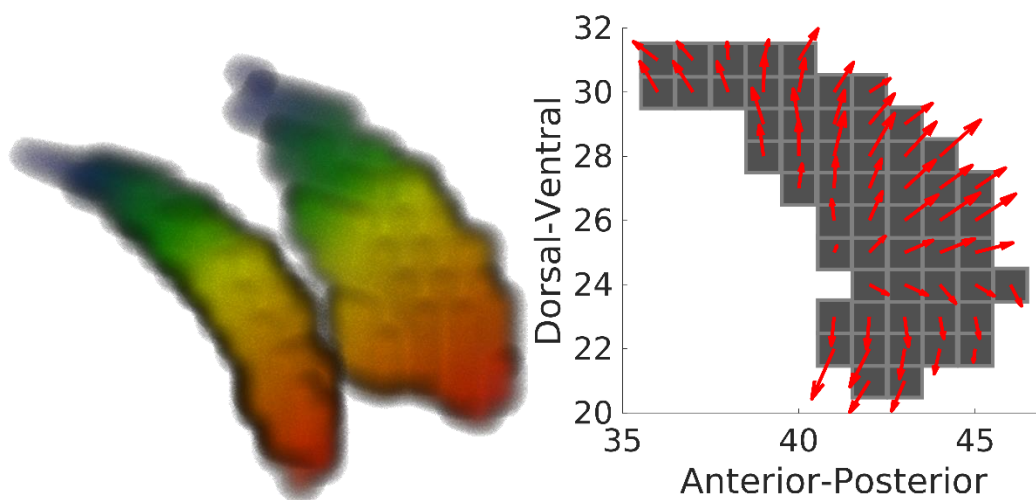


Fine Relational Spatial Topography

Toolbox Manual Version 1.0



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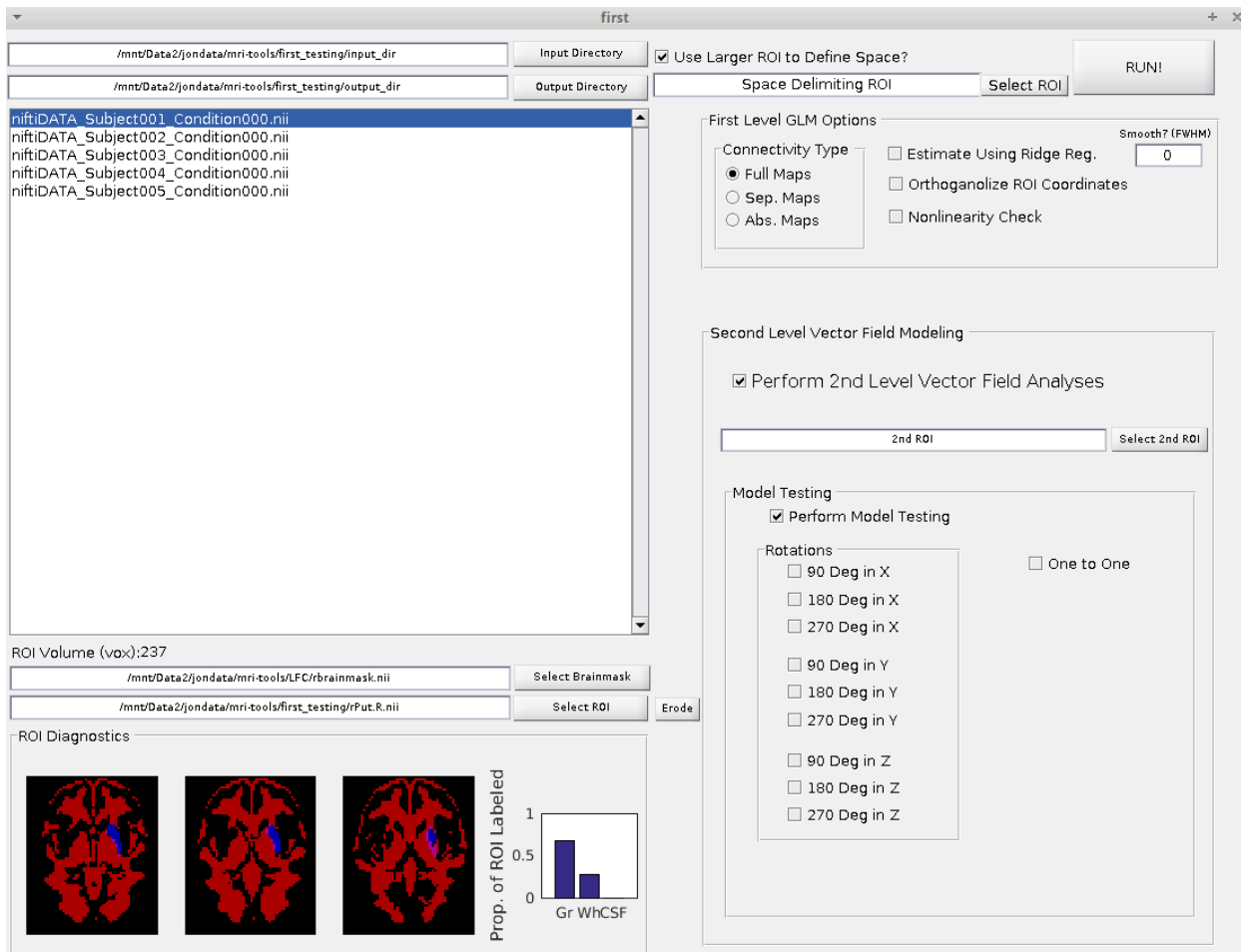
Cite for use: O'Rawe and Leung (in progress)

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Getting Oriented

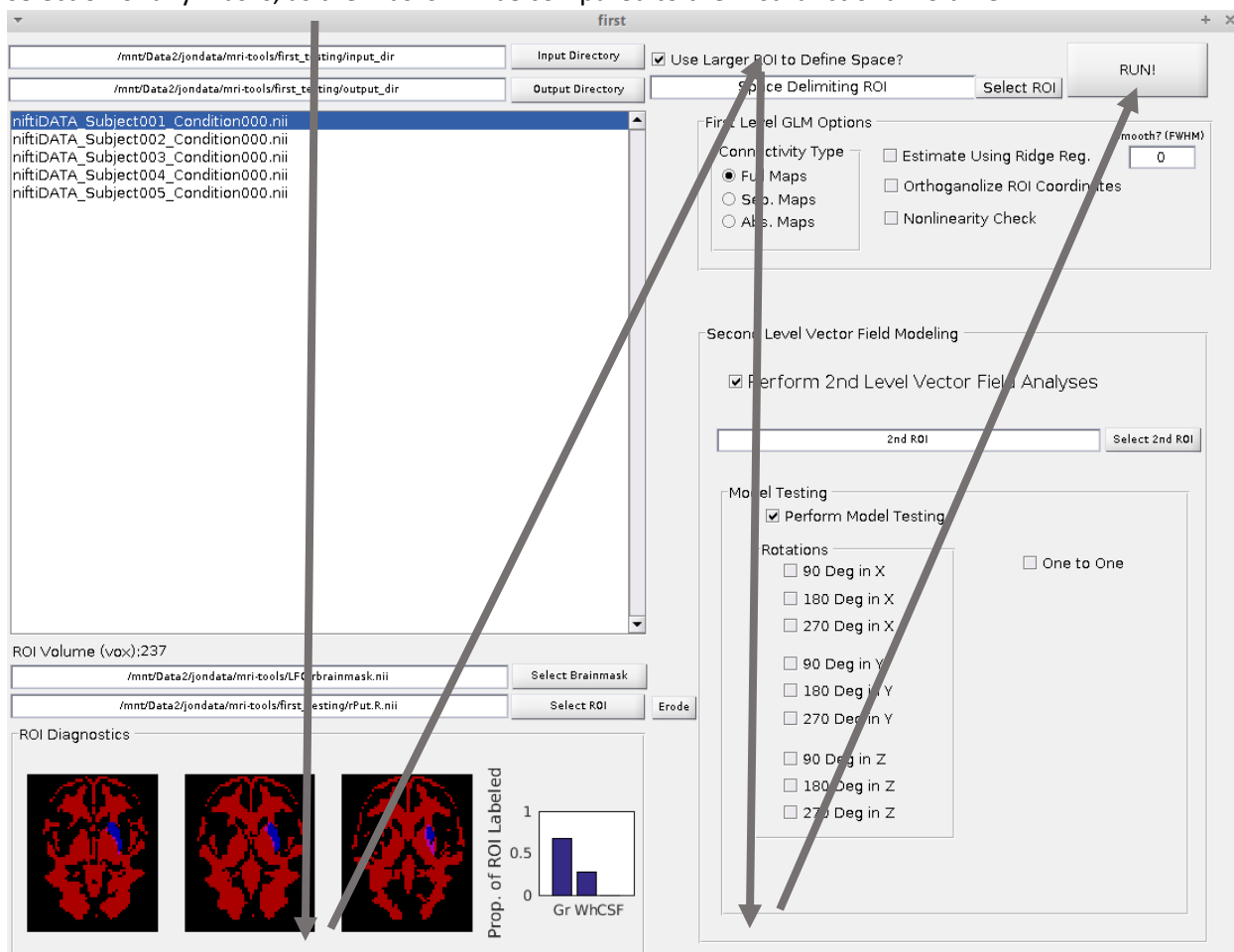
Throughout this manual, we will present portions of this screenshot to demonstrate where in the GUI the functionality we are discussing exists (first.m).



Order of Input

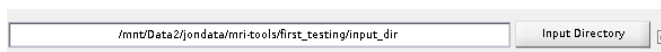
The current toolbox has been developed with some ordering effects due to dependencies across different functions, primarily to ensure all images are within the same space. The easiest procedure, as this is how the toolbox was developed, is to think of the toolbox as a two column paper, you start at the top left hand corner and perform actions until you've selected down to the bottom right hand corner.

However, in reality, the only necessary order is to have the functional volumes selected prior to the selection of any masks, as the masks will be compared to the first functional volume.



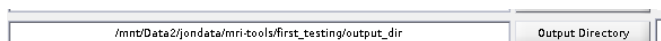
Input Directory

This should be a directory with one 4d NIfTI file per subject, each represented the subject's clean whole brain time-series.



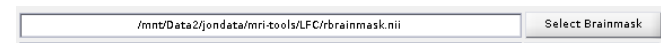
Output Directory

Select the directory in which you want F_{IRST} to output all the first level maps. Best to pick an empty directory created for this purpose, as a minimum of 6 NIfTI files are generated per subject.

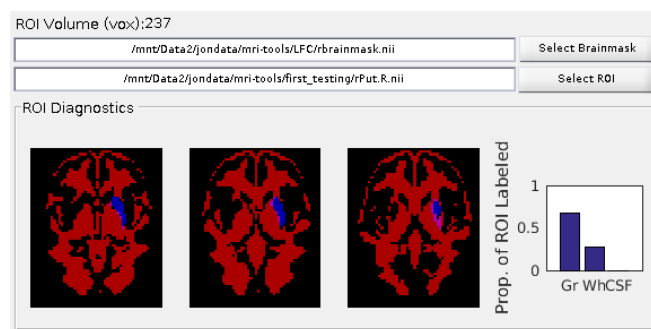


Brainmask

Select a binarized NIfTI file that will be used to mask out unimportant voxels to allow for efficient processing. A nonbinarized image will not produce an error, as any image input will be thresholded $>.5$, but may result in inappropriate results if $.5$ is an inappropriate threshold for the image.



ROI Panel



Select ROI

Here allows the selection of either a group ROI, in which case you select a single .nii file, or individual ROIs, in which you will select a .mat file whose first variable is an $[n \times 1]$ cellstr with each cell pointing to the full path of each subject's ROI, in the same order as the input data.

ROI Diagnostic Panel

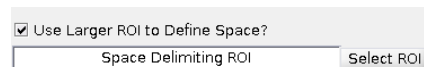
If you are using a single group level ROI, this panel plots your ROI in blue on top of the white matter and CSF masks from the MNI template thresholded at $.3$, the overlap in purple. To the right is the quantitative measure of how much of your ROI is labeled as grey matter, white matter, and CSF. If you find a large proportion overlapping with the MNI white matter and CSF masks, you may want to consider eroding your ROI.

Erode Button

Clicking the erode button strips a layer of voxels from the surface of your ROI and saves it as [roi_name]_eroded.nii within the same folder of your ROI. It's important to keep track of the number of voxels within your ROI, as the number of voxels within the ROI determine the degrees of freedom of the main GLM of F1RST, which is listed just above the brainmask input panel.

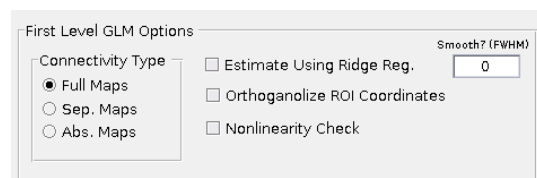
Use Larger ROI to define space?

There are very few reasons to use this option, the primary one being to examine whether or not an organizational feature remains consistent even after subsetting a region (see paper, analysis). The requirement is that your primary ROI must be a subset of the ROI selected in this option. This can be a .nii file or a .mat file like the previous ROI option.



First Level GLM Options

This panel sets various options for the input and output of the linear regression being performed.



Connectivity Type

This option delineates what to do with positive and negative correlations. There are 3 options, full maps, sep. maps, abs maps.

Full maps: Leaves the Fisher's z maps as is and performs the regression on them. Potential issue is that you might be seeing decreasing negative connectivity or increasing positive connectivity as the same parameter value. However, if GS regression isn't performed, there tends to be very few negative correlations in the data to begin with, so it's much less of a concern, and with GS regression the negative correlations can reflect positive correlations as well, so hard to say this option is ever truly too awful.

Sep. maps: Perform a separate regression on the positive and negative maps, allowing for the dissociation between positive and negative contributors to the end gradient connectivity maps.

Abs maps: Absolute values the Fisher's z maps, provided sign of correlation is uninterpretable, then only consider magnitude of correlation.

Ridge Regression

Instead of traditional OLS, this option solves the following equation:

$$\mathbf{b} = (\mathbf{X}^T\mathbf{X} + \lambda\mathbf{I})^{-1}\mathbf{X}^T\mathbf{y}$$

Where lambda is estimated as the lambda that minimizes the generalized cross validation function.

Orthogonalize ROI Coordinates

Inputs your Euclidean space into a PCA, rotating the coordinate system such that the axes are no longer correlated. Labels the axes based on their correlation structure with the original coordinate system, and thus might label incorrectly when your ROI is heavily rotated. We've also found that labeling is inconsistent in about ~10% of subjects when using individual ROIs, so manual inspection and relabeling is a necessary step if you use individual ROIs.

Nonlinearity Check

This pulls individual "rods", a set of voxels along one dimension with the other two dimensions held constant, out from your ROI and estimates whether or not the space determined by the linear correlations between voxels is linear in nature to the space of the voxels. Highly nonlinear relationships likely indicate an ROI that is ill-suited for this analysis, as it is likely composed of heterogeneous parcels. Produces a histogram of the percent variance accounted for in the ROI due to nonlinearity for all the subjects at the end of a run, allowing you to judge the validity of the analysis.

Smoothing Parameter

Enter in a smoothing parameter to apply to the parameter maps, in the metric of FWHM. It is recommended that you do not use smoothed time-series, and that you use this option to smooth the parameter maps after estimation. Utilizing smoothed time-course data likely artificially generates gradient like patterns, even when none exist.

Second Level Vector Field Modeling

Second Level Vector Field Modeling

Perform 2nd Level Vector Field Analyses

2nd ROI

Model Testing

Perform Model Testing

Rotations

90 Deg in X
 180 Deg in X
 270 Deg in X

90 Deg in Y
 180 Deg in Y
 270 Deg in Y

90 Deg in Z
 180 Deg in Z
 270 Deg in Z

One to One

Select 2nd ROI

This option can be a .nii or a .mat file, like previous ROI selection fields. This is the ROI in which the vector field will be extracted from in relation to the original ROI.

Model Testing

If you select this option, you must select at least one of the linear transformation options. This will produce outputs of model fit and basic vector field metrics such as divergence and curl.

List of Functions and Use (Alphabetical order)

divandcurl.m: Calculates divergence and curl (angular velocity) of a vector field.

divcurlformat.m: reformats output of divandcurl.m.

extract_timecourses.m: Given a set of ROIs and a functional volume, extracts $\{n \times 1\}$ cell, where each n contains a (time x voxel) size matrix containing the time-series of each voxel within the ROI.

extract_vectorfield.m: Extracts vector field from b-weight maps, plots group level vector field with permutation tests at the voxel level.

first.m: GUI Wrapper, contains functionality in-so-far as it ensures all images are within the same space before any operations are performed.

first_erode_roi.m: Strips off a single outer layer of voxels from an ROI.

FIRST_GLM.m: Performs first level regression analysis, primary function of FiRST.

generate_affine_matrix.m: Generate affine matrix to describe some arbitrary linear transformation.

model_vector_field.m: Given an extraction ROI and an affine matrix, generates an optimal vector field to describe a linear transformation.

optimize_roi.m: ROI optimization procedure from O'Rawe and Leung (in progress)

optimize_roi_spline.m: Generalization of ROI optimization procedure from O'Rawe and Leung (in progress)

orthoXYZ.m: Orthogonalizes coordinates using PCA, reselects and labels new axes by finding the maximal set of correlations between your original coordinates and the new coordinates.

plot_2d_vectorfields.m: Takes a 3 dimensional vector field and generates 3 2-dimensional vector field plots, collapsing across the unused dimension via mean.

ridgeReg.m: Performs ridge regression, estimates proper lambda based on minimizing the generalized cross validation function.

vector_model_selection.m: Compares model vectors (generated from model_vector_field.m) to empirical vector fields.

view_roi.m: Subcomponent of GUI wrapper, displays ROI ontop of TPM.