Manual for PyMVPA wrapper similarity analysis

fmriDsm.py
    [[[dataset <filename> mask <filename> samples <filename>]
     [select <list>]
     [detrend]
     [zscore]
     [average]] ||
     [datamat <filename>]]
     [dsm correlation <name> dsmsave <filename> dsmdisplay]
     [searchlight <radius> dsmmeasure <name>]
     [save <filename>]

###

dataset <filename> - parameter
       - option to specify the dataset file (string)
       - <filename> is the filename with .nii.gz extension

###

samples <filename> - parameter
       - option to specify the attributes file (string)
       - <filename> is the filename with .txt extension

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mask <filename>   - parameter
       - option to specify the mask file (string)
       - <filename> is the filename with .nii.gz extension

###

select <list> - label list

detrend - specify to detrend the dataset

zscore - specify to zscore the dataset

average - average across all labels

datamat <filename> - MATLAB filename

searchlight <radius> dsmmeasure <name> - searchlight measure with dsm and radius

save <filename> - to save the searchlight result

Example:
python fmriDsm.py dataset ../../data/sub1/wrbold1A.nii.gz mask ../../data/sub1/mask.img samples ../dsm/attrbDsmSetA.txt detrend zscore select [1.0,2.0,3.0,4.0,5.0,6.0,7.0,8.0] dsm correlation spearman dsmsave temp2.dat dsmdisplay average

python fmriDsm.py datamat ../rsa/hippo/avgsub1.mat dsm correlation spearman dsmsave temp.dat dsmdisplay

###

Average across all subjects
To execute this command, copy all the subject's dat files from previous command into a directory and run the following command:

fmriDsmAll.py shape <value> matfile <filename> save <filename>

shape <value> - mandatory parameter to reshape the dat files
matfile <filename> - to save result in matfile
save <filename> - save in dat file

Example:
python fmriDsmAll.py shape 8 [save tmp.dat matfile tmp.mat]