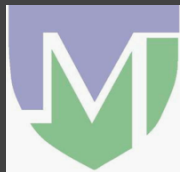# TRACULA:
Troubleshooting, visualization, and group analysis

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Directory structure

- Each subject has a TRACULA output directory, **`$dtroot/$subj/`**

- Under this directory:
  - **`dmri/`** : Raw diffusion images, outputs of tensor fit
  - **`dmri.bedpostX/`** : Outputs of ball-and stick model fit
  - **`dlabel/`** : Files that aid the tractography (from subject's own anatomical , *e.g.* aparc+aseg, or from tract atlas, *e.g.* anatomical priors, initialization)
  - **`dpath/`** : Outputs of tractography
 - **`scripts/`** : Log files

Ball-and-stick model fit

- Multiple diffusion compartments in each voxel:
  - Anisotropic compartments that model fibers (1, 2, ...)
  - One isotropic compartment that models everything left over (0)

- FSL/bedpostX infers from the data:
  - Orientation angles of anisotropic compartments
  - Volumes of all compartments
  - Overall diffusivity in the voxel

- Multiple fibers only if they are supported by data
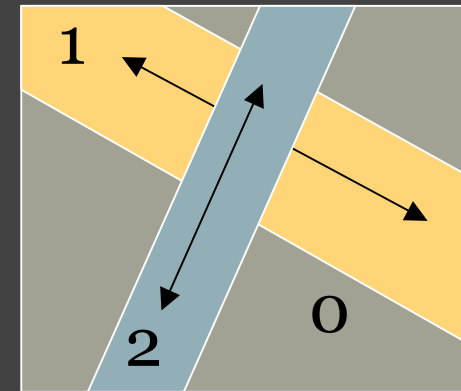
Troubleshooting: Gradient vectors

- Check that orientation of tensors follows corpus callosum, cingulum, corticospinal tract
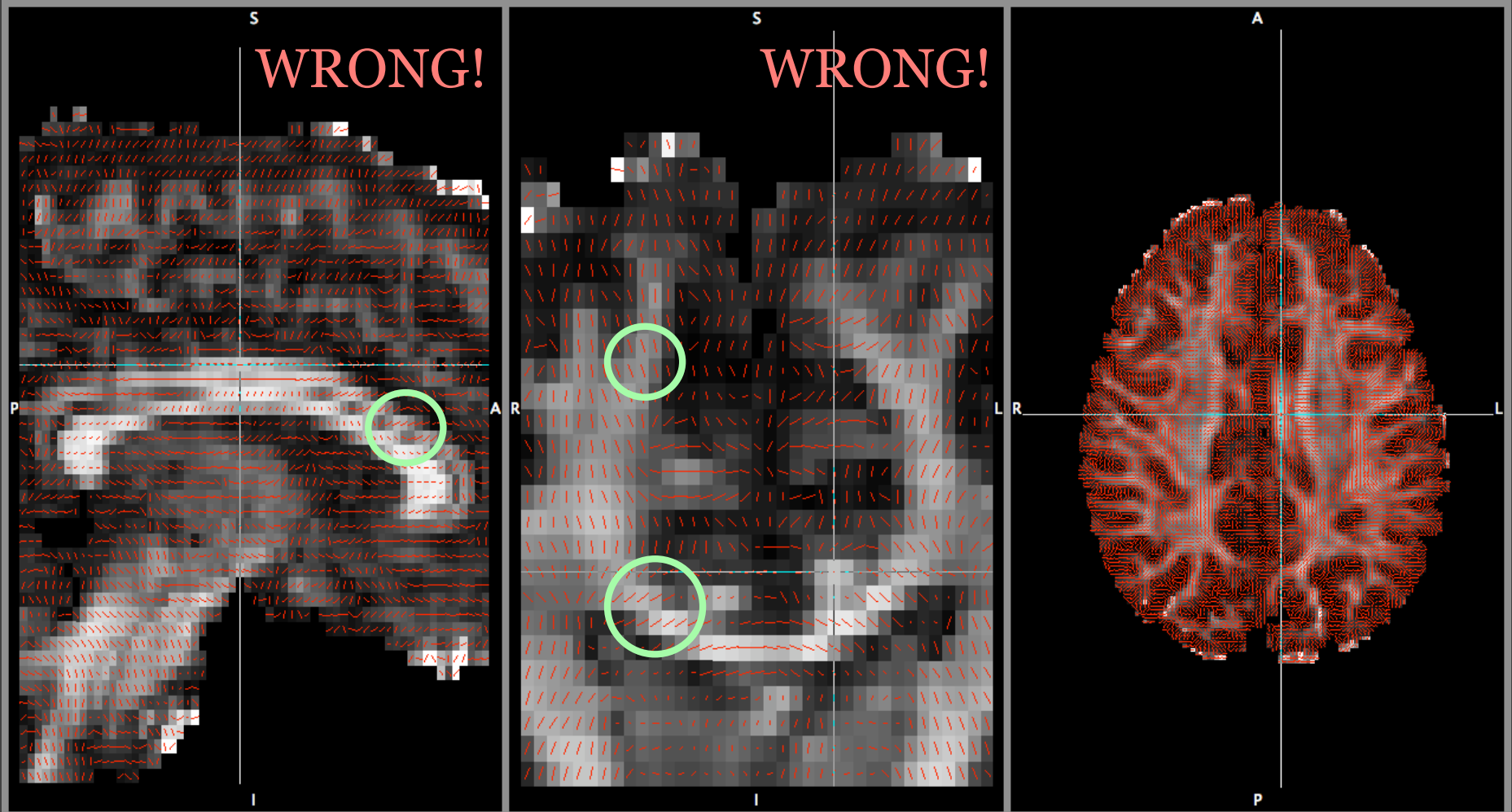
Troubleshooting: Registration to T_1

- Check aparc+aseg transformed to diffusion space, overlay on FA

- ```
  freeview dmri/dtifit_FA.nii.gz\
      dlabel/diff/aparc+aseg.bbr.nii.gz
  ```

- Also good for checking quality of aparc+aseg (perhaps recon-all brain mask includes too much or too little?)
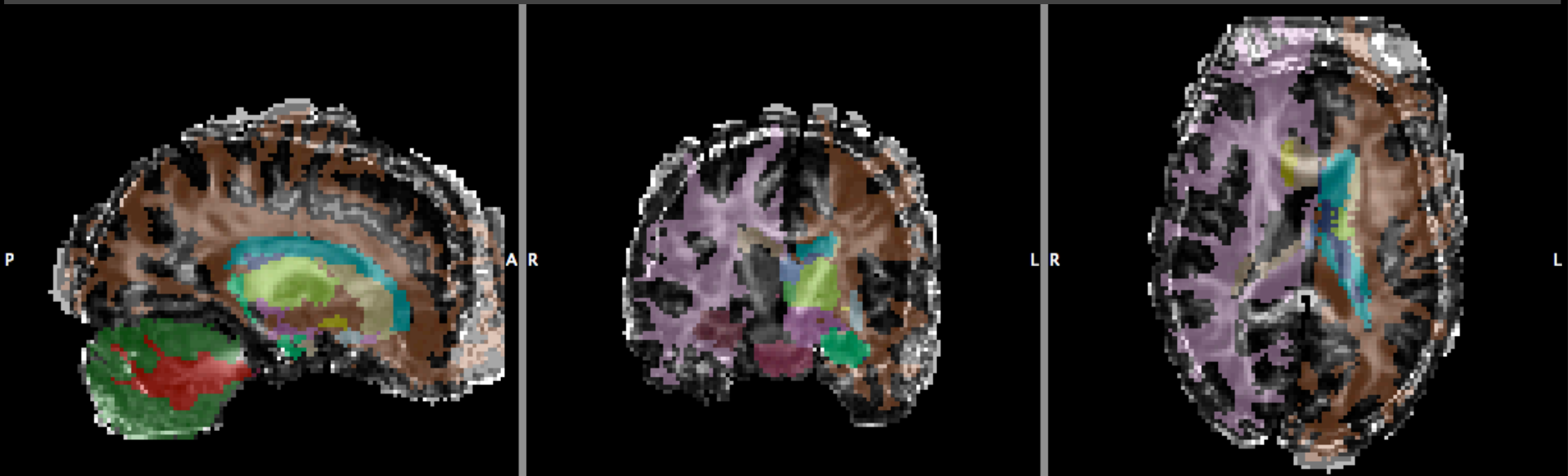
Troubleshooting: Initialization

- If path has not moved away from its initial position (reconstructed path looks like a 1D curve), there was something wrong with this initial position (maybe goes off white matter?)

- `freeview dmri/dtifit_FA.nii.gz \`
  `dlabel/diff/rh.slfp_PP_avg33_mni_bbr_cpts_5.nii.gz`

Troubleshooting: Initialization

- If initialization has failed for a specific pathway and subject, choose another initialization and repeat reconstruction (only repeat this particular pathway/subject)

- In configuration file:
  - `set reinit = 1`
  - Limit subjlist to this subject only
  - Limit pathlist to this pathway only

- Repeat:
  trac-all -prior -c dmrirc
  trac-all -path -c dmrirc

- Make sure to remove `set reinit = 1` when done with this!

Visualization with freeview

- There is a 4D volume where all the pathway distributions that were estimated have been merged

- Opening this file in freeview will display all distributions as isosurfaces, thresholded at 20% of their maximum value.

Visualization: 3D view

- ```
  freeview dmri/dtifit_FA.nii.gz \
       -tv dpath/merged_avg33_mni_bbr.mgz
  ```
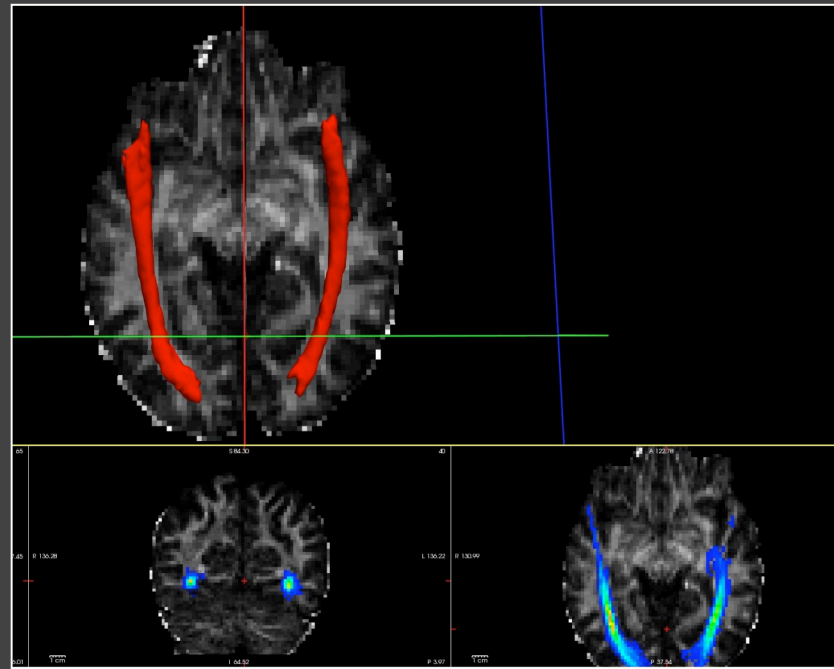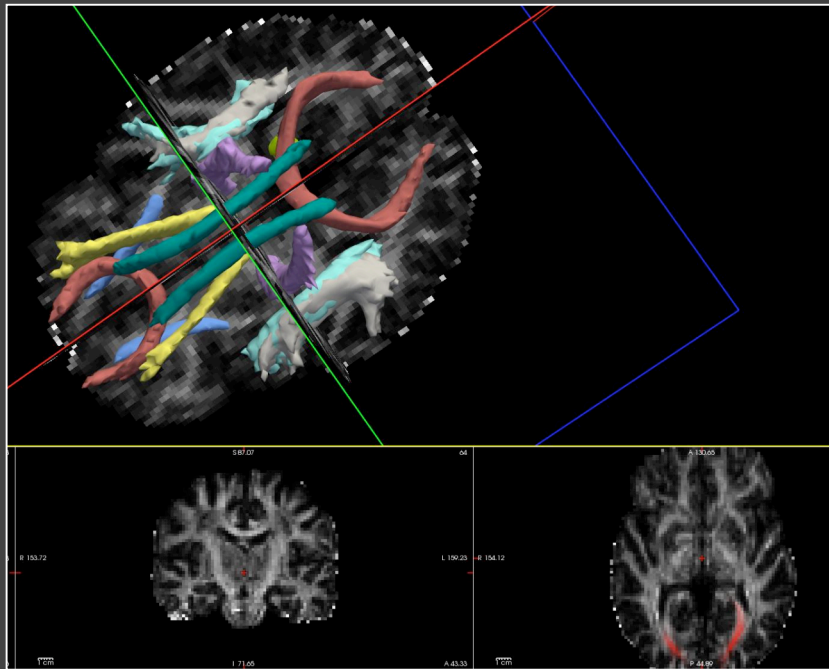

Change threshold for display

Visualization: 3D view

- `freeview dmri/dtifit_FA.nii.gz \`
    `-tv dpath/merged_avg33_mni_bbr.mgz`
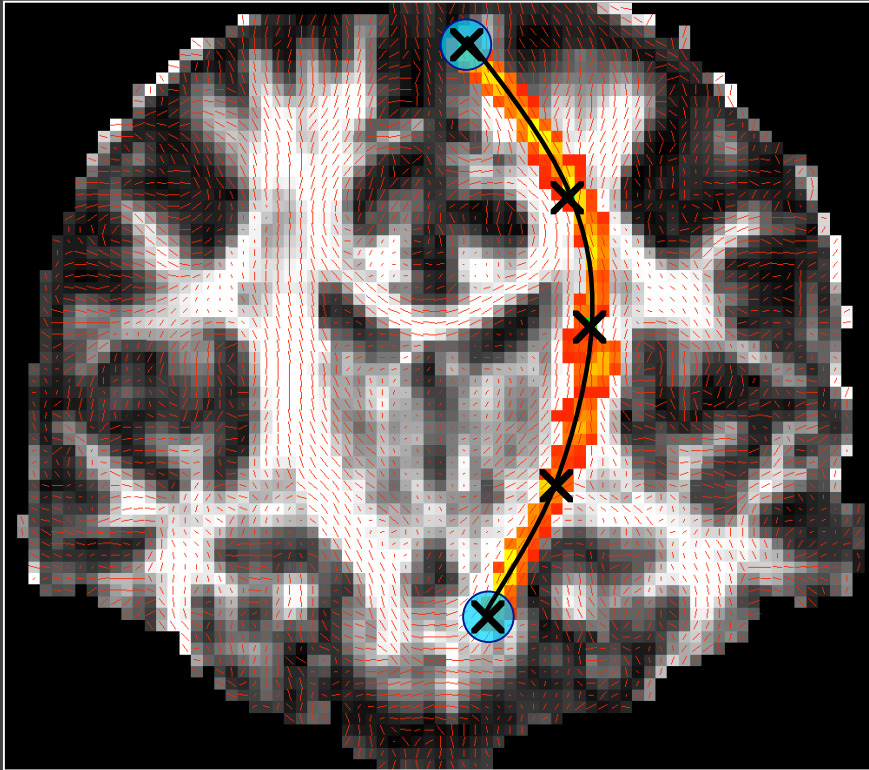
Change threshold for display

Visualization: Slice view

- `freeview dmri/dtifit_FA.nii.gz \`
  `    -tv dpath/merged_avg33_mni_bbr.mgz`
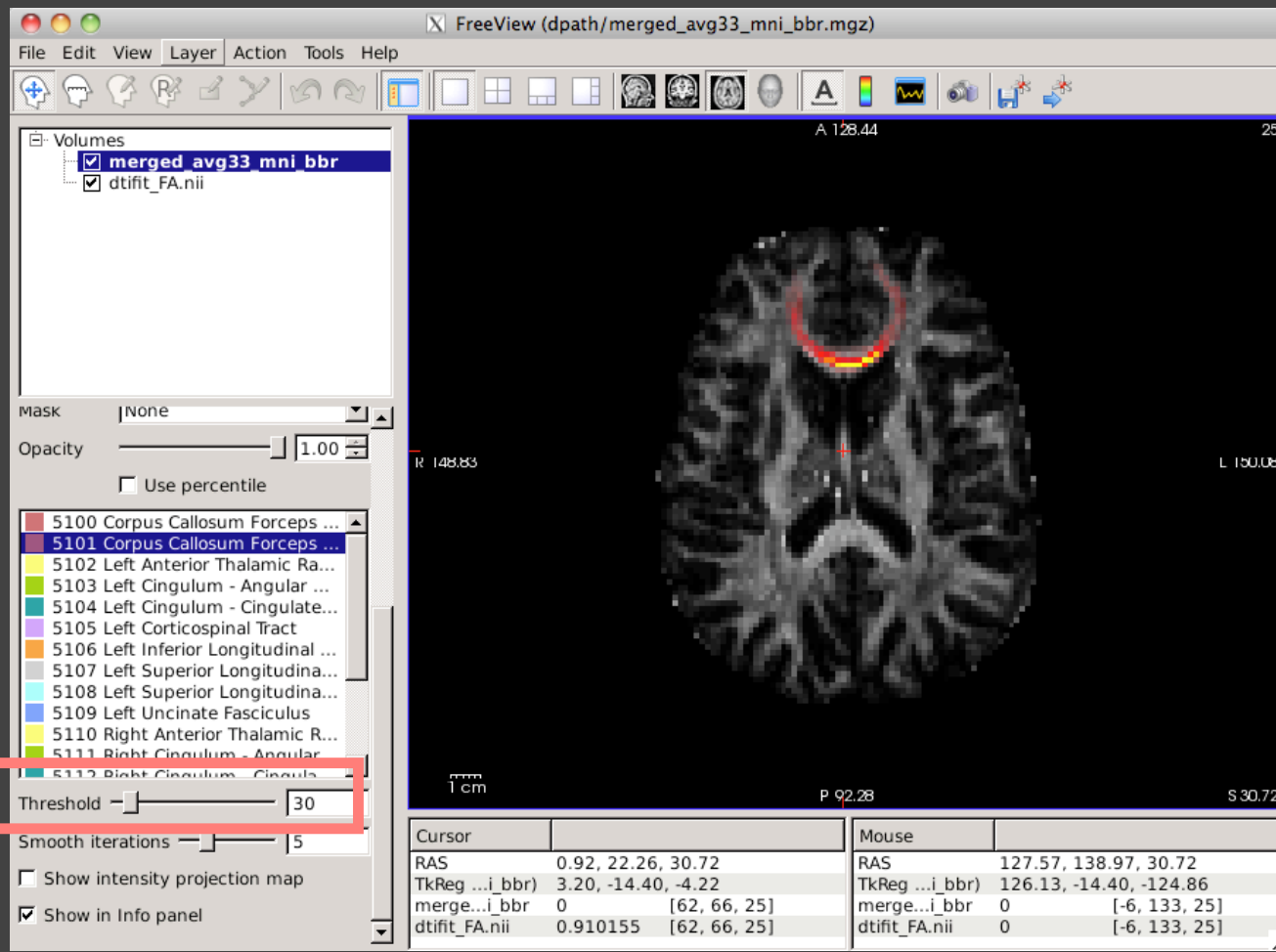
Change
threshold
for display

Tract-based measures

- Reconstruction outputs
  - Posterior probability distribution of pathway given data (3D):

    `paths.pd.nii.gz`
  - Maximum *a posteriori* pathway (1D):

    `path.map.nii.gz`
- Tract-based diffusion measures (FA, MD, RD, AD)
  - Averaged over the entire pathway distribution:

    `pathstats.overall.txt`
  - As a function of position along the pathway:

    `pathstats.byvoxel.txt`

Path stats (average values)

`pathstats.overall.txt`

```
# subjectname Diff001
# pathwayname lh.cst
#
Count 1000
Volume 327
Len_Min 35
Len_Max 70
Len_Avg 53.119
Len_Center 48
AD_Avg 0.00106102
AD_Avg_Weight 0.00108794
AD_Avg_Center 0.00105527
RD_Avg 0.000438781
RD_Avg_Weight 0.000430744
RD_Avg_Center 0.000441464
MD_Avg 0.000646195
MD_Avg_Weight 0.000649809
MD_Avg_Center 0.000646067
FA_Avg 0.519271
FA_Avg_Weight 0.539241
FA_Avg_Center 0.511358
```

- `*_Avg`: Average values of every voxel with probability > 20% of the maximum

- `*_Avg_Weight`: Multiply value at voxel with the probability at that voxel, sum over every voxel with probability > 20% of the maximum
  - This is closest to the notion of mean/expected value

- `*_Center`: Average values only on the 1-D path with the highest probability
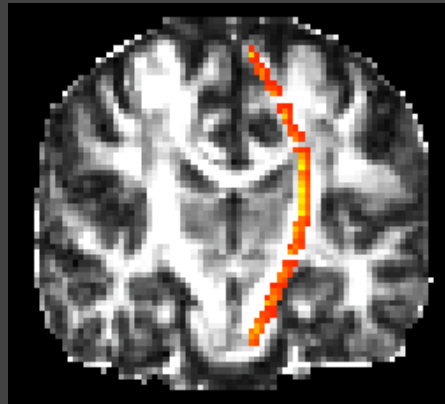
Path stats (values along the path)

pathstats.byvoxel.txt

```
# subjectname Diff001
# pathwayname lh.cst
#
# pathway start
x y z AD RD MD FA AD_Avg RD_Avg
66 63 13 0.00103657 0.000574918
66 63 14 0.00100453 0.000480365
67 64 15 0.000816154 0.00035986
67 64 16 0.000946625 0.00042132
68 64 17 0.000967142 0.00030569
68 64 18 0.00114626 0.000333594
69 65 19 0.00152806 0.000740932
69 65 20 0.00126399 0.000470638
69 65 21 0.00140243 0.000482392
70 65 21 0.00143949 0.000480912
70 65 22 0.00116007 0.000156374
70 66 23 0.00138642 0.000415134
71 66 24 0.00134187 0.000385197
71 66 25 0.00108983 0.000289931
71 66 26 0.00111074 0.000307493
```
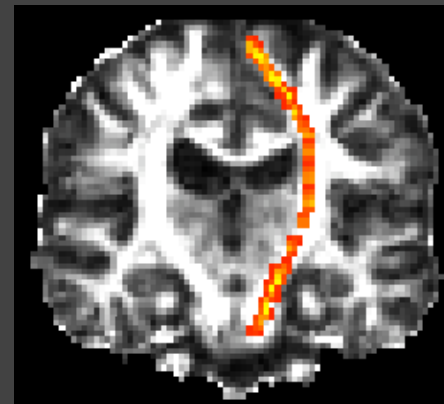
- At each position along the path
  - Value on 1-D path with the highest probability
  - `*_Avg`: Average value over nearest points from all sampled paths

- Coordinates are given in native diffusion space

- Paths from different subjects generally have different number of positions along path
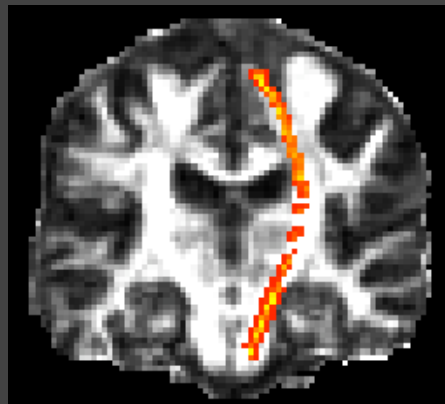
Example: Huntington's disease (HD)

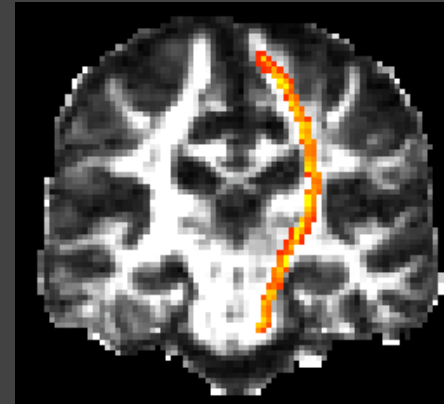Data courtesy of Dr. Diana Rosas, MGH
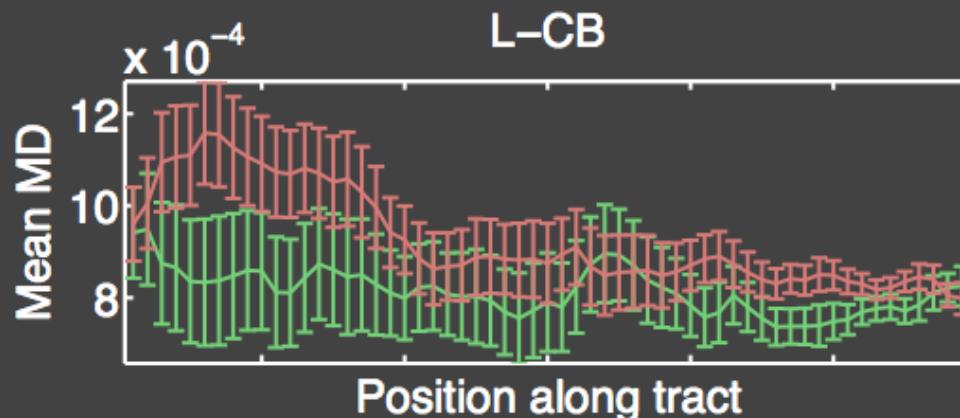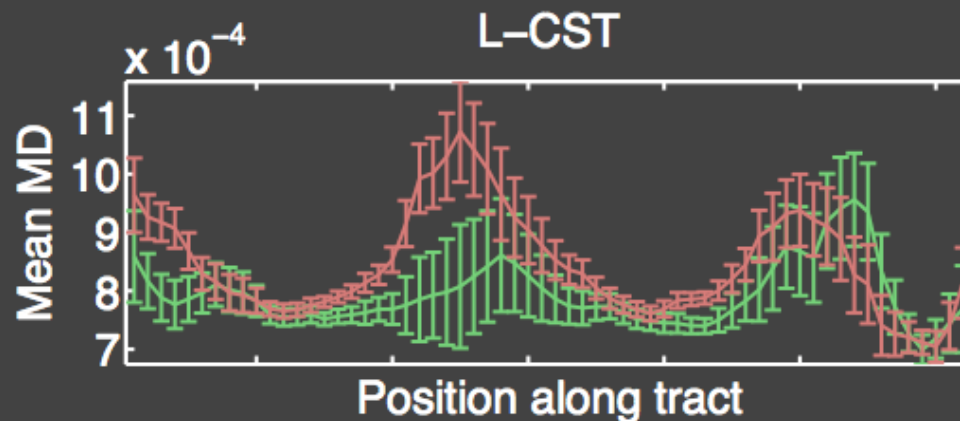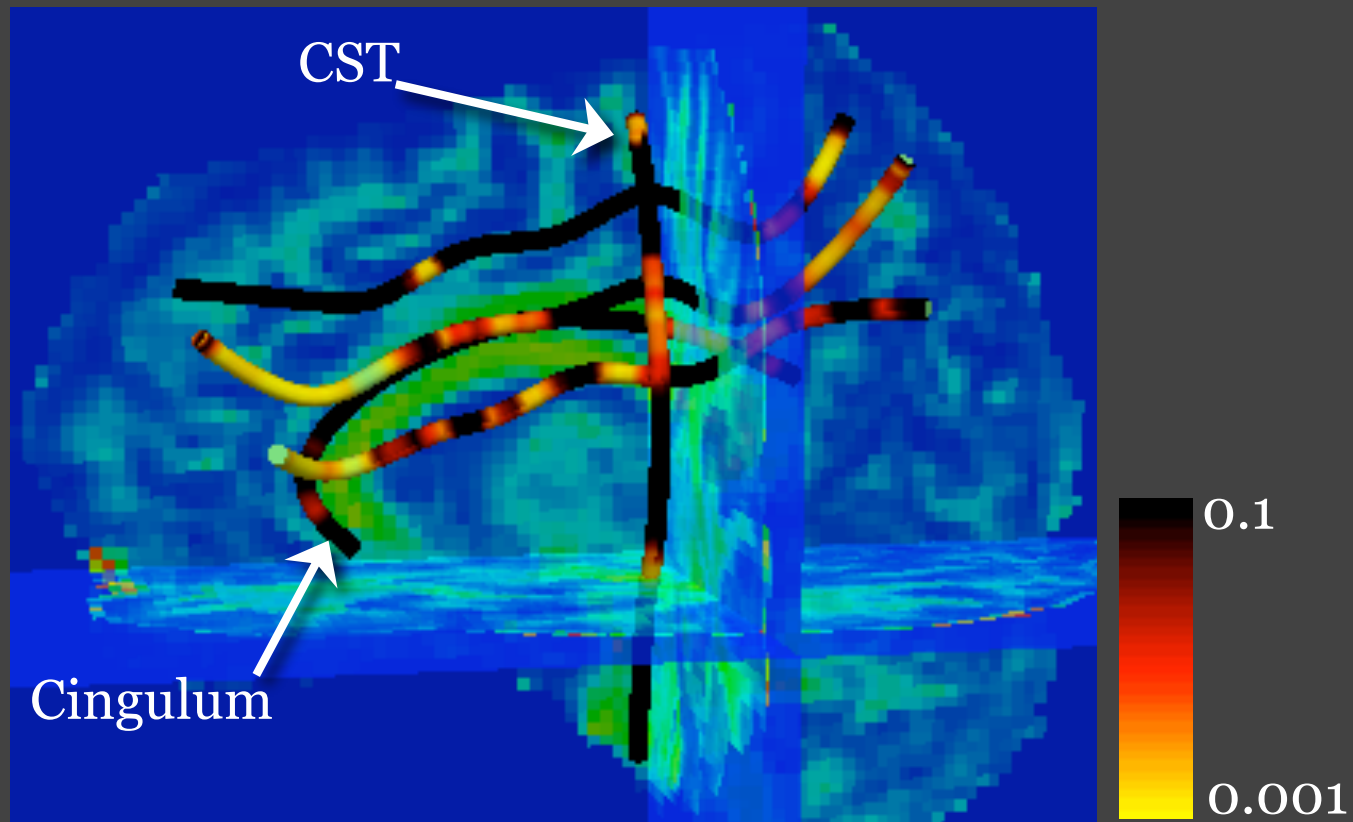

Healthy

HD stage 1

HD stage 2

HD stage 3

Plot measures along the pathway

Want to combine FA/MD/... along the path from multiple subjects, plot mean FA/MD/... for each group

Plot measures along the pathway

Want to display P-values for T-test on differences
in mean FA/MD/… between groups

New: Assemble group stats

```
trac-all -stat -c dmrirc
```

- Combine files of stats along the path from multiple subjects:
  - Find median path, set its mid-point to the origin (zero arc length along the path)
  - For every other path, find the closest point on this path to the mid-point of the median path, set this point to the origin
  - Now every point on every path is assigned an arc length
  - Interpolate values of FA/MD/... at the same arc lengths for all paths

- Outputs are saved under `$dtroot/stats/` and can be used for group studies on FA, MD, RD, AD along the pathway
  - One text file per pathway per measure (FA, MD, RD, AD)
  - Also produces average coordinates for each pathway in the template space (MNI or CVS) for visualization purposes
  - Log file shows which subjects are outliers (different shape-wise)

Display mean paths

- Use waypoint (-w) functionality of freeview
- `freeview $mnitemp \`
  `-w $dtroot/stats/*.path.mean.txt`
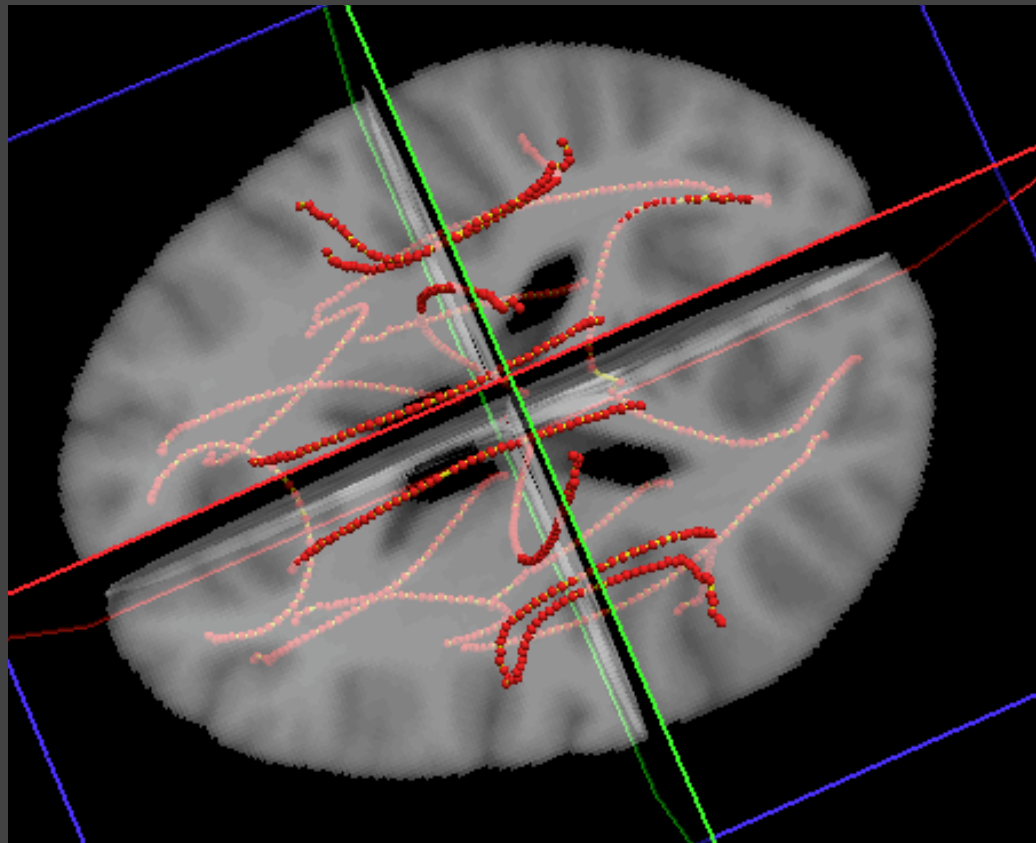
Paint *p*-values on mean paths

- Save *p*-values in a simple text file, load it as a "scalar map"