

# FreeSurfer Functional Analysis SStream (FS-FAST) Download and Installation

This gives instructions on how to download, install, and configure the environment for running FS-FAST, the fMRI analysis stream used by many of the researchers in the MGH-NMR Center. While designed to integrate with the FreeSurfer anatomical analysis package, FS-FAST can also be used without FreeSurfer. The FS-FAST package does not include the FreeSurfer software which can be downloaded from [www.nmr.mgh.harvard.edu/freesurfer](http://www.nmr.mgh.harvard.edu/freesurfer). For those in the Center, you do not need to Download or Install, just follow the instructions under Environment.

----- Download -----

Download the most recent version  
from <ftp://ftp.nmr.mgh.harvard.edu/pub/flat/fmri-analysis>

```
% ftp ftp.nmr.mgh.harvard.edu
user: anonymous
passwd: your email
```

```
ftp> cd pub/flat/fmri-analysis
```

```
ftp> binary
ftp> get fmri-YYMMDD.tar.gz
```

Where YYMMDD corresponds to the most recent date.

----- Install -----

Move `fmri-YYMMDD.tar.gz` to the directory under which you want the package to be installed.

```
Uncompress the tar file:
% gunzip fmri-YYMMDD.tar.gz
```

```
This creates fmri-YYMMDD.tar which can be detarred:
% tar xvf fmri-YYMMDD.tar
```

```
This will create a directory called fmri-YYMMDD under which there are 4 subdirectories: bin docs src toolbox. You may want to create a symbolic link to fmri-YYMMDD from fmri:
% ln -s fmri-YYMMDD fmri
```

----- Environment -----

```
In your .cshrc file (or equivalent), create a new environment variable:
setenv FMRI_ANALYSIS_DIR name-of-install-directory
```

For those in the MGH-NMR center, you can set  
setenv FMRI\_ANALYSIS\_DIR /homes/nmrnew/home/inverse/fmri

Add \$FMRI\_ANALYSIS\_DIR/bin and \$FMRI\_ANALYSIS\_DIR/bin/`uname -s`  
directories to your path.

Add the toolbox directory to your matlab path. This is done  
by adding following lines to the startup.m file in your  
matlab directory (ie, ~/matlab/startup.m):

```
fmri_analysis_dir = getenv('FMRI_ANALYSIS_DIR');  
fmritoolbox = sprintf('%s/toolbox',fmri_analysis_dir);  
path(path,fmritoolbox);
```

Note that you must have matlab 5.2 or higher to run the software.  
The software has been tested under Linux, IRIX, and Sun. The scripts  
first look for a command called "matlab5" then for "matlab". If  
it does not find either of those, it will exit.

To use the motion correction, you must have AFNI installed and its  
binaries in your path. For those in the MGH-NMR Center, you can  
add the following to your path:

```
/homes/nmrnew/home/inverse/afni/`uname -s`
```

```
----- Getting Started -----  
The file called overview.ps (or overview.tex) in the docs directory  
has information about what can be done with the software. There's  
also a lot more documentation in the docs as to how each program  
works.
```

```
----- Bugs, Comments, Questions -----  
Send comments or questions to analysis-bugs@nmr.mgh.harvard.edu.  
When making bug reports, please follow these steps:  
1. Specify what type of machine you were on when the problem occurred.  
2. Specify what program (along with command-line options) you were  
running when the problem occurred. NOTE: "program" means a program from the  
FAST package, not one that you have created that calls FAST programs.  
3. Specify the directory you were in when you ran the program.  
4. Include any text that the program printed out.  
5. Include the log file (if it exists).
```

```
----- Disclaimer -----  
See docs/DISCLAIMER
```

```
----- Copywrite -----  
See docs/COPYWRITE
```