1 Program fim2

1.1 Purpose

This program applies the correlation method to match an 'ideal' waveform to the MR intensity time series in each pixel [1]. The actual algorithm used is the recursive projection technique described in [2]. Features of fim2 include:

1. The ability to run several 'canonical' or 'ideal' waveforms, and select the results from the one most highly correlated in each pixel.

2. An 'ort' is a function of time that is orthogonally projected out of each data time series before the correlation is computed. The collection of orts is the matrix **S** in [2]. fim2 has the ability to use several 'orts' at once, and to generate internally polynomial functions of time to use as orts. This means that it is not necessary to provide a ramp time series file in order to remove linear trends in time from the data pixels; the -polort 1 option has the desired effect. (The name 'ort' was invented by Andrzej Jesmanowicz.)

3. The ability to output the contrast-to-noise-ratio (CNR) in each pixel. CNR is defined as α/σ, where α is the amplitude of the normalized ideal waveform, and σ is the standard deviation of the noise left after all ort and the ideal waveforms are projected out. In this context, 'normalized ideal waveform' means the waveform scaled so that the trough-to-peak height is 1. If the ideal waveform is a square wave, for example, then CNR will be the mean in the 'up' times minus the mean in the 'down' times, divided by σ.

4. The ability to output the standard deviation σ in each pixel, and the least squares fit coefficients of the ort and ideal waveforms.

5. The ability to clip to zero output correlations and functional intensities in pixels where the underlying images have low intensity. This is intended to help eliminate false positives that sometimes occur far outside the brain.

6. The ability to register and compensate for **in plane** movement between images by trying to match each image in the time series to a base image. Each image is resampled to the shifted and rotated grid estimated by the 'dfspace' filter. The usual correlation calculations then proceed using these registered images.

1.2 Usage

fim2 [options] imagefiles

where 'imagefiles ... ' is a sequence of MRI filenames. The options are:

1.3 Options

-pcnt # Correlation coefficient threshold will be 1 - 0.01 × '#' , where '#' should be between 1 and 100.

-pcthresh # Correlation coefficient threshold will be '#' (0.0 to 0.99).

-im1 # Index of image file to use as first in time series; default is 1; previous images are filled with this image to synchronize with the reference time series.

-num # Number of images to actually use, if more than this many are specified on the command line; default is to use all images.

-non This option turns off the default normalization of the output activation image; the user should provide a scaling factor via '-coef #', or '1' will be used.

-coef # The scaling factor used to convert the activation output from floats to short ints (if '-non' is also present).

-ort fname fname = filename of a time series to which the image data will be orthogonalized before correlations are computed; any number of '-ort' options (from 0 on up) may be used.

-ideal fname fname = filename of a time series to which the image data is to be correlated; at least one such time series is required; if the '-ideal' option is not used, then the first filename after all the options will be used (this is for compatibility with the older fim program by Andrzej Jesmanowicz of MCW).

This version of fim2 allows the specification of more than one ideal time series file. Each one is *separately* correlated with the image time series and the one most highly correlated is selected for each pixel. Multiple ideals are specified using more than one -ideal fname option, or by using the form

-ideal [fname1 fname2 ...]

This latter method allows the use of wildcarded ideal filenames. The '[' character that indicates the start of a group of ideals can actually be any *one* of these: $\boxed{[\ \{\ /\ \%}$ and the ']' that ends the group can be *one* of: $\boxed{]\ \}\ /\ \%}$. (The C-shell doesn't like the [or { characters, which is why the more innocuous / and % are available.)

The format of ort and ideal time series files:

ASCII; one number per line;
Same number of lines as images in the time series;
Value over 33333 means "don't use this image in the analysis".

Yet more options for fim2 are:

-polref # or -polort # Use polynomials of order 0..# as extra 'orts'; default is 0 (yielding a constant vector). Use # = -1 to suppress this feature.

-fimfile fname fname = filename to save activation magnitudes in; if not given, the last name on the command line will be used.

-corr If present, indicates to write correlation output to image file 'fimfile.CORR' (next option is better).

-corfile fname fname = filename to save correlation image in; if not present, and '-corr' is not present, correlation image is not saved.

-cnrfile fname fname = filename to save contrast-to-noise image in; if not present, will not be computed or saved; CNR is scaled by 100 if images are output as shorts and is written 'as-is' if output as floats (see '-flim').

-sigfile fname fname = filename to save standard deviation image in; the standard deviation is of what is left after the least squares removal of the -orts, -polrefs, and -ideal. **N.B.:** This is always output in the -flim format!

-fitfile fname Flag to save image files of the least squares fit coefficients of all the -orts and -polrefs series that are projected out of the data time series before the -ideal is fit. The actual filenames will be fname.01 fname.02 .... Their order is -orts, then -polrefs, and last -ideal. **N.B.:** These are always output in the -flim format!

-subort fname A new timeseries of images is written to disk, with names of the form 'fname.0001', etc. These images have the orts and polrefs (but not ideals) subtracted out. **N.B.:** These are always output in the -flim format.

-flim If present, write outputs in the libmri.a 'floating point' format, rather than scale and convert to integers. [The ftosh program can later convert to short integers.]

-clean If present, then output correlation and functional images won't have the +/- 10000 values forced into their corners for scaling purposes.

-clip If present, output correlations, etc., will be set to zero in regions of low intensity. 'Low intensity' is defined as follows: the maximum absolute intensity in the base image (see -regbase) is found; all pixels above 10% of this intensity are averaged; 10% of this average defines the -clip threshold. Pixels with intensity below this value in the base image will be set to zero in the -fimfile and -corfile.

-q If present, indicates 'quiet' operation.

-dfspace[:0] Indicates to use the 'dfspace' filter (*à la* program imreg) to register the images spatially before filtering. This uses the 'iterated differential spatial' method to align the images. The optional :0 indicates to skip the iteration of the method, and to use the simpler linear differential spatial alignment method.

-regbase fname Indicates to read the image in file 'fname' and use it for the base image to which other images are registered. If not present, then the first image in the time series that will be used in the correlation computations will be selected (e.g., skipping the -im1 images). This image is also used to define 'low intensity' if the -clip option is used.

1.4 Notes

1. Although I have spent a great deal of effort to make the alignment routines efficient, registration can easily double or triple the CPU time used by fim2. This is one reason for allowing multiple -ideal options, since the overhead of registration only need be performed once.

2. The MR imaging process is not as simple as just taking a picture with a camera. When the subject moves his/her head, not everything in the imaging process moves with it. Here are some things for which 'mere' spatial registration (-dfspace) will not compensate, especially in echo-planar imaging:

   Nonuniform B_z from magnet $\Longrightarrow$ Distortions caused by shimming errors don't move with head.

   Susceptibility changes to B_z are angle dependent $\Longrightarrow$ Rotation of head causes image distortions to change.

   B_1 inhomogeneities $\Longrightarrow$ Signal intensity at a given anatomical location will fluctuate with motion.

   Gradient field inhomogeneities $\Longrightarrow$ Yet more position dependent image distortions.

   Slice selection $\Longrightarrow$ $TR \approx T_1$ means that some tissue may have different relaxation histories as it moves in and out of the image slices.

   It is better to think of the MR image as a picture taken with a distorting pane of glass between the camera and the subject. If the subject moves, the pane of glass (the imager) doesn't, and so the distortions that were present in (say) the hippocampus are suddenly now at the parahippocampal gyrus. Simply moving the image back to the location it should have come from won't make the changed distortions go away.

3. There are at least two aspects to subject head motion in FMRI. First, if the motion is random, then the signal changes induced by movement will be a source of noise, and will tend to mask truly activated pixels (increase the false negative rate). Second,

if the motion is coherent with the task/stimulus protocol, then the signal changes induced by movement will tend to look like activated pixels (increase the false positive rate).

4. The file used in -regbase should be of the same character as the images which will be registered to it. By 'same character' I mean acquired with the same MR parameters under the same circumstances. It is crucial to note that the first image in an EPI sequence often does *not* meet this requirement, since the longitudinal magnetization has not previously been excited within a few T_1. It is also not likely to be possible to use the program imreg to register functional images with higher resolution anatomical images.

   In some cases, it may be practical to use -regbase to register a series of fim2 runs (from separate image sequences taken in the same scanning session) to a common image. This will be possible if there is no significant out-of-plane motion between scanning runs. For example, if the subject is in the scanner in the normal flat-on-his-back position, and he tends to slide along the tube during the scanning session, and the images are acquired in the sagittal plane, then the motion may mostly be in-plane and this application of -regbase may be appropriate. *I have not tried to do this*, as of today.

1.5 Example

Example 1. Below is a C-shell script to run fim2 and then to3d to create a collection of AFNI datasets.

- The time series image files (64 × 64) are in four directories (`v1`, `v2`, `v3`, and `v4`), 16 slices each, 68 images in each time series, with filenames such as `v1/v107.0033`, which is the 33$^{\text{rd}}$ image in time, in the 7$^{\text{th}}$ slice, in run `v1`.
- The C-shell 'foreach' command is used to loop over the runs and over the slices within the runs. The shell variable `$run` will successively be set to '`v1`', '`v2`', '`v3`', and '`v4`':

  foreach run (v1 v2 v3 v4)

  Similarly, the shell variable `$slice` will successively be set to '`01`', '`02`', . . . , '`16`':

  foreach slice(01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16)

- There are a number of ideal waveform files (cosine functions, with various phase shifts) in files with names like cos9.25. These are invoked by the option

  `-ideal % cos*.* %`

- The mean and linear trend in each pixel time series are projected out using:

  `-polort 1`

- The data is not thresholded on the correlation coefficient:

  `-pcthresh 0.0`

- The functional intensities are scaled to integers using the factor 100,000:

  `-non -coef 100000`

- Functional correlations and intensities will be set to zero in faint parts of the image time series:

  `-clip`

- The images are registered spatially:

  -

  dfspace

- The output functional images are stored in files with names like v1/07.FIM (for slice 7 of run `v1`); the correponding correlation coefficient image will be v1/07.COR:

  -fimfile $run/$slice.FIM -corfile $run/$slice.COR

- When all slices are done for a run, the .FIM and .COR files are put into an *AFNI* dataset using batch-mode to3d. The geometry parent dataset zzzz+orig was created earlier using the interactive mode of to3d.

- This script is executed from the directory that contains the `v1`, `v2`, `v3`, and `v4` data directories. The .FIM and .COR files are left in those directories.

The Actual Script!

```
#!/bin/csh
# set part of the prefix for the output AFNI bricks
set prefix = dfst
foreach run ( v1 v2 v3 v4 )
 echo ''----- starting run $run -----''
 foreach slice( 01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 )
 fim2 -ideal % cos*.* % \
 -polort 1 \
 -pcthresh 0.0 \
 -non -coef 100000 \
 -clip \
 -dfspace \
 -fimfile ${run}/${slice}.FIM -corfile ${run}/${slice}.COR \
 ${run}/${run}${slice}.0*
 end
 set pref = ${run}:${prefix}
 to3d -fith -geomparent zzzz+orig \
 -dname $pref -dlabel $pref -prefix $pref \
 ${run}/*.FIM ${run}/*.COR
end
```

1.6 References

[1] P.A. Bandettini, A. Jesmanowicz, E.C. Wong, and J.S. Hyde. Processing strategies for time-course data sets in functional MRI of the human brain. *Magn. Reson. Med.* **30**, 161–173 (1993).

[2] R.W. Cox, A. Jesmanowicz, and J.S. Hyde. Real-time functional magnetic resonance imaging. *Magn. Reson. Med.* **33**, 230–236 (1995).