# Spike Analyzer - identifying bad scans in fMRI

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# Problem and common solutions

- **movement** in the scanner causes

  1. displacement of voxels

  2. large (unphysiological) peaks in the BOLD signal

- **realignment** solves the displacement problem

- **inclusion of movement parameters** "filters out" variance in the BOLD signal that corresponds to the exact movement trajectory of the subject in the scanner

- **unwarping** solves the problem of stimulus-correlated movement by building a linear model to adjust the data

# But …

- some large spikes in the BOLD time series may persist …

- removing these unphysiological peaks in the BOLD signal **can (!!!)** improve the model fit and the detection of experimental effects

- crude approach: remove "bad scans" from the time series and interpolated missing volumes from previous and subsequent scan(s)

- more elegant approach: build a regressor for each bad scan and include it in the design matrix -> this will capture the singular peak of the bad scan

# However …

- if you "exclude" too many bad scans through modeling, you lose a certain amount of your trials -> estimates of experimental effects may be less reliable (= higher variance) -> diminish the power to detect the effect of interest

- finding the right balance is a matter of experience with multiple data sets -> defaults can be sue as a first pass, but results should be critically examined and defaults can be adjusted.

# How to detect "bad scans" in the data?

- examination and analysis of the global signal time series for fast changes and correlations with movement parameters

- diagnostic indices:

    1. derivative of global signal

    2. movement velocity

    3. correlation with movement parameters

    4. thresholds on movement parameters

# spike analyzer

- provides several diagnostic plots and automatically flags "bad scans" and outputs them as nuisance regressors to be included in the 1st level design matrix (option additional regressors)

- selecting voxels for computation of global signal

  1. Segment EPI images and create a GW matter mask - slow, but most accurate

  2. constant number of voxels - requires several passes through the data - slow, but fairly accurate

  3. ROI mask image - if the interest is focus on a specific anatomical region (could be also a whole brain mask)

  4. spm_global: includes several outliers in computational of global mean, leads to exclusion of too many bad scans (depreciated)

# Spike Analyzer 1.6

Subject Directory: /Users/glaescher/tmp/15097/epi/level_1
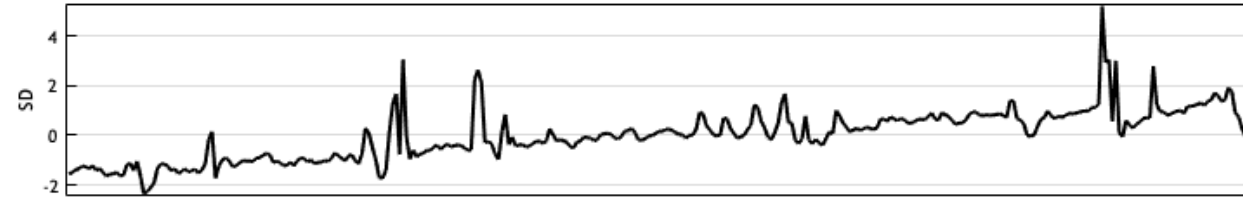
global mean

1st derivative
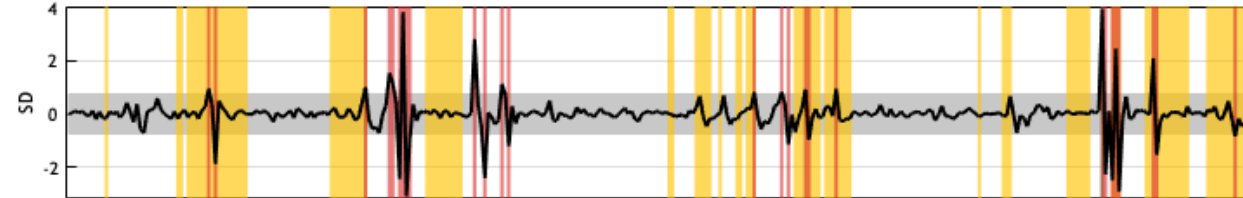
local correlation b/w global
mean and mvmt params

Movement parameter
(translation)

Movement parameter
(rotation)
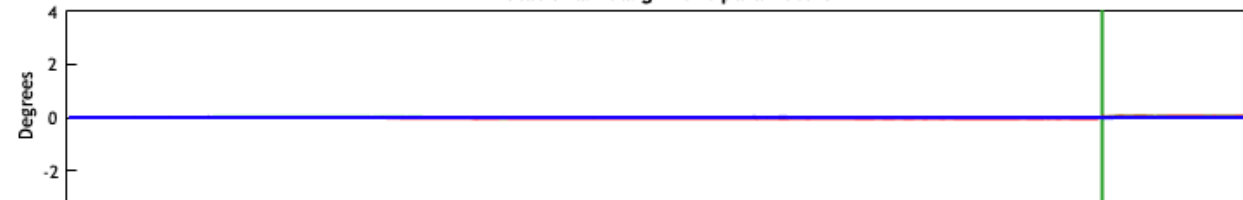
Movement velocity
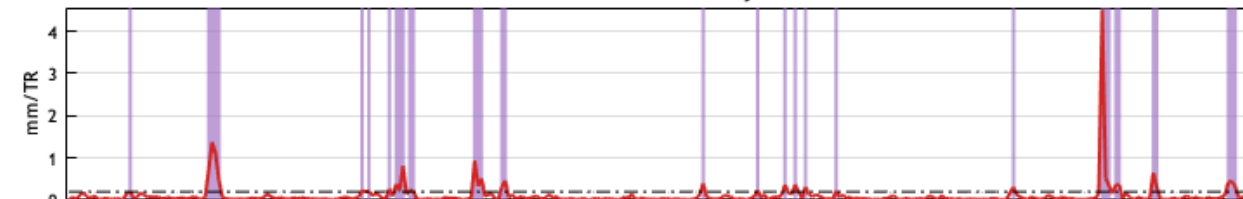
corrected global mean
(mvmt params regressed out)
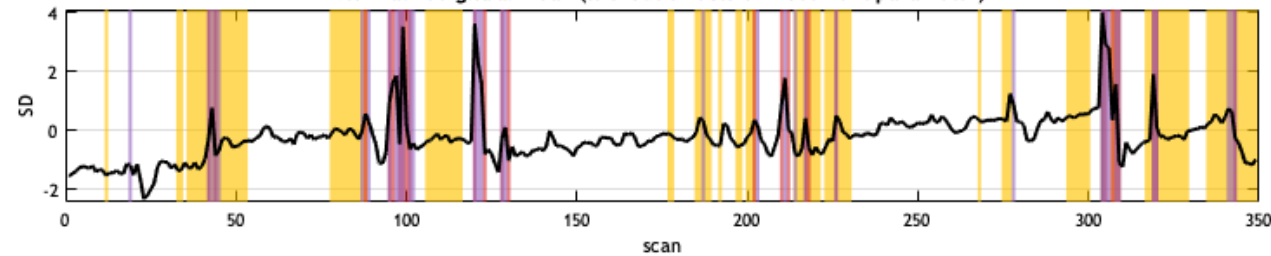
no. of scans excluded
by different diagnostic indices



No. of candidate scans suggested for removal through separate modeling:
global mean/mvmt correlation (0.8): 114/349 (32.66%)
1st derivative of global mean (0.8 SD): 27/349 (7.74%)
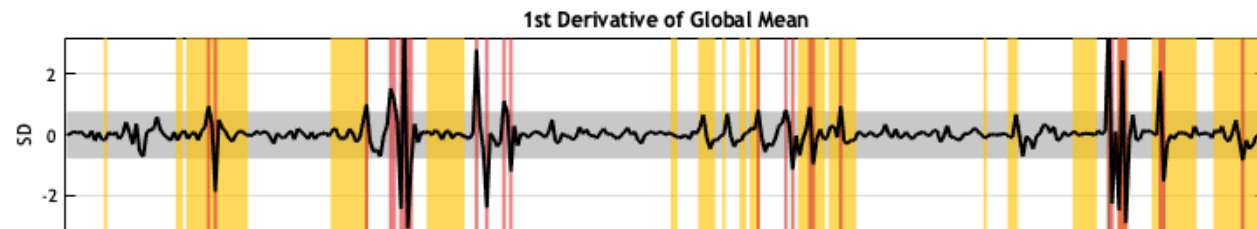movement parameters (0.8 * voxsize): 1/349 (0.29%)
movement velocity (0.20 mm/TR): 35/349 (0.10%)
TOTAL: 139/349 (39.83%)

# spike analyzer detection thresholds

`cfg.globthr (0.75)`

± SD deviation from 0

**1st Derivative of Global Mean**

`cfg.rsqrthr (0.8)`
`cfg.winsize (20)`

80% of the variance is explained by mvmt

**Correlation between global mean and movement parameters (window: 20 scans)**
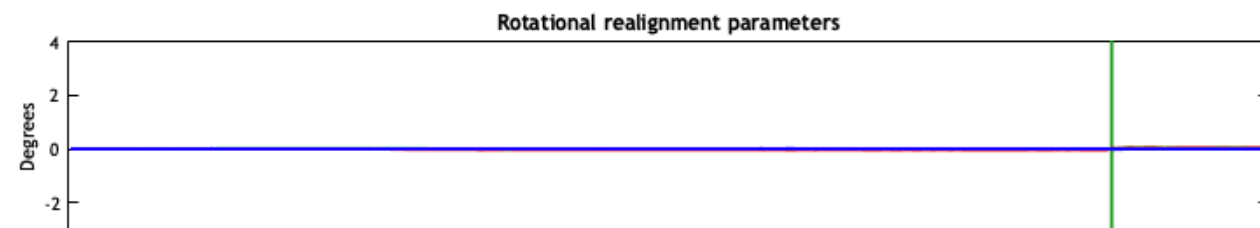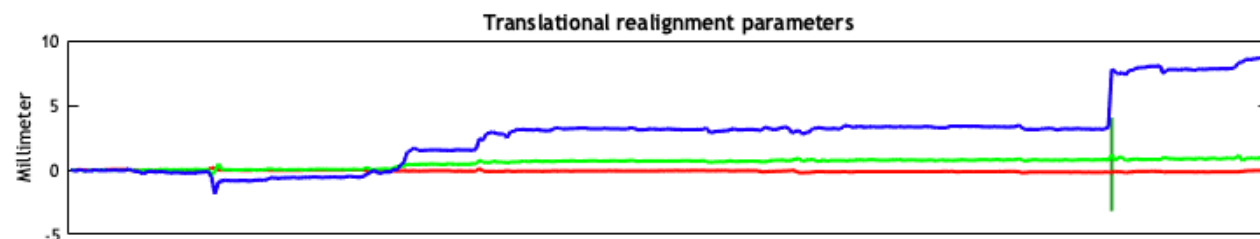
`cfg.realignthr (1)`

stringent threshold:
1mm translation / 1 degree rotation
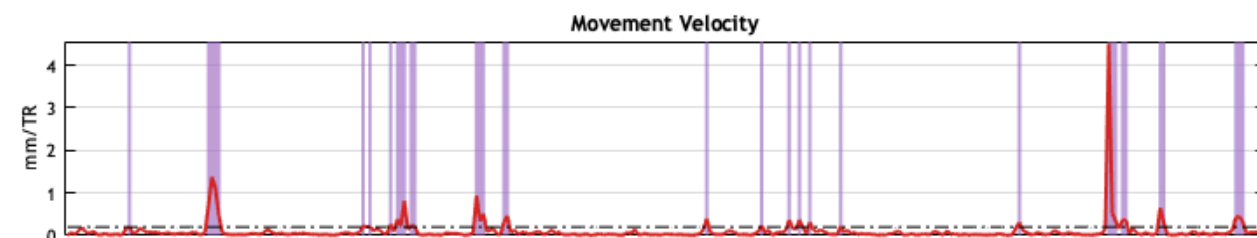lenient threshold:
2mm translation / 2 degrees rotation
old rule of thumb:
voxel size in translation / rotation

**Translational realignment parameters**

**Rotational realignment parameters**

`cfg.movethr (0.2)`

0.2 mm/TR

**Movement Velocity**

# How to call spike analyzer

**Attention: use only resliced volumes as input (either are realignment or normalization) !!!**

```
P = spm_select('ExtFPList','epi/level_1','^rvol_0.*\.nii',inf);
rp = spm_select('FPList','epi/level_1/','^rp.*\.txt')
[nuis, cfg] = spike_analyzer(P, rp);
```

To re-use the created EPI brainmask during threshold adjustment:

```
cfg.voxselect = 'roi';
cfg.globthr = 1;
[nuis, cfg] = spike_analyzer(P, rp, cfg);
```
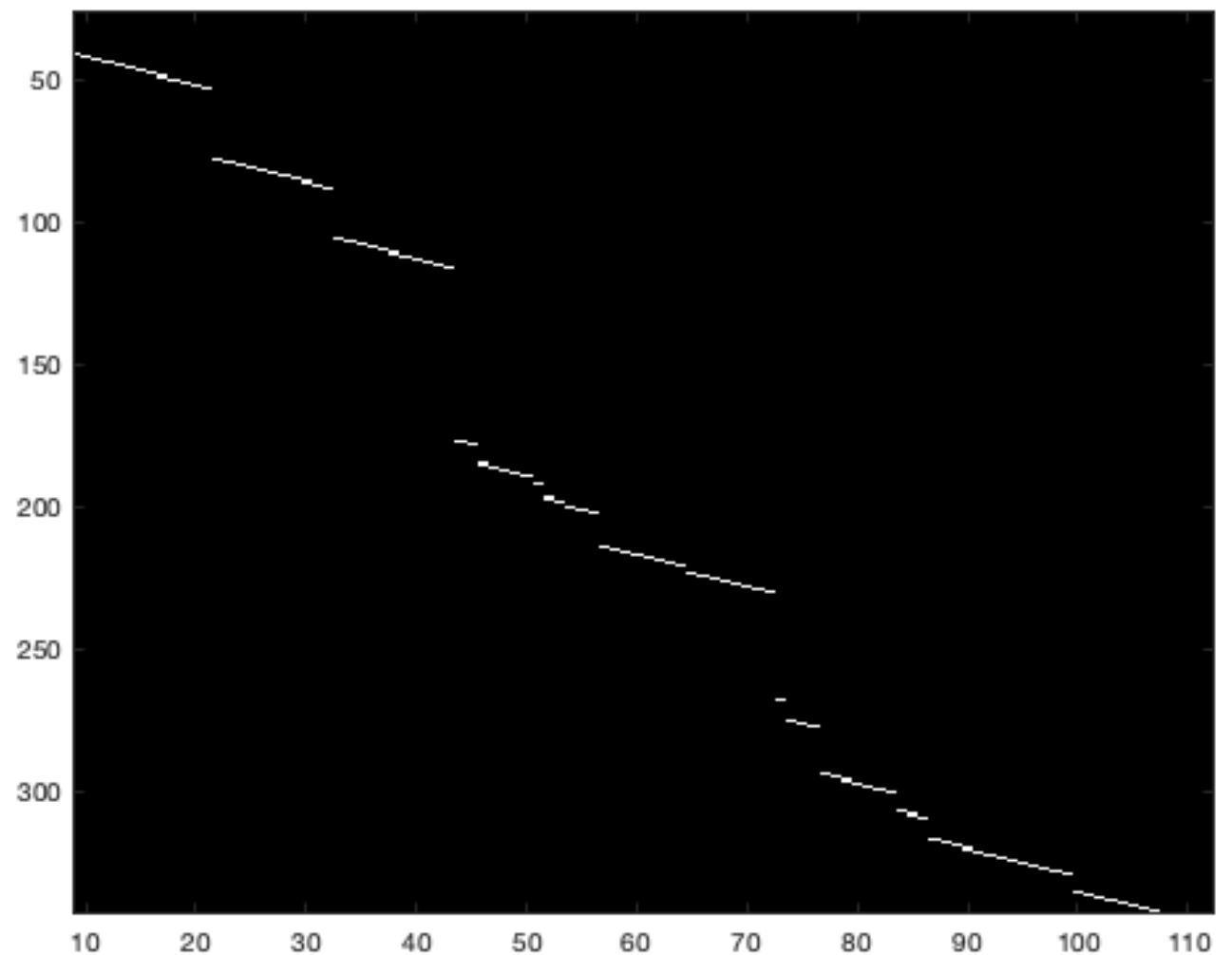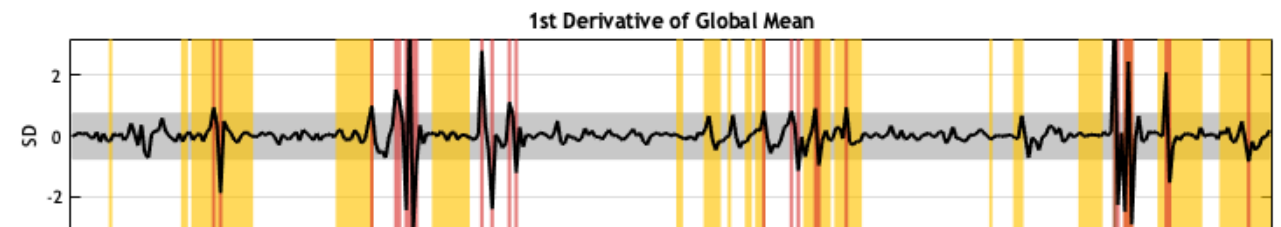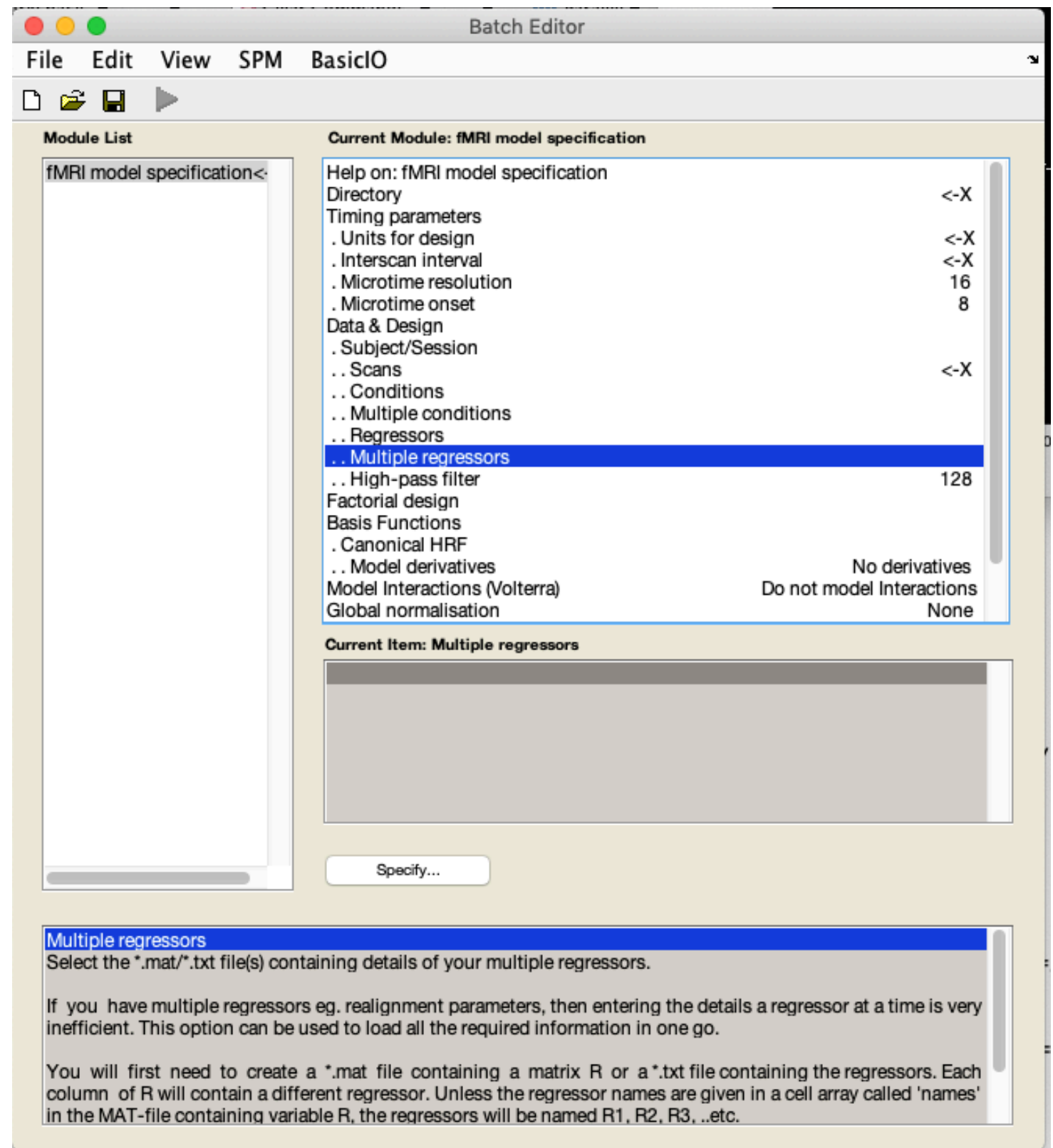
# Output of spike analyzer

# How to include output in 1st level design

```
>> R = nuis.all;
>> save bad_scans.mat R
```

**Attention:** all calls to spike analyzer are session-specific, i.e. you have to loop over runs

Inclusion in 1st level design is also done per session. Bad scan
regressors will be names R1 R2 etc.

# When should I use it and where can I get it?

- Limited success with univariate analyses (sometimes it helps, sometimes it doesn't)

- Good success with multivariate analyses (leaving bad scans in the time series can screw up your activation patterns)

Download Spike Analyzer here:

https://github.com/GlascherLab/SpikeAnalyzer