NEURO M203 & BIOMED M263 WINTER 2014

MRI Lab 2: Neuroimaging Connectivity Lab

In today's lab we will work with sample diffusion imaging data and the group averaged fMRI data collected during your scanning session.

We will again use Brainsuite software to view and interact with the data, so you will not need to reinstall this program (provided you haven't deleted it from last week).

We will provide an intro to diffusion imaging and functional connectivity analyses at the start of class. A brief into to DTI is also provided at the end of these lab notes.

Instructions For Downloading Data:

Downloading Data

1. Open a browser, go to http://users.bmap.ucla.edu/~narr/M203_NEUROANATOMY_LAB/

a. Find the zipped folders containing sample DTI data labeled "Neuroanatomy_DTI.zip" Download this folder.

b. Find the zipped folder containing sample functional connectivity data labeled "Neuroanatomy_FC.zip" Download this folder.

c. Unzip these 2 folders on your computer desktop. This will take many megabytes of space.

Note: If you have problems downloading, let us know and we will upload your data from a flash drive.

Imaging Data

1. You should see the following files in the "Neuroanatomy_Class_DTI" folder:

    a. brainsuite_tracts.bst (BrainSuite study file)

    b. class.nii.gz (T1 image)

    c. tracts.dft (tractography file)

    d. class.svreg.corr.label.nii.gz (BrainSuite generated subcortical labels)

    e. label_descriptions.xml (BrainSuite Label descriptions)

    f. class.left.pial.cortex.svreg.dfs (left hemisphere surface)

    g. class.right.pial.cortex.svreg.dfs (right hemisphere surface)

    h. class.mask.nii.gz (mask file)

    i. brainsuite_light.bst (BrainSuite Study file with less tracts)

    j. tracts_LIGHT.dft (tractography file)

2. You should have the following files in the "Neuroanatomy_Class_FC" folder:

    k. ICA_statsmapA.nii.gz

    l. ICA_statsmapB.nii.gz

    m. ICA_statsmapC.nii.gz

    n. ICA_statsmapD.nii.gz

    o. ICA_statsmapE.nii.gz

    p. bg_image.nii.gz

1. Tractography:

A. Drop **BrainSuite_tracts.bst** onto BrainSuite. This bst file loads the following files into BrainSuite:
- o Structural volume (class.nii.gz)
- o Structural mask (class.mask.nii.gz)
- o Left hemisphere surface rendering (class.left.pial.cortex.svreg.dfs)
- o Right hemisphere surface rendering class.right.pial.cortex.svreg.dfs
- o Structural segmentation label (class.svreg.corr.label.nii.gz)
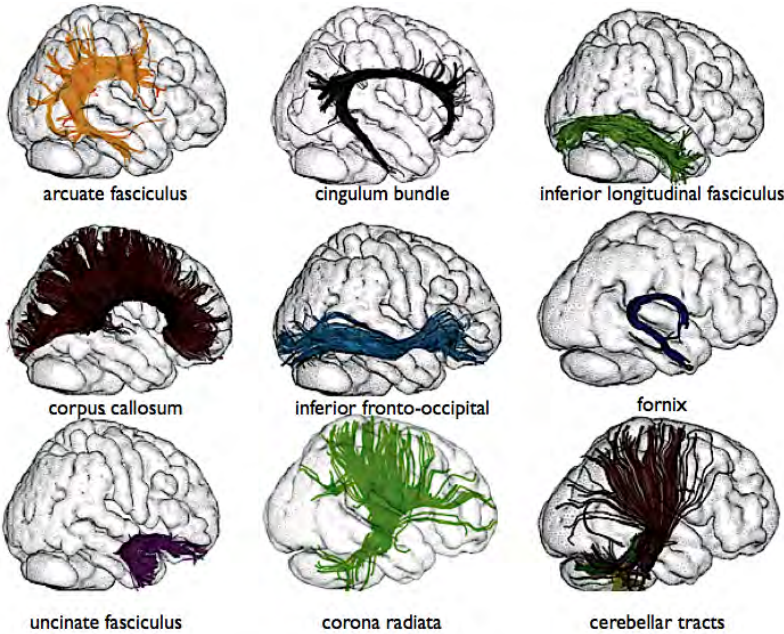- o Label Description file (label_descriptions.xml)
- o Diffusion tracts (tracts.dft)

   *use BrainSuite_LIGHT.bst if your system crashes or lag

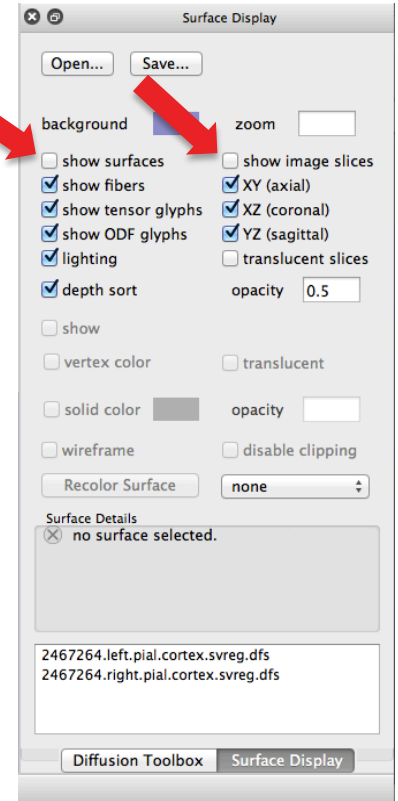B. Adjust the display to view tractography:
1. Hide the surfaces by deselecting **show surfaces** on **Surface Display Menu** ('S')
2. Hide the slices by deselecting **show image slices** on **Surface Display Menu** ('S')
3. Zoom in on the 3D view (Command + scroll)

C. Explore the tracts by scrolling through. View different planes using the **x**, **y**, and **z** keys to make cuts.
1. Make a cut using the "x" key. Scroll through the sagittal view to identify the tracts
2. Use the "y" and "z" keys to view tracts from alternative **angles**.
3. Try to identify the following tracts

arcuate fasciculus   cingulum bundle   inferior longitudinal fasciculus

corpus callosum   inferior fronto-occipital   fornix

uncinate fasciculus   corona radiata   cerebellar tracts

Catani and Thiebaut de Schotten 2008

D. For the tracts that are not easily identifiable, use **Tract filtering** on the **Diffusion Toolbox** ('D') to only view fibers that go through a region of interest (ROI). Explore the tracts using spherical ROIs
1. Select the **Spherical ROI1** checkbox
2. Scroll through the image to see tracts connected to the sphere
3. Adjust the sphere **radius** to see larger regions
4. Adjust other parameters (e.g. wireframe)
5. Move the ROI by adjusting its position in the 3 other **views**
6. Deselect **ROI1** checkbox when finished
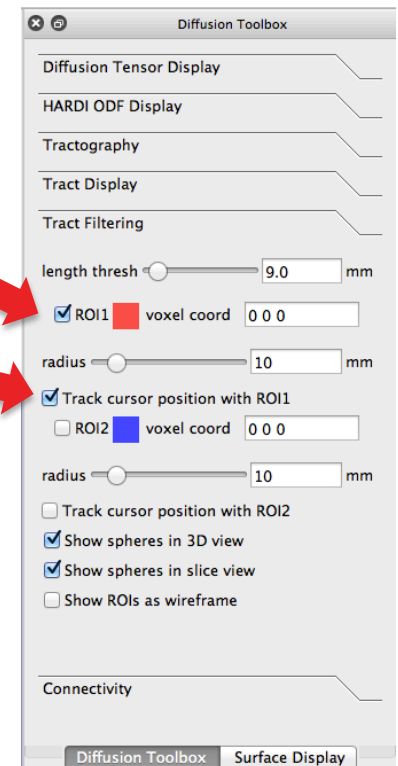
E. The Connectivity Viewer allows you to explore connections between different ROIs
   1. In the **Diffusion toolbox** ('D'):
      (1) Open the **Connectivity** tab.
      (2) Press the **Compute Connectivity** button (may take 1-2 minutes).
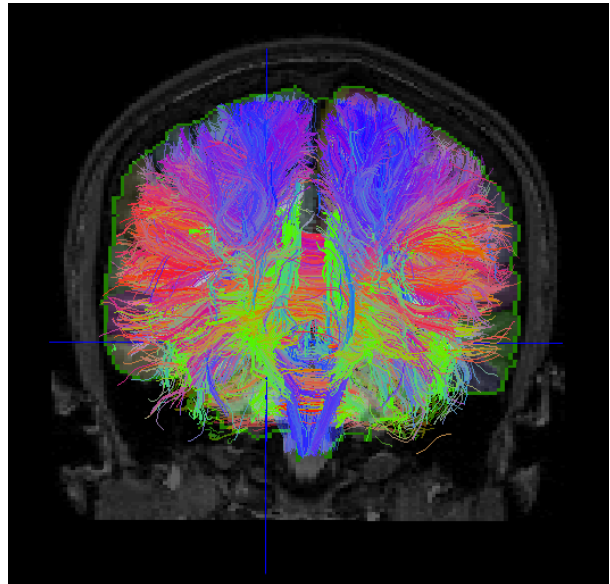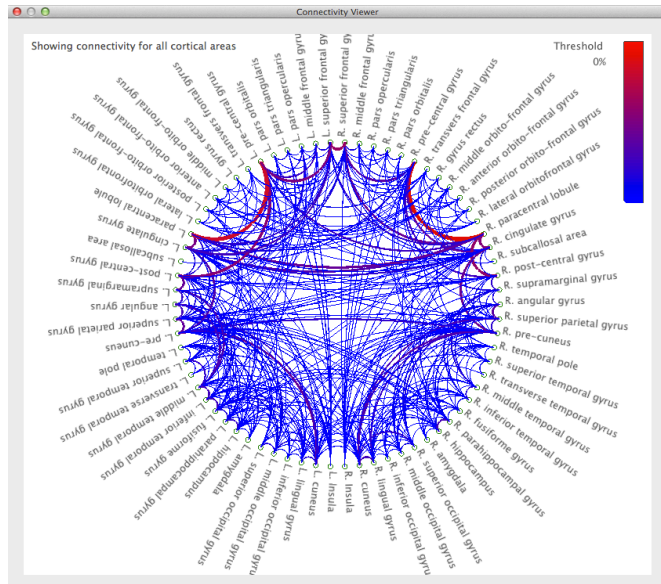
   2. Select nodes along the wheel
   3. Command-select to view connections between only 2 ROIs, note which tracts exits between the two selected ROIs.
   4. Shift-select to view multiple connections, Command-select to view fibers between two ROIs
   5. Press keys **1,2,3,4,5** and **6** to observe different subsets (e.g., lobes). Each key corresponds with the following subsets.
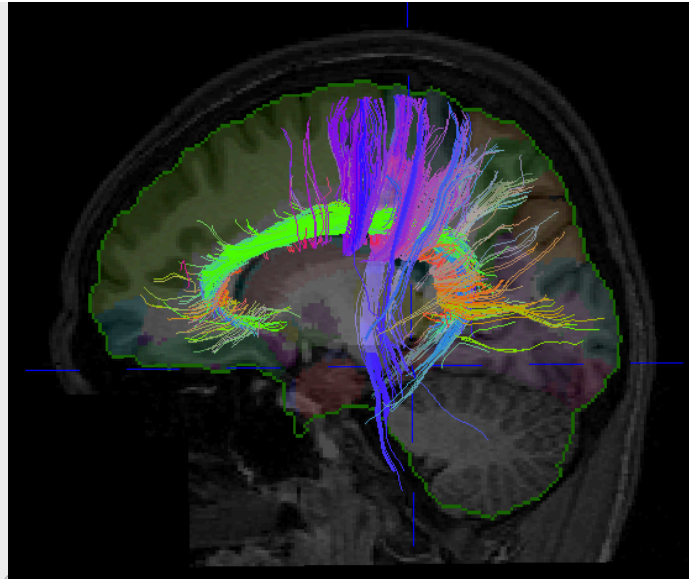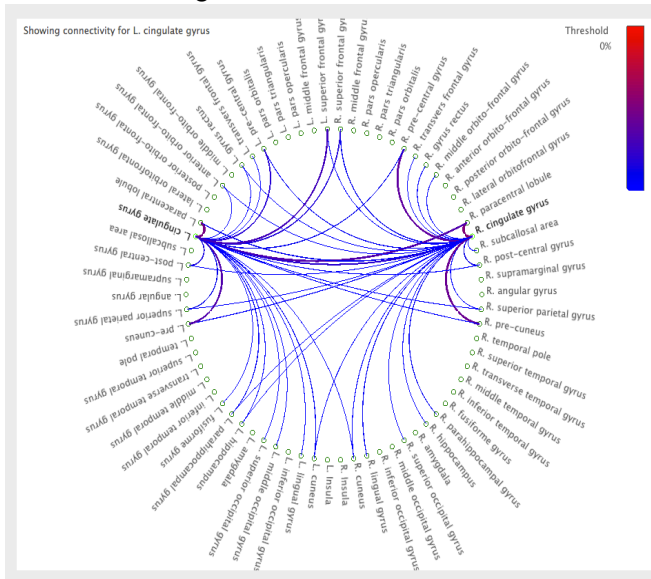
      (1) All cortical areas
      (2) Frontal lobe ROIs
      (3) Parietal lobe ROIs
      (4) Temporal lobe ROIs
      (5) Occipital lobe ROIs
      (6) Subcortical areas

2. Independent Component Analysis, finger-tapping fMRI data

In this exercise, we'll look at partial results from an independent component analysis (ICA) of the combined fMRI data for the whole class (i.e., group-level statistics). As we discussed during the lecture/intro, ICA can identify functionally co-active brain networks based on their mutual spatio-temporal similarity. In other words, ICA groups together voxels that share similar timecourses and spatial distrubtions across subjects into different "independent components", and is used to measure functional connectivity.

In our data, the results of the ICA are heavily influenced by the BOLD response to different aspects of the finger-tapping task. On the next page are 5 timecourses for components identified by the ICA (red solid lines), overlayed with the timecourse of the task (black dahsed lines). Your job is to match each timecourse with the corresponding statistical map. (*Hint: Only one of these components is **not** related to the task.*)

To load statistical maps:

- Drag **bg_image.nii** into "Overlay 2" in the "Image Display Properties" window. This is your reference for anatomy.

- Drag each statistical map (**ICA_statsmapA.nii, ICA_statsmapB.nii, ICA_statsmapC.nii, ICA_statsmapD.nii, ICA_statsmapE.nii**) into "Volume" in "Image Display Properties."

- To change the map colors, go to *Image, Volume LUT, Jet.*

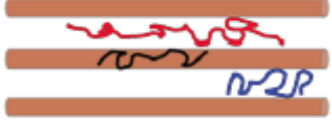If you'd like to check your answers (or you want hints), let Amber know. Enjoy!

	Timecourse	Map
	A	A
	B	B
	C	C
	D	D
	E	E

Timecourse A

Timecourse B

Timecourse C
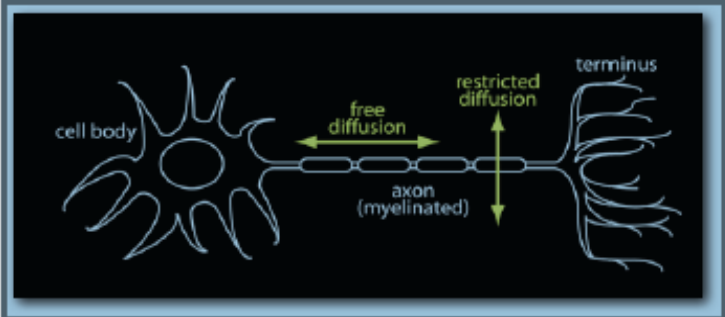

Timecourse D

Timecourse E
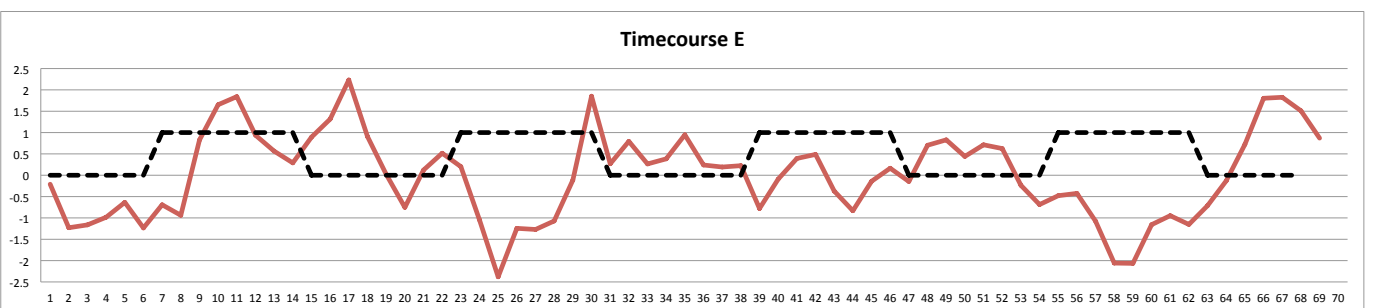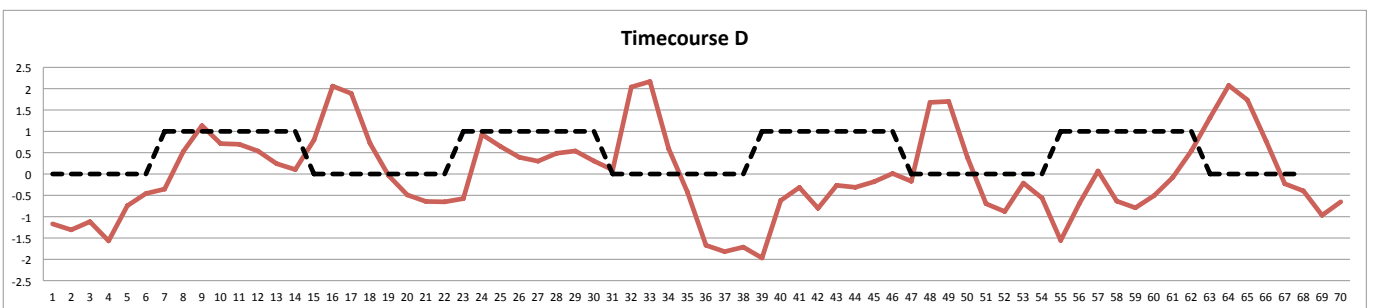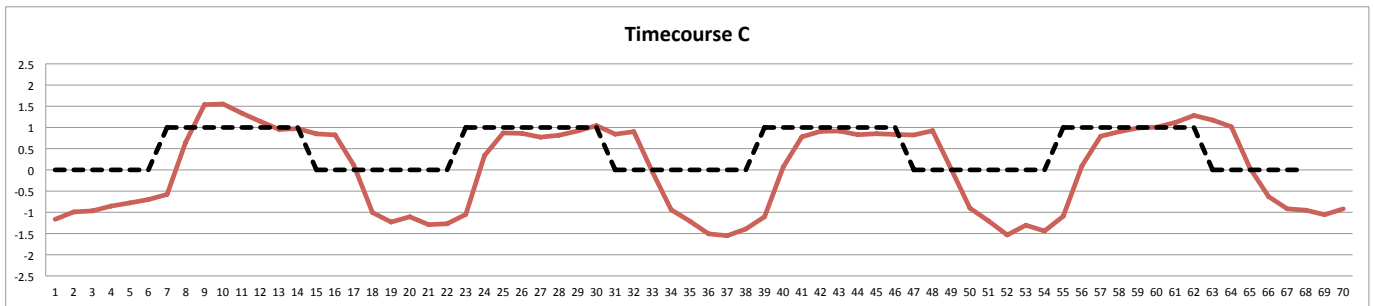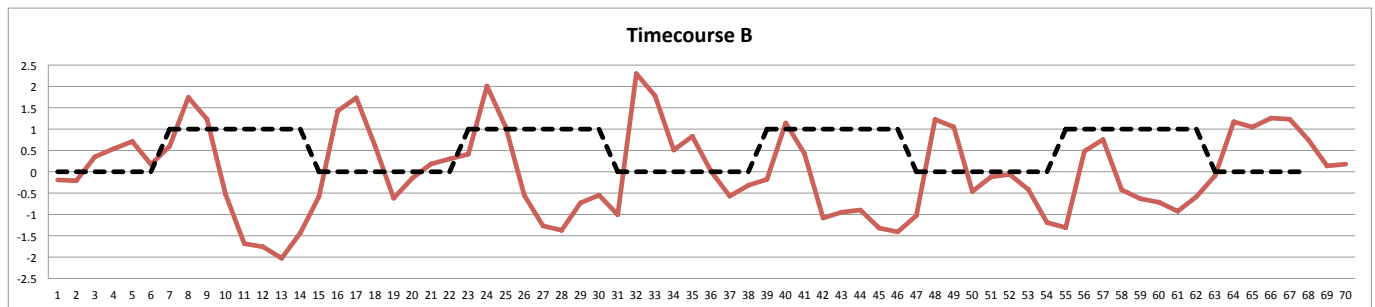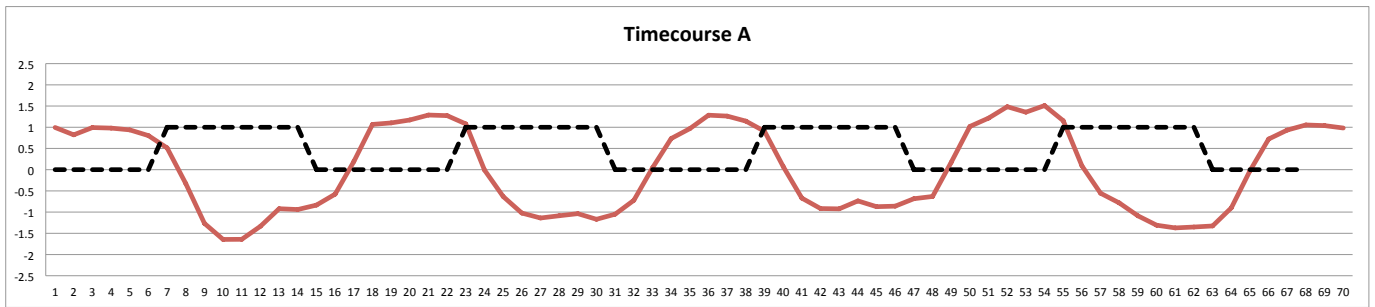
BRIEF INTRO TO DTI

- Water diffusion is anisotropic in coherently organized fibers (muscle and large axon bundles). Diffusivity is largest parallel to, and smallest perpendicular to fiber orientation.

- To describe anisotropic diffusion, diffusivity must be measured in more than one direction. In diffusion imaging, the MR signal is thus made sensitive to the random diffusion motions of water molecules. Applying linear gradient fields in different axes allows diffusivity may be measured in different directions.

- In the mid 1990's, the *diffusion tensor model* (Basser et al., 1994) was devised to describe both the shape and orientation (the diffusion ellipsoid) of anisotropic diffusion.

- By applying at least 6 gradient directions, the diffusion tensor provides measures of the three principal diffusivities (eigenvalues) and directions (eigenvectors) to characterize the 3D shape of diffusion.


Diffusion in the Brain. Why is it Interesting?

Free Diffusion	Diffusion in GM	Diffusion in WM
Isotropic	Isotropic	Anisotropic

Diffusion is hindered by tissue boundaries, membranes, etc.
Marker for tissue microstructure (healthy and pathology)
Diffusion is anisotropic in white matter

The Diffusion Tensor Ellipsoid
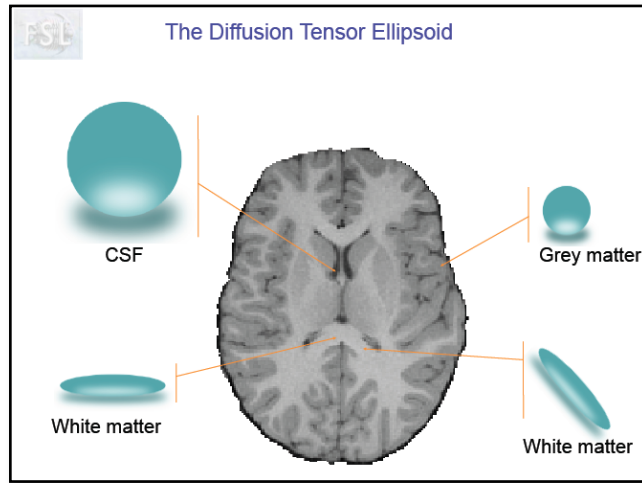
- The diffusion tensor thus estimates magnitude and preferred direction of water diffusion in each voxel. Although six directions are sufficient, more directions produce more accurate tensor estimates.

- NOTE: More advanced 'non-tensor' based models such as HARDI and DSI allow more precise fitting of diffusion properties and typically utilize >60 diffusion directions.

- Fiber direction is indicated by the tensor's main eigenvector. This vector can be color-coded to map the position and orientation of a white matter pathway.

- Different tractography methods may be used to identify specific pathways in the brain.

- Scalar metrics derived from the diffusion tensor (fractional anisotropy, mean, radial and axial diffusivity) within particular white matter pathways or other regions of interest can be compared across subjects.
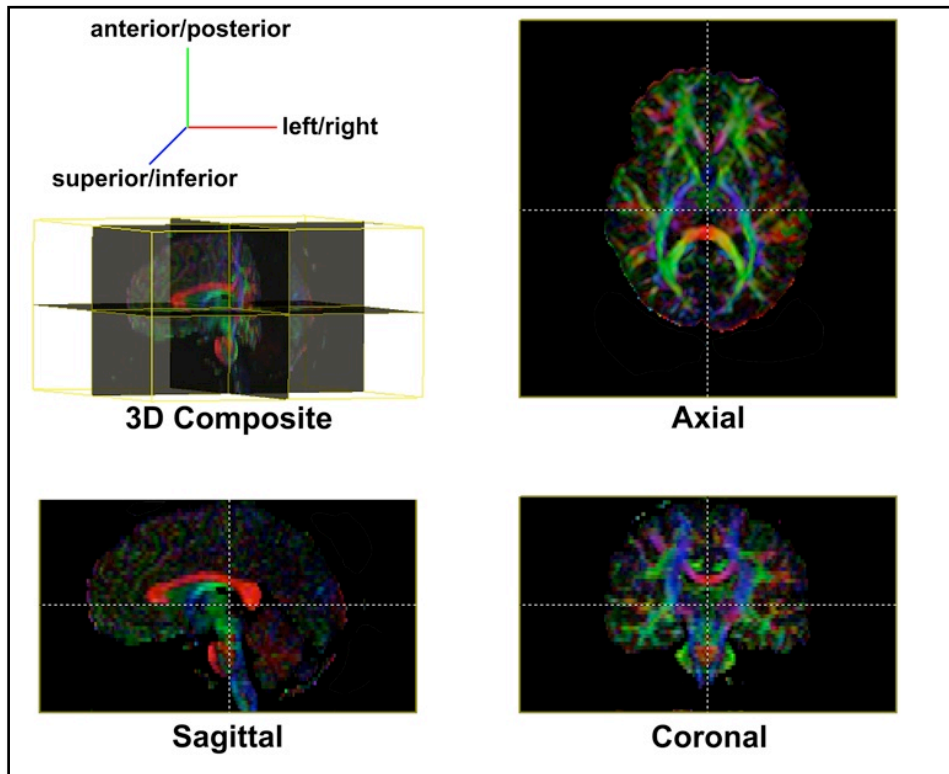
FA-weighted color direction map