

Title: generalized canonical correlation analysis in NPAIRS framework (gCCA)

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Description: It is a multivariate method based on generalized canonical correlation analysis (gCCA) to maximize SPM reproducibility without adopting any model for the hemodynamic response or other temporal brain responses. The underlying assumption is that there are multiple subjects that share an unknown spatial response (or spatial map) to the common experimental manipulation but may show different temporal responses to external stimulation. For each subject, our gCCA explores a broad, potentially inconsistent range of temporal responses in fMRI time-series space while maximizing the mean of correlation coefficients between the pair-wise spatial maps of the subjects

Syntax:

[r] = gCCA(Data_FileName,MaskFile,num_resample,num_pc,outputdirectory,var_mode)

Inputs:

Data_FileName: is a cell array containing the name of nifti files.
MaskFile: Mask file name, which is used to remove non-brain voxels.
num_resample: the number of split-half resampling in npairs framework
num_pc: Number of principle component in
dimension reduction step used in main gCCA
num_pc=0 ---> Determine the number of pc,
based on leave-one out cross validation
(This option would be very slow very slow)
num_pc=-1 Laplacian dimension reduction
(See Minka T, "Automatic choice of
dimensionality for PCA", In 13th Annual
Conference on Neural Information
Processing Systems, 2000).
num_pc=-2 No dimension reduction
0 <num_pc<1---> Runs dimension reduction and keeps
100num_pc percent of energy of each subject
num_pc>=1 ---> Runs dimension reduction and keeps
num_pc principle components

outputdirectory: The output directory will contain the output nifti file and a mat
file. Mat file includes r (reproducibility metric) and time-domain
response.
VV in the nifti filename means voxel-wise variance estimation
PV in the output nifti filename means pooled variance estimation
(NPAIRS-Like)
var_mode: The z-map estimation algorithm.
variance estimation mode 0: voxel-wise
variance estimation , 1:pooled variance estimation
(NPAIRS-Like), 2: Both Strategies (default)

Output:

r: reproducibility values per components, components saved in output directories

Output files:

- 1) A MAT file will be saved after the split-half resampling is performed. This Mat file contains four variables:

Avect_avg: Subject x Time points x num_pc

It contains the average of temporal response of each subject over all split-half resamplings.

A_full: is a cell array, each component is the temporal responses of each subject, when we run the gCCA on full data (without split-half resampling)

Zm_full: is the z-map acquired from full data. The pooled estimation of variance used to calculate the z-map.

- 2) Group_Z_Map_(xx)_(nn)subjects_(pp).nii
xx: PV (Z-map acquired using pooled variance estimation)
VV (Z-map acquired using voxel based variance estimation)
nn: Number of subjects used in the analysis
pp: num_pc*100 (num_pc is the input parameter)

Contents:

It is Nifti file, containing all the z-maps acquired using gCCA in NPAIRS framework.

Reference:

B Afshin-Pour, GA Hossein-Zadeh, SC Strother, H Soltanian-Zadeh (2012): Enhancing reproducibility of fMRI statistical maps using generalized canonical correlation analysis in NPAIRS framework, NeuroImage.

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