
fc_ComputeGBC3.m

```
function [] = fc_ComputeGBC3(flist, command, mask, verbose, target, targetf, rsmooth, rdilate, ignore, time, cv, vstep)
```

Computes GBC maps for individuals as well as group maps.

INPUT

flist	- conc-like style list of subject image files or conc files: subject id:<subject_id> roi:<path to the individual's ROI file> file:<path to bold files - one per line>
command	- the type of gbc to run: mFz, aFz, pFz, nFz, aD, pD, nD, mFzp, aFzp, ... <type of gbc>:<parameter> <type of gbc>:<parameter> ...
mask	- An array mask defining which frames to use (1) and which not (0). All if empty.
verbose	- Report what is going on. [false]
target	- Array of ROI codes that define target ROI [default: FreeSurfer cortex codes]
targetf	- Target folder for results.
rsmooth	- Radius for smoothing (no smoothing if empty). []
rdilate	- Radius for dilating mask (no dilation if empty). []
ignore	- The column in *_scrub.txt file that matches bold file to be used for ignore mask. All if empty. []
time	- Whether to print timing information. [false]
cv	- Whether to compute covariances instead of correlations. [false]
vstep	- How many voxels to process in a single step. [1200]

USE

This function is a wrapper for `gmrmimage.mri_ComputeGBC` method. It enables computing GBC for a list of subjects. `flist` specifies the subject identities, bold files to compute GBC on and `roi` to use for specifying the volume mask, voxels over which to compute GBC. `mask` specifies what frames of an image to work on. `target` specifies the ROI codes that define ROI from the subject specific ROI files over which to compute GBC for. Usually the subject specific `roi` file would be that subject's FreeSurfer `aseg` or `aseg+aparc` segmentation. And if no `target` is specified all gray matter voxels are used for computing GBC.

What specifically gets computed is defined in the `command` string. For specifics see help for the `gmrmimage.mri_ComputeGBC` method.

In addition, if `rsmooth` and `rdilate` are specified, each subjects bold image will be 3D smoothed with the specified FWHM in voxels. As subjects gray matter masks differ and do not overlap precisely, `rdilate` will dilate the borders with the provided number of voxels. Here it is important to note that values from the expanded mask will not be used, rather the values from the valid mask will be smeared into the dilated area.

The results will be saved in the `targetf` folder. The results of each command will be saved in a separate file holding the computed GBC values for all the subjects. The files will be named with the root of the `flist` with `gbc` and code for the specific gbc computed added.

For more information see documentation for `gmrmimage.mri_ComputeGBC` method.

--- (c) Grega RepovÅ¡ on 2009-11-04.

Change log

2009-11-04 - Created by Grega RepovÅ¡.

2010-11-16 - Modified by Grega RepovÅ¡.

2010-11-22 - Modified by Grega RepovÅ¡.

2010-12-01 - Modified by Grega RepovÅ¡ - added in smoothing and dilation of images.

2014-01-22 - Modified by Grega Repovs - took care of commands that return multiple volumes (e.g. mFzp)

2016-02-08 - Modified by Grega RepovÅ¡ - added an option to specify how many voxels to work with in a single step.

2016-11-26 - Modified by Grega RepovÅ¡ - updated documentation.

Published with MATLAB® R2016b