

IIT Human Brain Atlas v.5.0

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Last updated: December 24, 2021

Table of Contents

RESOURCES.....	4
MEAN DTI TEMPLATE FILES	4
MEDIAN DTI TEMPLATE FILES.....	6
HARDI TEMPLATE FILES.....	7
GRAY MATTER ATLAS FILES	7
WHITE MATTER ATLAS FILES.....	10
LABELS FOR THE DESIKAN GRAY MATTER ATLAS.....	14
LABELS FOR THE DESTRIEUX GRAY MATTER ATLAS.....	16
CODES FOR THE WHITE MATTER ATLAS.....	20
LIST OF WHITE MATTER BUNDLES.....	22
<u>HOW TO SPATIALLY NORMALIZE INDIVIDUAL DTI DATA TO THE IIT HUMAN BRAIN ATLAS USING DTI-TK.....</u>	<u>24</u>
<u>HOW TO USE THE IIT HUMAN BRAIN ATLAS IN TBSS.....</u>	<u>31</u>
<u>HOW TO VISUALIZE FIBER ORIENTATION DISTRIBUTION FUNCTIONS OF THE IIT HUMAN BRAIN ATLAS USING MRTRIX.....</u>	<u>35</u>
<u>HOW TO DO HARDI TRACTOGRAPHY ON THE IIT HUMAN BRAIN ATLAS USING MRTRIX</u>	<u>37</u>
<u>HOW TO VISUALIZE THE GRAY MATTER LABELS OF THE IIT HUMAN BRAIN ATLAS USING FSLEYES</u>	<u>39</u>
<u>HOW TO VISUALIZE THE GRAY MATTER LABELS OF THE IIT HUMAN BRAIN ATLAS USING ITK-SNAP....</u>	<u>41</u>
<u>HOW TO INTERPRET THE INFORMATION IN THE IIT WHITE MATTER ATLAS.....</u>	<u>43</u>
<u>HOW TO VISUALIZE THE MOST PROBABLE WHITE MATTER CONNECTION IN EACH VOXEL OF THE IIT HUMAN BRAIN ATLAS USING FSLEYES</u>	<u>46</u>
<u>HOW TO VISUALIZE THE MOST PROBABLE WHITE MATTER CONNECTION IN EACH VOXEL OF THE IIT HUMAN BRAIN ATLAS USING ITK-SNAP</u>	<u>49</u>
<u>HOW TO USE THE IIT HUMAN BRAIN ATLAS TO EXTRACT INFORMATION ABOUT THE CONNECTIVITY OF A GRAY MATTER LABEL A TO ANOTHER GRAY MATTER LABEL B</u>	<u>52</u>
<u>REGIONCONNECT: HOW TO USE THE IIT HUMAN BRAIN ATLAS TO FIND OUT WHICH PAIRS OF GRAY MATTER LABELS HAVE CONNECTIONS THROUGH A USER-DEFINED WHITE MATTER REGION OF INTEREST (ROI).....</u>	<u>54</u>

HOW TO CONDUCT ROI-BASED ANALYSES IN WHITE MATTER USING THE IIT HUMAN BRAIN ATLAS...57

HOW TO USE THE SKELETONIZED VERSION OF THE IIT WHITE MATTER ATLAS.....59

Resources

- Summary: The IIT Human Brain Atlas contains anatomical, DTI, and HARDI templates, probabilistic gray matter labels, probabilistic connectivity-based white matter labels and files containing information about the quality of the templates. In addition, files that make the IIT Human Brain Atlas directly compatible with common neuroimaging tools such as FSL, TBSS, DTI-TK, ITK-SNAP, MRtrix etc. are provided.
- Matrix size: All files are available in two matrix sizes: 182x218x182 and 256x256x256. The spatial resolution is the same in both versions. The 256x256x256 is simply a zero-padded version of the 182x218x182 (the units for some of the files are different between versions; see details below). The origin of the 256x256x256 files is set to (0,0,0). The orientation of the 182x218x182 files is RPI and that of the 256x256x256 files is LPI.
- Space: The IIT Human Brain Atlas is in ICBM-152 space. More specifically, in FSL, the 182x218x182 files of the atlas are in MNI152, or MNI152_T1_1mm space.
- Naming: All files listed below are in 182x218x182 matrix size. The corresponding files in 256x256x256 matrix size are named the same way as the files in native matrix size with a “_256” suffix. For example, the FA volume of the mean DTI template in 182x218x182 matrix size is called “IITmean_FA.nii”, and the same FA volume in 256x256x256 matrix size is called “IITmean_FA_256.nii”. The *_256.nii files are not discussed separately in this document because they have the same contents as the corresponding files listed below.

Mean DTI template files

- | | |
|----------------------------|---|
| - IITmean_b0.nii: | Average of the normalized $b=0$ sec/mm ² (mean T2-weighted) images over all subjects. |
| - IITmean_colormap.tif: | FA-weighted orientation color maps produced from the tensors of the mean DTI template. |
| - IITmean_cou.nii: | Cone of uncertainty for the mean DTI template. (Produced based on 100 mean tensor templates generated with a bootstrap approach). (Units: degrees). |
| - IITmean_dw.nii: | Average normalized mean DW images over all subjects. |
| - IITmean_FA.nii: | FA maps produced from the tensors of the mean DTI template. |
| - IITmean_FA_skeleton.nii: | White matter skeleton derived from IITmean_FA.nii, for use with TBSS. This skeleton was thresholded at $FA > 0.25$. |

- IITmean_fastd.nii: Standard deviation of FA of the mean DTI template. (Produced based on 100 mean tensor templates generated with a bootstrap approach).
- IITmean_L(1,2,3).nii: 1st, 2nd, and 3rd eigenvalues of the mean DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmean_lower_cingulum.nii: Mask of the inferior portion of the cingulum corresponding to IITmean_FA.nii, for use with TBSS.
- IITmean_tensor.nii: Full tensors of the mean DTI template. The matrix size of this file is 182x218x182x6. (Units: mm²/sec). (The 256x256x256x6 version is compatible with DTI-TK and has Units: 10⁻³ mm²/sec).
- IITmean_tensor_mask_256.nii: Binary mask corresponding to the tensor file of the mean DTI template "IITmean_tensor_256.nii", for use in the non-linear registration step of DTI-TK.
- IITmean_tr.nii: Trace maps produced from the tensors of the mean DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmean_trstd.nii: Standard deviation of trace of the mean DTI template. (Produced based on 100 mean tensor templates generated with a bootstrap approach). (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmean_tvdt_scl.nii: Total variance of the diffusion tensor of the mean DTI template. (Produced based on 100 mean tensor templates generated with a bootstrap approach). (Units: 10⁻⁸(mm²/sec)²).
- IITmean_V(1,2,3).nii: 1st, 2nd, and 3rd eigenvectors of the mean DTI template. The dimensions of the three eigenvector files are 182x218x182x3. (For the 256x256x256 version of the atlas, the dimensions of the three eigenvector files are 256x256x256x3).
- IITmean_(xx,yx,yy,zx,zy,zz).nii: The xx, yx, yy, zx, zy, zz tensor elements of the mean DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- tbss_3_postreg_iit(_256): Script allowing use of the IIT Human Brain Atlas in TBSS. More specifically, this script applies the nonlinear transformations.
- tbss_4_prestats_iit(_256): Script allowing use of the IIT Human Brain Atlas in TBSS. More specifically, this script completes the final steps before statistical analysis.

- tbss_non_FA_iit(_256): Script allowing use of the IIT Human Brain Atlas in TBSS. More specifically, this script applies the nonlinear transformations and projection parameters to non-FA data.

Median DTI template files

- IITmedian_colormap.tif: FA-weighted orientation color maps produced from the tensors of the median DTI template.
- IITmedian_cou.nii: Cone of uncertainty for the median DTI template. (Produced based on 100 median tensor templates generated with a bootstrap approach). (Units: degrees).
- IITmedian_FA.nii: FA maps produced from the tensors of the median DTI template.
- IITmedian_fastd.nii: Standard deviation of FA of the median DTI template. (Produced based on 100 median tensor templates generated with a bootstrap approach).
- IITmedian_L(1,2,3).nii: 1st, 2nd, and 3rd eigenvalues of the median DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmedian_tr.nii: Trace maps produced from the tensors of the median DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmedian_trstd.nii: Standard deviation of trace of the median DTI template. (Produced based on 100 median tensor templates generated with a bootstrap approach). (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).
- IITmedian_tvdt_scl.nii: Total variance of the diffusion tensor of the median DTI template. (Produced based on 100 median tensor templates generated with a bootstrap approach). (Units: 10⁻⁸(mm²/sec)²).
- IITmedian_V(1,2,3).nii: 1st, 2nd, and 3rd eigenvectors of the median DTI template. The dimensions of the three eigenvector files are 182x218x182x3. (For the 256x256x256 version of the atlas, the dimensions of the three eigenvector files are 256x256x256x3).
- IITmedian_(xx,yx,yy,zx,zy,zz).nii: The xx, yx, yy, zx, zy, zz tensor elements of the median DTI template. (Units: mm²/sec). (For the 256x256x256 version, Units: 10⁻³ mm²/sec).

HARDI template files

- IIT_HARDI.nii: Spherical harmonic (SH) coefficients representing the fiber orientation distribution (FOD) function (produced using constrained spherical deconvolution with $l=6$). The dimensions of the file are 182x218x182x28. (For the 256x256x256 version of the atlas, the dimensions of the file are 256x256x256x28). Each of the 28 volumes corresponds to a single spherical harmonic component, in the following order:
 - [1] $Y(0,0)$
 - [2] $\text{Im}\{Y(2,2)\}$
 - [3] $\text{Im}\{Y(2,1)\}$
 - [4] $Y(2,0)$
 - [5] $\text{Re}\{Y(2,1)\}$
 - [6] $\text{Re}\{Y(2,2)\}$
 - [7] $\text{Im}\{Y(4,4)\}$
 - [8] $\text{Im}\{Y(4,3)\}$ etc.(Note: SH coefficients are stored in a format compatible with the MRtrix toolbox, i.e. the $(-1)^m$ factor in SH basis was omitted).

- IIT_GFA.nii: Generalized FA maps produced from the spherical harmonic coefficients of the HARDI template.

- IIT_correlation.nii: Maps of the average correlation of neighboring FODs (6 neighbors) of the HARDI template. FOD correlation was defined in: "Anderson, A.W., 2005. Measurement of fiber orientation distributions using high angular resolution diffusion imaging. *Magn Reson Med* 54, 1194-1206".

Gray matter atlas files

- IIT_(CSF,GM,WM)_tissue_prob.nii: Probability maps for cerebrospinal fluid (CSF), gray matter (GM), white matter (WM).

- IITmean_t1.nii: Mean T1-weighted template.

- IITstd_t1.nii: Standard deviation of the T1-weighted template.

- IITcv_t1.nii: Coefficient of variation of the T1-weighted template.

- IIT_GM_Desikan_atlas.nii: 84 GM labels of the IIT Human Brain Atlas. (Based on the Desikan atlas, Neuroimage 2006;31:968-980). See [“Labels for the Desikan Gray Matter atlas”](#) below.
- IIT_GM_Desikan_confidence.nii: Confidence index map for the Desikan GM labels.
- IIT_GM_Desikan_mask.nii: GM mask corresponding to the IIT Human Brain Atlas with the Desikan labels.
- IIT_GM_Desikan_prob.nii: Maps of the probability that a GM voxel belongs to a GM label, for each Desikan GM label separately (thus this file contains 84 volumes, one for each label). The dimensions of this file are 182x218x182x84. (For the 256x256x256 version of the atlas, the dimensions of this file are 256x256x256x84). The order of the 84 GM labels in this file is shown in the [“Labels for the Desikan Gray Matter atlas”](#) section below (1st column). When opened in FSL, the "volume" index in FSL corresponds to the "order" shown in the [“Labels for the Desikan Gray Matter atlas”](#) section below. NOTE: DO NOT UNZIP THIS FILE WITHOUT ENOUGH SPACE (~2.5GB) IN THE TARGET DIRECTORY; IF YOU HAVE TROUBLE VIEWING THIS FILE IN FSLVIEW DUE TO ITS LARGE SIZE, YOU CAN OPEN THE INDIVIDUAL PROBABILITY MAPS FOR EACH LABEL AS DESCRIBED NEXT.
- label_probabilities_Desikan.zip: This zipped directory contains individual maps of the probability that a GM voxel belongs to a Desikan GM label. There is one file per label, named label-(labelID).nii. This is the same information as in the IIT_GM_Desikan_prob.nii file above, but divided into 84 files, one for each GM label. The dimensions of each file are 182x218x182. (For the 256x256x256 version of the atlas, the dimensions of each file are 256x256x256). The files are named using the labelID listed in the [“Labels for the Desikan Gray Matter atlas”](#) section below.
- LUT_GM_Desikan_0to255.txt: Text file containing an appropriate look-up table that allows visualization of all gray matter labels of the atlas in color in ITK-SNAP. This look-up table should be used in conjunction with the IIT_GM_Desikan_atlas.nii.
- LUT_GM_Desikan_0to1.txt: Text file containing an appropriate look-up table that allows visualization of all gray matter labels of the atlas in color in FSLeyes. This look-up table should be used in conjunction with the IIT_GM_Desikan_atlas.nii.
- IIT_GM_Destrieux_atlas.nii: 164 GM labels of the IIT Human Brain Atlas. (Based on the Destrieux atlas, Neuroimage 2010;53:1-15). See [“Labels for the Destrieux Gray Matter atlas”](#) below.

- IIT_GM_Destrieux_confidence.nii: Confidence index map for the Destrieux GM labels.

- IIT_GM_Destrieux_mask.nii: GM mask corresponding to the IIT Human Brain Atlas with the Destrieux labels.

- IIT_GM_Destrieux_prob.nii: Maps of the probability that a GM voxel belongs to a GM label, for each Destrieux GM label separately (thus this file contains 164 volumes, one for each label). The dimensions of this file are 182x218x182x164. (For the 256x256x256 version of the atlas, the dimensions of this file are 256x256x256x164). The order of the 164 GM labels in this file is shown in the "[Labels for the Destrieux Gray Matter atlas](#)" section below (1st column). When opened in FSL, the "volume" index in FSL corresponds to the "order" shown in the "[Labels for the Destrieux Gray Matter atlas](#)" section below. NOTE: DO NOT UNZIP THIS FILE WITHOUT ENOUGH SPACE (~4GB) IN THE TARGET DIRECTORY; IF YOU HAVE TROUBLE VIEWING THIS FILE IN FSLVIEW DUE TO ITS LARGE SIZE, YOU CAN OPEN THE INDIVIDUAL PROBABILITY MAPS FOR EACH LABEL AS DESCRIBED NEXT.

- label_probabilities_Destrieux.zip: This zipped directory contains individual maps of the probability that a GM voxel belongs to a Destrieux GM label. There is one file per label, named label-(labelID).nii. This is the same information as in the IIT_GM_Destrieux_prob.nii file above, but divided into 164 files, one for each GM label. The dimensions of each file are 182x218x182. (For the 256x256x256 version of the atlas, the dimensions of each file are 256x256x256). The files are named using the labelID listed in the "[Labels for the Destrieux Gray Matter atlas](#)" section below.

- LUT_GM_Destrieux_0to255.txt: Text file containing an appropriate look-up table that allows visualization of all gray matter labels of the atlas in color in ITK-SNAP. This look-up table should be used in conjunction with the IIT_GM_Destrieux_atlas.nii.

- LUT_GM_Destrieux_0to1.txt: Text file containing an appropriate look-up table that allows visualization of all gray matter labels of the atlas in color in FSLeyes. This look-up table should be used in conjunction with the IIT_GM_Destrieux_atlas.nii.

White matter atlas files

- IIT_WM_atlas.nii: 4D white matter labels of the IIT Human Brain Atlas (based on tractography on the HARDI template and connectivity of pairs of gray matter Desikan labels). This file contains 60 3D volumes, and for each WM voxel it provides a list of the top 60 most probable fiber connections passing through that voxel (in descending confidence order). These connections are between pairs of gray matter labels. The 60 values corresponding to each WM voxel in this file represent the “names” of the most probable connections. These “names” are defined as follows:
name = $GM1 \times 100 + GM2$, where GM1 and GM2 are codes assigned to the two gray matter labels (see list of [Codes for the white matter atlas](#)).
Example #1: if the code for GM1 = 4 and for GM2 = 9, then the “name” for the connection between GM1 and GM2 is 409.
Example #2: if the code for GM1 = 7 and for GM2 = 35, then the “name” for the connection between GM1 and GM2 is 735.
The dimensions of the file are 182x218x182x60. The confidence index corresponding to each connection is included in the IIT_WM_atlas_confidence file (which shares the same architecture).
- IIT_WM_atlas_60_top_layers.zip: This folder contains the same information as the IIT_WM_atlas.nii file split in 60 separate 3D volumes named IIT_WM_atlas_I1.nii, IIT_WM_atlas_I2.nii, ..., IIT_WM_atlas_I60.nii.
- IIT_WM_atlas_skeletonized.nii: Skeletonized version of the IIT_WM_atlas.nii.
- IIT_WM_atlas_60_top_layers_skeletonized.zip: This folder contains the same information as the IIT_WM_atlas_skeletonized.nii file split in 60 separate 3D volumes named IIT_WM_atlas_I1_skeletonized.nii, IIT_WM_atlas_I2_skeletonized.nii, ..., IIT_WM_atlas_I60_skeletonized.nii.
- IIT_WM_atlas_confidence.nii: 4D confidence index corresponding to the white matter labels of the IIT Human Brain Atlas (IIT_WM_atlas.nii). This file contains 60 3D volumes, and for each WM voxel it provides the confidence index for the top 60 most probable fiber connections passing through that voxel (in descending confidence order) (these connections

are between pairs of gray matter labels). In each voxel, the confidence corresponding to a certain connection is defined as the ratio of the number of streamlines that go through that voxel and belong to that connection divided by the total number of streamlines going through that voxel. This file does not contain the names of the connections. The names of the connections can be found in the IIT_WM_atlas.nii file. The dimensions of the file are 182x218x182x60.

- IIT_WM_atlas_confidence_60_top_layers.zip: This folder contains the same information as the IIT_WM_atlas_confidence.nii file split in 60 separate 3D volumes named IIT_WM_atlas_confidence_l1.nii, IIT_WM_atlas_confidence_l2.nii, ..., IIT_WM_atlas_confidence_l60.nii.
- IIT_WM_atlas_confidence_skeletonized.nii: Skeletonized version of the IIT_WM_atlas_confidence.nii file.
- IIT_WM_atlas_confidence_60_top_layers_skeletonized.zip: This folder contains the same information as the IIT_WM_atlas_confidence_skeletonized.nii file split in 60 separate 3D volumes named IIT_WM_atlas_confidence_l1_skeletonized.nii, IIT_WM_atlas_confidence_l2_skeletonized.nii, ..., IIT_WM_atlas_confidence_l60_skeletonized.nii.
- IIT_TDI.zip: This zipped directory contains individual track density (TDI) maps for all possible pairs of GM labels. There is one file per pair of GM labels, named: label(code of GM1)_(code of GM2).nii. For example, "label41_4.nii" is a TDI map of connectivity between left amygdala (code 41) and left cuneus (code 4). For the full list of GM codes see the "[Codes for the white matter atlas](#)".
- IIT_TDI_sum.nii: A sum of TDI maps of all possible pairs of GM labels.
- IIT_TDI_sum_skeletonized.nii: Skeletonized version of the IIT_TDI_sum.nii file.
- IIT_WM_atlas_length.nii: 4D file containing the average length of the fiber connections corresponding to the white matter labels of the IIT Human Brain Atlas (IIT_WM_atlas.nii). This file contains 60 3D volumes, and for each WM voxel it provides the average length for the top 60 most probable fiber connections passing through that voxel (in

descending confidence order). The names of the connections can be found in the IIT_WM_atlas.nii file. The dimensions of the file are 182x218x182x60.

- IIT_connectivity_matrix.txt:

Connectivity matrix of the IIT Human Brain Atlas connectome. The connectivity matrix is based on tractography on the HARDI template and connectivity of pairs of gray matter Desikan labels. Each row corresponds to a seed GM label and each column to a target GM label. Each element of the connectivity matrix contains the number of streamlines that originated from the seed gray matter label (row) and terminated in the target gray matter label (column). The matrix is symmetric. The order of GM labels in the matrix is the same as that in the table of [“Codes for the white matter atlas”](#).

- regionconnect.py:

This python script provides a list of pairs of GM labels that have connections through a user-defined white matter ROI, along with the probabilities that fibers passing through the ROI belong to these connections. Details on how to use this script can be found in the [“regionconnect: How to use the IIT Human Brain Atlas to find out which pairs of gray matter labels have connections through a user-defined white matter region of interest \(ROI\)”](#) chapter.

- IIT_bundles.zip:

This directory contains track density images for 42 fiber bundles. The full list of bundles is shown in the [“List of white matter bundles”](#) below. Bundles were segmented using RecoBundles (Neuroimage 2018;170:283-295). The recommended thresholds for generating masks of the bundles are also provided in the [“List of white matter bundles”](#) below.

- IIT_bundles_skeletonized.zip:

Skeletonized version of the IIT_bundles files.

- LUT_WM_0to255.txt:

Text file containing an appropriate look-up table that allows visualization of the most probable white matter connection in each voxel of the atlas in color in ITK-SNAP. This look-up table should be used in conjunction with the IIT_WM_atlas_I1.nii file included in IIT_WM_atlas_60_top_layers.zip. (Note that this look-up table may not be appropriate for visualization of the 2nd, 3rd, ..., 60th most probable connections).

- LUT_WM_0to1.txt: Text file containing an appropriate look-up table that allows visualization of the most probable white matter connection in each voxel of the atlas in color in FSLEyes. This look-up table should be used in conjunction with the IIT_WM_atlas_I1.nii file included in IIT_WM_atlas_60_top_layers.zip. (Note that this look-up table may not be appropriate for visualization of the 2nd, 3rd, ..., 60th most probable connections).
- LUT_Connectome_Nodes.txt: Text file containing an appropriate look-up table for the GM labels used to generate the WM connectivity matrix.
- IIT_HARDI_tractogram_256.tck: The whole brain tractogram in “.tck” format generated by MRtrix3. This file exists only in the 256x256x256 matrix size.
- IIT_fornix_fixed_5tt_file_for_ACT_tractography.nii: Tissue probability maps with manually edited fornix. This image can be used for Anatomically-Constrained Tractography.

Labels for the Desikan Gray Matter atlas

(Neuroimage 2006;31:968-980)

IMPORTANT NOTE: The following information should be used in combination with the IIT GRAY matter Desikan atlas only. If you are using the IIT gray matter Destrieux atlas, OR the IIT white matter atlas, scroll down to the next two lists.

order	labelID	label-name
0	8	Left-Cerebellum-Cortex
1	47	Right-Cerebellum-Cortex
2	10	Left-Thalamus-Proper
3	49	Right-Thalamus-Proper
4	11	Left-Caudate
5	50	Right-Caudate
6	12	Left-Putamen
7	51	Right-Putamen
8	13	Left-Pallidum
9	52	Right-Pallidum
10	17	Left-Hippocampus
11	53	Right-Hippocampus
12	18	Left-Amygdala
13	54	Right-Amygdala
14	26	Left-Accumbens-area
15	58	Right-Accumbens-area
16	1001	ctx-lh-bankssts
17	2001	ctx-rh-bankssts
18	1002	ctx-lh-caudalanteriorcingulate
19	2002	ctx-rh-caudalanteriorcingulate
20	1003	ctx-lh-caudalmiddlefrontal
21	2003	ctx-rh-caudalmiddlefrontal
22	1005	ctx-lh-cuneus
23	2005	ctx-rh-cuneus
24	1006	ctx-lh-entorhinal
25	2006	ctx-rh-entorhinal
26	1007	ctx-lh-fusiform
27	2007	ctx-rh-fusiform
28	1008	ctx-lh-inferiorparietal
29	2008	ctx-rh-inferiorparietal
30	1009	ctx-lh-inferiortemporal
31	2009	ctx-rh-inferiortemporal
32	1010	ctx-lh-isthmuscingulate
33	2010	ctx-rh-isthmuscingulate
34	1011	ctx-lh-lateraloccipital
35	2011	ctx-rh-lateraloccipital
36	1012	ctx-lh-lateralorbitofrontal
37	2012	ctx-rh-lateralorbitofrontal
38	1013	ctx-lh-lingual
39	2013	ctx-rh-lingual
40	1014	ctx-lh-medialorbitofrontal
41	2014	ctx-rh-medialorbitofrontal

42	1015	ctx-lh-middletemporal
43	2015	ctx-rh-middletemporal
44	1016	ctx-lh-parahippocampal
45	2016	ctx-rh-parahippocampal
46	1017	ctx-lh-paracentral
47	2017	ctx-rh-paracentral
48	1018	ctx-lh-parsopercularis
49	2018	ctx-rh-parsopercularis
50	1019	ctx-lh-parsorbitalis
51	2019	ctx-rh-parsorbitalis
52	1020	ctx-lh-parstriangularis
53	2020	ctx-rh-parstriangularis
54	1021	ctx-lh-pericalcarine
55	2021	ctx-rh-pericalcarine
56	1022	ctx-lh-postcentral
57	2022	ctx-rh-postcentral
58	1023	ctx-lh-posteriorcingulate
59	2023	ctx-rh-posteriorcingulate
60	1024	ctx-lh-precentral
61	2024	ctx-rh-precentral
62	1025	ctx-lh-precuneus
63	2025	ctx-rh-precuneus
64	1026	ctx-lh-rostralanteriorcingulate
65	2026	ctx-rh-rostralanteriorcingulate
66	1027	ctx-lh-rostralmiddlefrontal
67	2027	ctx-rh-rostralmiddlefrontal
68	1028	ctx-lh-superiorfrontal
69	2028	ctx-rh-superiorfrontal
70	1029	ctx-lh-superiorparietal
71	2029	ctx-rh-superiorparietal
72	1030	ctx-lh-superiortemporal
73	2030	ctx-rh-superiortemporal
74	1031	ctx-lh-supramarginal
75	2031	ctx-rh-supramarginal
76	1032	ctx-lh-frontalpole
77	2032	ctx-rh-frontalpole
78	1033	ctx-lh-temporalpole
79	2033	ctx-rh-temporalpole
80	1034	ctx-lh-transversetemporal
81	2034	ctx-rh-transversetemporal
82	1035	ctx-lh-insula
83	2035	ctx-rh-insula

Labels for the Destrieux Gray Matter atlas

(Neuroimage 2010;53:1-15)

IMPORTANT NOTE: The following information should be used in combination with the IIT GRAY matter Destrieux atlas only. If you are using the IIT gray matter Desikan atlas, scroll up to the previous list. If you are using the IIT white matter atlas, scroll down to the next list.

order	labelID	label-name
0	8	Left-Cerebellum-Cortex
1	47	Right-Cerebellum-Cortex
2	10	Left-Thalamus-Proper
3	49	Right-Thalamus-Proper
4	11	Left-Caudate
5	50	Right-Caudate
6	12	Left-Putamen
7	51	Right-Putamen
8	13	Left-Pallidum
9	52	Right-Pallidum
10	17	Left-Hippocampus
11	53	Right-Hippocampus
12	18	Left-Amygdala
13	54	Right-Amygdala
14	26	Left-Accumbens-area
15	58	Right-Accumbens-area
16	11101	ctx_lh_G_and_S_frontomargin
17	12101	ctx_rh_G_and_S_frontomargin
18	11102	ctx_lh_G_and_S_occipital_inf
19	12102	ctx_rh_G_and_S_occipital_inf
20	11103	ctx_lh_G_and_S_paracentral
21	12103	ctx_rh_G_and_S_paracentral
22	11104	ctx_lh_G_and_S_subcentral
23	12104	ctx_rh_G_and_S_subcentral
24	11105	ctx_lh_G_and_S_transv_frontopol
25	12105	ctx_rh_G_and_S_transv_frontopol
26	11106	ctx_lh_G_and_S_cingul-Ant
27	12106	ctx_rh_G_and_S_cingul-Ant
28	11107	ctx_lh_G_and_S_cingul-Mid-Ant
29	12107	ctx_rh_G_and_S_cingul-Mid-Ant
30	11108	ctx_lh_G_and_S_cingul-Mid-Post
31	12108	ctx_rh_G_and_S_cingul-Mid-Post
32	11109	ctx_lh_G_cingul-Post-dorsal
33	12109	ctx_rh_G_cingul-Post-dorsal
34	11110	ctx_lh_G_cingul-Post-ventral
35	12110	ctx_rh_G_cingul-Post-ventral
36	11111	ctx_lh_G_cuneus
37	12111	ctx_rh_G_cuneus
38	11112	ctx_lh_G_front_inf-Opercular
39	12112	ctx_rh_G_front_inf-Opercular
40	11113	ctx_lh_G_front_inf-Orbital
41	12113	ctx_rh_G_front_inf-Orbital

42 11114 ctx_lh_G_front_inf-Triangul
43 12114 ctx_rh_G_front_inf-Triangul
44 11115 ctx_lh_G_front_middle
45 12115 ctx_rh_G_front_middle
46 11116 ctx_lh_G_front_sup
47 12116 ctx_rh_G_front_sup
48 11117 ctx_lh_G_Ins_lg_and_S_cent_ins
49 12117 ctx_rh_G_Ins_lg_and_S_cent_ins
50 11118 ctx_lh_G_insular_short
51 12118 ctx_rh_G_insular_short
52 11119 ctx_lh_G_occipital_middle
53 12119 ctx_rh_G_occipital_middle
54 11120 ctx_lh_G_occipital_sup
55 12120 ctx_rh_G_occipital_sup
56 11121 ctx_lh_G_oc-temp_lat-fusifor
57 12121 ctx_rh_G_oc-temp_lat-fusifor
58 11122 ctx_lh_G_oc-temp_med-Lingual
59 12122 ctx_rh_G_oc-temp_med-Lingual
60 11123 ctx_lh_G_oc-temp_med-Parahip
61 12123 ctx_rh_G_oc-temp_med-Parahip
62 11124 ctx_lh_G_orbital
63 12124 ctx_rh_G_orbital
64 11125 ctx_lh_G_pariet_inf-Angular
65 12125 ctx_rh_G_pariet_inf-Angular
66 11126 ctx_lh_G_pariet_inf-Supramar
67 12126 ctx_rh_G_pariet_inf-Supramar
68 11127 ctx_lh_G_parietal_sup
69 12127 ctx_rh_G_parietal_sup
70 11128 ctx_lh_G_postcentral
71 12128 ctx_rh_G_postcentral
72 11129 ctx_lh_G_precentral
73 12129 ctx_rh_G_precentral
74 11130 ctx_lh_G_precuneus
75 12130 ctx_rh_G_precuneus
76 11131 ctx_lh_G_rectus
77 12131 ctx_rh_G_rectus
78 11132 ctx_lh_G_subcallosal
79 12132 ctx_rh_G_subcallosal
80 11133 ctx_lh_G_temp_sup-G_T_transv
81 12133 ctx_rh_G_temp_sup-G_T_transv
82 11134 ctx_lh_G_temp_sup-Lateral
83 12134 ctx_rh_G_temp_sup-Lateral
84 11135 ctx_lh_G_temp_sup-Plan_polar
85 12135 ctx_rh_G_temp_sup-Plan_polar
86 11136 ctx_lh_G_temp_sup-Plan_tempo
87 12136 ctx_rh_G_temp_sup-Plan_tempo
88 11137 ctx_lh_G_temporal_inf
89 12137 ctx_rh_G_temporal_inf
90 11138 ctx_lh_G_temporal_middle
91 12138 ctx_rh_G_temporal_middle
92 11139 ctx_lh_Lat_Fis-ant-Horizont

93 12139 ctx_rh_Lat_Fis-ant-Horizont
 94 11140 ctx_lh_Lat_Fis-ant-Vertical
 95 12140 ctx_rh_Lat_Fis-ant-Vertical
 96 11141 ctx_lh_Lat_Fis-post
 97 12141 ctx_rh_Lat_Fis-post
 98 11143 ctx_lh_Pole_occipital
 99 12143 ctx_rh_Pole_occipital
 100 11144 ctx_lh_Pole_temporal
 101 12144 ctx_rh_Pole_temporal
 102 11145 ctx_lh_S_calcarine
 103 12145 ctx_rh_S_calcarine
 104 11146 ctx_lh_S_central
 105 12146 ctx_rh_S_central
 106 11147 ctx_lh_S_cingul-Marginalis
 107 12147 ctx_rh_S_cingul-Marginalis
 108 11148 ctx_lh_S_circular_insula_ant
 109 12148 ctx_rh_S_circular_insula_ant
 110 11149 ctx_lh_S_circular_insula_inf
 111 12149 ctx_rh_S_circular_insula_inf
 112 11150 ctx_lh_S_circular_insula_sup
 113 12150 ctx_rh_S_circular_insula_sup
 114 11151 ctx_lh_S_collat_transv_ant
 115 12151 ctx_rh_S_collat_transv_ant
 116 11152 ctx_lh_S_collat_transv_post
 117 12152 ctx_rh_S_collat_transv_post
 118 11153 ctx_lh_S_front_inf
 119 12153 ctx_rh_S_front_inf
 120 11154 ctx_lh_S_front_middle
 121 12154 ctx_rh_S_front_middle
 122 11155 ctx_lh_S_front_sup
 123 12155 ctx_rh_S_front_sup
 124 11156 ctx_lh_S_interm_prim-Jensen
 125 12156 ctx_rh_S_interm_prim-Jensen
 126 11157 ctx_lh_S_intrapariet_and_P_tran
 127 12157 ctx_rh_S_intrapariet_and_P_tran
 128 11158 ctx_lh_S_oc_middle_and_Lunatus
 129 12158 ctx_rh_S_oc_middle_and_Lunatus
 130 11159 ctx_lh_S_oc_sup_and_transversal
 131 12159 ctx_rh_S_oc_sup_and_transversal
 132 11160 ctx_lh_S_occipital_ant
 133 12160 ctx_rh_S_occipital_ant
 134 11161 ctx_lh_S_oc-temp_lat
 135 12161 ctx_rh_S_oc-temp_lat
 136 11162 ctx_lh_S_oc-temp_med_and_Lingual
 137 12162 ctx_rh_S_oc-temp_med_and_Lingual
 138 11163 ctx_lh_S_orbital_lateral
 139 12163 ctx_rh_S_orbital_lateral
 140 11164 ctx_lh_S_orbital_med-olfact
 141 12164 ctx_rh_S_orbital_med-olfact
 142 11165 ctx_lh_S_orbital-H_Shaped
 143 12165 ctx_rh_S_orbital-H_Shaped

144 11166 ctx_lh_S_parieto_occipital
145 12166 ctx_rh_S_parieto_occipital
146 11167 ctx_lh_S_pericallosal
147 12167 ctx_rh_S_pericallosal
148 11168 ctx_lh_S_postcentral
149 12168 ctx_rh_S_postcentral
150 11169 ctx_lh_S_precentral-inf-part
151 12169 ctx_rh_S_precentral-inf-part
152 11170 ctx_lh_S_precentral-sup-part
153 12170 ctx_rh_S_precentral-sup-part
154 11171 ctx_lh_S_suborbital
155 12171 ctx_rh_S_suborbital
156 11172 ctx_lh_S_subparietal
157 12172 ctx_rh_S_subparietal
158 11173 ctx_lh_S_temporal_inf
159 12173 ctx_rh_S_temporal_inf
160 11174 ctx_lh_S_temporal_sup
161 12174 ctx_rh_S_temporal_sup
162 11175 ctx_lh_S_temporal_transverse
163 12175 ctx_rh_S_temporal_transverse

Codes for the White Matter atlas

IMPORTANT NOTE: The following information should be used in combination with the IIT WHITE matter atlas only. If you are using the IIT gray matter Desikan atlas, OR the IIT gray matter Destrieux atlas, scroll up to the previous two lists.

code	label-name
1	ctx-lh-bankssts
2	ctx-lh-caudalanteriorcingulate
3	ctx-lh-caudalmiddlefrontal
4	ctx-lh-cuneus
5	ctx-lh-entorhinal
6	ctx-lh-fusiform
7	ctx-lh-inferiorparietal
8	ctx-lh-inferiortemporal
9	ctx-lh-isthmuscingulate
10	ctx-lh-lateraloccipital
11	ctx-lh-lateralorbitofrontal
12	ctx-lh-lingual
13	ctx-lh-medialorbitofrontal
14	ctx-lh-middletemporal
15	ctx-lh-parahippocampal
16	ctx-lh-paracentral
17	ctx-lh-parsopercularis
18	ctx-lh-parsorbitalis
19	ctx-lh-parstriangularis
20	ctx-lh-pericalcarine
21	ctx-lh-postcentral
22	ctx-lh-posteriorcingulate
23	ctx-lh-precentral
24	ctx-lh-precuneus
25	ctx-lh-rostralanteriorcingulate
26	ctx-lh-rostralmiddlefrontal
27	ctx-lh-superiorfrontal
28	ctx-lh-superiorparietal
29	ctx-lh-superiortemporal
30	ctx-lh-supramarginal
31	ctx-lh-frontalpole
32	ctx-lh-temporalpole
33	ctx-lh-transversetemporal
34	ctx-lh-insula
35	Left-Cerebellum-Cortex
36	Left-Thalamus-Proper
37	Left-Caudate
38	Left-Putamen
39	Left-Pallidum
40	Left-Hippocampus
41	Left-Amygdala
42	Left-Accumbens-area
43	Right-Thalamus-Proper

44 Right-Caudate
45 Right-Putamen
46 Right-Pallidum
47 Right-Hippocampus
48 Right-Amygdala
49 Right-Accumbens-area
50 ctx-rh-bankssts
51 ctx-rh-caudalanteriorcingulate
52 ctx-rh-caudalmiddlefrontal
53 ctx-rh-cuneus
54 ctx-rh-entorhinal
55 ctx-rh-fusiform
56 ctx-rh-inferiorparietal
57 ctx-rh-inferiortemporal
58 ctx-rh-isthmuscingulate
59 ctx-rh-lateraloccipital
60 ctx-rh-lateralorbitofrontal
61 ctx-rh-lingual
62 ctx-rh-medialorbitofrontal
63 ctx-rh-middletemporal
64 ctx-rh-parahippocampal
65 ctx-rh-paracentral
66 ctx-rh-parsopercularis
67 ctx-rh-parsorbitalis
68 ctx-rh-parstriangularis
69 ctx-rh-pericalcarine
70 ctx-rh-postcentral
71 ctx-rh-posteriorcingulate
72 ctx-rh-precentral
73 ctx-rh-precuneus
74 ctx-rh-rostralanteriorcingulate
75 ctx-rh-rostralmiddlefrontal
76 ctx-rh-superiorfrontal
77 ctx-rh-superiorparietal
78 ctx-rh-superiortemporal
79 ctx-rh-supramarginal
80 ctx-rh-frontalpole
81 ctx-rh-temporalpole
82 ctx-rh-transversetemporal
83 ctx-rh-insula
84 Right-Cerebellum-Cortex
85 Axial-section-through-medulla
86 Fornix-body
87 Left-optic-tract
88 Right-optic-tract

List of white matter bundles

(using Recobundles on whole brain tractogram, Neuroimage 2018;170:283-295)

Bundle abbreviation	Bundle name	Recommended track density threshold for generating bundle mask (see notes below)
AC	anterior commissure	3
AF_L	left arcuate fasciculus	2
AF_R	right arcuate fasciculus	2
AST_L	left frontal aslant tract	5
AST_R	right frontal aslant tract	5
C_L	left cingulum	3
C_R	right cingulum	3
CC_ForcepsMajor	forceps major	5
CC_ForcepsMinor	forceps minor	2
CC	corpus callosum	1
CCMid	middle of corpus callosum	4
CST_L	left corticospinal tract	0
CST_R	right corticospinal tract	0
F_L_R	fornix	0
FPT_L	left frontopontine	1
FPT_R	right frontopontine	1
ICP_L	left inferior cerebellar peduncle	5
ICP_R	right inferior cerebellar peduncle	5
IFOF_L	left inferior frontooccipital fasciculus	0
IFOF_R	right inferior frontooccipital fasciculus	0
ILF_L	left inferior longitudinal fasciculus	5
ILF_R	right inferior longitudinal fasciculus	2
MCP	middle cerebellar peduncle	5
MdLF_L	left middle longitudinal fasciculus	5
MdLF_R	right middle longitudinal fasciculus	5
ML_L	left medial lemniscus	150
ML_R	right medial lemniscus	150
OPT_L	left occipitopontine tract	0
OPT_R	right occipitopontine tract	0
OR_L	left optic radiation	5
OR_R	right optic radiation	10
PPT_L	left parietopontine tract	2
PPT_R	right parietopontine tract	2
SCP	superior cerebellar peduncle	50
SLF_L	left superior longitudinal fasciculus	10
SLF_R	right superior longitudinal fasciculus	5
STT_L	left spinothalamic tract	150
STT_R	right spinothalamic tract	150

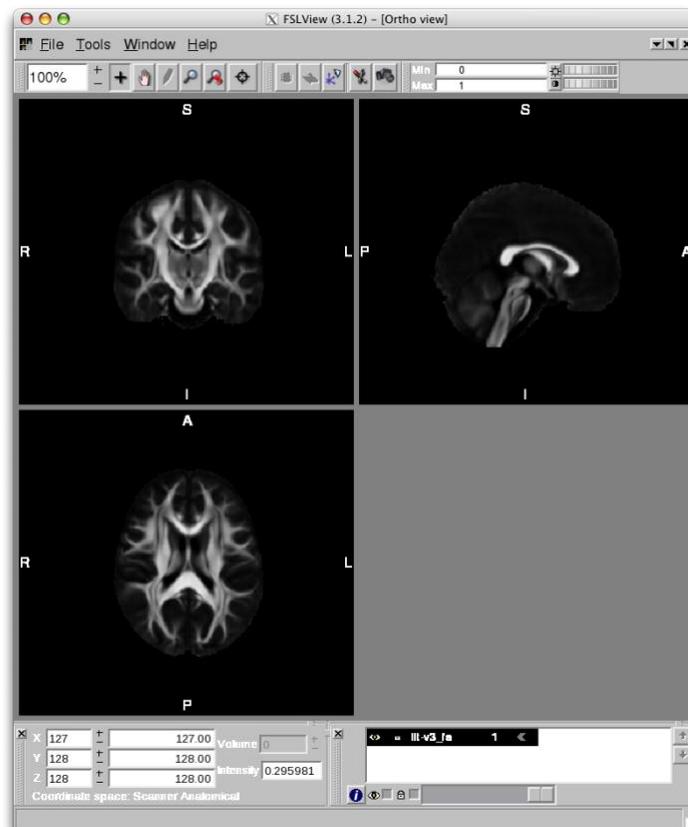
UF_L	left uncinat fasciculus	0
UF_R	right uncinat fasciculus	0
VOF_L	left vertical occipital fasciculus	15
VOF_R	right vertical occipital fasciculus	3

Notes: To generate masks of these bundles, apply the thresholds shown in this table to the TDIs of the corresponding bundles (IIT_bundles.zip) and convert the thresholded TDIs to masks of zeroes and ones. For a better result, smooth the resulting masks and apply a threshold of 0.5 to obtain new masks.

How to spatially normalize individual DTI data to the IIT Human Brain Atlas using DTI-TK

Step 1. Download the mean DTI template of the IIT Human Brain Atlas

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit. The 256x256x256 version of the mean DTI template of the IIT Human Brain Atlas (i.e. the IITmean_*_256.nii files) is directly compatible with DTI-TK tools (no pre-processing needed). The orientation of the 256x256x256 files is LPI. The only files required for spatial normalization of individual DTI data to the IIT Human Brain Atlas using DTI-TK, are **IITmean_tensor_256.nii** and **IITmean_tensor_mask_256.nii**. The rest of the IITmean_*_256.nii files can be used for other purposes (e.g. in a clinical study where all data is normalized to the IIT Human Brain Atlas and voxel-wise analysis is conducted in that space, the 256x256x256 version of the GM atlas can be used for localization purposes). NOTE: Do not confuse the files of the mean DTI template with those of the median DTI template.



FA maps of IITmean_tensor_256.nii displayed in FSL

Step 2. Download and install DTI-TK

DTI-TK can be downloaded from here:

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Downloads.Downloads>

Installation instructions for DTI-TK can be found here:

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.Install>

Step 3. Organize the data

If the individual DWI dataset were processed via FSL, the processed DTI outputs could be converted to DTI-TK tensor format and preprocessed using the DTI-TK script `fsl_to_dtitk`:

```
fsl_to_dtitk <FSL_basename>
```

Let's assume that the individual DTI dataset to be registered to the IIT Human Brain Atlas is named "tensor.nii.gz". For convenience, copy "tensor.nii.gz", "IITmean_tensor_256.nii.gz", and "IITmean_tensor_mask_256.nii.gz" to a new directory of your choice. Then go to that directory and run the following commands.

Step 4. Perform rigid body registration

The command to use is:

```
dti_rigid_reg IITmean_tensor_256.nii.gz tensor.nii.gz EDS 4 4 4 0.01
```

The detailed usage of the command is given here:

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.Registration>

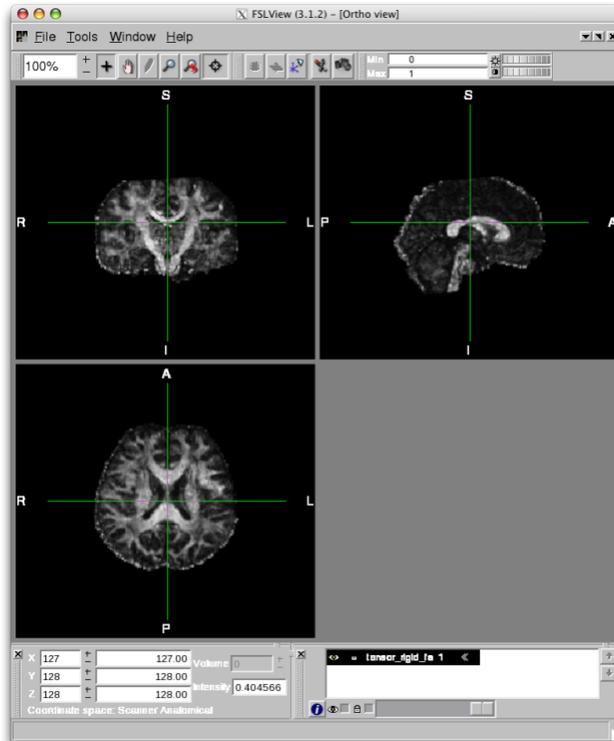
The output in the command window should look like this:

```
Rigid Registration of tensor.nii.gz to IITmean_tensor_256.nii.gz
Similarity Measure : EDS
Reorient Option : FS
Reading IITmean_tensor_256.nii.gz ... Done in 1.81s
sampling step size = [4, 4, 4]
Gaussian smoothing: sigma = [1.64, 1.64, 1.64] ... Done in 12.7s
Reading tensor.nii.gz ... Done in 0.09s
Gaussian smoothing: sigma = [0.736, 0.736, 0.736] ... Done in 0.29s
Initial Difference = 1.16e+07
initial estimate provided by center of mass alignment
cgm optimizer ftol = 0.01
both iteration 0 : 3.9e+06
both iteration 1 : 3.61e+06
both iteration 2 : 3.56e+06
both iteration 3 : 3.51e+06
both iteration 4 : 3.49e+06
cpu time consumed in seconds: 4.61
Final Registration Parameters = 91.7 -87.1 -106 0.0708 -0.0467 -0.0835
Final Difference = 3.48e+06
Total Difference Computation = 38
Total Gradient Computation = 5
Output the rigid transformation as tensor.aff
```

```

inFile = tensor.nii.gz
outFile = tensor_aff.nii.gz
interpolation option is LEI
reorientOption = PPD
Reading tensor.nii.gz ... Done in 0.09s
trans (inverse) applied = [108.372, -106.017, -101.090]
[ 0.996, -0.080, -0.047; 0.083, 0.994, 0.071; 0.041, -0.074, 0.996]
reading output volume specification from IITmean_tensor_256.nii.gz
backward resampling ...time consumed = 6.380
Writing tensor_aff.nii.gz ... Done in 7.480s
done

```



FA map of the individual dataset after rigid registration to the IITmean_tensor_256.nii.gz

This step takes less than a minute to run on a 2.26GHz Intel Xeon Quad-core machine. Two new files are generated in this step: "tensor_aff.nii.gz" is the rigidly-aligned individual DTI dataset, and "tensor.aff" is the corresponding rigid transformation.

Step 5. Perform affine registration

The command to use is:

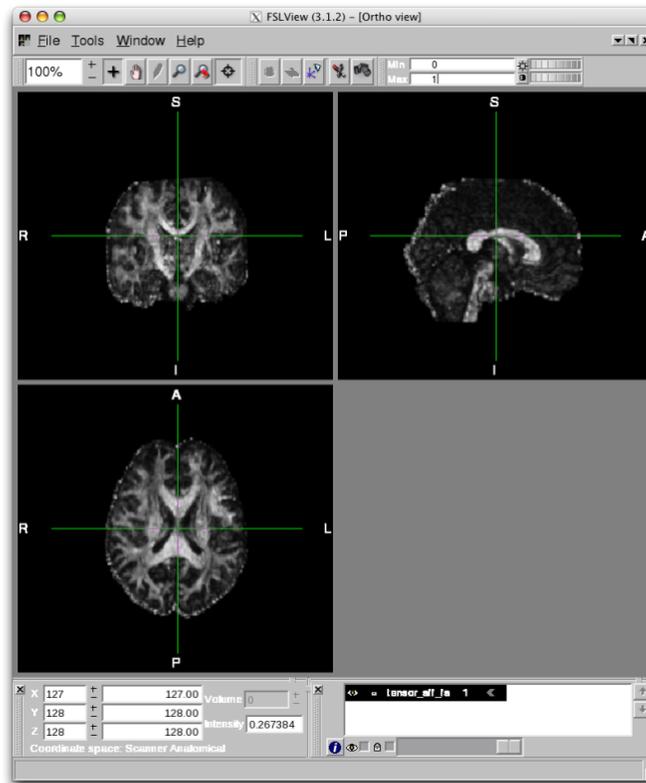
```
dti_affine_reg IITmean_tensor_256.nii.gz tensor.nii.gz EDS 4 4 4 0.01 1
```

The detailed usage of the command is given here:

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.Registration>

The output in the command window looks very similar to that of rigid registration.

This step takes about a minute to run and will overwrite the "tensor_aff.nii.gz" and "tensor.aff" with the newer versions, i.e., the affine-aligned individual DTI dataset, and the corresponding affine transformation.



FA map of the individual dataset after affine registration to the IITmean_tensor_256.nii.gz

Step 6. Perform diffeomorphic registration

The command to use is:

```
dti_diffeomorphic_reg IITmean_tensor_256.nii.gz tensor_aff.nii.gz  
IITmean_tensor_mask_256.nii.gz 1 5 0.002
```

(this command should be entered in one line)

The detailed usage of the command is given here:

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.Registration>

This step registers the affine-transformed version of the individual DTI dataset to the IITmean_tensor_256.nii template in an iterative process. For one iteration, the output in the command window looks like this:

```
registering tensor_aff.nii.gz to IITmean_tensor_256.nii.gz ...  
starting at Tue May 7 16:33:27 CDT 2013
```

```
iteration 1 begins ...
```

```
Similarity Measure : DDS, Reorient Option : FS  
Reading IITmean_tensor_256.nii.gz ... Done in 1.89s  
Reading tensor_aff_diffeo.nii.gz ... Done in 1.62s
```

Reading IITmean_tensor_mask_256.nii.gz ... Done in 0.13s

starting level 2, ending level 5

Level 2

Piecewise Affine Setup: size = 8, 8, 4; vsize = 32, 32, 64

pDim = 3072; scalings : img = 0.06, prior = 0.1, reg = 0.04; ftol = 0.002

before : sum = 15509.2, img = 258487, prior = 0, reg = 0

iter 0: sum = 15509.2, img = 258487, prior = 0, reg = 0

iter 1: sum = 14040.1, img = 225335, prior = 254.063, reg = 12364.7

iter 2: sum = 13672.8, img = 223239, prior = 227.157, reg = 6393.85

iter 3: sum = 13198.6, img = 212977, prior = 548.367, reg = 9128.77

iter 4: sum = 12732, img = 200672, prior = 1289.2, reg = 14069

iter 5: sum = 12574.9, img = 197684, prior = 1518.83, reg = 14049.8

iter 6: sum = 12468.7, img = 196470, prior = 1647.2, reg = 12893.9

iter 7: sum = 12358.1, img = 195045, prior = 1874.1, reg = 11699.7

iter 8: sum = 12297.9, img = 194559, prior = 1957.36, reg = 10714.3

iter 9: sum = 12254.1, img = 193994, prior = 2026.8, reg = 10295.4

iter 10: sum = 12219, img = 193229, prior = 2129.24, reg = 10309.6

iter 11: sum = 12188.8, img = 192319, prior = 2233.08, reg = 10658.2

iter 12: sum = 12166, img = 191744, prior = 2331.71, reg = 10704.2

iter = 87, iterGrad = 13

after : sum = 12149.9, img = 191871, prior = 2304.51, reg = 10182.5

Level 3

Piecewise Affine Setup: size = 16, 16, 8; vsize = 16, 16, 32

pDim = 24576; scalings : img = 0.06, prior = 0.1, reg = 0.04; ftol = 0.002

before : sum = 12154.3, img = 191937, prior = 2305.54, reg = 10189.4

iter 0: sum = 12154.3, img = 191937, prior = 2305.54, reg = 10189.4

iter 1: sum = 11730.3, img = 186602, prior = 2279.07, reg = 7656.99

iter 2: sum = 11614.8, img = 185925, prior = 2232.42, reg = 5900.45

iter 3: sum = 11492.8, img = 182509, prior = 2452.02, reg = 7427.49

iter 4: sum = 11429.9, img = 180030, prior = 2787.96, reg = 8732.57

iter 5: sum = 11394.4, img = 178737, prior = 3035.96, reg = 9165.4

iter 6: sum = 11356, img = 177586, prior = 3355.81, reg = 9131.26

iter 7: sum = 11337.9, img = 177114, prior = 3508.34, reg = 9004.82

iter = 57, iterGrad = 8

after : sum = 11329.9, img = 177029, prior = 3493.93, reg = 8970.23

Level 4

Piecewise Affine Setup: size = 32, 32, 16; vsize = 8, 8, 16

pDim = 196608; scalings : img = 0.06, prior = 0.1, reg = 0.04; ftol = 0.002

before : sum = 11329.9, img = 177031, prior = 3494.42, reg = 8964.41

iter 0: sum = 11329.9, img = 177031, prior = 3494.42, reg = 8964.41

iter 1: sum = 10852.6, img = 168989, prior = 3145.04, reg = 9969.28

iter 2: sum = 10731.2, img = 168369, prior = 3106.01, reg = 7961.53

iter 3: sum = 10626.8, img = 165274, prior = 3330.83, reg = 9432.21

iter 4: sum = 10564.1, img = 162380, prior = 3703, reg = 11274.4

iter 5: sum = 10537.1, img = 161074, prior = 3982.62, reg = 11859.1

iter 6: sum = 10508.6, img = 160059, prior = 4343.56, reg = 11768.8

iter 7: sum = 10492.4, img = 159505, prior = 4582.44, reg = 11597.1

iter = 65, iterGrad = 8

after : sum = 10485.8, img = 159427, prior = 4557.95, reg = 11609.7

Level 5

Piecewise Affine Setup: size = 64, 64, 32; vsize = 4, 4, 8

pDim = 1572864; scalings : img = 0.06, prior = 0.1, reg = 0.04; ftol = 0.002

before : sum = 10485.8, img = 159429, prior = 4558.86, reg = 11604.2

iter 0: sum = 10485.8, img = 159429, prior = 4558.86, reg = 11604.2

iter 1: sum = 9900.49, img = 149254, prior = 3821.13, reg = 14079.2

iter 2: sum = 9740.68, img = 148365, prior = 3691.82, reg = 11739.4

iter 3: sum = 9589.32, img = 143974, prior = 3651.05, reg = 14644.6

iter 4: sum = 9495.53, img = 140067, prior = 3874.69, reg = 17601

iter 5: sum = 9459.15, img = 138330, prior = 4113.64, reg = 18699.1

iter 6: sum = 9427.8, img = 137154, prior = 4481.06, reg = 18762.1

iter 7: sum = 9406.07, img = 136599, prior = 4781.94, reg = 18298.6

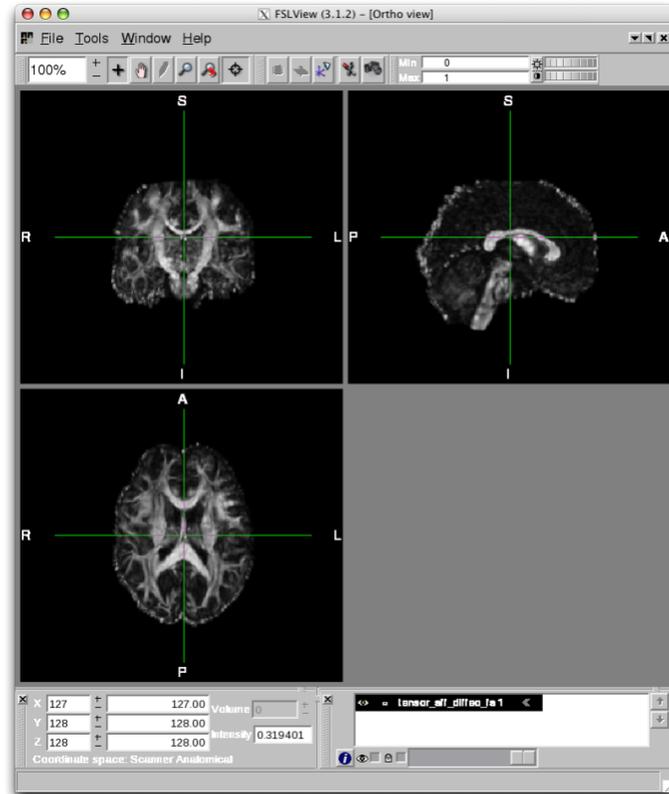
iter 8: sum = 9392.96, img = 136200, prior = 4972.44, reg = 18093

```

iter = 73, iterGrad = 9
after : sum = 9386.49, img = 136089, prior = 4956.36, reg = 18137.6
Little Endian System
Writing VECTORS ...
size is currently determined internally.
vsize = 1, 1, 1
origin is currently default to [0, 0, 0].
outFile = tensor_aff_to_IITmean_tensor_256.5.df.nii.gz
Little Endian System
Reading VECTORS ...
Writing tensor_aff_to_IITmean_tensor_256.5.df.nii.gz ... Done in 15.51s
converting to the diffeomorphic deformation field: ...
Reading tensor_aff_to_IITmean_tensor_256.5.df.nii.gz ... Done in 1.72s
Gaussian smoothing: sigma = [ 1, 1, 1] ... Done in 6.88s
Gaussian smoothing: sigma = [ 1, 1, 1] ... Done in 6.72s
maxNorm = 7.38 iterations = 14
Voxelwise scaling tensor_aff_to_IITmean_tensor_256.5.df.nii.gz by 6.1e-05 ... Done in 0.12s
.....
Writing tensor_aff_to_IITmean_tensor_256.5.df.nii.gz ... Done in 15.5s
Reading IITmean_tensor_mask_256.nii.gz ... Done in 0.12s
input volume IITmean_tensor_mask_256.nii.gz
size: 256x256x256, voxel size: 1x1x1, origin: [0, 0, -0]
reading output volume specification from tensor_aff_to_IITmean_tensor_256.5.df.nii.gz
output volume specification: size: 256x256x256, voxel size: 1x1x1, origin: [0, 0, 0]
matching the center of the old and the new voxel spaces
Writing tensor_aff_jac_mask.nii.gz ... Done in 0.93s
inFile = tensor_aff_to_IITmean_tensor_256.5.df.nii.gz
Reading tensor_aff_to_IITmean_tensor_256.5.df.nii.gz ... Done in 1.79s
outFile = tensor_aff_to_IITmean_tensor_256.5.df_jac.nii.gz
Writing tensor_aff_to_IITmean_tensor_256.5.df_jac.nii.gz ... Done in 10.48s
JACOBIAN STATISTICS: after current iteration mean = 1.02413 min = 0.479575 max = 2.72716 # of voxels =
2.21872e+06
inFile = tensor_aff.nii.gz
outFile = tensor_aff_diffo_current.nii.gz
transFile = tensor_aff_to_IITmean_tensor_256.5.df.nii.gz
df option is FD
interpolation option is LEI
reorientOption = PPD
Reading tensor_aff.nii.gz ... Done in 1.52s
Reading tensor_aff_to_IITmean_tensor_256.5.df.nii.gz ... Done in 1.72s
backward resampling ...time consumed = 62.48
Writing tensor_aff_diffo_current.nii.gz ... Done in 17.61s
IMAGE SIMILARITY: after previous iteration = 261832 after current iteration = 153080
iteration 1 done

```

This step takes about 18 minutes to complete for each iteration (on a 2.26GHz Intel Xeon Quad-core machine). The number of iterations is an input argument that can be adjusted according to your needs. The example given above uses 5 iterations. This step will generate two new files: "tensor_aff_diffo.nii.gz" is the diffeomorphic-aligned volume, and "tensor_aff_diffo.df.nii.gz" is the corresponding deformation field.



FA map of the individual dataset after diffeomorphic registration to the IITmean_tensor_256.nii.gz

Step 7. Combine affine and diffeomorphic transformation

The command to use is:

```
dti_warp_to_template tensor.nii.gz IITmean_tensor_256.nii.gz 1 1 1
```

The detailed usage of the command is given here (see section “Mapping the subject data to the template space”):

<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.OptionspostReg>

This step combines the affine transformation and diffeomorphic displacement field into one single displacement field and brings the original data from raw space to the space of the IIT Human Brain Atlas using a single interpolation.

How to use the IIT Human Brain Atlas in TBSS

In this chapter it is assumed that you have already installed TBSS.

Step 1. Download necessary files and scripts

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit.

Download the mean FA template

(**IITmean_FA.nii.gz** OR **IITmean_FA_256.nii.gz**),

the corresponding FA skeleton

(**IITmean_FA_skeleton.nii.gz** OR **IITmean_FA_skeleton_256.nii.gz**),

and the corresponding lower cingulum mask

(**IITmean_lower_cingulum.nii.gz** OR **IITmean_lower_cingulum_256.nii.gz**).

If tensor-based registration is used to replace Steps 3 to 5 below, also download the following file:

(**IITmean_tensor.nii.gz** OR **IITmean_tensor_256.nii.gz**)

Note: The *_256 files correspond to the 256x256x256 version of the atlas. The files without the _256 at the end of their filenames are in the original 182x218x182 space. You only need to download one of the two versions of the above files.

Download the following scripts:

tbss_3_postreg_iit,

tbss_4_prestats_iit,

tbss_non_FA_iit,

OR the equivalent scripts appropriate for TBSS analysis on the 256x256x256 version of the IIT Human Brain Atlas:

tbss_3_postreg_iit_256,

tbss_4_prestats_iit_256,

tbss_non_FA_iit_256

Note: These are modified versions of the original TBSS scripts `tbss_3_postreg`, `tbss_4_prestats`, `tbss_non_FA`. The modified scripts perform the same tasks as the original scripts, with the difference that they use the IIT Human Brain Atlas.

Note: You only need to download one of the two versions of the above scripts (i.e. with or without the _256 extension). Just make sure you are consistent in terms of the version of the atlas you are working with (i.e. 182x218x182 or 256x256x256).

Step 2. Move the downloaded files to the parent directory

Move the files you downloaded in Step 1 above, to the parent directory of your TBSS study (i.e. mytbss/ according to the TBSS user guide).

Step 3. Run the TBSS pre-processing step (See alternative approach below)

The TBSS user guide can be found at:

<http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/TBSS/UserGuide>

Execute the first step described in the TBSS user guide (i.e. tbss_1_preproc).

Step 4. Nonlinear registration to the mean FA template of the IIT Human Brain Atlas (See alternative approach below)

To register the FA data from all subjects to the mean FA template of the IIT Human Brain Atlas, run the following command from inside the parent directory (i.e. mytbss/ according to the TBSS user guide):

```
tbss_2_reg -t ./IITmean_FA.nii.gz
```

OR

```
tbss_2_reg -t ./IITmean_FA_256.nii.gz (for the 256x256x256 version of the atlas)
```

Step 5. Apply the nonlinear transformations (See alternative approach below)

Run the following command from the parent directory:

```
./tbss_3_postreg_iit -t
```

OR

```
./tbss_3_postreg_iit_256 -t (for the 256x256x256 version of the atlas)
```

Note: Make sure you include the “.” at the start of the command, so that the script downloaded in Step 1 is used. This script is a modified version of the original tbss_3_postreg script that allows use of the IIT Human Brain Atlas.

Note: Make sure you use –t at the end of the command, and not –T. The –t option allows use of the IIT Human Brain Atlas.

ALTERNATIVE APPROACH

Tensor-based registration could be applied (e.g. using DTI-TK) instead of FA-based non-linear registration. For tensor-based registration replace steps 3-5 above with the following steps I and II. It is also recommended to refer to the DTI-TK web page

(<http://dti-tk.sourceforge.net/pmwiki/pmwiki.php?n=Documentation.TBSS>) for further details.

Skip steps 3 to 5 above.

Step I. Pre-processing and nonlinear tensor-based registration to the DTI template of the IIT Human Brain Atlas

To pre-process and register the DTI data from all subjects to the DTI template of the IIT Human Brain Atlas using tensor-based registration (assuming they are in the same directory), refer to the [“How to spatially normalize individual DTI data to the IIT Human Brain Atlas using DTI-TK”](#) chapter.

Step II. Prepare images from registered DTI data for TBSS

Move the normalized DTI data to ./FA directory.

Go to ./FA directory:
cd ./FA

Generate the FA maps of the spatially normalized DTI data:
TVtool -in [subj?_normalized].nii.gz -fa

Merge the FA maps of the spatially normalized DTI data into a 4D volume.
mkdir -p ../stats
fslmerge -a ../stats/all_FA [subj1_normalized_fa subj2_normalized_fa ...]

Some masking steps:

```
cd ../stats
fslmaths all_FA -max 0 -Tmin -bin mean_FA_mask -odt char
fslmaths ../IITmean_FA -mas mean_FA_mask mean_FA
(OR fslmaths ../IITmean_FA_256 -mas mean_FA_mask mean_FA, for the 256x256x256 version
of the atlas)
fslmaths mean_FA -bin mean_FA_mask
fslmaths all_FA -mas mean_FA_mask all_FA

cp ../IITmean_FA_skeleton mean_FA_skeleton
(OR cp ../IITmean_FA_skeleton_256 mean_FA_skeleton, for the 256x256x256 version of the
atlas)
fslmaths mean_FA_skeleton -mas mean_FA_mask mean_FA_skeleton
```

Step 6. Final steps before statistical analysis

Run the following command from the parent directory:

```
./tbss_4_prestats_iit 0.25
OR
./tbss_4_prestats_iit_256 0.25 (for the 256x256x256 version of the atlas)
```

Note: Make sure you include the “.” at the start of the command so that the script downloaded in Step 1 is used. This script is a modified version of the original tbss_4_prestats script that allows use of the IIT Human Brain Atlas.

Note: The skeleton downloaded in Step 1 is already thresholded at 0.25 (i.e. only voxels with $FA > 0.25$ are included in the skeleton). Therefore, threshold values for the command of Step 6 should range from 0.25 to 1. A threshold value of 0.2 or 0.1 would generate the same skeleton as a threshold of 0.25.

Step 7. (OPTIONAL STEP for TBSS analysis of non-FA data) Apply the non-linear transformations and projection parameters to non-FA data

If you want to project non-FA data (e.g. L2) to the white matter skeleton, run the following command from the parent directory:

```
./tbss_non_FA_iit -t L2
```

OR

```
./tbss_non_FA_iit_256 -t L2 (for the 256x256x256 version of the atlas)
```

Note: Make sure you include the “.” at the start of the command so that the script downloaded in Step 1 is used. This script is a modified version of the original `tbss_non_FA` script that allows use of the IIT Human Brain Atlas.

Note: Make sure you use the `-t` option.

Note: Follow the rest of the TBSS instructions for this step. For example, before running the command above, you need to make the L2 data available in a directory named “L2” within the parent directory. Also, the filenames of the L2 data must be exactly the same as those of the FA data.

Step 8. Proceed with the rest of the TBSS analysis

Proceed with the rest of the TBSS analysis as described in the TBSS user guide.

How to visualize fiber orientation distribution functions of the IIT Human Brain Atlas using MRtrix

Step 1. Download the spherical harmonics representation of fiber orientation distribution functions of the IIT Human Brain Atlas

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit.

The spherical harmonics representation of fiber orientation distribution functions (FODs) is contained in **IIT_HARDI.nii.gz** (in 182x218x182x28 matrix size) **OR** in **IIT_HARDI_256.nii.gz** (in 256x256x256x28 matrix size).

For the background you can use the mean FA template (**IITmean_FA.nii.gz**) or the GFA template (**IIT_GFA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

Step 2. Download and install MRtrix

MRtrix can be downloaded from here:

<http://www.mrtrix.org/>

Documentation for MRtrix can be found here:

<http://userdocs.mrtrix.org/en/latest/>

Step 3. Open the background images

Open MRview of MRtrix (type "mrview" in the command line), go to File > Open.

Locate and select the template you would like to use as background (e.g. IITmean_FA.nii.gz downloaded in Step 1 above).

Step 4. Open the file containing the fiber orientation distribution information.

In MRview, select 'Tool->ODF display' to display the sidebar.

From the menu in the sidebar click the 'Open SH Image' button and locate the file containing the spherical harmonics representation of the FODs (i.e. IIT_HARDI.nii.gz for the 182x218x182 matrix size, or IIT_HARDI_256.nii.gz for the 256x256x256 matrix size). The FOD will be

displayed in the viewing plane.

Detailed MRview instructions can be found here:

<https://mrtrix.readthedocs.io/en/latest/reference/commands/mrview.html>

How to do HARDI tractography on the IIT Human Brain Atlas using MRtrix

Step 1. Download the necessary files

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit.

The spherical harmonics representation of fiber orientation distribution functions (FODs) is contained in **IIT_HARDI.nii.gz** (in 182x218x182x28 matrix size) **OR** in **IIT_HARDI_256.nii.gz** (in 256x256x256x28 matrix size).

For the background you can use the mean FA template (**IITmean_FA.nii.gz**) or the GFA template (**IIT_GFA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

The tissue segmentation file for Anatomically-Constrained Tractography (ACT) on the IIT HARDI template is **IIT_fornix_fixed_5tt_file_for_ACT_tractography.nii.gz** (in 182x218x182x5 matrix size) **OR** **IIT_fornix_fixed_5tt_file_for_ACT_tractography_256.nii.gz** (in 256x256x256x5 matrix size).

Step 2. Download and install MRtrix

MRtrix can be downloaded from here:

<http://www.mrtrix.org/>

Documentation for MRtrix can be found here:

<http://userdocs.mrtrix.org/en/latest/>

Step 3. Perform fiber tracking

Instructions for MRtrix Anatomically-Constrained Tractography (ACT) can be found here:

https://mrtrix.readthedocs.io/en/latest/quantitative_structural_connectivity/act.html

Instructions for MRtrix Spherical-deconvolution Informed Filtering of Tractograms (SIFT) can be found here:

https://mrtrix.readthedocs.io/en/latest/quantitative_structural_connectivity/sift.html

Instructions for MRtrix structural connectome construction can be found here:

https://mrtrix.readthedocs.io/en/latest/quantitative_structural_connectivity/structural_connectome.html

Step 4. Open the background images

Open MRview of MRtrix (type “mrview” in the command line), go to File > Open.

Locate and select the template you would like to use as background (e.g. IITmean_FA.nii.gz downloaded in Step 1 above).

Step 5. Open the file containing tractography results

In MRview, select 'Tool->tractography' to display the sidebar.

From the menu in the sidebar choose 'Open tractogram' button and locate the *.tck file with the tractography results.

Detailed MRview instructions can be found here:

<https://mrtrix.readthedocs.io/en/latest/reference/commands/mrview.html>

How to visualize the gray matter labels of the IIT Human Brain Atlas using FSLeYes

Step 1. Download the gray matter labels and look-up tables of the IIT Human Brain Atlas

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit.

The labels of the gray matter atlas in 182x218x182 matrix size are contained in:

IIT_GM_Desikan_atlas.nii.gz (for Desikan labels; Desikan et al. Neuroimage 2006;31:968-980) and

IIT_GM_Destrieux_atlas.nii.gz (for Destrieux labels; Destrieux et al. Neuroimage 2010;53:1-15),

OR in 256x256x256 matrix size in:

IIT_GM_Desikan_atlas_256.nii.gz (for Desikan labels) and

IIT_GM_Destrieux_atlas_256.nii.gz (for Destrieux labels).

For the background you can use the mean T1-weighted template (**IITmean_t1.nii.gz**) or the mean FA template (**IITmean_FA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

Also download the corresponding look-up tables **LUT_GM_Desikan_0to1.txt** and **LUT_GM_Destrieux_0to1.txt**.

Step 2. Download and install FSL

Documentation for FSLeYes can be found here:

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLeYes>

Step 3. Open the background images

In FSLeYes, go to File >Add overlay from file.

Click Browse to locate and select the template you would like to use as background (e.g. `IITmean_t1.nii.gz` downloaded in Step 1 above).

Click Open, and then Finish.

Step 4. Open the file containing the gray matter labels

In FSleyes, go to File > Add overlay from file.

Click Browse to locate and select the file containing the gray matter labels (i.e. IIT_GM_Destrieux_atlas.nii.gz for the 182x218x182 matrix size, or IIT_GM_Destrieux_atlas_256.nii.gz for the 256x256x256 matrix size; this needs to match the matrix size of the background image you already loaded).

Select the gray matter label file in “Overlay list” panel. In the menu bar, change “3D/4D volume” to “Label image”

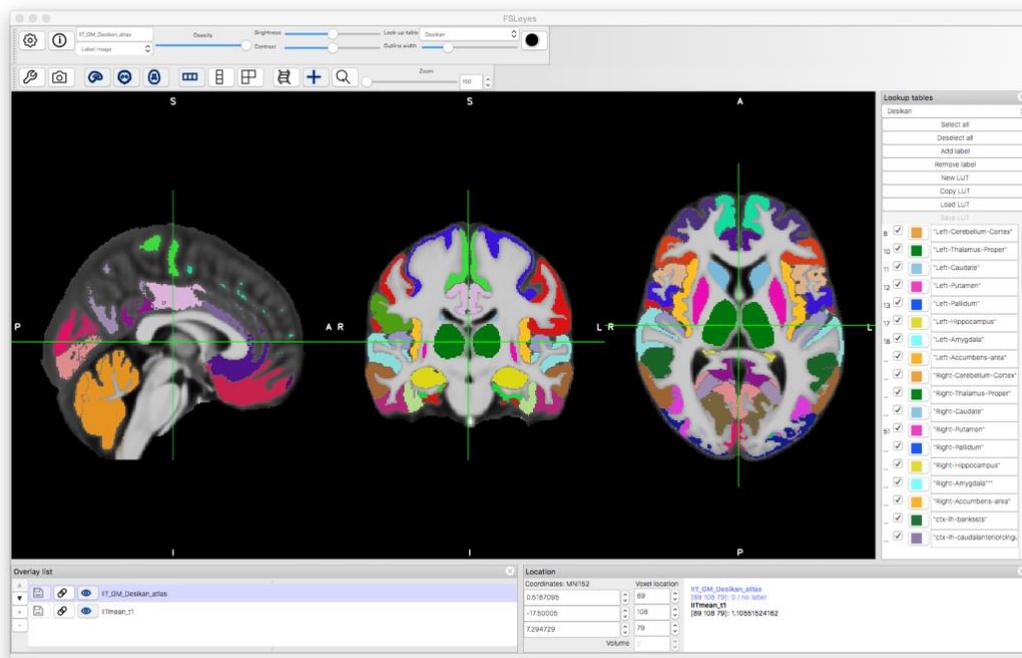
Step 5. Load an appropriate look-up table

In FSleyes, go to Setting > Ortho View 1 > Lookup tables.

In the “Lookup tables” panel, click Load LUT to load a new lookup table. Enter the name of the new lookup table and click “ok” to select the file named LUT_GM_Destrieux_0to1.txt or LUT_GM_Desikan_0to1.txt (depending on the atlas you loaded in the previous step).

Click OK and make sure the new lookup table is chosen in the “Lookup tables” Panel. You should be able to see the images below.

Also note that, if you click on a label, the name of it appears in the “Location” textbox in FSleyes.



How to visualize the gray matter labels of the IIT Human Brain Atlas using ITK-SNAP

Step 1. Download the gray matter labels and look-up tables of the IIT Human Brain Atlas

To download the IIT Human Brain Atlas, visit www.nitrc.org/projects/iit.

The labels of the gray matter atlas in 182x218x182 matrix size are contained in:

IIT_GM_Desikan_atlas.nii.gz (for Desikan labels; Desikan et al. Neuroimage 2006;31:968-980) and

IIT_GM_Destrieux_atlas.nii.gz (for Destrieux labels; Destrieux et al. Neuroimage 2010;53:1-15),

OR in 256x256x256 matrix size in:

IIT_GM_Desikan_atlas_256.nii.gz (for Desikan labels) and

IIT_GM_Destrieux_atlas_256.nii.gz (for Destrieux labels).

For the background you can use the mean T1-weighted template (**IITmean_t1.nii.gz**) or the mean FA template (**IITmean_FA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

Also download the corresponding look-up tables **LUT_GM_Desikan_0to255.txt** and **LUT_GM_Destrieux_0to255.txt**.

Step 2. Download and install ITK-SNAP

ITK-SNAP can be downloaded from here:

<http://www.itksnap.org/pmwiki/pmwiki.php?n=Main.Downloads>

Documentation for ITK-SNAP can be found here:

<http://www.itksnap.org/pmwiki/pmwiki.php?n=Documentation.HomePage>

Step 3. Open the background images

In ITK-SNAP, go to File > Open Main Image.

Click Browse to locate and select the template you would like to use as background (e.g. `IITmean_t1.nii.gz` downloaded in Step 1 above).

Click Next, and then Finish.

Step 4. Open the file containing the gray matter labels

In ITK-SNAP, go to Segmentation > Open Segmentation.

Click Browse to locate and select the file containing the gray matter labels (i.e. IIT_GM_Destrieux_atlas.nii.gz for the 182x218x182 matrix size, or IIT_GM_Destrieux_atlas_256.nii.gz for the 256x256x256 matrix size; this needs to match the matrix size of the background image you already loaded).

Click Next, and then Finish.

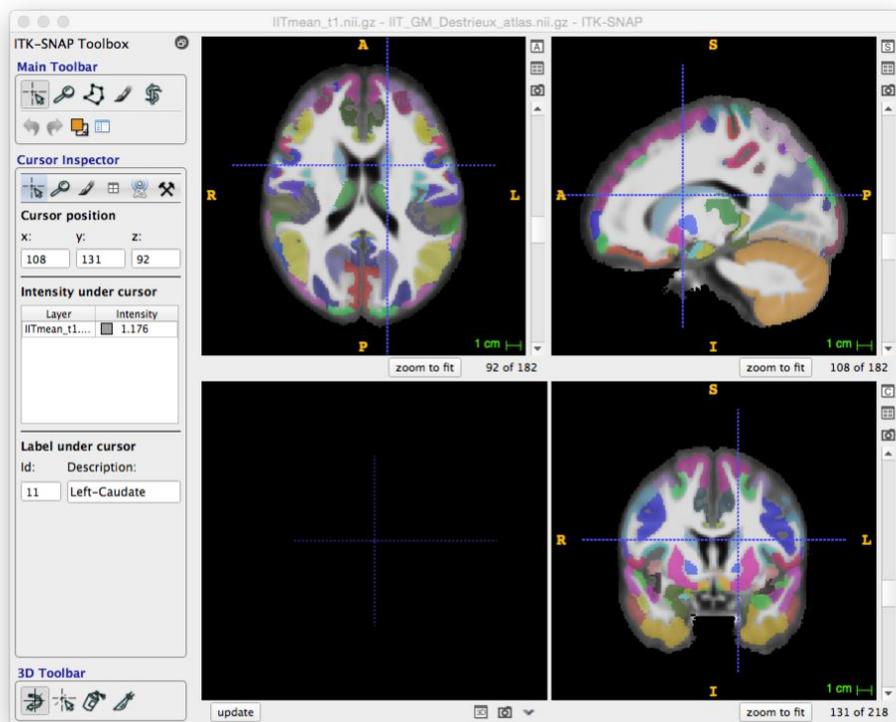
Step 5. Load an appropriate look-up table

In ITK-SNAP, go to Segmentation > Import Label Descriptions.

Click Browse to locate and select the file named LUT_GM_Destrieux_0to255.txt or LUT_GM_Desikan_0to255.txt (depending on the atlas you loaded in the previous step).

Click OK and you are done. You should be able to see the images below.

Also note that, if you click on a label, the name of it appears in the “Label under cursor: Description” textbox in ITK-SNAP.



How to interpret the information in the IIT white matter atlas

The purpose of this chapter is to explain how to interpret the information included in the files of the IIT white matter atlas.

First, the IIT white matter atlas is a cortical-parcellation-based atlas. For its construction, a whole brain tractogram was constructed using the framework of Anatomically-Constrained Tractography (ACT) and was filtered by the Spherical-deconvolution Informed Filtering of Tractograms (SIFT) algorithm. The Desikan gray matter labels were used to group streamlines connecting pairs of labels (see “[Codes for the white matter atlas](#)”).

Second, the IIT white matter atlas contains multi-layer white matter labels. This means that each white matter voxel is assigned a list of gray matter label-pairs with the most probable connections through that voxel. The reason behind the multi-layer labels is that multiple fiber populations often share the same voxels, and therefore white matter voxels must be given the chance to have multiple labels.

Note: Maps of major fiber-bundles (IIT_bundles.zip and the skeletonized version IIT_bundles_skeletonized.zip) are also available in addition to the multi-layer white matter labels discussed above. Major fiber-bundles were parcellated using a well-established white matter fiber clustering method (RecoBundles, Neuroimage 2018;170:283-295).

Step 1. Download files

Download the following files of the IIT Human Brain Atlas from www.nitrc.org/projects/iit

IIT_WM_atlas.nii.gz
IIT_WM_atlas_confidence.nii.gz } (in 182x218x182x60 matrix size)

OR

IIT_WM_atlas_256.nii.gz
IIT_WM_atlas_confidence_256.nii.gz } (in 256x256x256x60 matrix size)

Step 2. Display both files simultaneously

Display the IIT_WM_atlas.nii and IIT_WM_atlas_confidence.nii files simultaneously, using FSL or any other visualization software that allows you to sync both images.

Both the IIT_WM_atlas.nii and IIT_WM_atlas_confidence.nii files are 4D. They contain 60 3D volumes. For each white matter voxel, the file IIT_WM_atlas.nii provides a list of the top 60 most

probable fiber connections passing through that voxel (in descending confidence order). These connections are between pairs of gray matter labels. The IIT_WM_atlas_confidence.nii file provides the confidence index for the top 60 most probable fiber connections passing through that voxel.

(Note: The *_256 versions of these files are large and certain visualization software packages may fail. Consider using the versions of the files without the _256 extension. Alternatively, you can open only one or few volumes of the atlas at a time. Individual volumes can be found in 60 separate files within the:

IIT_WM_atlas_60_top_layers.zip, and

IIT_WM_atlas_confidence_60_top_layers.zip,

OR

IIT_WM_atlas_60_top_layers_256.zip, and IIT_WM_atlas_confidence_60_top_layers_256.zip)

Step 3. How to interpret the information in IIT_WM_atlas.nii

The 60 values corresponding to a white matter voxel in this file represent the names of the 60 most probable connections in that voxel. These names are constructed as follows:

name = $GM_1 \times 100 + GM_2$, where GM_1 and GM_2 are codes assigned to the two gray matter labels participating in the connection (see list of [“Codes for the white matter atlas”](#)).

Example #1: if the code for $GM_1 = 4$ and for $GM_2 = 9$, then the name for the connection between GM_1 and GM_2 is 409.

Example #2: if the code for $GM_1 = 7$ and for $GM_2 = 35$, then the name for the connection between GM_1 and GM_2 is 735.

The IIT_WM_atlas.nii file gives the names of the most probable connections. Given the name i of the i -th most probable connection, you can extract the codes of the corresponding pair of gray matter labels as follows:

$$GM_{1i} = \text{Floor}(\text{name}_i / 100)$$

$$GM_{2i} = \text{name}_i - 100 \times \text{Floor}(\text{name}_i / 100)$$

Example

If the first volume of the 4D IIT_WM_atlas.nii has a value of 3842 in voxel $[x, y, z]$, then the most probable fiber connection passing through that voxel is the connection between gray matter labels with codes:

$$GM_1 = \text{Floor}(3842/100) = \text{Floor}(38.42) = 38 \text{ (corresponding to Left-Putamen),}$$

and

$$GM_2 = 3842 - 100 \times \text{Floor}(3842/100) = 3842 - 100 \times \text{Floor}(38.42) = 3842 - 100 \times 38 = 3842 - 3800 = 42 \text{ (corresponding to Left-Accumbens-area).}$$

If for the same voxel, the second volume of the IIT_WM_atlas.nii file has a value of 4211, then the second most probable fiber connection passing through that voxel is the connection between gray matter labels with codes:

$$GM_1 = \text{Floor}(4211/100) = \text{Floor}(42.11) = 42 \text{ (corresponding to Left-Accumbens-area)}$$

and

$$GM_2 = 4211 - 100 \times \text{Floor}(4211/100) = 4211 - 100 \times \text{Floor}(42.11) = 4211 - 100 \times 42 = 4211 - 4200 = 11 \text{ (corresponding to ctx-lh-lateralorbitofrontal).}$$

Step 4. How to interpret the information in IIT_WM_atlas_confidence.nii

The 60 values in each white matter voxel of this file represent the confidence values corresponding to the 60 most probable connections listed in IIT_WM_atlas.nii. In each voxel, the confidence corresponding to a certain connection is defined as the ratio of the number of streamlines that go through that voxel and belong to that connection divided by the total number of streamlines going through that voxel.

How to visualize the most probable white matter connection in each voxel of the IIT Human Brain Atlas using FSLeves

The IIT white matter atlas contains multi-layer white matter labels. This means that each white matter voxel is assigned a list of gray matter label-pairs with the most probable connections through that voxel. The reason behind the multi-layer labels is that multiple fiber populations often share the same voxels, and therefore white matter voxels must be given the chance to have multiple labels. The current version of the atlas includes for each white matter voxel the top 60 most probable fiber connections passing through that voxel (in descending confidence order). These connections are between pairs of gray matter labels. This chapter explains how to visualize the most probable white matter connection in each voxel of the atlas using FSLeves.

Step 1. Download the white matter labels and corresponding look-up table

Download the following files of the IIT Human Brain Atlas from:

www.nitrc.org/projects/iit

IIT_WM_atlas_60_top_layers.zip

OR in 256x256x256 matrix size:

IIT_WM_atlas_60_top_layers_256.zip

For the background you can use the mean T1-weighted template (**IITmean_t1.nii.gz**) or the mean FA template (**IITmean_FA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

Download the look-up table **LUT_WM_0to1.txt**

Step 2. Unzip the white matter labels file

Unzip the **IIT_WM_atlas_60_top_layers.zip**
(or **IIT_WM_atlas_60_top_layers_256.zip**)

You now have access to 60 volumes named **IIT_WM_atlas_IXX.nii.gz**, where **XX** is a number from 1 to 60.

Example: **IIT_WM_atlas_I1.nii.gz** includes for each voxel the most probable fiber connection passing through that voxel.

Example: IIT_WM_atlas_l60.nii.gz includes for each voxel the 60th most probable fiber connection passing through that voxel (i.e. the least probable out of the 60 options provided).

Step 3. Download and install FSL

Documentation for FSLEyes can be found here:

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLEyes>

Step 4. Open the background images

In FSLEyes, go to File > Add overlay from file.

Click Browse to locate and select the template you would like to use as background (e.g. IITmean_t1.nii.gz downloaded in Step 1 above).

Click Open, and then Finish.

Step 5. Open the file containing the white matter labels

In FSLEyes, go to File > Add overlay from file.

Click Browse to locate and select IIT_WM_atlas_l1.nii.gz, which contains the most probable white matter connection in each voxel.

Select the gray matter label file in “Overlay list” panel. In the menu bar, change “3D/4D volume” to “Label image”

Step 6. Load the look-up table

In FSLEyes, go to Setting > Ortho View 1 > Lookup tables.

In the “Lookup tables” panel, click Load LUT to load a new lookup table. Enter the name of the new lookup table and click “ok” to select the file named LUT_WM_0to1.txt.

Click OK and make sure the new lookup table is chosen in the “Lookup tables” Panel. You should be able to see the images below.

How to visualize the most probable white matter connection in each voxel of the IIT Human Brain Atlas using ITK-SNAP

The IIT white matter atlas contains multi-layer white matter labels. This means that each white matter voxel is assigned a list of gray matter label-pairs with the most probable connections through that voxel. The reason behind the multi-layer labels is that multiple fiber populations often share the same voxels, and therefore white matter voxels must be given the chance to have multiple labels. The current version of the atlas includes for each white matter voxel the top 60 most probable fiber connections passing through that voxel (in descending confidence order). These connections are between pairs of gray matter labels. This chapter explains how to visualize the most probable white matter connection in each voxel of the atlas using ITK-SNAP.

Step 1. Download the white matter labels and corresponding look-up table

Download the following files of the IIT Human Brain Atlas from:

www.nitrc.org/projects/iit

IIT_WM_atlas_60_top_layers.zip

OR in 256x256x256 matrix size:

IIT_WM_atlas_60_top_layers_256.zip

For the background you can use the mean T1-weighted template (**IITmean_t1.nii.gz**) or the mean FA template (**IITmean_FA.nii.gz**), or any other template you wish, since they are all in the same space (just make sure to pick the appropriate matrix size; files in the 182x218x182 matrix size don't contain any numbers at the end of their filenames; files in the 256x256x256 matrix size have filenames that end with `_256`).

Download the look-up table **LUT_WM_0to255.txt**

Step 2. Unzip the white matter labels file

Unzip the **IIT_WM_atlas_60_top_layers.zip**
(or **IIT_WM_atlas_60_top_layers_256.zip**)

You now have access to 60 volumes named **IIT_WM_atlas_IXX.nii.gz**, where **XX** is a number from 1 to 60.

Example: **IIT_WM_atlas_I1.nii.gz** includes for each voxel the most probable fiber connection passing through that voxel.

Example: IIT_WM_atlas_l60.nii.gz includes for each voxel the 60th most probable fiber connection passing through that voxel (i.e. the least probable out of the 60 options provided).

Step 3. Download and install ITK-SNAP

ITK-SNAP can be downloaded from here:

<http://www.itksnap.org/pmwiki/pmwiki.php?n=Main.Downloads>

Documentation for ITK-SNAP can be found here:

<http://www.itksnap.org/pmwiki/pmwiki.php?n=Documentation.HomePage>

Step 4. Open the background images

In ITK-SNAP, go to File > Open Main Image.

Click Browse to locate and select the template you would like to use as background (e.g. IITmean_t1.nii.gz downloaded in Step 1 above).

Click Next, and then Finish.

Step 5. Open the file containing the white matter labels

In ITK-SNAP, go to Segmentation > Open Segmentation.

Click Browse to locate and select IIT_WM_atlas_l1.nii.gz, which contains the most probable white matter connection in each voxel.

Click Next, and then Finish.

Step 6. Load the look-up table

In ITK-SNAP, go to Segmentation > Import Label Descriptions.

Click Browse to locate and select the file named LUT_WM_0to255.txt.

Click OK and you are done. You should be able to see the images below.



If you click in a white matter voxel, the name of the most probable label (most probable connection) in that voxel appears in the “Label under cursor” textbox in ITK-SNAP. The numerical label ID is also shown in the “Label under cursor” textbox.

(Note: A similar approach can be used to visualize the 2nd, 3rd etc. most probable connections. However, the look-up table may not be appropriate).

How to use the IIT Human Brain Atlas to extract information about the connectivity of a gray matter label A to another gray matter label B

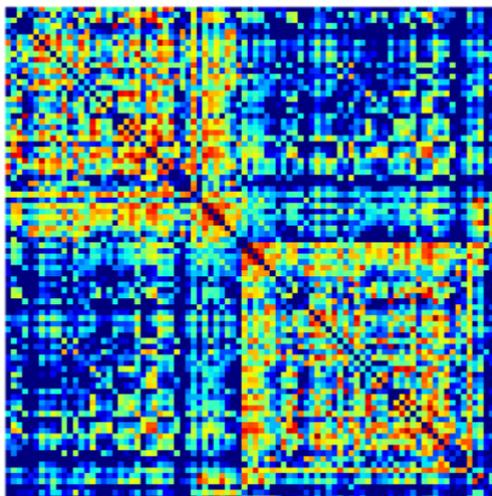
The purpose of this chapter is to explain how to use the IIT Human Brain Atlas to find the number of streamlines that originate from a gray matter label A and terminate in another gray matter label B. In the construction of the IIT white matter atlas, a whole brain tractogram was constructed using the framework of Anatomically-Constrained Tractography (ACT) and was filtered by the Spherical-deconvolution Informed Filtering of Tractograms (SIFT) algorithm. The Desikan gray matter labels of the IIT Human Brain Atlas were used to group streamlines connecting pairs of labels. A connectivity matrix was generated from this process and is made available as part of the IIT white matter atlas. We can use this connectivity matrix to find the number of streamlines that originated from a gray matter label A and terminated in another gray matter label B.

Step 1. Download necessary files

Download the following file of the IIT Human Brain Atlas from www.nitrc.org/projects/iit:
IIT_connectivity_matrix.txt

Step 2. Read connectivity matrix

This connectivity matrix is a table written in a plain text file and can be opened in multiple ways, even in Excel. The rows and columns of the connectivity matrix correspond to gray matter labels (in the same order). The value in each element of the connectivity matrix is equal to the number of streamlines that connect one gray matter label (row) with another gray matter label (column). The connectivity matrix is symmetric.



Connectivity matrix

The diagonal elements of the connectivity matrix have been set to 0. The order of gray matter labels in the connectivity matrix is the same as that in the table "[Codes for the white matter atlas](#)". The top left element of the connectivity matrix corresponds to the label with code=1. To find the number of streamlines that connect e.g. the left middle temporal label (code 14) and the left fusiform label (code 6) we need to look in row 14 and column 6.

Note: In addition to the gray matter labels of the IIT Human Brain Atlas (Desikan labels), the "[Codes for the white matter atlas](#)" also contains a label for an axial section through the medulla (code 85), one label for the Fornix body (code 86), and two labels for coronal sections through the right and left optic tracts proximal to the optic chiasm (codes 87 & 88). These four labels were added so that the connectivity matrix includes connections to the spinal cord, fornix, and eyes, which are not included in the gray matter labels of the atlas (Desikan labels) and would otherwise not be represented.

regionconnect: How to use the IIT Human Brain Atlas to find out which pairs of gray matter labels have connections through a user-defined white matter region of interest (ROI)

The purpose of this chapter is to explain how to use the IIT Human Brain Atlas to uncover the pairs of gray matter labels that have connections through a user-defined white matter region of interest (ROI). For example, when a voxel-wise analysis generates a white matter cluster with significant findings, you can follow the steps described in this chapter to find out which pairs of gray matter labels have connections that occupy that cluster. The same can be done if the white matter ROI is a section of the IIT white matter skeleton (from TBSS analysis). Similarly, you can extract the list of connections located inside any user-defined ROI. More details regarding the output are provided in Step 4 below.

Step 1. Download files

Download the following files of the IIT Human Brain Atlas from www.nitrc.org/projects/iit:

IIT_WM_atlas.nii.gz
IIT_WM_atlas_confidence.nii.gz
IIT_TDI_sum.nii.gz

} (in 182x218x182 matrix size)

OR

IIT_WM_atlas_256.nii.gz
IIT_WM_atlas_confidence_256.nii.gz
IIT_TDI_sum_256.nii.gz

} (in 256x256x256 matrix size)

Also download:
regionconnect.py

Make sure to place all the downloaded files in the same folder.

Step 2. Define the white matter ROI

Create a mask of the white matter ROI in the space of the IIT Human Brain Atlas, and save it in .nii (or .hdr, .img) file format. The value of the mask should be 1 inside the ROI, and 0

elsewhere.

- If the ROI was generated from an analysis conducted in IIT space, then your ROI is already in the correct space.

- If the ROI is in a different space, you will need to transform it to IIT space first.

- If you want to select/draw an ROI in IIT space, you can use the mean FA template (IITmean_FA.nii.gz), or the mean T₁ template (IITmean_t1.nii.gz), or any other template of the IIT atlas as reference (just make sure you use the matrix size you are interested in, 182x218x182 or 256x256x256; the latter templates have filenames that end with _256). By using an IIT template as a reference, you ensure that the generated ROI is located in IIT space.

Step 3. Perform ROI-based analysis

Install `numpy` and `nibabel` in your python environment and run the `regionconnect.py` script.

```
python3 -m pip install numpy nibabel
```

```
python /your_path/regionconnect.py path_to_ROI_mask path_to_output_text_file
```

regionconnect provides a list of pairs of gray matter labels that have connections through a user-defined white matter ROI (it does that by searching through the 4D labels of the white matter atlas, which makes it fast). For each connection, this script also returns the probability that a fiber passing through a voxel of the ROI belongs to that connection. This information is presented in a text file (`path_to_output_text_file`) in the form of a table. In this table, each line corresponds to connectivity of a pair of gray matter labels, and connections are arranged in the order of importance (i.e. top line in the table corresponds to the pair of gray matter labels with the highest probability that a fiber passing through a voxel of the ROI belongs to that connection) (see examples below).

Example using a test ROI "roi.nii.gz":

- *Command:*

```
python ./IITatlas/regionconnect.py ./data/roi.nii.gz ./data/results_roi.txt
```

- *Contents of the output file " ./data/results_roi.txt":*

```

1  ###77.69%of the selected ROI is used in this analysis
2  ###22.31%of the ROI is located outside of the white matter
3
4  ###MOST PROBABLE CONNECTIONS:
5
6  9.021299853587% - ctx-lh-supramarginal AND ctx-lh-insula
7  6.857814592495% - ctx-lh-precuneus AND Left-Thalamus-Proper
8  6.794296568621% - ctx-lh-transversetemporal AND ctx-lh-insula
9  6.336889452614% - ctx-lh-postcentral AND ctx-lh-insula
10 5.923441452803% - ctx-lh-superiorparietal AND ctx-lh-insula
11 4.943753625577% - ctx-lh-superiorparietal AND Left-Thalamus-Proper
12 4.608928523431% - ctx-lh-postcentral AND Left-Thalamus-Proper
13 4.085873216454% - ctx-lh-superiorparietal AND Left-Putamen
14 3.943344998947% - ctx-lh-paracentral AND Left-Thalamus-Proper
15 3.623818439938% - ctx-lh-postcentral AND Left-Putamen
16 3.496007841224% - ctx-lh-supramarginal AND Left-Putamen
17 3.320946084750% - ctx-lh-precuneus AND ctx-lh-insula
18 2.881935870991% - ctx-lh-precuneus AND Left-Putamen
19 1.657084037986% - ctx-lh-supramarginal AND Left-Thalamus-Proper
20 1.419666150754% - ctx-lh-isthmuscingulate AND Left-Thalamus-Proper
21 1.364668852165% - ctx-lh-paracentral AND Left-Putamen
22 1.269585504835% - ctx-lh-precuneus AND Axial-section-through-medulla
23 1.189413407005% - Left-Thalamus-Proper AND Left-Caudate
24 1.179730801578% - ctx-lh-paracentral AND ctx-lh-insula
25 1.154362324697% - ctx-lh-postcentral AND Left-Pallidum
26 1.122215995308% - ctx-lh-superiorparietal AND Axial-section-through-medulla
27 1.114469897296% - ctx-lh-superiortemporal AND ctx-lh-insula
28 1.031780302105% - ctx-lh-precentral AND Left-Thalamus-Proper
29 0.873953478686% - ctx-lh-superiorparietal AND Left-Pallidum
30 0.823410238721% - ctx-lh-paracentral AND Axial-section-through-medulla
31 0.815857799471% - ctx-lh-postcentral AND Axial-section-through-medulla
32 0.794556050687% - ctx-lh-precuneus AND Left-Pallidum
33 0.622011663978% - ctx-lh-paracentral AND Left-Pallidum
34 0.583668455822% - ctx-lh-supramarginal AND Axial-section-through-medulla
35 0.524604518764% - ctx-lh-supramarginal AND Left-Pallidum

```

In this example, we get the information that 77.69% of the voxels contained in the user-defined ROI were used in the analysis, and 22.31% of the voxels in the ROI were ignored because they were located outside white matter (no connectivity information could be generated for that portion of the ROI).

The top connection is between the ctx-lh-supramarginal and ctx-lh-insula. The value “9.021299” in the first column is the probability (in %) that a fiber passing through a voxel of the ROI belongs to this connection. Similarly, the second most probable connection is between ctx-lh-precuneus and left_thalamus_proper. The probability (in %) that a fiber passing through a voxel of the ROI belongs to this connection is ~6.8578%.

You can identify which voxels of the ROI were located outside white matter by comparing the image of the ROI to the IIT_WM_atlas.nii.gz (or IIT_WM_atlas_256.nii.gz). You can then, either modify your ROI so that 100% of it overlaps with white matter, or you can use the original results of regionconnect(.py), keeping in mind that they correspond to only that portion of the ROI that overlaps with white matter.

How to conduct ROI-based analyses in white matter using the IIT Human Brain Atlas

The purpose of this chapter is to explain how to use the white matter resources of the IIT Human Brain Atlas to conduct region of interest (ROI) analyses in white matter. The IIT Human Brain Atlas offers at least 3 options for white matter parcellation. All 3 options are connectivity-based, and not focused on anatomical structures (e.g. external capsule, internal capsule). The 3 connectivity-based parcellation options provided by the IIT Human Brain Atlas are:

- 1) the top layer of the multi-layer white matter labels (in the following we will refer to this as the “top layer” approach),
- 2) masks of the TDI maps for all connections in the IIT connectome (we will call this the “connectome” approach),
- 3) masks of major bundles (we will call this the “bundles” approach).

In the following, we explain the 3 options in more detail.

“Top layer” approach

The IIT white matter atlas contains multi-layer white matter labels. This means that each white matter voxel is assigned a list of gray matter label-pairs with the most probable connections through that voxel (for more information see [“How to interpret the information in the IIT white matter atlas”](#)). In each voxel of the atlas, the first (top) layer of the multi-layer label represents the most probable white matter connection through that voxel. The map that shows the top layer for each voxel can be accessed by downloading:

IIT_WM_atlas_60_top_layers.zip

(or **IIT_WM_atlas_60_top_layers_256.zip** in 256x256x256 matrix size).

After unzipping this file, there will be a folder that contains maps of the top 60 layers. The map of the top layer is named:

IIT_WM_atlas_l1.nii.gz

(or **IIT_WM_atlas_l1_256.nii.gz** in 256x256x256 matrix size)

(see how to visualize the top layer using [FSLeyes](#) or [ITK-SNAP](#)) and provides a WM parcellation that can be used for region of interest analyses.

To transfer this parcellation to data from individual subjects, one would need to spatially normalize the individual subject data to the IIT Human Brain Atlas (see [“How to spatially normalize individual DTI data to the IIT Human Brain Atlas using DTI-TK”](#)).

[Skeletonized versions of the above files](#) are also available:

IIT_WM_atlas_60_top_layers_skeletonized.zip

(or **IIT_WM_atlas_60_top_layers_skeletonized_256.zip** in 256x256x256 matrix size)
and

IIT_WM_atlas_I1_skeletonized.nii.gz

(or **IIT_WM_atlas_I1_skeletonized_256.nii.gz** in 256x256x256 matrix size).

These provide the “top layer” parcellations of the IIT white matter skeleton and could be used in skeletonized ROI analyses. To project individual subject data to the IIT white matter skeleton follow the steps in the [“How to use the IIT Human Brain Atlas in TBSS”](#).

“Connectome” approach

The IIT Human Brain Atlas includes track density images (TDI) for all connections in the IIT connectome. The TDI maps can be obtained by downloading:

IIT_TDI.zip

(or **IIT_TDI_256.zip** in 256x256x256 matrix size).

This zipped directory contains one file per connection (for more information, see the description of IIT_TDI.zip in the [“White matter atlas files”](#)). The TDI files can be masked according to the user’s requirements (e.g. 5% of the maximum track density), and can be converted to masks for use in ROI analyses. To transfer these masks to data from individual subjects, one would need to first spatially normalize the individual subject data to the IIT Human Brain Atlas (see [“How to spatially normalize individual DTI data to the IIT Human Brain Atlas using DTI-TK”](#)).

“Bundles” approach

The IIT Human Brain Atlas also includes TDI maps for major bundles. The bundles are included in the zip file:

IIT_bundles.zip

(or **IIT_bundles_256.zip** in 256x256x256 matrix size).

This zipped directory contains one file per bundle (for more information, see the description of IIT_bundles.zip in the [“White matter atlas files”](#)). The TDI files of the bundles can be masked according to the user’s requirements and be converted to masks for use in region of interest analyses. To transfer these masks to data from individual subjects, one would need to first spatially normalize the individual subject data to the IIT Human Brain Atlas (see [“How to spatially normalize individual DTI data to the IIT Human Brain Atlas using DTI-TK”](#)).

[Skeletonized versions of these files](#) are also available:

IIT_bundles_skeletonized.zip

(or **IIT_bundles_skeletonized_256.zip** in 256x256x256 matrix size).

These provide TDI information about the bundles along the IIT white matter skeleton. Once masked to the user’s preference, they can be used as skeletonized masks of the bundles in skeletonized ROI analyses. To project individual subject data to the IIT white matter skeleton follow the steps in the [“How to use the IIT Human Brain Atlas in TBSS”](#).

How to use the skeletonized version of the IIT white matter atlas

The purpose of the skeletonized version of the IIT white matter atlas is to simplify use of the atlas in combination with TBSS analyses on the IIT skeleton (IITmean_FA_skeleton.nii). The skeletonized atlas can be used in the same ways as the regular white matter atlas.

Skeletonized versions of the following files of the IIT white matter atlas are available at www.nitrc.org/projects/iit:

IIT_WM_atlas.nii	IIT_WM_atlas_ skeletonized .nii
IIT_WM_atlas_confidence.nii	IIT_WM_atlas_confidence_ skeletonized .nii
IIT_WM_atlas_60_top_layers.zip	IIT_WM_atlas_60_top_layers_ skeletonized .zip
IIT_WM_atlas_confidence_60_top_layers.zip	IIT_WM_atlas_confidence_60_top_layers_ skeletonized .zip
IIT_TDI_sum.nii	IIT_TDI_sum_ skeletonized .nii
IIT_bundles.zip	IIT_bundles_ skeletonized .zip

OR in 256x256x256 matrix size:

IIT_WM_atlas_256.nii	IIT_WM_atlas_ skeletonized _256.nii
IIT_WM_atlas_confidence_256.nii	IIT_WM_atlas_confidence_ skeletonized _256.nii
IIT_WM_atlas_60_top_layers_256.zip	IIT_WM_atlas_60_top_layers_ skeletonized _256.zip
IIT_WM_atlas_confidence_60_top_layers_256.zip	IIT_WM_atlas_confidence_60_top_layers_ skeletonized _256.zip
IIT_TDI_sum_256.nii	IIT_TDI_sum_ skeletonized _256.nii
IIT_bundles_256.zip	IIT_bundles_ skeletonized _256.zip

