

mkcontrast

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1 Introduction

mkcontrast is a program for creating a contrast matrix. The output of `mkcontrast` can be used to specify contrasts for `stxgrinder` and for `isxavg-re`. The contrast matrix R is used to test the hypothesis

$$H_0 : R\hat{\beta} = 0 \quad (1)$$

where $\hat{\beta}$ is the vector of input variables. For example, if the variables come as the output of `selxavg`, then $\hat{\beta}$ is the set of hemodynamic averages for all conditions. The number of columns in R must be equal to the number of elements in $\hat{\beta}$. The number of rows in R will be determined by the type of statistic to be computed. If R has only one row, the resulting test must be a t-test. One can think of the rows of R as vectors used to correlate with the input variables.

While the contrast matrix created by `mkcontrast` can be used with arbitrary data sets, it is geared toward being applied to the output of `selxavg` which produces a hemodynamic average for each non-null condition, with N_h post-stimulus averages per condition, where $N_h = \frac{\text{TimeWindow}}{\text{TER}}$ (TimeWindow and TER are input variables to `selxavg`). If the number of non-null conditions is N_c , then the vector $\hat{\beta}$ can then be conceptually divided into a string of N_c subvectors each with N_h components. When invoking `mkcontrast`, the `-nconds` options should be set to N_c , the `-ndelays` options should be set to N_h . `mkcontrast` provides the ability to set up contrasts both between conditions and between time points within a condition, or a combination of both.

2 Usage

Typing `mkcontrast` at the command-line without any options will give the following message:

```
USAGE: mkcontrast [-options] -o cmtxmatfile
```

Option Set 1:

```
-nconds nconds      : number of conditions (excl fix)
-wcond  cw1 cw2 ... : weight of each condition
-sumconds           : sum conditions
-ndelays ndelays    : number of delays points in HDR
-wdelay  dw1 dw2 ... : weight of each delay
-sumdelays         : sum delays
-showcmtx          : display contrast matrix
-sxadat file       : dat file from selxavg
```

Option Set 2:

```
-TER TER           : Estimation resolution (sec)
-estim TPreStim    : Estimation prestimulus period (0) (sec)
-nconds nconds     : number of conditions (excl fix)
-wcond  cw1 cw2 ... : weight of each condition
```

```

-sumconds          : sum conditions
-ndelays ndelays   : number of delays points in HDR
-sumdelays         : sum delays
-ircorr nircorr    : correlate with nircorr ideal HDRs
-deltarange dmin dmax ... : delta range of ideal HDIR
-taurange tmin tmax ... : tau range of ideal HDIR
-sxadat file       : dat file from selxavg

```

The two option sets differ in the ways that the weights for correlating with the average hemodynamic response are set. Most of the options are common between the two.

3 Command-line Arguments – Option Sets 1 and 2

-nconds: number of conditions (as found in the paradigm file), excluding the null or fixation condition. See also `-sxadat`.

-wcond: list of weightings for each condition. The number in the list must be equal to *nconds*. For example, if there are 3 non-null conditions, then setting `-wcond 0 -1 1` would subtract condition 2 from condition 3 and ignore condition 1. If one wanted to subtract the average of conditions 1 and 3 from condition 2, then set `-wcond -.5 1 -.5`. The weight can be any real number, positive or negative.

-sumconds: sum the (weighted) averages of each condition together *before* computing the F-statistic.

-ndelays: number of averages per condition. This is the same as the number of components in the time window as set during invocation of *selxavg*. For a time window of 20 seconds and TR of 2 seconds, there would be $\frac{20}{2} = 10$ averages per condition. See also `-sxadat`.

-sumdelays: sum the (weighted) averages of each delay together *before* computing the F-statistic.

-showmtx: display an image of the contrast matrix.

-sxadat: specify a dat file as created by *selxavg*. The dat file has information about the number of conditions (`-nconds`), the number of delays (`-ndelays`), the TER (`-TER`), and the prestimulus baseline duration (`-prestim`) so that those parameters do not have to be placed on the command-line.

-monly: only generate the matlab file which would accomplish the analysis but do not actually execute it. This is mainly good for debugging purposes.

4 Command-line Arguments – Option Set 1

-wdelay: list of weights for each average. The number in the list must be equal to *ndelays*. The weight can be any real number, positive or negative. For example, let the number of delays equal 10. If one wanted to compute the average of the first three delay averages against

the average of the last four delay averages, then set `-wdelay -0.3 -0.3 -0.3 0 0 0 0.25 0.25 0.25 .25`.

5 Command-line Arguments – Option Set 2

-TER: temporal estimation resolution in seconds. This is the same as the value supplied to `selxavg`. If a `-TER` flag was not passed to `selxavg`, then use the TR. See also `-sxadat`.

-prestim: prestimulus baseline in seconds. This is the same as the value supplied to `selxavg`. If a `-prestim` flag was not passed to `selxavg`, then use 0.

-ircorr: specify the number of ideal HemoDynamic Response Impulse Functions (HDRIF) with which to correlate the average hemodynamic response. The ideal response is modeled as a gamma function of the form

$$h(t) = \begin{cases} 0 & t < \Delta \\ \left(\frac{\tau e^2}{4}\right)\left(\frac{t-\Delta}{\tau}\right)^2 e^{-\left(\frac{t-\Delta}{\tau}\right)} & t > \Delta \end{cases} \quad (2)$$

Note that there are two parameters, *Delta* and *tau*. Each of the *nircorr* functions is given a unique parameter set through the `-deltarange` and `-taurange` options.

-deltarange: minimum and maximum ranges of *Delta*. The values that *Delta* assumes will be *nircorr* values evenly spread through the minimum and maximum. Each *Delta* will be paired with the corresponding *tau*.

-taurange: minimum and maximum ranges of *tau*. The values that *tau* assumes will be *nircorr* values evenly spread through the minimum and maximum. Each τ will be paired with the corresponding Δ .