fMRI Signal Processing Toolbox v1.1
Release Notes

Ameera X. Patel

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Acknowledgements

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1 Parcellation

1.1 parcellate.sh

This function has been amended to ensure exclusion of zero voxels during computation of regional time series and centroid coordinates.

How does it work? The parcellation template is copied into your working directory and resampled to the functional image resolution. A brain mask of the standard space pre-processed functional image is then computed to exclude all zero voxels. This is applied to the resampled parcellation template to clip off no-data voxels. This modified parcellation template is used for parcellation (called "xxxxx_clipped+tlrc"). The selected parcellation template is thus tailored to each subject separately.

If entire parcels have been clipped off from the template due to variations in subject anatomy, these will be represented in all outputs as columns of zeros. The program will also output an error in the terminal (as in v1.0) to warn that zero parcels have been detected, and will create an error file "par_error_xxxxx.txt" containing information about which parcels to remove from your analysis.

Due to inter-subject variability after standard space transformation, parcels on the surface of the brain are likely to contain different numbers of voxels from subject to subject. The program output containing information on the number of voxels in each parcel, now outputs the number of non-zero voxels in each parcel that were used to parcellate that brain. This is in contrast to v1.0, which simply stated the number of voxels in each parcel of the original (unclipped) parcellation template.

Do I need to re-parcellate my data? Yes. Although this modification is likely to have a small impact on your group analysis, it will likely affect your results at the single subject level, so you should re-parcellate all of your data.

How does this change affect computation time? It has no noticeable impact on the computation time stated in the toolbox documentation.

1.2 templates

Due to popular demand, a new template has been added to this release of the toobox. This template is a sub-parcellated anatomical template (based on the AAL template) that contains 638 parcels. It works best with the MNI brain, so please select this option for standard space transformation during parcellation. This template omits the cerebellum.

A summary of parcellation templates included in the toolbox can be found below:

- AT116.nii (116 regions, anatomical parcellation)

- AT150.nii (150 regions, random parcellation)

- AT230.nii (230 regions, random parcellation)

- AT325.nii (325 regions, random parcellation)

- SP638.nii (638 regions, sub-parcellated anatomical template)

2 speedypp.py

This function has been amended to improve CSF masking, and consequently, the estimation of CSF signal for inclusion in the regression matrix.

How does the new masking work? The toolbox now contains a new "master template" based on a segmented standard space MNI brain to mask out all regions except the ventricles. For each subject, this "master template" is then trasformed to native space and combined with the original segmented anatomical and brain mask for that subject. The end result is a CSF mask based on each individual subject's anatomy that only retains non-zero ventricular voxels. For each subject, the mask is output in the directory "spp.rest" with the suffix _csfmask.

How does this affect computation time? There is no noticeable impact on computation time.

Do I need to re-process my data? If you have used the –rcsf flag in v1.0, yes, you will need to re-process your data.

3 checkmysubject.sh

This is a new function that takes as input: the regional time series, FD and DVARS. The output is a 3-word statement in the terminal, which tells you whether to keep or reject the subject from further analysis. Subjects are rejected if they contain a high proportion of movement-corrupted frames of data (r=0.45 is the default).

Users are given the option of whether to use the DVARS threshold proposed in Power *et al.*, 2012, or to use a threshold more relevant to the pre-processing methods used in this toolbox. The former states that a frame is "bad" if DVARS exceeds an absolute value of 0.5%. This threshold cannot be used for pre-processing methods other than that proposed in Power *et al.*. The default thresholding method in this function computes the baseline DVARS value (from all frames of data) and allows for a 0.3% increase in signal intensity from this baseline. For the Power *et al.*, 2012 data, this yields a similar threshold to that proposed in their paper of 0.5%. The default method is strongly recommended, as it accomodates different pre-processing methods and inter-subject variation in DVARS baseline.

4 FD.sh

A small modification has been made to the computation of the Framewise Displacement. Rotational movement parameters are now converted to displacements about a sphere of radius 50mm.

5 scrub.sh

A modification has been made to how frames are removed from time series in the process of scrubbing. In v1.0, all bad frames (with either high FD or high DVARS) were masked out. This has been changed to replicate exactly the frame removal method used in Power *et al.*, 2012. The program now scrubs

frames only if both FD **and** DVARS are above the threshold set (i.e. the intersection of the two vectors, rather than the union). It will also remove one frame prior and two frames after those frames masked for removal.

6 correlate.sh

This function now includes a plotting option (-p) to plot the distribution of correlation values from the upper triangle of the correlation matrix.