MRI Analysis Methods

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These pages describe some general analyses that will likely be completed for every MR session. Many of these methods are also good for checking data and processing.

Quality check

Main page: Quality check

After completing the pre-analysis steps, compute a coherence analysis and mean map to check the data. The coherence analysis checks that the BOLD signal change is in phase with the stimulus presentation, while the mean map shows the average signal across the scan. Both are good for identifying areas with signal dropout or signal distortion. Plus if anything went wrong in the above steps, these will look crazy. Includes instructions for computer coronal and mean map through the GUI or by script.

General linear model (GLM)

The General Linear Model is a standard fMRI analysis that allows for determining the "contribution" of different conditions to the BOLD signal-- in other words, how much a certain category or type of stimuli drives the BOLD signal. The resulting beta weights for each condition in each voxel can then be compared using contrasts. The variance explained by the model can also be computed.

Standard general linear model

Main page: General linear model

Fitting standard general linear model is implemented in mrVista and can be computed via the GUI or by script. Subsequent analyses, such as computing linear contrasts (statistical comparisons among two or more conditions) and viewing the time series are implemented as well. The disadvantage is that the analysis code is fairly complicated and it can be hard to figure out what exactly it is doing. This page also includes background on the general linear model and references for understanding mathematical basis and instructions for running GLM by script and for computer contrasts with the resulting betas.

Denoised GLM

Main page: Denoised GLM

GLMdenoise (Kay et al, 2013) is a variation of the standard GLM that denoises data using nuisance regressors derived from PCA on noise voxels. This denoising improves GLM model fit and SNR. The denoising code is open source and hosted in a GitHub repository. It also does not require further data acquisition. This page describes the GLMdenoise procedure in brief, running GLMdenoise, and checking data using the GLMdenoise figures. It also provides example scripts for running GLMdenoise, creating nifti files from the outputs, creating parameter maps from the outputs, and computing linear contrasts from the outputs.

Retinotopy: population receptive fields (pRF)

Main page: Retinotopy **under construction**

Early visual cortex is retinotopic, meaning that adjacent points in the cortex are stimulated by adjacent points on the retina and building a distorted image of the visual field on the cortex. These retinotopic areas can be mapped using high contrast bars moving across the visual field and then modeling each voxel's population receptive field (pRF) as a 2D gaussian defined by two parameters: (1) x y coordinates defining the center of the pRF, the point in the visual field that best drives the activity of the voxel; and (2) sigma, corresponding to the size of the pRF in visual degrees. The pRF centers can then be visualized on the surface of a 3D mesh and used to define retinotopic maps. In the lab, we ascribe to the Wandell+Brewer+Witthoft description of maps, which include

- Ventral maps: V2v, V3v, V4, VO1, VO2, PHC-1, PHC-2
- Dorsal maps: V2d, V3d, V3ab, LO1, LO2, TO1, TO2

This page includes background and references for the pRF model, instructions for fitting the pRF model, and instructions and references for defining retinotopic maps. Note the intention of these instructions is to provide a general guide and reference, and are probably insufficient for learning to define retinotopy for the first time.
Selecting ROIs & visualizing time course
under construction

Defining ROIs from anatomical templates

Currently we use two methods to derive visual field map ROIs from anatomical data:

- The V1-V3 retinotopy model from Benson, Butt, Brainard, Aguirre (PLoS CB, 2014)

The way we currently implement these ROIs in vistasoft is the vistasoft ROIs from anatomical templates