Program 3dfim+

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1 Program 3dfim+

1.1 Purpose

Program 3dfim+ calculates the cross-correlation of an ideal reference waveform with the measured FMRI time series data for each voxel.

The input to program 3dfim+ consists of an *AFNI* 3d+time data set, along with one or more ideal (reference) time series, and possibly one or more "ort" time series (see definition below). Output consists of a "bucket" dataset, containing sub-bricks for various user specified parameters, such as the fit coefficient, the Pearson product moment correlation coefficient, % change relative to baseline, the Spearman rank correlation coefficient, etc.

This program is the command line version of the *AFNI* fim+ function. Although the algorithms used by these two programs are different, the output results should agree up to roundoff error. There are two exceptions: the programs use somewhat different definitions in computing the Spearman rank correlation coefficient, and the Quadrant correlation coefficient. Hence, the user should not expect agreement between the programs for these two parameters.

1.2 Theory

1.2.1 Fit Coefficient

The measured FMRI data will be modeled as the sum of a polynomial function of time, plus a linear combination of "ort" functions, plus an ideal reference function, plus noise. For example, if we use a linear polynomial ort (i.e., $polort = 1$), three separate ort time series functions ($\phi(n)$, $\theta(n)$, and $\psi(n)$), and the ideal time series $r(n)$, then the measured response can be modeled by:

$$y(n) = \underbrace{\beta_0 + \beta_1 n}_{\text{polynomial ort}} + \underbrace{\gamma_1\phi(n) + \gamma_2\theta(n) + \gamma_3\psi(n)}_{\text{ort functions}} + \underbrace{\alpha r(n)}_{\text{ideal}} + \underbrace{\varepsilon(n)}_{\text{noise}}$$

where $\varepsilon(n) \overset{iid}{\sim} N(0, \sigma^2)$.

Using the matrix notation

$$\mathbf{X} = \begin{bmatrix} 1 & 0 & \phi(0) & \theta(0) & \psi(0) & r(0) \\ 1 & 1 & \phi(1) & \theta(1) & \psi(1) & r(1) \\ 1 & 2 & \phi(2) & \theta(2) & \psi(2) & r(2) \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & N-1 & \phi(N-1) & \theta(N-1) & \psi(N-1) & r(N-1) \end{bmatrix}$$

$$\mathbf{y} = \begin{bmatrix} y(0) \\ y(1) \\ y(2) \\ \vdots \\ y(N-1) \end{bmatrix}, \quad \boldsymbol{\beta} = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \gamma_1 \\ \gamma_2 \\ \gamma_3 \\ \alpha \end{bmatrix} \quad \boldsymbol{\varepsilon} = \begin{bmatrix} \varepsilon(0) \\ \varepsilon(1) \\ \vdots \\ \varepsilon(N-1) \end{bmatrix}$$

the above equation can be written:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}.$$

The linear regression problem is then to find an estimate $\mathbf{b}$ of the vector of unknown parameters

$$\mathbf{b} = \hat{\boldsymbol{\beta}} = \begin{bmatrix} \hat{\beta}_0 & \hat{\beta}_1 & \hat{\gamma}_1 & \hat{\gamma}_2 & \hat{\gamma}_3 & \hat{\alpha} \end{bmatrix}^t$$

which provides a good "fit" to the data. For this fit to the model, the time series data is then estimated by:

$$\widehat{\mathbf{y}} = \mathbf{X}\mathbf{b}$$

The usual criterion for estimating $\mathbf{b}$ is to minimize the error sum of squares between the fit and the data:

$$\begin{aligned} SSE &= Q(\mathbf{b}) = \sum_{n=0}^{N-1} \left(y(n) - \widehat{y}(n)\right)^2 \\ &= \left(\mathbf{y} - \widehat{\mathbf{y}}\right)^t \left(\mathbf{y} - \widehat{\mathbf{y}}\right) \end{aligned}$$

(Unless otherwise specified, the summation symbol $\sum$ will imply summation over the time index n; $n = 0, ..., N-1$.) It is easy to show that

$$\mathbf{b} = \left(\mathbf{X}^t\mathbf{X}\right)^{-1} \mathbf{X}^t\mathbf{y}$$

is the least squares estimate of $\boldsymbol{\beta}$. The estimated "fit" is then given by:

$$
\begin{aligned}
\widehat{\mathbf{y}} &= \mathbf{Xb} \\
&= \mathbf{X}\left(\mathbf{X}^t\mathbf{X}\right)^{-1}\mathbf{X}^t\mathbf{y}
\end{aligned}
$$

A more general representation of the $\mathbf{X}$ matrix is:

$$
\mathbf{X} = \left[\ \mathbf{P} \ \mid\ \mathbf{S} \ \mid\ \mathbf{r}\ \right]
$$

where the columns of sub-matrix $\mathbf{P}$ correspond to the polynomial orts; the columns of sub-matrix $\mathbf{S}$ contain the "ort" functions; and $\mathbf{r}$ is the column vector which represents the ideal (reference) function.

Program 3dfim+ estimates the parameter vector $\boldsymbol{\beta}$ at each voxel location, and appends the $\hat{\alpha}$ fit coefficient as one of the sub-bricks of an *AFNI* "bucket" dataset, if so requested by the user.

1.2.2 Pearson Product Moment Correlation Coefficient

Suppose that the *polynomial ort* is just a constant (i.e., *polort* $= 0$), and suppose that there are no *ort functions*. Then the Pearson product moment correlation coefficient between random variables $\mathbf{r}$ and $\mathbf{y}$ is calculated by (see Ref.[1]):

$$
\rho = \frac{\sum\left(r(n) - \overline{r}\right)\left(y(n) - \overline{y}\right)}{\left[\sum\left(r(n) - \overline{r}\right)\right)^2 \sum\left(y(n) - \overline{y}\right)^2\right]^{\frac{1}{2}}}
$$

where $\overline{r}$ and $\overline{y}$ are the sample means:

$$
\begin{aligned}
\overline{r} &\equiv \frac{1}{N}\sum r(n) \\
\overline{y} &\equiv \frac{1}{N}\sum y(n)
\end{aligned}
$$

However, if *ort functions* are present, or if *polort* > 0, then the above formula for calculating the correlation coefficient must be modified to remove the variation which is explained by the orts. This is done by first constructing the matrix $\mathbf{X}_{base}$ whose columns consist of the polynomial orts and ort functions:

$$
\mathbf{X}_{base} = \left[\ \mathbf{P} \ \mid\ \mathbf{S}\ \right]
$$

Then, both the ideal $\mathbf{r}$ and the data $\mathbf{y}$ are fitted using $\mathbf{X}_{base}$:

$$
\begin{aligned}
\mathbf{r}_{base} &= \mathbf{X}_{base}\left(\mathbf{X}^t_{base}\mathbf{X}_{base}\right)^{-1}\mathbf{X}^t_{base}\mathbf{r} \\
\mathbf{y}_{base} &= \mathbf{X}_{base}\left(\mathbf{X}^t_{base}\mathbf{X}_{base}\right)^{-1}\mathbf{X}^t_{base}\mathbf{y}
\end{aligned}
$$

The partial correlation coefficient (that is, the correlation between $\mathbf{r}$ and $\mathbf{y}$, after the linear association of each with the ort functions has been removed) is given by:

$$\rho = \frac{\sum (r(n) - r_{base}(n))\,(y(n) - y_{base}(n))}{\left[\sum (r(n) - r_{base}(n))^2 \sum (y(n) - y_{base}(n))^2\right]^{\frac{1}{2}}}$$

If we define the residuals r_{res} and y_{res}

$$\begin{aligned} r_{res}(n) &\equiv r(n) - r_{base}(n) \\ y_{res}(n) &\equiv y(n) - y_{base}(n) \end{aligned}$$

then the partial correlation coefficient can be written:

$$\rho = \frac{\sum (r_{res}(n))\,(y_{res}(n))}{\left[\sum (r_{res}(n))^2 \sum (y_{res}(n))^2\right]^{\frac{1}{2}}}$$

Program 3dfim+ calculates the partial correlation coefficient ρ for each voxel, and, if so requested by the user, appends these values as one of the sub-bricks of an *AFNI* "bucket" dataset.

1.2.3 Multiple Ideals

Thus far, we have considered only a single ideal function. However, the extension to multiple ideals is straightforward. Consider the q ideals, $\mathbf{r}_1, ..., \mathbf{r}_q$. The fit coefficient α and the partial correlation coefficient ρ are evaluated for each ideal:

$$\begin{aligned} \alpha(\mathbf{r}_i) &= \alpha(\mathbf{r})\,|_{\mathbf{r}=\mathbf{r}_i} \\ \rho(\mathbf{r}_i) &= \rho(\mathbf{r})\,|_{\mathbf{r}=\mathbf{r}_i} \end{aligned}$$

Let

$$k = \arg\max_{i=1,...,q} |\rho(\mathbf{r}_i)|$$

then define

$$\begin{aligned} \alpha &\equiv \alpha(\mathbf{r}_k) \\ \rho &\equiv \rho(\mathbf{r}_k) \end{aligned}$$

In this case, the kth ideal is referred to as the "Best Index", and the program reports the parameters α, ρ, etc., for the Best Index only.

1.2.4 Residual Error

As mentioned above, the error sum of squares between the (best) fit and the data is given by:

$$SSE = \sum_{n=0}^{N-1} (y(n) - \widehat{y}(n))^2$$

Letting

$$\begin{aligned} p &= \text{number of polynomial ort coefficients} = polort + 1 \\ s &= \text{number of ort time series} \\ r &= \begin{cases} 1 & \text{if} \quad \text{number of ideal time series} = 1 \\ 2 & \text{if} \quad \text{number of ideal time series} > 1 \end{cases} \end{aligned}$$

then the mean square error is defined:

$$MSE = \frac{SSE}{N - p - s - r}$$

and the standard deviation of the residuals is:

$$\widehat{\sigma} = \sqrt{MSE}$$

Program 3dfim+ calculates the standard deviation $\widehat{\sigma}$ for each voxel, and, if so requested by the user, appends these values as one of the sub-bricks of an *AFNI* "bucket" dataset.

1.2.5 Percent Change

As described above, the quantity $\widehat{\alpha}$ estimates the fit coefficient for the (best) ideal time series. If we define the peak-to-peak (PP) variation of the ideal time series:

$$PP(ideal\ T.S.) = \max(ideal\ T.S.) - \min(ideal\ T.S.)$$

then the actual variation in the measured response due to the ideal time series is:

$$\widehat{\alpha} \cdot PP(ideal\ T.S.)$$

So, if we define the $Baseline$, $Average$, and $Topline$:

$$Baseline = \sum_i \widehat{\beta}_i \cdot ave(polynomial\ ort\ \#i) + \sum_j \widehat{\gamma}_j \cdot ave(ort\ T.S.\ \#j) + \widehat{\alpha} \cdot \min(ideal\ T.S.)$$

$$Average = \sum_i \widehat{\beta}_i \cdot ave(polynomial\ ort\ \#i) + \sum_j \widehat{\gamma}_j \cdot ave(ort\ T.S.\ \#j) + \widehat{\alpha} \cdot ave(ideal\ T.S.)$$

$$Topline = \sum_i \widehat{\beta}_i \cdot ave(polynomial\ ort\ \#i) + \sum_j \widehat{\gamma}_j \cdot ave(ort\ T.S.\ \#j) + \widehat{\alpha} \cdot \max(ideal\ T.S.)$$

then the $\%\ Change$ relative to the $Baseline$, $Average$, and $Topline$ can be defined as follows:

$$\%\ Change = 100 \cdot \frac{\widehat{\alpha} \cdot PP(ideal\ T.S.)}{Baseline}$$

$$\%\ From\ Ave = 100 \cdot \frac{\widehat{\alpha} \cdot PP(ideal\ T.S.)}{Average}$$

$$\%\ From\ Top = 100 \cdot \frac{\widehat{\alpha} \cdot PP(ideal\ T.S.)}{Topline}$$

Program 3dfim+ calculates the quantities $\%\ Change$, $\%\ From\ Ave$, $\%\ From\ Top$ for each voxel, and, if so requested by the user, appends these values as sub-bricks of an *AFNI* "bucket" dataset.

1.2.6 Other Correlation Coefficients

Spearman rank correlation coefficient The Spearman rank correlation coefficient uses the ranks of the data, rather than the data itself, in calculating the cross-correlation. For example, if

$$y(n) = \{432, 212, 790, 635, 583, 606\}$$

then

$$Rank(y(n)) = \{2, 1, 6, 5, 3, 4\}.$$

The average rank is determined by the number of data points N :

$$\overline{Rank} = \frac{N+1}{2}.$$

The Spearman rank correlation coefficient is then defined (see Ref.[2]) as follows (assuming $polort = 0$, and assuming no ort time series):

$$\rho_S = \frac{\sum \left(Rank\,(r(n)) - \overline{Rank}\right)\left(Rank\,(y(n)) - \overline{Rank}\right)}{\left[\sum \left(Rank\,(r(n)) - \overline{Rank}\right)^2 \sum \left(Rank\,(y(n)) - \overline{Rank}\right)^2\right]^{\frac{1}{2}}}$$

However, when $polort > 0$, or when ort time series are entered, we define the Spearman rank correlation coefficient using the residuals r_{res} and y_{res}, (as previously defined), as follows:

$$\rho_S = \frac{\sum \left(Rank\left(r_{res}(n)\right) - \overline{Rank}\right)\left(Rank\left(y_{res}(n)\right) - \overline{Rank}\right)}{\left[\sum \left(Rank\left(r_{res}(n)\right) - \overline{Rank}\right)^2 \sum \left(Rank\left(y_{res}(n)\right) - \overline{Rank}\right)^2\right]^{\frac{1}{2}}}$$

If so requested by the user, program 3dfim+ calculates ρ_S for each voxel, and appends these values as one of the sub-bricks of an *AFNI* "bucket" dataset. Note: If multiple ideals are used, then ρ_S is calculated for each ideal, but only the largest (in absolute value) is reported.

Quadrant correlation coefficient The Quadrant correlation coefficient is defined similarly to the Spearman rank correlation coefficient, except that the *sign* function is applied to the different factors:

$$\rho_Q = \frac{\sum \left(sign\left(Rank\left(r(n)\right) - \overline{Rank}\right)\right)\left(sign\left(Rank\left(y(n)\right) - \overline{Rank}\right)\right)}{\left[\sum \left(sign\left(Rank\left(r(n)\right) - \overline{Rank}\right)\right)^2 \sum \left(sign\left(Rank\left(y(n)\right) - \overline{Rank}\right)\right)^2\right]^{\frac{1}{2}}}$$

where

$$sign(x) \equiv \begin{cases} 1 & \text{if} \quad x > 0 \\ 0 & \text{if} \quad x = 0 \\ -1 & \text{if} \quad x < 0 \end{cases}$$

However, when $polort > 0$, or when ort time series are entered, we define the Quadrant correlation coefficient using the residuals r_{res} and y_{res}, (as previously defined), as follows:

$$\rho_Q = \frac{\sum \left(sign\left(Rank\left(r_{res}(n)\right) - \overline{Rank}\right)\right)\left(sign\left(Rank\left(y_{res}(n)\right) - \overline{Rank}\right)\right)}{\left[\sum \left(sign\left(Rank\left(r_{res}(n)\right) - \overline{Rank}\right)\right)^2 \sum \left(sign\left(Rank\left(y_{res}(n)\right) - \overline{Rank}\right)\right)^2\right]^{\frac{1}{2}}}$$

If so requested by the user, program 3dfim+ calculates ρ_Q for each voxel, and appends these values as one of the sub-bricks of an *AFNI* "bucket" dataset. Note: If multiple ideals are used, then ρ_Q is calculated for each ideal, but only the largest (in absolute value) is reported.

1.3 Usage

The syntax for execution of program 3dfim+ is as follows:

3dfim+ [**-input** *fname* | **-input1D** *dname*] [**-mask** *mname*]
[**-nfirst** *fnum*] [**-nlast** *lnum*] [**-polort** *pnum*] [**-fim_thr** *p*] [**-cdisp** *cval*]
[**-ort_file** *sname*] **...** [**-ort_file** '*sname[i,j,k]*']
-ideal_file *rname* **...** [**-ideal_file** '*rname[i,j,k]*']
[**-out** *param*] [**-out** *param*] [**-bucket** *bprefix*]

The different command line options are explained below.

1.4 Options

-input *fname*

The -input command specifies that $fname$ is the filename of the *AFNI* 3d + time data set to be used as input for the 3dfim+ program. The -input command is mandatory *except* when the -input1D command is used in its place.

-input1D *dname*

The -input1D command specifies that *dname* is the filename of the *AFNI* .1D time series data file to be used as input for the 3dfim+ program. That is, instead of a 3d+time dataset, the input consists of only a single FMRI time series as the measured data. In this case, all output is directed to the screen. Commands which would otherwise generate output files (such as the -bucket command) are ignored. This option allows analysis of, e.g., time series obtained from selected voxels, or time series obtained as the average over an ROI.

-mask *mname*

The optional -mask command specifies that *mname* is the filename of the *AFNI* 3d dataset to be used for "masking " the input data. That is, if a voxel in the mask dataset has value zero, then the corresponding voxel in the 3d+time input dataset will be ignored for computational purposes. All output corresponding to that particular voxel will be set to zero. If the mask dataset represents the brain, i.e., if the mask contains 1's only at locations inside the brain, and 0's at locations outside the brain, this will greatly improve the program execution speed. (See program 3dIntracranial.)

Of course, the mask dataset must have the same voxel dimensions as the input 3d+time dataset.

-nfirst *fnum*

The optional -nfirst command specifies that $fnum$ is the number of the first image to be used in the analysis. (Note: the first image in the dataset is numbered 0.) The default value is $fnum = 0$.

-nlast *lnum*

The optional -nlast command specifies that *lnum* is the number of the last image to be used in the analysis (Note: the first image in the dataset is numbered 0). The default value is *lnum* = number of the last image in the dataset. (The program 3dinfo can be used to print out information about a dataset.)

-polort *pnum*

The optional -polort command specifies that *pnum* (*pnum* $= 0, 1$, or 2) is the degree of the polynomial in the baseline model (corresponding to the null hypothesis). The default value is *pnum* $= 1$ (corresponding to the baseline model: $Z_n = \gamma_0 + \gamma_1 n + \varepsilon_n$; i.e., the signal is a constant plus linear trend plus noise).

-fim_thr *p*
The optional -fim_thr command is used set the threshold for an internally generated mask. The program first calculates the average image intensity for the first volume in the time series. Then, any voxel whose intensity is less than $p * average$, where $0 \leq p \leq 1$, will be excluded from the analysis. This helps to speed up program execution by excluding voxels which lie (roughly) outside the brain. Default: $p = 0.0999$.

-cdisp *cval*
The optional -cdisp command is used to control output to the user's terminal during program execution. For each voxel in the data set, if the absolute value of the correlation coefficient is greater than or equal to *cval*, then the estimated parameters are written to the screen; otherwise, nothing is written to the screen for that particular voxel. Note that the -cdisp command effects screen output only, and has absolutely no effect upon the data file output generated by the program.

-ort_file *sname*
The optional -ort_file command specifies that *sname* is the filename of the .1D time series representing a time series function to which the estimated response is to be orthogonalized.

For multi-column .1D files, this command has the alternative format:

-ort_file *'sname[i,j,k]'*
In this case, the -ort_file command specifies that columns i, j, and k of file *sname* are to be used as "ort" time series functions. The column indexing begins with 0. Note that the square brackets around the column index must be enclosed within quotation marks. Also, if no column selector is used, then all columns in file *sname* will be used as "ort" functions.

-ideal_file *rname*
The mandatory -ideal_file command specifies that *rname* is the filename of the .1D time series representing an "ideal" (i.e., reference) time series function. Note: A value ≥ 33333 in any ideal time series means "don't use this time point in the analysis".

For multi-column .1D files, this command has the alternative format:

-ideal_file *'rname[i,j,k]'*
In this case, the -ideal_file command specifies that columns i, j, and k of file *rname* are to be used as "ideal" time series functions. The column indexing begins with 0. Note that the square brackets around the column index must be enclosed within quotation marks. Also, if no column selector is used, then all columns in file *rname* will be used as "ideal" functions.

-out *param* The following character strings can be used as *param* for generating sub-bricks of the output bucket dataset:

param	Meaning	Section
'Fit Coef'	$\widehat{\alpha}$ = L.S. fit coefficient for Best Index	1.2.1
'Best Index'	k = Index number for Best Index	1.2.3
'% Change'	100 * P-P amplitude of signal response / Baseline	1.2.5
Baseline	Average of Baseline response	1.2.5
Correlation	ρ = product moment correlation coefficient for Best Index	1.2.2
'% From Ave'	100 * P-P amplitude of signal response / Average	1.2.5
Average	Baseline + average of signal response	1.2.5
'% From Top'	100 * P-P amplitude of signal response / Topline	1.2.5
Topline	Baseline + P-P amplitude of signal response	1.2.5
'Sigma Resid'	$\widehat{\sigma}$ = Std. Dev. of residuals from best fit	1.2.4
All	This specifies all of the above parameters	
'Spearman CC'	ρ_S = Spearman correlation coefficient	1.2.6
'Quadrant CC'	ρ_Q = Quadrant correlation coefficient	1.2.6

Note that *param* character strings which contain blank spaces *must* be enclosed by quotes.

-bucket *bprefix*

The -bucket command is used to create a single *AFNI* "bucket" type dataset having multiple sub-bricks. The output is written to the file with the user specified prefix filename bprefix. Each of the individual sub-bricks can then be accessed for display within program afni. See Example 2 below for illustration of the format of the bucket dataset.

1.5 Examples

Example 1. Evaluation of a Single Time Series

A researcher has used *AFNI* to write the contents (time series) of one voxel to file 042_033_001.1D. This single time series can be analyzed using the -input1D option, as shown below.

Program 3dfim+ Batch Command File for Example 1

```
3dfim+ \
-input1D 042_033_001.1D \
-nfirst 3 \
-polort 1 \
-ideal_file stim05.all.1D \
-out 'Fit Coef' \
-out 'Best Index' \
-out '% Change' \
-out Baseline \
-out Correlation \
-out '% From Ave' \
```

```
-out Average \
-out '% From Top' \
-out Topline \
-out 'Sigma Resid' \
-out 'Spearman CC' \
-out 'Quadrant CC'
```

■

The -input1D command indicates that the measurement data consists of a single time series, which is to be read from file 042_033_001.1D. The command -nfirst specifies that time point #3 is the first to be used in the analysis, i.e., to allow for transients, the first three data points in the time series are to be discarded. The command -polort 1 indicates that the baseline model should include a constant offset plus linear trend terms.

The command -ideal_file indicates that the ideal time series is to be read from file stim05.all.1D. Since this file contains 15 columns, corresponding to 15 different time lags for the stimulus function, the measurement data will be correlated with each of these 15 ideal time series.

This is followed by 12 -out commands, specifying which parameters are to be reported. Note that the first 10 of these commands could be replaced by the single command: -out all.

Since the input measurement data consists of a single FMRI time series, all output is directed to the screen, for example:

Program 3dfim+ Screen Output for Example 1

Program:	3dfim+
Author:	B. Douglas Ward
Date:	26 April 2000

Results for Voxel #0:

Fit Coef	=	711.1375
Best Index	=	5.0000
% Change	=	4.4626
% From Ave	=	4.3606
Baseline	=	15935.4082
Average	=	16308.2891
Correlation	=	0.8266
% From Top	=	4.2720
Topline	=	16646.5449
Sigma Resid	=	242.9861
Spearman CC	=	0.7268
Quadrant CC	=	0.8459

■

Example 2. Evaluation of a 3d+time Dataset

A researcher wants to locate voxels which respond to an ideal reference function, by means of cross-correlation. The measured FMRI data is contained in the 3d+time dataset v2:time+orig (.HEAD and .BRIK). The ideal time series function is recorded in file cosall.1D. This file actually contains 8 columns, corresponding to 8 different time delayed versions of the stimulus function. Also, the -dfile option of program 3dvolreg was previously used to write the estimated motion parameters to file v2.motion.1D. This file contains 9 columns, of which columns 1 – 6 correspond to the estimated motion parameters.

In order to calculate the cross-correlation, at each voxel location, program 3dfim+ can be executed with the following batch commands:

Program 3dfim+ Batch Command File for Example 2

```
3dfim+ \
-input v2:time+orig \
-nfirst 3 \
-polort 1 \
-ort_file 'v2.motion.1D[1..6]' \
-ideal_file cosall.1D \
-cdisp 0.5 \
-out All \
-out 'Spearman CC' \
-out 'Quadrant CC' \
-bucket v2.3dfim.bucket
```

■

The first batch command specifies that the input 3d+time dataset is to be read from file v2:time+orig (.HEAD and .BRIK). The command -nfirst specifies that image #3 is the first to be used in the analysis, i.e., to allow for transients, the first three data points in each time series are to be discarded.

The command -polort 1 indicates that the baseline model should include a constant offset plus linear trend terms (this is the default condition). The following command, -ort_file 'v2.motion.1D[1..6]', indicates that the baseline model should also include, as 6 separate ort time series functions, the 6 motion parameters estimated by program 3dvolreg. The purpose of including the estimated motion parameters as ort functions is to reduce the number of false positives due to motion-correlated activation, and to increase the number of true positives by reducing the amount of measurement error due to motion.

The command -ideal_file indicates that the ideal time series is to be read from file cosall.1D. Since this file contains 8 columns, and since no columns were specified using the '[]' notation, all 8 columns will be used as 8 separate ideal time series.

The command -cdisp 0.5 is used to specify that, during execution of the program, screen output is generated for voxels whose product-moment correlation coefficient exceeds 0.5.

The next three -out commands specify the contents of the program output.

Finally, the command -bucket v2.3dfim.bucket is used to generate the "bucket" type dataset v2.3dfim.bucket+orig (.HEAD and .BRIK) containing the user specified parameter estimates.

After program 3dfim+ has finished execution, program afni can be used to view the output file.

The format for the bucket dataset v2.3dfim.bucket is illustrated below.

Brick #	Label	Contents
0	Fit Coef	Least squares fit coefficient for Best Index
1	Best Index	Index number for best ideal
2	% Change	100 * P-P amplitude of signal response / Baseline
3	% From Ave	100 * P-P amplitude of signal response / Average
4	Baseline	Average of Baseline response
5	Average	Baseline + average of signal response
6	Correlation	Product-moment correlation coefficient for Best Index
7	% From Top	100 * P-P amplitude of signal response / Topline
8	Topline	Baseline + P-P amplitude of signal response
9	Sigma Resid	Std. dev. of residuals from best fit
10	Spearman CC	Spearman correlation coefficient
11	Quadrant CC	Quadrant correlation coefficient

Note that the output of this program can be used as input to other programs, such as 3dANOVA, for comparing results across subjects, runs, experimental conditions, etc.

■

1.6 References

[1] J. Neter, W. Wasserman, M. H. Kutner, *Applied Linear Statistical Models*, 2nd edition. Homewood, Illinois: Irwin (1985).

[2] E. L. Lehmann, *Nonparametrics: Statistical Methods Based on Ranks.* Oakland, CA: McGraw-Hill (1975).