

# The NMR-MGH fMRI Processing Stream

This document gives a short overview of the functional MRI processing used at the NMR Center at Massachusetts General Hospital. Pointers to other documents are indicated in *italics*. Please send questions or comments to **analysis-bugs@nmr.mgh.harvard.edu**. The package is available via ftp from **ftp://ftp.nmr.mgh.harvard.edu/pub/flat/fmri-analysis**.

## 1 Summary

The NMR-MGH fMRI processing stream is based on selective averaging (Dale and Buckner, 1997) and deconvolution (Buroc, et al, 1998). The method models the BOLD signal as a linear combination of time-invariant hemodynamic responses imbedded in Gaussian noise. For event-related designs, the hemodynamic responses to different event types are modeled as a sum of delayed delta functions (regressors) with unknown weights (regression coefficients). No assumptions about the form of the hemodynamic shape (delay or dispersion) are made. For block designs, the shape of the hemodynamic response (ie, the regressor) is assumed but its weight is unknown. In both cases, the regressors are estimated using a least-squares method (Hamilton, 1994). For event-related designs, this method results the optimal *unbiased* estimator of the hemodynamic response. The covariance matrix of the regression coefficients is maintained and used to compute multivariate statistics. Individual subjects can be combined using either a random-effects or fixed-effects model (after appropriate spatial normalization). The package includes a tool for aiding in the design of rapid-presentation event related designs. The package also includes visualization tools for overlaying functional activation on structural images as well as to view the hemodynamic responses for different conditions in a “point-and-click” environment.

## 2 Computational Requirements

The software will run under Linux, Sun, and SGI operating systems. *Matlab*<sup>TM</sup> 5.2 or higher is required to run the software. Note, however, knowledge of matlab is not required as all of the programs run directly from the unix command-line. Note: the motion correction program is a front-end for running the AFNI motion correction (see <http://varda.biophysics.mcg.edu/cox/> for more information about AFNI). You must have the AFNI software package installed on your computer and the binaries in your path.

## 3 File Formats

Input images are assumed to be stored in *bfile* format. The *bfile* format divides each volume into a number of files, one for each anatomical slice. Each slice may contain multiple planes corresponding to the slice image at different times. Each slice file has a name conforming to the format stem\_XXX.btype, where “XXX” is the three-digit, zero padded slice number, and “btype” is either “bshort” or “bfloat”. Bshorts store signed 16 bit integers. Bfloats store 32 bit floating point numbers. Each slice has a corresponding header file with a name conforming to the format “stem\_XXX.hdr”. This header has four numbers: number of columns, number of rows, number of planes, and endianness. The endianness is either 0 (big-endian) or 1 (little-endian).

The scheduling of stimuli is indicated in the *paradigm* file. This is a file with (at least) two columns of numbers. The first column indicates the time at which a stimulus was presented, and

the second indicates the type of stimulus that was presented at that time. The stimulus types are defined by this file.

## 4 Rapid-Presentation Event-Related Experimental Design

Rapid-Presentation Event-Related (RPER) is a type of fMRI experimental design where the stimuli are presented closely enough in time that their hemodynamic responses can overlap. In contrast, fixed-interval event-related (FIER) designs require that stimulus presentations be separated enough in time that the hemodynamic responses do not overlap. RPER can result in experiments with significantly more statistical power than FIER (Dale, et al, 1999). RPER allows for better randomization of events. Analysis of RPER does make the assumption that the overlap is linear. The validity of linear overlap has been explored in several experiments (eg, Dale and Buckner, 1997; Miezin, et al, 1999).

The scheduling of events in RPER is a non-trivial task because events can occur at any time during the run. However, different schedules may result in different statistical power. Accordingly, we have devised a technique to search for sequences that will offer the most power. See *optseq*.

## 5 Processing Stream

Individual Subject Processing Stream Summary:

1. Motion Correction (mc-afni)
2. Intensity Normalization (inorm)
3. Selective Averaging (selxavg)
4. Statistical Analysis (stxgrinder)
5. Visualization (yakview)

Group Processing Stream Summary:

1. Motion Correction (mc-afni)
2. Intensity Normalization (inorm)
3. Selective Averaging (selxavg)
4. Spatial Normalization, eg Talairach
5. Inter-Subject Averaging, Fixed (isxavg-fe) and Random (isxavg-fe) Effects.
6. Visualization (yakview)

## 6 The Sessions Environment

All of the functional processing can be performed on data arbitrary file names in arbitrary directories. However, it can be a tedious process to specify all of these command-line parameters. To alleviate this problem, we have developed a file and directory naming structure that we call the *Sessions Environment*. Commands that exploit this environment typically end with *-sess* suffix.

### References:

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