Analyze This! Practicalities of fMRI and Diffusion Data Analysis
Data Download Instructions

Weekday Educational Course, ISMRM 23rd Annual Meeting and Exhibition
Tuesday 2nd June 2015, 10:00-12:00, Room 718A
http://ismrm.org/15/program_files/Tu03.htm

Purpose of the Course

The aim of this course is to help attendees better understand how to use the various software packages that are made freely available for fMRI and diffusion MRI data analysis. Attendees will be invited to download some data and analyze it using their favorite freeware software package(s). Experts in the use of each package will present their analysis of the data, and will showcase the capabilities of the software. ISMRM attendees will be invited to submit a slide summarizing their results along with any questions they have. A selection of these will be answered during the Discussion periods.

Software Packages

The following data analysis software packages will be showcased:

fMRI analysis packages

FSL: http://www.fmrib.ox.ac.uk/fsl
SPM: http://www.fil.ion.ucl.ac.uk/spm
AFNI: http://afni.nimh.nih.gov/afni

Diffusion analysis packages

FSL: http://fsl.fmrib.ox.ac.uk/fsl
Camino: http://cmic.cs.ucl.ac.uk/camino
MRtrix3: https://github.com/jdtournier/mrtrix3
Track Vis: http://trackvis.org
MRI Studio: http://www.mristudio.org

Data Download

Prof. David van Essen, joint head of the Human Connectome Project (HCP), has given permission for ISMRM delegates to use data from the NIH-funded Human Connectome Project, provided they are willing to agree to the HCP Open Access Data Use Terms. The following pages describe instructions to download the data that will be used for this ISMRM educational course. Some suggested questions that could be asked using these datasets are also appended.

Submitting a Question or Data Analysis Summary

During the Educational Session we aim to have two discussion periods. You are invited to send a one-slide summary of your data analysis and/or a question you might have about these software packages to Peter Jezzard (peter.jezzard@univ.ox.ac.uk). The deadline for submitting questions is Friday 29th May 2015. As many of these questions as possible will be included during the Discussion periods.

Instructions for Data Download

All data that will be used during the educational session can be obtained from the Human Connectome Project web site, http://humanconnectome.org

To access the data, first visit the site http://db.humanconnectome.org

There you will be prompted to 'Create an Account', if you do not already have one.

Once you have an account, log in via the http://db.humanconnectome.org web site.

As a first step, you will need to accept the Open Access Terms, by clicking on the relevant button.

fMRI Data

fMRI data will be taken from the **WU-Minn HCP Data – 500 Subjects + MEG2** cohort dataset. Access the data via the Download Image Data button on the top right of the respective panel, selecting the "Single Subject" option. Under "Processing Level", either select the "Unprocessed" option (if you wish to run your own preprocessing) or "Preprocessed" (if you want to start your analysis from data that has already been processed using the HCP pipelines) and click on the relevant + queue for download button. If working with unprocessed data you will then need to grab at least one of the resting-state downloads, and quite likely will also want the second resting-state session as well as the structural data. Also select the "Language Task fMRI" data by clicking on its + queue for download button. To start the download process, press the Download Packages button. Note that the HCP website uses the Aspera Connect protocol to speed up data transfer from their server to your computer. You will be prompted to download this software plugin and install it, if you do not already have it.

For working with HCP-preprocessed data, you will want either one or both of the minimally-preprocessed fMRI datasets, or the FIX-denoised datasets (which have the minimal-preprocessing applied as well as ICA-based structured noise removal), as well as (probably) the structural data. If you want to focus your analysis on finding resting-state networks and you're not interested in doing your own preprocessing and noise removal, we recommend working from the FIX-denoised datasets. Many of these different downloads have data in two "spaces" - both volumetric (3D/4D NIFTI files) and "grayordinates" (a combination of surface vertices and subcortical voxels: CIFTI files). The NIFTI files are more compatible with a wider range of software, but the CIFTI files allow for a more natural representation of the data, where (for example) cross-subject alignment will be better.

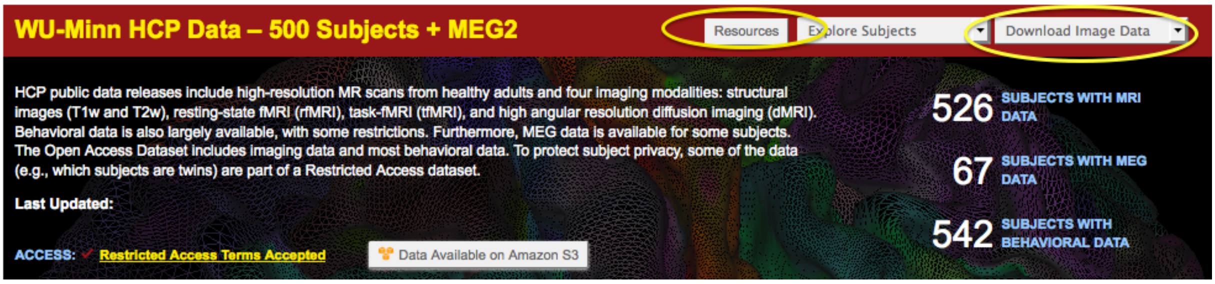
Diffusion Data

You can choose different datasets for the diffusion data, depending on whether you wish to download unprocessed or processed data, and depending on the size of dataset that you want to access.

Higher resolution diffusion data: The **WU-Minn HCP Data – 500 Subjects + MEG2** cohort dataset contains high-resolution data (1.25mm^3) in both Preprocessed and Unprocessed formats. This is a 3-shell diffusion series (3 different q-space diffusion tables, each collected with the phase encode gradients in L>R and R>L to invert any geometric distortion). Access the data via the Download Image Data button, selecting the "Single Subject" option. Under "Processing Level", you can either select the "Preprocessed" option, or the "Unprocessed" option. This provides data with or without any pre-processing applied (mostly geometric distortion correction). Now select the "Diffusion Preprocessed" or "Diffusion Unprocessed" data by clicking on the relevant + queue for download button. To start the download process, press the Download Packages button. Note that the HCP website uses the Aspera Connect protocol to speed up data transfer from their server to your computer. You will be prompted to download this software plugin and install it, if you do not already have it.

Lower resolution diffusion data: The **WU-Minn HCP Lifespan Pilot Data** cohort dataset contains lower-resolution data (1.5mm^3) in only Unprocessed format, which might be more manageable to analyze. This is a 2-shell diffusion series (2 different q-space diffusion tables, each collected with the phase encode gradients in L>R and R>L to invert any geometric distortion). First select the "All HCP Lifespan Subjects" from the Explore Subjects button. This should list a series of subjects in different age ranges. We suggest that you aim to analyze the first of the adults (Subject LS4025) by clicking on the LS4025 selection. Next press the Download Images button to show the available data. Select the "Diffusion Unprocessed" data by clicking on the relevant + queue for download button. To start the download process, press the Download Packages button. Note that the HCP website uses the Aspera Connect protocol to speed up data transfer from their server to your computer. You will be prompted to download this software if you do not already have it.

Detailed information on the data acquisition and fMRI task parameters may be found via the HCP website at http://www.humanconnectome.org/documentation or via the Resources option on the respective project panel.



HCP public data releases include high-resolution MR scans from healthy adults and four imaging modalities: structural images (T1w and T2w), resting-state fMRI (rfMRI), task-fMRI (tfMRI), and high angular resolution diffusion imaging (dMRI). Behavioral data is also largely available, with some restrictions. Furthermore, MEG data is available for some subjects. The Open Access Dataset includes imaging data and most behavioral data. To protect subject privacy, some of the data (e.g., which subjects are twins) are part of a Restricted Access dataset.

Last Updated:

ACCESS: ✓ Restricted Access Terms Accepted

Data Available on Amazon S3

526 SUBJECTS WITH MRI DATA

67 SUBJECTS WITH MEG DATA

542 SUBJECTS WITH BEHAVIORAL DATA

Data Analysis Suggestions

Here are some suggestions for what sort of analysis you might want to try with the different software packages:

fMRI analysis packages

FSL:

We will demonstrate how the HCP/FSL core pipelines are used to preprocess and denoise the resting-state fMRI data, including mapping the data onto "grayordinates", a combination of cortical-surface-vertices and subcortical-voxels. We will then show example connectivity and RSN analyses with the HCP rfMRI data.

SPM:

The SPM presentation will use both the HCP language task and resting state datasets for three different demonstrations. The HCP language data will be used to show a standard task-related GLM analysis stream. That dataset will also be used to explore task-related functional connectivity effects using the SPM psychophysiological analysis functions. The HCP resting state dataset will be used to demonstrate intrinsic functional connectivity effects using CONN, the SPM connectivity toolbox.
Full step-by-step tutorials for all three exercises will be posted at:
http://neurometrika.org/fMRI_Analysis_SPM

AFNI:

We plan to demonstrate Resting-State FMRI processing tools on the single-subject HCP data made available for this class and explore the results with AFNI's InstaCorr. For a more complete connectivity picture we also plan on generating anatomical connectivity results alongside functional connectivity ones with FATCAT & SUMA.
For those interested in task-based analysis we recommend using uber_subject.py to analyze the preprocessed task data.
We have setup a message board (http://afni.nimh.nih.gov/bootcamp/board/list.php?3) for the class where we will be posting processing instructions and where users can raise questions before the class.

Diffusion analysis packages

FSL:

FSL includes tools for advanced distortion correction (topup, eddy). You can use these tools to pre-process the raw Lifespan data (or a subset of it). Then, you can perform fiber orientation modelling (use bedpostx –model 2). You can perform tractography (for instance try reconstructing the optic radiation or the corticospinal tract), but can also use the tractography results to perform connectivity-based segmentation of gray matter regions. You can follow the steps outlined in the FSL course practical to achieve this (http://fsl.fmrib.ox.ac.uk/fslcourse/lectures/practicals/fdt2/index.html#conseg).

Camino:

Camino offers a variety of tools for model fitting and tractography; as well as data synthesis and simulation. The presentation at the conference will focus on model fitting and tractography. Pre-processing such as motion and distortion correction is required before using Camino; you may do this yourself or download the preprocessed HCP data from the instructions above.

Some of the model fitting routines in Camino can account for the spatially varying b-values in the HCP data. See http://cmic.cs.ucl.ac.uk/camino//index.php?n=Tutorials.HCP for more information and for example diffusion tensor reconstruction.

Tractography is performed with the **track** tool, using deterministic or probabilistic algorithms. Track will accept input from Camino model reconstructions; NIFTI diffusion tensors (from Camino or elsewhere), or the output of FSL's **bedpostx** program. Tractography results may be filtered within Camino using **procstreamlines**, and exported to VTK for visualization. The Track Vis developers have provided a converter tool to import Camino tracts into the Track Vis format for visualization in Track Vis. http://www.nitrc.org/projects/camino-trackvis

Please see the main Camino tutorial page for more examples: http://cmic.cs.ucl.ac.uk/camino//index.php?n=Main.Tutorials

MRtrix3:

MRtrix provides a set of tools to perform various types of analysis of diffusion-weighted MRI data. Here we will demonstrate the latest version of the software, MRtrix3 (https://github.com/jdtournier/mrtrix3). We will describe the use of MRtrix3 to reconstruct various major white matter pathways, as well as its use in generating a connectivity matrix. For this, we recommend you use the Preprocessed HCP data, and also download the Structural Preprocessed data (used for visualisation, Anatomically Constrained Tractography, SIFT, connectome construction, and Multi-Tissue CSD). You can use the FreeSurfer parcellations (in the Structural Preprocessed data) to build the connectivity matrix. You'll find information related to software installation, basic usage, and tutorials for the more advanced analyses on the MRtrix3 wiki: https://github.com/jdtournier/mrtrix3

Track Vis:

1) Download the preprocessed high-resolution diffusion data from the "WU-Minn HCP Data – 500 Subjects + MEG2" dataset.

2) Unzip the "data" and "nodif_brain_mask" files so that the file suffixes are ".nii" as opposed to ".nii.gz" (Diffusion Toolkit prefers unzipped nifti files).

3) To reconstruct deterministic fiber tracts with Diffusion Toolkit, use the following parameters: Imaging Model = DTI, Raw data file = "data.nii", Maximum b value = 3010, Number of b0 volumes = 1, Image orientation = auto, Apply gradient orientation

correction = checked, Mask image = nodif_brain_mask.nii (mask threshold will automatically change to 0.01 to 1.01 once this file is uploaded), angle threshold = 60, Orientation patch = Invert Z with No Swap.

4) For the Gradient table, upload the attached gradient table (see Appendix), in which the vectors have been scaled according to the b values at which they were acquired (press the "file" icon to the right of the Gradient table menu, then click the "+" button, then name your new gradient table, then copy and paste the gradient table from the Appendix, then click the "save" icon).

5) Once Diffusion Toolkit is finished reconstructing the fiber tracts, open TrackVis and load the ".trk" file. Under "Image," click the "+" button and add the "dti_b0.nii", "dti_dwi.nii", "dti_adc.nii", "dti_fa.nii", and "dti_fa_color.nii" files.

6) To confirm that the tracts are in the appropriate neuroanatomic orientation, manually trace a region of interest (ROI) in the corpus callosum and create a new track group to visualize the transcallosal fibers; also trace ROIs in the posterior limbs of the internal capsules and the cerebral peduncles, and create a track group that contains both of these ROIs (right click on the track file and select "toggle existing ROI") to visualize the corticospinal tracts.

7) During the presentation, we will identify connections between nodes of the Default Mode Network and nodes of the Ascending Reticular Activating System to demonstrate TrackVis' features. Experiment on your own with tractography analyses of these networks before the presentation!

MriStudio / MriCloud:

MriStudio (http://www.mristudio.org) consists of three programs that run in the Windows platform. It offers an integrative pipeline for artifact corrections, outlier rejection, comprehensive quality control reports, tensor calculation, and tract reconstruction. It also offers quantitative analysis tools based on image normalization using diffeomorphic transformation and atlas-based white matter segmentation. A new image analysis platform, MriCloud (http://www.mricloud.org), is web-based platform-free software, which was introduced in 2014. It offers fully automated DTI analysis pipelines including multi-atlas brain segmentation, which utilizes publicly available supercomputing resources for the CPU-demanding tasks.

Appendix. Gradient table values needed for TrackVis.

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