

Extended HCP Atlas (HCPex) User Guide v1.1

The extended HCP-MMP atlas (HCPex) is described by Huang, Rolls et al (2022).

The extended HCP-MMP atlas is provided in the asymmetric MNI standard space of the ICBM152 2009c T1 template. The cortical regions in this atlas are those defined by Glasser et al (2016), and are reordered based on the HCP-MMP v1.0 atlas (Huang *et al.* 2022) and the CortexID provided in the Supplementary Material File NIHMS68870-supplement-Neuroanatomical_Supplementary_Results.pdf of Glasser et al (2016). 66 new subcortical parcellations (33 in each hemisphere) are added in HCPex, after the cortical regions.

The connectivity of most of the cortical regions in the HCPex atlas as analysed with effective connectivity, functional connectivity, and diffusion tractography has been described (Huang et al. 2021; Ma et al. 2022; Rolls et al. 2022d, 2022c, 2022a, 2022b; Rolls et al. 2022f, 2022e; Rolls et al. 2022g; Rolls et al. 2022h; Rolls 2023; Rolls et al. 2023), and these sources provide much evidence about the functions as well as connectivity of the cortical regions as defined in both the HCP-MMP1 (Glasser *et al.* 2016) and HCPex (Huang, Rolls et al (2022)) atlases.

Note: In practice, we have found that for group data, taking the average of 172 participants' functional connectivity (Rolls *et al.* 2022e), the correlation between the average functional connectivity map for 360 cortical areas between HCPex and surface-based registration is 0.94, but is less good for single subjects, for which surface-based analysis is better, as set out in Huang, Rolls et al (2022). On the other hand, HCPex is likely to be helpful for activation studies in which the analysis is frequently performed in volumetric space; and is very helpful for diffusion tractography studies (Huang *et al.* 2021), which are usually performed in volumetric space.

Update Log

2022.12.23 Correction for the output in the HCPexOrdering.m function. 2D slices in coronal (from Huang, Rolls et al (2022)), and sagittal and axial (Rolls *et al.* 2023) views are provided with the toolbox. Please cite the toolbox as Huang, Rolls et al (2022).

Download

HCPex was released on 18 November 2021. The latest version can be downloaded from <https://www.oxcns.org/NeuronalNetworkSimulationSoftware.html> or <https://github.com/wayalan/HCPex> as HCPex_v1.1.zip.

User Guide

This HCPex atlas is mainly based on the HCP-MMP v1.0 (Glasser *et al.* 2016), but adds 33 subcortical regions in each hemisphere, and provides a reordering of the 360 cortical regions based on the cortical division that each region belong to. The regions are re-ordered as follows: *primary visual, early visual, dorsal stream visual, ventral stream visual, MT + complex and neighboring visual areas, somatosensory and motor, paracentral lobular and middle cingulate, premotor, posterior opercular, early auditory, auditory association, insular and frontal opercular, medial temporal, temporo-parieto-occipital junction, superior parietal, inferior parietal, posterior cingulate, anterior cingulate and medial prefrontal, orbital and polar frontal, inferior frontal, dorsolateral prefrontal, and subcortical regions.*

The new atlas is available as a toolbox for SPM (Results > Atlas), MRICroGL (MRICroGL should be used and not MRICron, for the latter cannot handle more than 255 regions), FreeSurfer viewer (Freeview), and is also compatible with AAL3 software. The HCPex atlas is provided with isotropic voxel size 1x1x1 mm. In addition, a lower resolution version of HCPex is provided with 2x2x2 mm voxel size for use in for example functional MRI studies.

Contents of the package

This HCPex archive contains NIfTI files for HCPex in two different resolutions (1x1x1mm & 2x2x2mm), a skull-stripped ICBM152 T1 template for atlas overlapping, and necessary files for MRICroGL, FreeSurfer, SPM, and AAL3 software. We also provide a useful function “HCPexOrdering.m” for users to alter the connectivity matrix from the HCPex to the original HCP-MMP v1.0 label ordering.

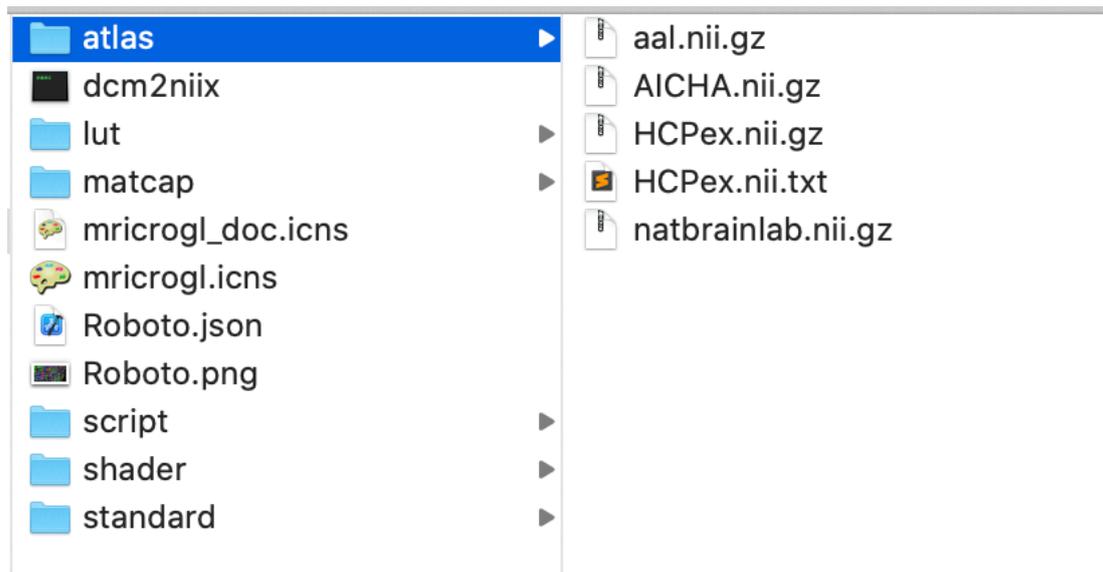
File Type	Filename	Description
1x1x1 mm ³	HCPex.nii.gz	Atlas file; Required for MRICroGL, Freeview, and SPM software
	HCPex.nii.txt	Required for MRICroGL
	HCPex.xml	Required for SPM12
	HCPex_LookUpTable.txt	Required for Freeview
	HCPex_LookUpTable.lut	Required for FSL
	mni_icbm152_t1_tal_nlin_asym_09c_brain.nii.gz	Skull-stripped T1 template
2x2x2 mm ³	HCPex_2mm.nii	Atlas file; Required for MRICroGL, Freeview, SPM, and AAL3 software
	HCPex_2mm.txt	Required for MRICroGL
	HCPex_2mm.xml	Required for SPM12

Matlab files	HCPexOrdering.m	Reordering function
	HCPex_LabelID.mat	Required for the reordering function
	HCPex_2mm_Border.mat	Required for AAL3 software
	HCPex_2mm_vol.mat	Required for AAL3 software
	HCPex_2mm_List.mat	Required for AAL3 software

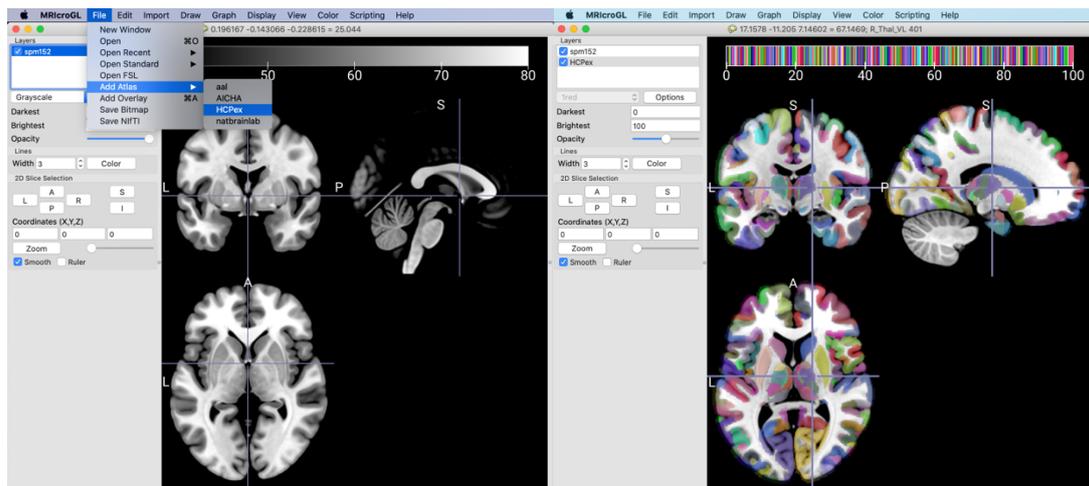
You can find HCPex ordering (1st column), HCP-MMP ordering (2nd column), the Region name in two different formats (3rd and 4th column), cortex division numbers (5th column), and cortex division names (6th column) (as defined by Glasser et al (2016)) in the HCPex_LabelID.mat file.

Tutorial for use of HCPex with MRICroGL

1. Copy HCPex.nii.gz and HCPex.nii.txt files to the MRICroGL/atlas directory



2. Open the MRICroGL application
3. Add Atlas > HCPex
4. Done! Drag the mouse to navigate the atlas labels.

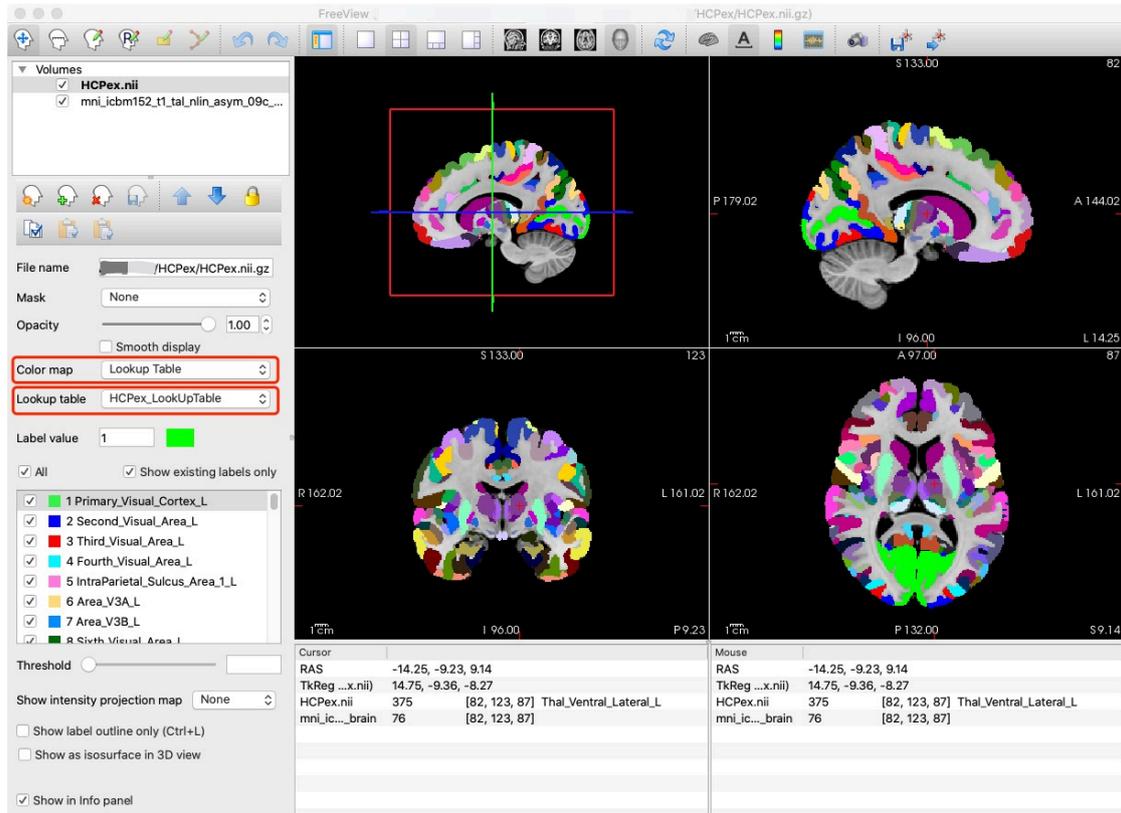


Please confirm that the HCPex.nii.txt file is in the same directory with HCPex.nii.gz, so that MRICroGL can automatically detect the labelling file.

HCPex is defined in the MNI ICBM152 2009c asymmetric T1 template. Please open "mni_icbm152_t1_tal_nlin_asym_09c_brain.nii" as the background T1 image if you wish for more accurate overlapping visualization.

Tutorial for Freesurfer viewer (freeview)

1. Open the freeview application (with command line tool ↵ freeview)
2. File → Load Volume → Select volume file
“mni_icbm152_t1_tal_nlin_asym_09c_brain.nii” → OK
3. File → Load Volume → Select volume file “HCPex.nii.gz” → OK
4. Color map popup menu: Lookup Table
5. Lookup table: HCPex_LookUpTable.txt
5. Done! Drag the mouse to navigate the atlas labels.



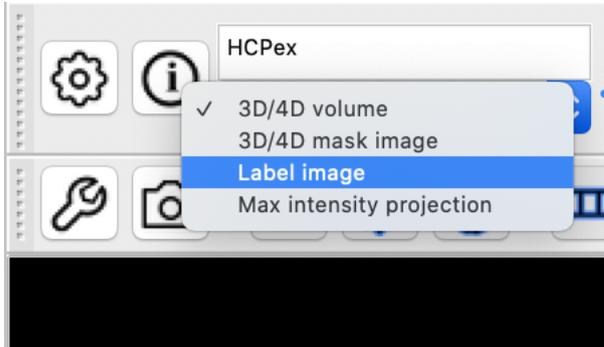
Note: Freeview command line is also supported:

```
freeview -v mni_icbm152_t1_tal_nlin_asym_09c_brain.nii.gz
```

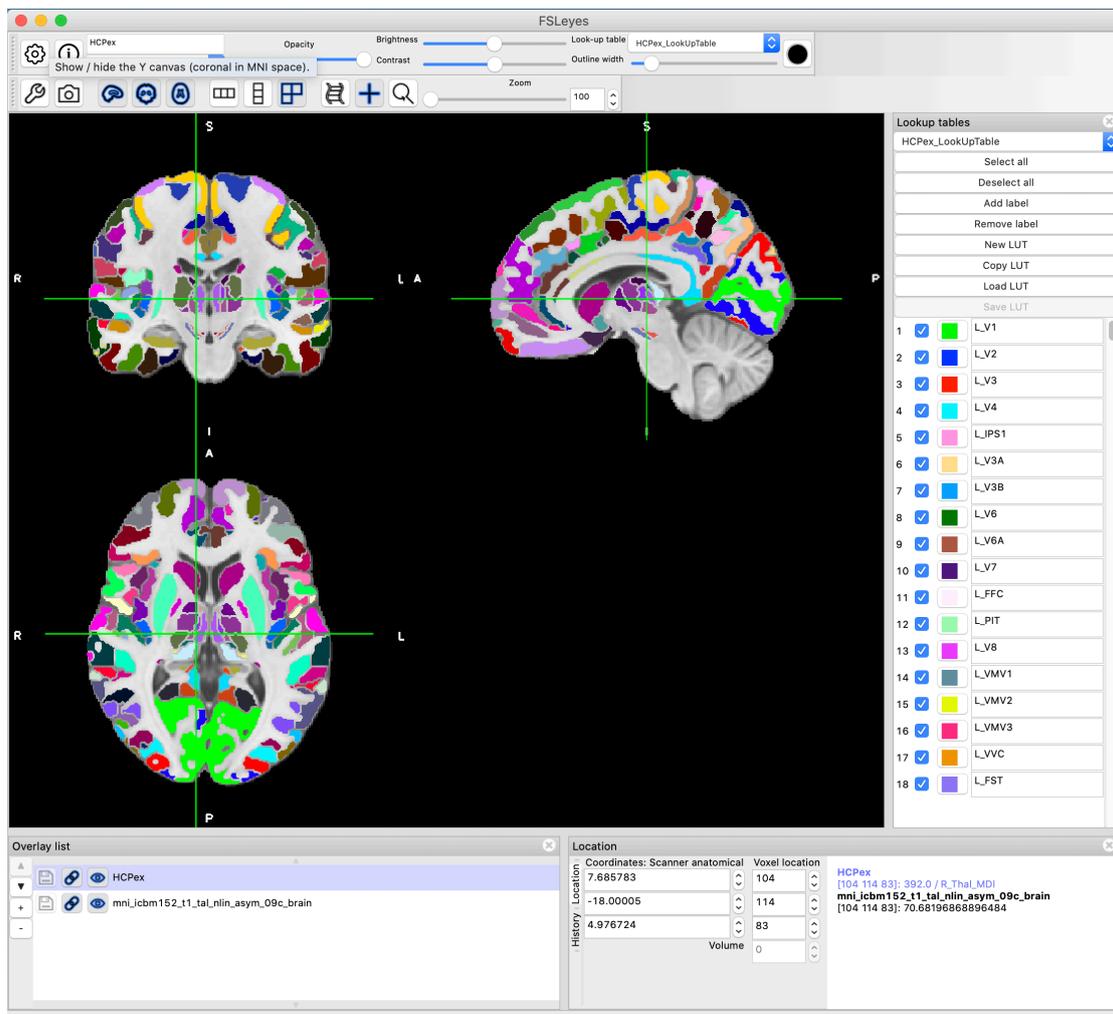
```
-v HCPex.nii.gz:colormap=lut:lut=HCPex_LookUpTable.txt
```

Tutorial for use of HCPex with FSL

1. Launch FSLEYES
2. File > Add from file > mni_icbm152_t1_tal_nlin_asym_09c_brain.nii.gz
3. File > Add from file > HCPex.nii.gz
4. Overlay type > Label image

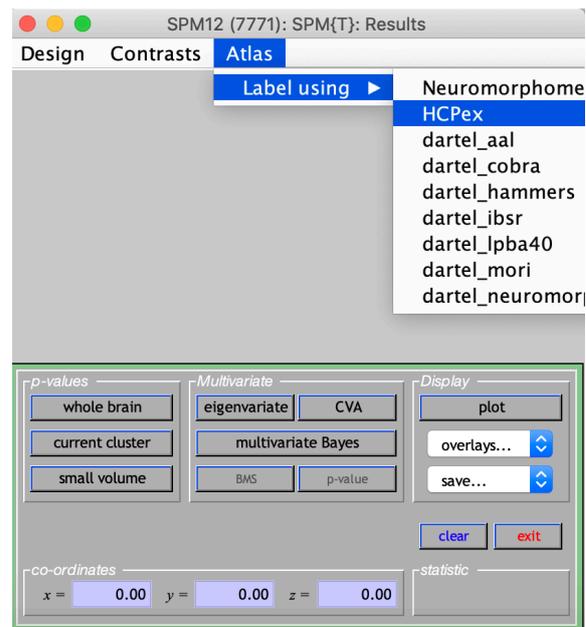


5. Settings > Ortho View 1 > Lookup tables > Load LUT > HCPex_LookUpTable.lut

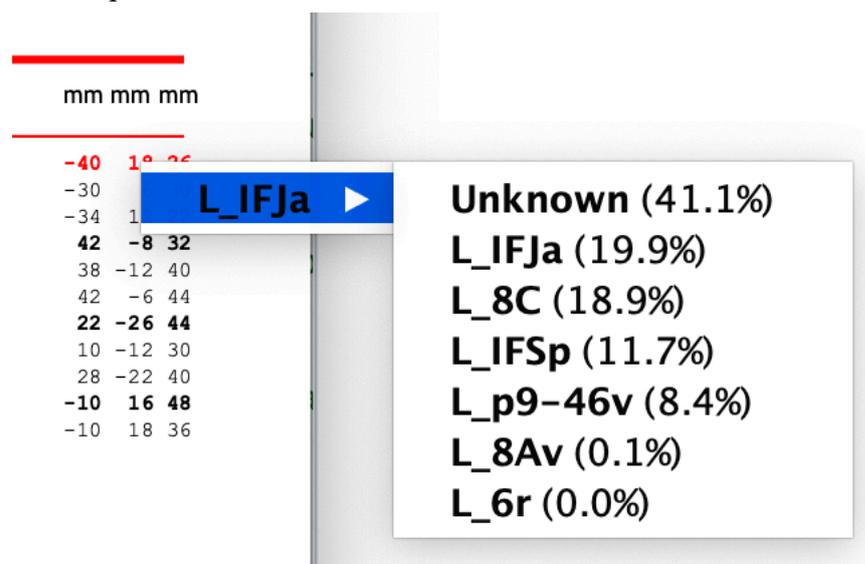


Tutorial for SPM (Results)

1. Copy the HCPex.nii and HCPex.xml into your SPM12/atlas directory
2. Launch SPM12 from the command window in Matlab
 >> spm_fmri
3. Select the desired contrast, mask, probability and extent threshold in the regular “Results”.
4. In the SPM12 Results window: Atlas/ Label using/ HCPex

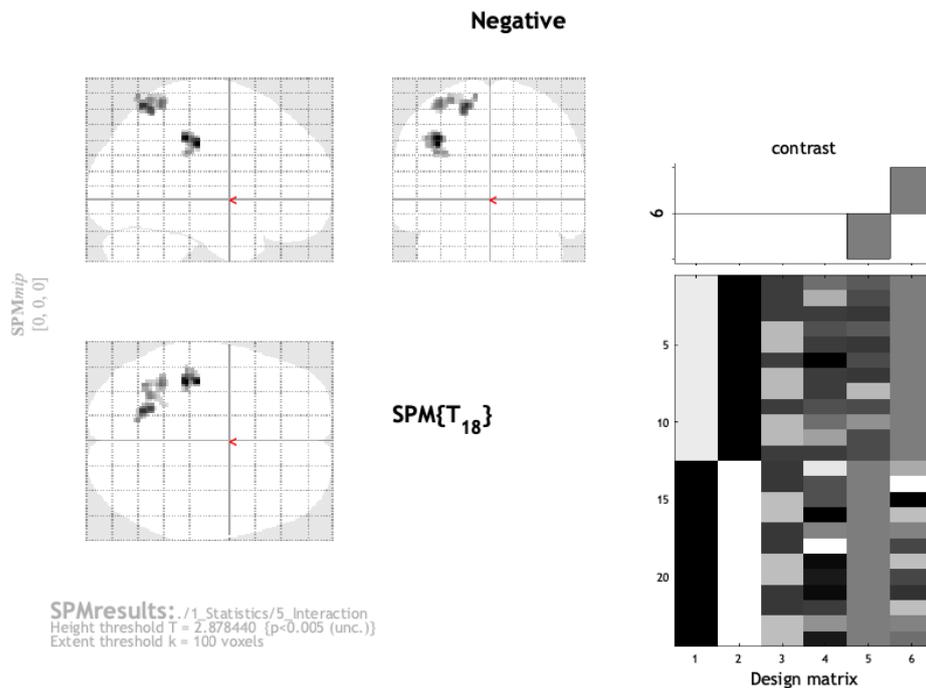


5. You can get the label with a right click on the coordinates in the right of the Graphic window



Tutorial for SPM (with AAL3 software)

- Download AAL3 from the website:
<https://www.oxcns.org/NeuronalNetworkSimulationSoftware.html>
Or
<http://www.gin.cnrs.fr/tools/aal>
- Gunzip and untar the archive will create an AAL3 directory
- Add the extracted directory to your Matlab path
- Launch AAL3 function from the Matlab command window
`>> AAL3`
- Choose a labeling procedure. Three choices are explained and documented in the paper (Tzourio-Mazoyer et al. 2002): Local maxima labeling, Extended local maxima labeling and Cluster labeling. For "Extended local maxima labeling" input the local maxima radius of the sphere in millimeters (default 10 mm).
- Select the desired contrast, mask, probability and extent threshold like in the regular spm Results.
- Select the anatomical parcellation: HCPex_2mm.nii
- Then you get the label on the coordinates in the Graphic window.



Negative

Labels : *volume summary (labels and distances for entire volume)*

x,y,z mm	label	dist mm				
-38 -32 40	Area_2_L	0.00	Anterior_IntraParietal_Area_L	2.00	Area_PFT_L	8.25
-38 -24 36	Area_3a_L	4.47	Area_2_L	4.90	Primary_Sensory_Cortex_L	6.00
-38 -32 30	RetroInsular_Cortex_L	4.00	Area_OP1-SII_L	6.00	Area_PFCm_L	6.32
-18 -62 62	Ventral_IntraParietal_Complex_L	2.00	Medial_Area_7A_L	2.83	Lateral_Area_7P_L	2.83
-36 -30 62	Area_7PC_L	2.00	Area_Lateral_IntraParietal_ventral	18.5	Area_PFM_Complex_L	6.00
-28 -38 66	Ventral_IntraParietal_Complex_L	0.00	Lateral_Area_7A_L	4.47	Area_7PC_L	4.47

Tutorial for the matrix reordering function (HCPexOrdering.m)

1. Load matrix file from the Matlab command window. Here, we provide an example connectivity matrix for demonstration.
Example: > load ExampleMatrix.mat
2. Run the HCPexOrdering.m function from the Matlab command window to reorder the input matrix from the original HCP-MMP ordering to the new HCPex ordering (*forward*).

```
> rMatrix = HCPexOrdering(ExampleMatrix, 1);
```

or

3. Run the HCPexOrdering.m function from the Matlab command window to reorder the input matrix from the new HCPex ordering to the original HCP-MMP ordering (*backward*).

```
> OrigMat = HCPexOrdering(rMatrix, -1);
```

Note: HCPex_LabelID.mat is needed when running the HCPexOrdering.m function (should be placed in the same folder). You can find HCPex ordering (1st column), HCP-MMP1 ordering (2nd column), Region name in two different formats (3rd and 4th column), cortex labels (5th column), and cortex names (6th column) in the HCPex_LabelID.mat file.

Notes for atlas resampling

The current HCPex atlas is established based on the ICBM152 2009c asymmetric template in MNI standard space with the dimensions of 193x229x193 (1mm³ atlas). Although the atlas in 2x2x2mm³ is provided, we noticed that there are many variants of MNI space images found in different studies, especially fMRI, and most of the software handles images with identical resolution and dimension only. In this regard, we would like to suggest a hint for users who want to resample the atlas by themselves.

Taking FSL *flirt* function for example, to resample the HCPex to MNI152 T1 template provided by FSL:

```
flirt -in mni_icbm152_t1_tal_nlin_asym_09c_brain.nii.gz
      -ref MNI152_T1_1mm_brain.nii.gz -omat icbm2fsl.mat -dof 6

flirt -ref MNI152_T1_1mm_brain.nii.gz -in HCPex.nii.gz
      -applyxfm -init icbm2fsl.mat -out HCPex_FSLspace.nii.gz
      -interp nearestneighbour
```

However, resampling is not recommended if you want to keep the useful subcortical regions, such as the thalamic nuclei. The best solution will be using the ICBM152 2009c asymmetric template (Fonov et al. 2011) for normalization in the first place so to keep the small subcortical regions. Moreover, surface-based or diffeomorphic image registration techniques are highly recommended during MNI standard space mapping, so that the feature of gray matter ribbon can be largely preserved.

Note on registration.

To obtain optimal spatial normalization at the individual level, we recommend nonlinear registration using the brain-extracted T1w volume to the brain-extracted ICBM 2009c asymmetrical template in MNI152 space.

References

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