STACMR

STACMR is a set of Matlab functions that conduct CMR analyses of state-trace data. CMR stands for "coupled monotonic regression". This is a quick guide to its use.

Java

The current implementation of STACMR calls code written in java. While this speeds up the analysis to a very great extent, it does require (at this point) some extra housekeeping. This is itemized below:

1. Java is usually pre-installed in Matlab. To check, type:

   ```
   >> version -java
   ```
   Any version on or after version 1.7 is good. If java is not installed, you will have to do this yourself from http://www.oracle.com/technetwork/java/javase/downloads/jre8-downloads-2133155.html.

2. The appropriate CMR java runtime library also needs to be acquired and stored in a convenient directory. The current version is called `fxMR-0.3.25.jar.`

3. Before running any of the STACMR programs, the CMR java runtime library needs to be made available to Matlab. This requires the command:

   ```
   javaclasspath(path);
   ```
   where path is the full pathname of the library. An example (omitting stuff in the middle) is:
   ```
   javaclasspath('C:\Users\LAPTOP\Documents\...\fxMR-
   0.3.25.jar');
   ```

Input data structures

The basic idea is that we have a set of data (called a *data structure*) that is organised as a set of observations on $d > 1$ *dependent variables* across levels of two or more *independent variables*. From the point of view of *state-trace analysis* (STA), the number of different independent variables is not important – rather, it is the total number of conditions (combinations of levels). For example, if there are two independent variables, one with 2 levels, the other with 3 levels, then there will be a total of 2 x 3 = 6 conditions. These conditions will be numbered from 1 to 6.

For this reason, STACMR distinguishes only between conditions defined between-subjects and conditions defined within-subjects. If there are b between-subjects conditions and w within-subjects conditions then there is a total of bw conditions ordered by the set of between-subjects conditions. That is, the first w conditions correspond to the set of within-subjects conditions under the first between-subjects condition, the next w conditions correspond to the set of within-subjects conditions under the second between-subjects condition, and so on.

At present, STACMR accepts two kinds of data structure:

1. **Cell array format**. In this format, the data are organised in a *b* x *d* cell array where *b* is the number of between-subjects groups and *d* is the number of dependent variables. Each component of this cell array is itself an *n* x *w* matrix of observations where *n* is the number of subjects (which may vary across groups and dependent variables) and *w* is the number of within-subjects conditions (fixed across groups and dependent variables). The dependent variable may be either within-subjects or between-subjects – it doesn't matter because the correlation between dependent variables is assumed to be zero (although this might be up for grabs in future implementations).

2. **General format**. This structure is useful if the data are already in some kind of fixed column format. It is organised as a matrix in which each row corresponds to an observation and each column is defined as follows:
   column 1 = subject number (for identification only, not used directly)
   column 2 = between-subjects condition or group (if none, then column 2 = 1)
   column 3 = dependent variable (1 or 2)
   columns 4 to end = values for each within-subjects condition

   While STACMR accepts data in general format it always converts it to cell array format using the function,
   ```
   >> y = gen2cell (data);
   ```

Partial order

As well as data, the various STACMR functions often make use of an optional partial order. A partial order on a vector, *x*, is a set of pairs, (*i*, *j*), such that $x_i < x_j$.

A partial order is represented in STACMR in two (equivalent) ways:

1. As a cell array containing the set of (*i*, *j*) pairs, e.g., `{[1 2] [2 3] [1 4]}`. There is a shorthand for a linear order such as `{[1 2] [2 3]}` which can be written as `{[1 2 3]}` or, even more simply, as `{1:3}`.

2. As an adjacency matrix in which entry (*i*, *j*) = 1 if (*i*, *j*) is an element of a partial order, otherwise (*i*, *j*) = 0.

The function, `cell2adj`, converts a partial order in cell array form into its corresponding adjacency matrix form. For example,

```
>> E = {[1 2] [2 3] [1 4]};
>> A = cell2adj (1:4, E)
A =
```

```
     0     1     0     1
     0     0     1     0
     0     0     0     0
     0     0     0     0
```

In the above call to `cell2adj`, the vector, `1:4`, specifies the set of nodes or points that the partial order applies to. It is almost invariably the sequence of numbers, 1 to *n*, where, in this case, *n* = 4. The function `adj2cell` converts an adjacency matrix into its corresponding cell array.

The principal functions

The operation of the principal functions will be illustrated with respect to two data sets.

The first, called `delay`, is a data set discussed by Dunn, J. C., Newell, B. R., & Kalish, M. L. (2012). The effect of feedback delay and feedback type on perceptual category learning. *Journal of Experimental Psychology: Learning, Memory and Cognition, 38*(4), 840-859. It is in general format and is contained in the file, `delay.dat`. That is,

```
>> delay = load('delay.dat'); % read the data file

>> y = gen2cell(delay); % convert to cell array format
```

staSTATS.m

This function computes summary statistics of a data structure in cell array format.

Example call:

```
>> delaystats = staSTATS (y, shrink);
```

Here, `y` is the `delay` data in cell array format and `shrink` is an optional parameter denoting how much shrinkage to apply to the estimated covariance matrix. Generally, the covariance matrix needs to be shrunk during the bootstrap cycle to avoid ill-conditioning.

If `shrink = 0` then no shrinkage is applied. If `shrink = 1` then maximum shrinkage is applied. This means that the covariance matrix is diagonalized with all off-diagonal entries set to zero. If `shrink < 0` (the default) then an optimal shrinkage value is estimated for each within-subjects block and applied according to an algorithm developed by Ledoit, O. & Wolf, M. (2004). Honey, I shrunk the sample covariance matrix, *The Journal of Portfolio Management*, *30*(4), 110-119.

`staSTATS` returns, in `delaystats`, a cell array of length equal to the number of dependent variables in `y`. Each component of `delaystats` is a structured array. For the dependent variable, `ivar`:

- `delaystats{ivar}.means` = vector of means across all conditions
- `delaystats{ivar}.cov =` the covariance matrix (for information only)
- `delaystats{ivar}.regcov =` the adjusted covariance matrix following application of shrinkage
- `delaystats{ivar}.n =` matrix of number of observations (subjects) in each within-subjects block
- `delaystats{ivar}.lm =` matrix of Loftus-Masson within-subjects standard errors (used by `staPLOT` below)
- `delaystats{ivar}.weights =` matrix of weights defined by: `delaystats{ivar}.n.* delaystats{ivar}.regcov^-1`
- `shrinkage` = a vector of length *b* (where *b* is the number of levels of the between-subject independent variable) containing the specified or estimated shrinkage values

Thus, delaystats has two elements. If you look at the means, they look like this:

```
>> disp(delaystats{1}.means)
0.3676  0.4676  0.5757  0.6118  0.3445  0.4434  0.5081  0.5169

>> disp(delaystats{2}.means)
0.3308  0.4550  0.5346  0.5492  0.2836  0.3031  0.3180  0.3098
```

staMR.m

This function conducts monotonic regression on a data structure according to a given partial order. We say it fits the *partial order model* to the data (i.e., the set of dependent variables).

Example call:

```
>> [x, f, shrinkage] = staMR (data, E, shrink);
```

Input:

Here, `data` is either a data structure (in cell array or general format) or structured output from `staSTATS`; `E` is a partial order (required) in either cell array or adjacency matrix format; `shrink` is an optional shrinkage parameter (defined previously). If `data` is a cell array of structured output from `staSTATS`, then the shrinkage specified by this output is used whether the argument `shrink` is specified or not.

Output:

`x` is a *d*-element cell array of that contains the best-fitting values for each dependent variable; `f` is the value of the least squares fit; `shrinkage` is a *b* x *d* matrix of shrinkage values (where *b* is the number of levels of the between-subject independent variable).

Try this with `delay`. To do so, we have to specify a partial order. Use the following:

```
>> E = {1:4, 5:8, [5 1], [6 2], [7 3], [8 4]};
```

```
>> [x2, f2, s2] = staMR (delay, E);
```

```
>> disp([x2{:}]);
    0.3676    0.3308
    0.4676    0.4550
    0.5757    0.5346
    0.6118    0.5492
    0.3445    0.2830
    0.4434    0.3034
    0.5081    0.3149
    0.5169    0.3149

>> disp(f2);
    0.1721

>> disp(s2);
    0.0520    0.0491
    0.0314    0.2650
```

staCMR.m

This is the main function that conducts the CMR (state-trace) analysis. It takes a data structure or a cell array of structured output from `staSTATS` and an optional partial order and returns the best fitting values (to the data means) and the least squares fit. We say it fits the *conjoint partial order and monotonic model* to the data.

Example call:

```
>> [x, f, s] = staCMR (data, E, shrink);
```

On the input side, `data` is the data structure, `model` is an optional model (explained above), `E` is an optional partial order, `shrink` is an optional shrinkage parameter (defined previously).

On the output side, `x` is a cell array of the best-fitting values, `f` is the value of the least squares fit, and `s` is a structured array of fit statistics. The component, `s.shrinkage`, is a *b* x *d* matrix of shrinkage values.

Now try this with `delay`:

```
>> [x1, f1, s1] = staCMR (delay, E);
```

```
>> disp([x1{:}]);
    0.3759    0.3150
    0.4850    0.4358
    0.5898    0.5167
    0.6265    0.5318
    0.3353    0.2856
    0.4186    0.3150
    0.4806    0.3227
    0.4850    0.3227

>> disp(f1);
    1.7493

>> disp(s1.shrinkage);
    0.0520    0.0491
    0.0314    0.2650
```

staCMRFIT.m

This function estimates the empirical distribution (and hence *p*-value) of the fit of the conjoint monotonic and partial order model against the fit of the partial order model.

Example call:

```
>> [p, datafit, fits] = staCMRFIT (nsample, data, model, E,
shrink, proc);
```

Input:

- `nsample` is the number of Monte-Carlo samples (about 10,000 should be good)
- `data` is a data structure (which can be in general format, cell array format, or structured output from `staSTATS`). If data is non-summary data in general or cell array format then the bootstrap resampling is non-parametric, otherwise it is parametric (assumes a normal distribution).
- `model` is an optional model (default = STA)
- `E` is an optional partial order (default = none)
- `shrink` is an optional shrinkage parameter (default = -1)
- `proc` is an optional specification of maximum number of processors to be used (default = maximum available)

Output:

- `p` is the estimated *p*-value
- `datafit` is the observed fit value (see below)
- `fits` is a vector of empirical fit values (see below)

Important note:

`staCMRFIT` operates on the difference in fit values between a partial order model (calculated using `staMR.m,` e.g., `f2` above) and the combined partial order + monotonic model (calculated using `staCMR.m,` e.g., `f1` above).

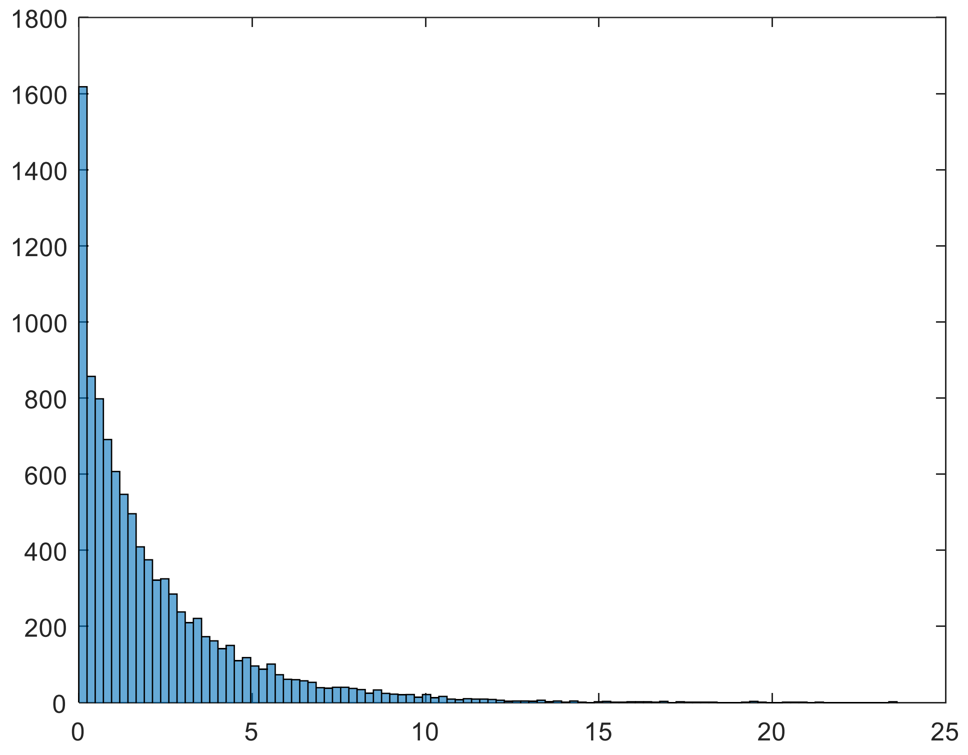
Example output (note that p and fits will be approximate only):

```
>> [p, datafit, fits] = staCMRFIT (10000, delay, [], E);

>> disp([p, datafit])

     0.4538    1.5772

>> histogram (fits, 100)
```



staPLOT.m

This function generates a state-trace plot of a data structure.

Example call:

`>> staPLOT (data,` *optional argument pairs*`);`

Here, `data` is a data structure or a cell array of structured output from `staSTATS`. The optional argument pairs are of the form; *'keyword'*, *value*. The following are the set of keywords (valid alternatives in parentheses);

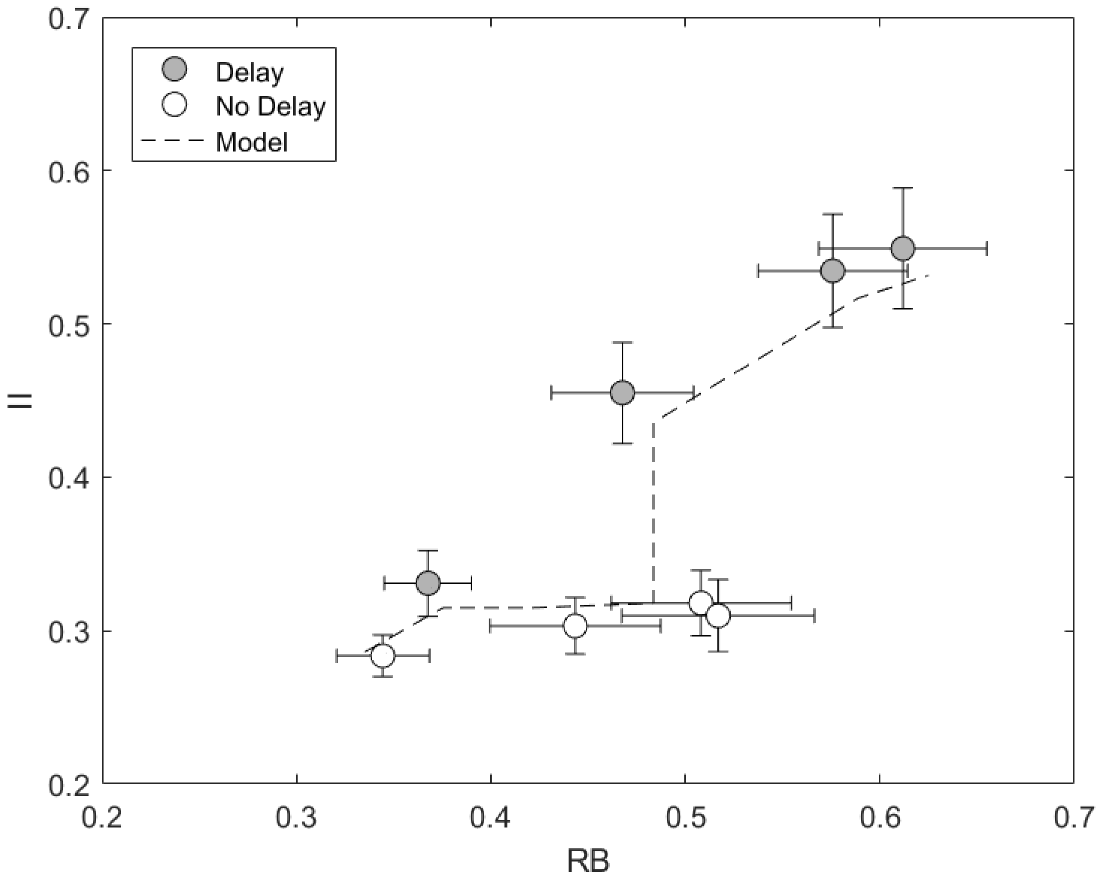
- `predictions (prediction, pred, p)` is a *d*-element cell array that defines a set of fitted values (output from `staMR` or `staCMR`)
- `vars (v, dv)` is a 2-vector that defines two dependent variables for plotting (default = `[1, 2]`)
- `groups (group, g)` is a cell array that defines a structure on the conditions. For example if there are 2 between-subjects conditions and 3 within subjects conditions then one group structure might be `{1:3, 4:6}`. At present, only one factor can be identified in this way.
- `labels (label, lab, l)` is a cell array that defines the labels of the levels defined by `groups`
- `axislabels (axislabel, axislab, axis)` is a cell array that defines the labels of the x- and y-axes
- `axislimits (axislimit, axislim, limits, limit, lim)` is a cell array that defines the upper and lower limits of the axes
- `axisticks (axistick, ticks, tick, t)` is a cell array that defines tick marks for x- and y-axes (if specified then `axislimits` is redundant)
- `location (loc)` is a Matlab value for the location of the legend (default = `'northwest'`)
- `color  (col, c)` is a 3-element RGB vector specifying the color of the plot of predicted values (default is black)
- `line` is a flag to indicate if the predicted values are connected by a line. If set a line is drawn (default) otherwise no line is drawn.

Example output:

To see how this works, we use `delay` and the results of the earlier call to `staCMR`.

```
>> staPLOT(delay, 'pred', x1, 'groups', {1:4 5:8}, 'labels',
{'Delay' 'No Delay'}, 'axislabels', {'RB' 'II'}, 'axisticks',
{.2:.1:.7, .2:.1:.7});
```

This should produce the following graph:


0.7
0.6
0.5
0.4
0.3
0.2
II
0.2
0.3
0.4
0.5
0.6
0.7
RB
Delay
No Delay
Model