

TractoR and Other Software

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TractoR

- A **platform** for multimodal image analysis
- A set of R **packages**, some of which are individually on CRAN
- A series of R **scripts** for performing common tasks
- A simple command-line **interface** for running these scripts
- A set of **self-tests** and **example data**
- A dissemination route for methodological work

```

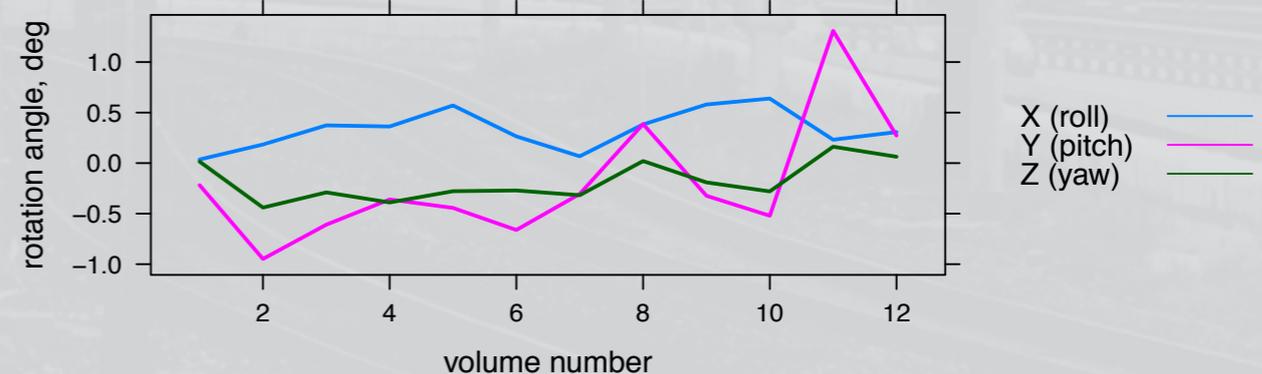
tractor — fish /Users/jon/Documents/Development/Git/tractor
Last login: Tue May 24 10:55:05 on ttys027
Welcome to fish, the friendly interactive shell
Type help for instructions on how to use fish
[[jon@mc244-182 ~]$ cd git/tractor
[[jon@mc244-182 ~/Documents/Development/Git/tractor]$ tractor status tests/data/session
Starting TractoR environment...
GENERAL:
  Session directory      : /Users/jon/Documents/Development/Git/tractor/tests/data/session
  Working directory exists : TRUE

DIFFUSION:
  Preprocessing complete : TRUE
  Data dimensions        : 96 x 96 x 60 x 12 voxels
  Voxel dimensions       : 2.5 x 2.5 x 2.5 mm x 1 s
  Number of shells        : 1
  Diffusion b-values      : 0, 1000 s/mm^2
  Number of gradient directions : 2, 10
  Diffusion tensors fitted : TRUE
  Fibre orientation model  : FSL-BEDPOSTX (1 fibre per voxel)

FUNCTIONAL:
  Data dimensions        : 64 x 64 x 30 x 15 voxels
  Voxel dimensions       : 3.28125 x 3.28125 x 3.99 mm x 2.16 s
  Sampling frequency     : 0.463 Hz
  Total time              : 32.4 s

STRUCTURAL:
  Number of T1w volumes : 1
  T1w space dimensions  : 176 x 232 x 256 voxels
  T1w voxel dimensions  : 1 x 1 x 1 mm
  Parcellation created  : TRUE
  Number of T2w volumes : 0
  Number of PDw volumes : 0
Experiment completed with 0 warning(s) and 0 error(s)
[[jon@mc244-182 ~/Documents/Development/Git/tractor]$ tractor plotcorrections tests/data/session Mode:all
Starting TractoR environment...
[* QUESTION: Copy figure to pdf file? [yn] y
Experiment completed with 0 warning(s) and 0 error(s)
[[jon@mc244-182 ~/Documents/Development/Git/tractor]$ ]

```

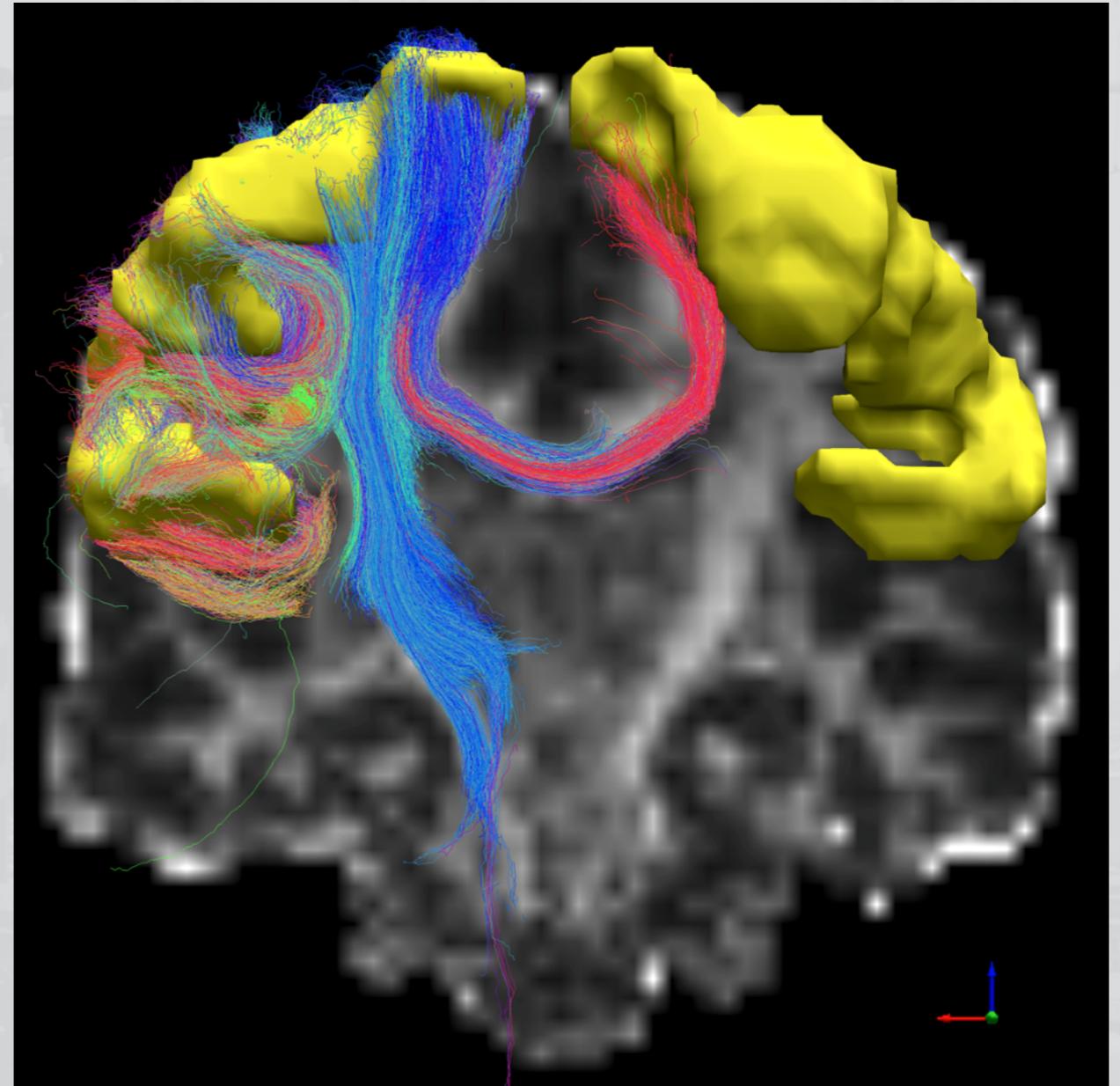


Capabilities

- **DICOM** processing: read, sort, convert to NIfTI format
- **Diffusion** processing: brain masking (FSL-BET or *k*-means); eddy current correction (FSL or NiftyReg); tensor fitting; calculation of FA, MD, etc.
- FSL-BEDPOSTX interface for diffusion **modelling**
- Probabilistic **tractography** (seed-based, mask-based or whole-brain)
- Neighbourhood tractography methods for consistent **tract segmentation** in groups; model-based streamline pruning
- Structural and functional **connectome** analysis; graph metrics
- Graph **subnetwork** analysis
- Linear and nonlinear **registration** (FSL or NiftyReg)
- Image and tract **visualisation**

New in TractoR 3

- Support for **multishell** diffusion data
- Much more efficient **tractography**
- Native **TrackVis** file format support
- Improved **image processing**
- Much more consistent **parallelisation**
- Better **visualisation**
- Fewer core scripts, less duplication
- No need for a **Fortran** compiler or **ImageMagick**



Getting help

- How do I use the command line interface?

```
#sh> tractor -h
```

```
#sh> man tractor
```

- What scripts are available?

```
#sh> tractor list
```

- What does the *track* script do, and what options can I give it?

```
#sh> tractor -o track
```

- What version of TractoR and R am I running?

```
#sh> tractor platform
```

The session

- TractoR favours using a convention over making people specify lots of files
- Data sets are stored in a managed directory structure, whose top-level directory is called a “session”

session	top-level session directory
-/tractor	main managed directory
--/transforms	stored transformations between different spaces
--/diffusion	diffusion-weighted images and their derivatives
--/fdt	images and other files used by FSL's diffusion toolbox
--/fdt.bedpostX	images and other files produced by FSL-BEDPOSTX
--/structural	structural (e.g. T_1 -weighted) images
--/freesurfer	output from the Freesurfer pipeline
--/functional	functional (generally T_2^* -weighted BOLD) images
-[other subdirectories]	unmanaged files, such as DICOM-format files

- TractoR scripts that need data require the top-level session directory (only) to be specified

Starting with DICOM files

- First sort into directories of related files (slices or volumes of the same series)

```
#sh> tractor dicomsort
```

- Then convert a directory of files into a standalone NIfTI file

```
#sh> tractor dicomread flashT1
```

- Or import into an existing session directory

```
#sh> tractor import /data/session  
flashT1 ImageWeighting:t1
```

- TractoR can also read the Siemens CSA private header:

```
#sh> tractor dicomtags dicom/01.dcm  
SiemensAscii:true
```

Diffusion preprocessing

- Read from DICOM, correct for susceptibility distortion (optional), choose a reference $b=0$ volume, mask the brain, correct for eddy-current distortions
- Standard pipeline in TractoR 2.x would now be

```
#sh> tractor dpreproc UseTopup:false MaskingMethod:kmeans  
EddyCorrectionMethod:eddycorrect
```

- For datasets with no phase-reversed $b=0$ volume, you probably want

```
#sh> tractor dpreproc UseTopup:false
```

- For the standard two-shell Prisma protocol with one phase-reversed $b=0$, it's

```
#sh> tractor dpreproc DicomDirectories:mainDiffusion,reversePEDiffusion  
ReversePEVolumes:auto
```

- Note that FSL's **topup** and **eddy** tools take a long time (hours) to run
- **Flipping** gradient directions in the A-P direction is now done by default

Tractography

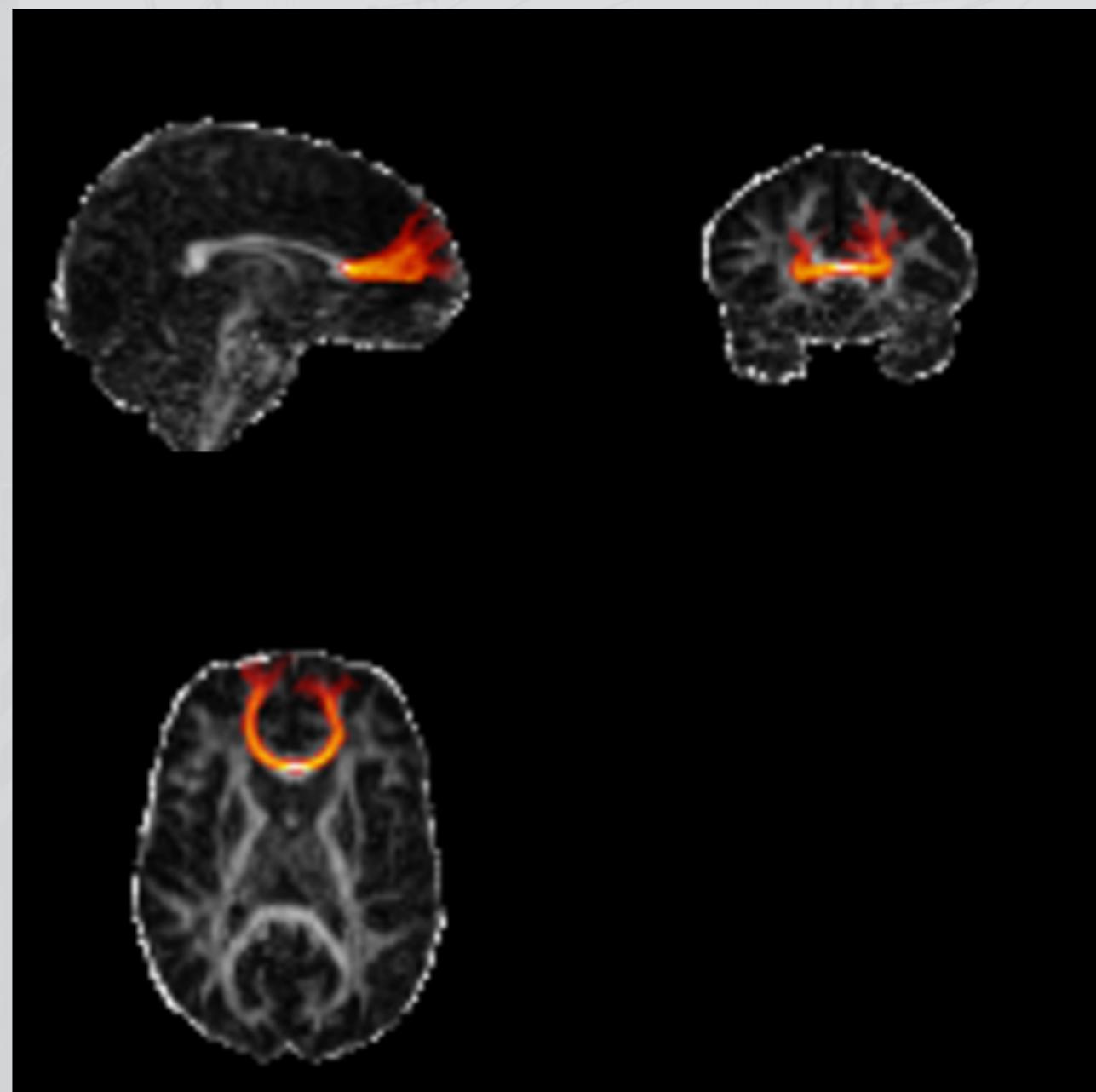
- TractoR currently uses **FSL-BEDPOSTX** as its diffusion model
- Multishell supported
- Tracking from seed points, masks or named regions, with or without constraints
- Streamline counts limited by disk space, not memory; written straight to TrackVis **.trk format**
- Random seeding within regions, seed jittering, length thresholding

Single-seed tractography

- Tract images created using (very flexible) `slice` script
- Handles overlays (with transparency), projections, multiple views

```
#sh> tractor track session 50 59 33
Streamlines:5000 RequireMap:true
```

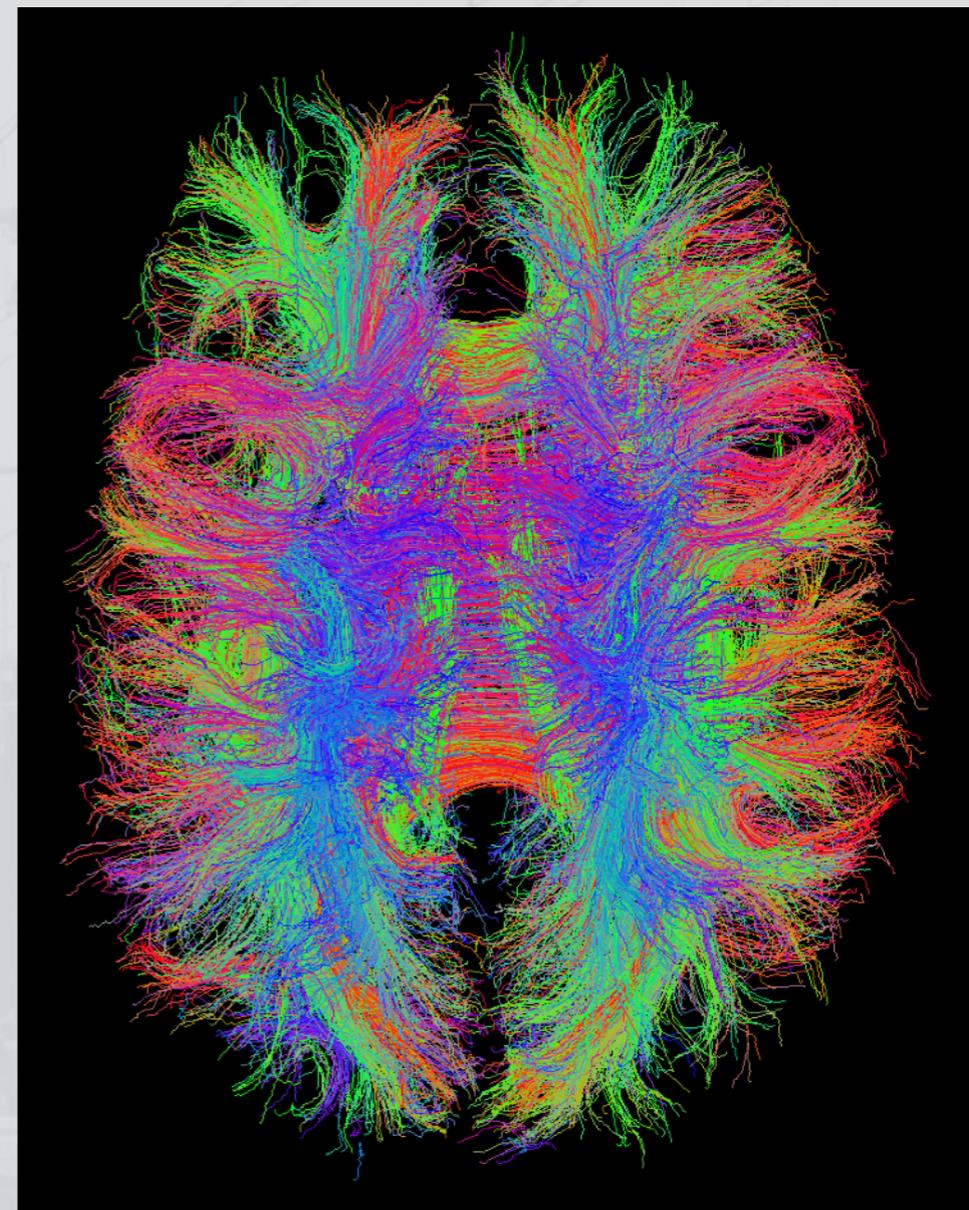
```
#sh> tractor slice session@FA tract
X:50 Y:59 Z:33 Alpha:log
```



Whole-brain tractography

- If a parcellation is available, we can explicitly seed from white matter voxels
- Length thresholding is easy (units are millimetres)
- Load streamlines directly in TrackVis

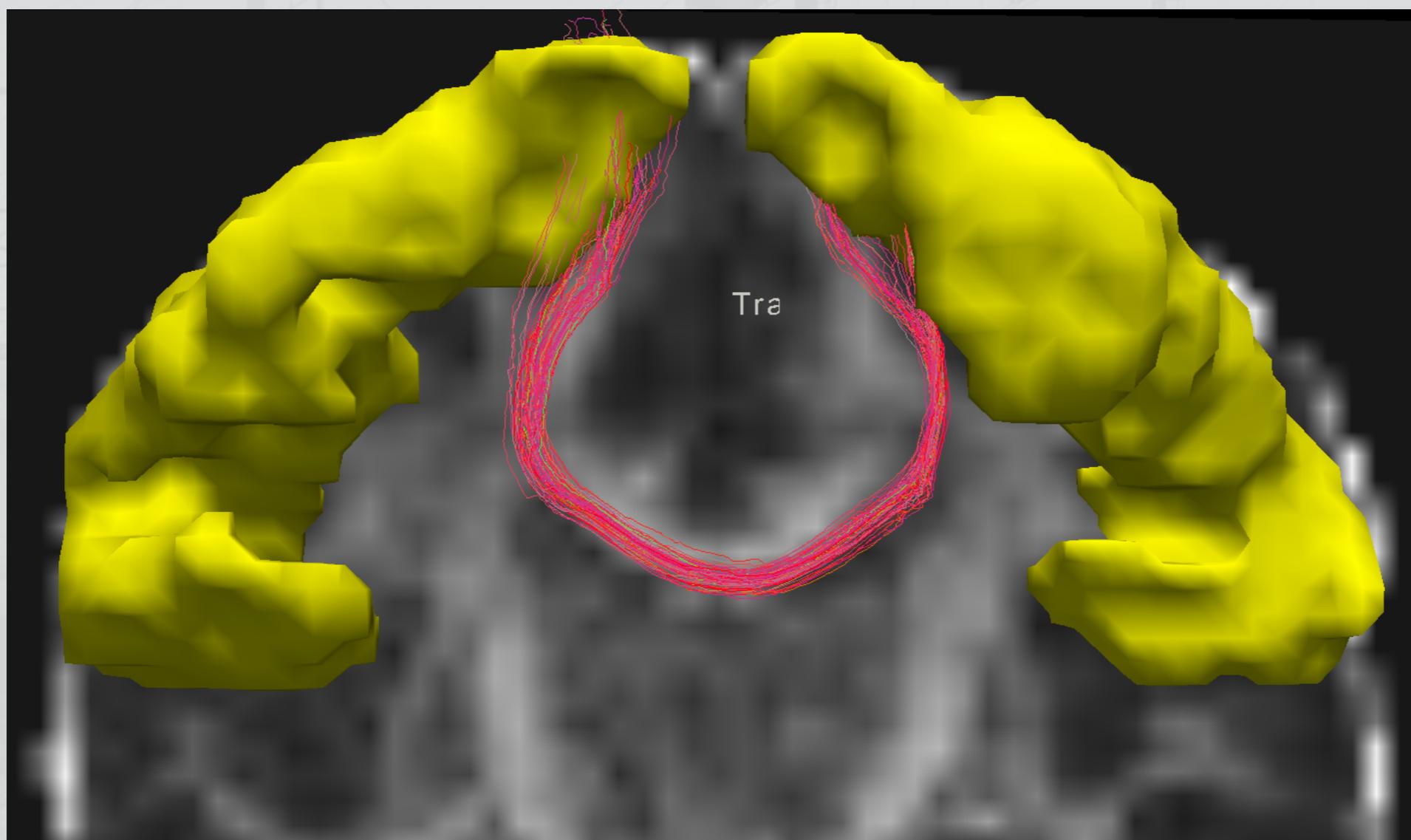
```
#sh> tractor track session
white_matter MinLength:20
RequirePaths:true
```



```
[jon@mc244-182 ~/Documents/Development/Git/tractor/tests/data]$ time tractor track session white_matter MinLength:20 RequirePaths:true
Starting TractoR environment...
* INFO: Performing sequential global tractography with 33053 seed(s), 100 streamlines per seed
* * INFO: 1397359 streamlines (42.3%) were retained after filtering
Experiment completed with 0 warning(s) and 0 error(s)
    135.80 real        132.50 user         2.46 sys
```

Region-to-region tractography

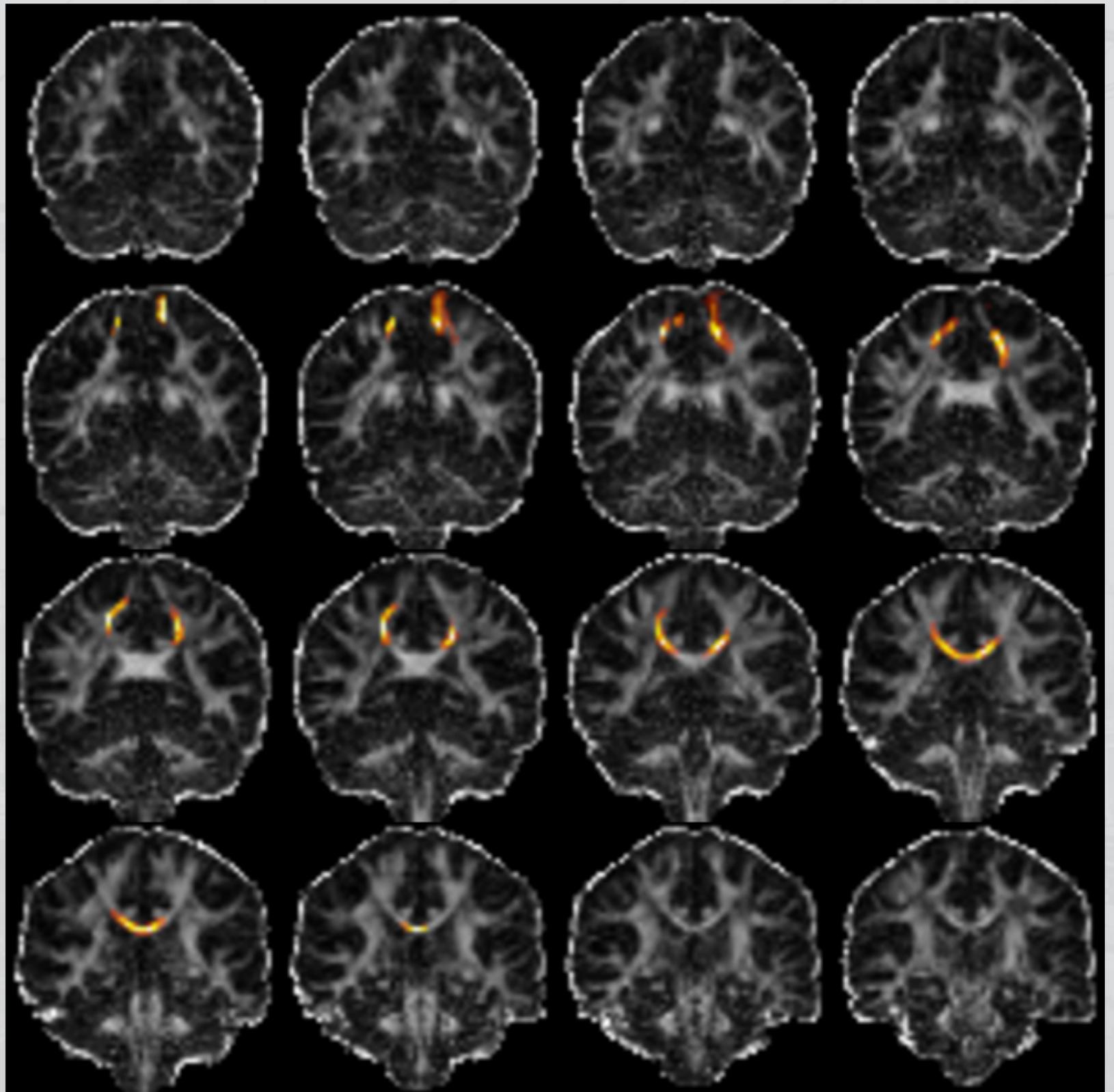
```
#sh> tractor track session postcentral_gyrus_left BoundaryManipulation:outer  
Streamlines:1000x TargetRegions:postcentral_gyrus_right  
TerminateAtTargets:true MinTargetHits:1 RequirePaths:true
```



More “slice”ing

- Contact sheet type graphic generated when multiple slices on a single axis given

```
#sh> tractor slice
      session@FA tract
      Y:25-40 Alpha:log
      Clearance:2
```

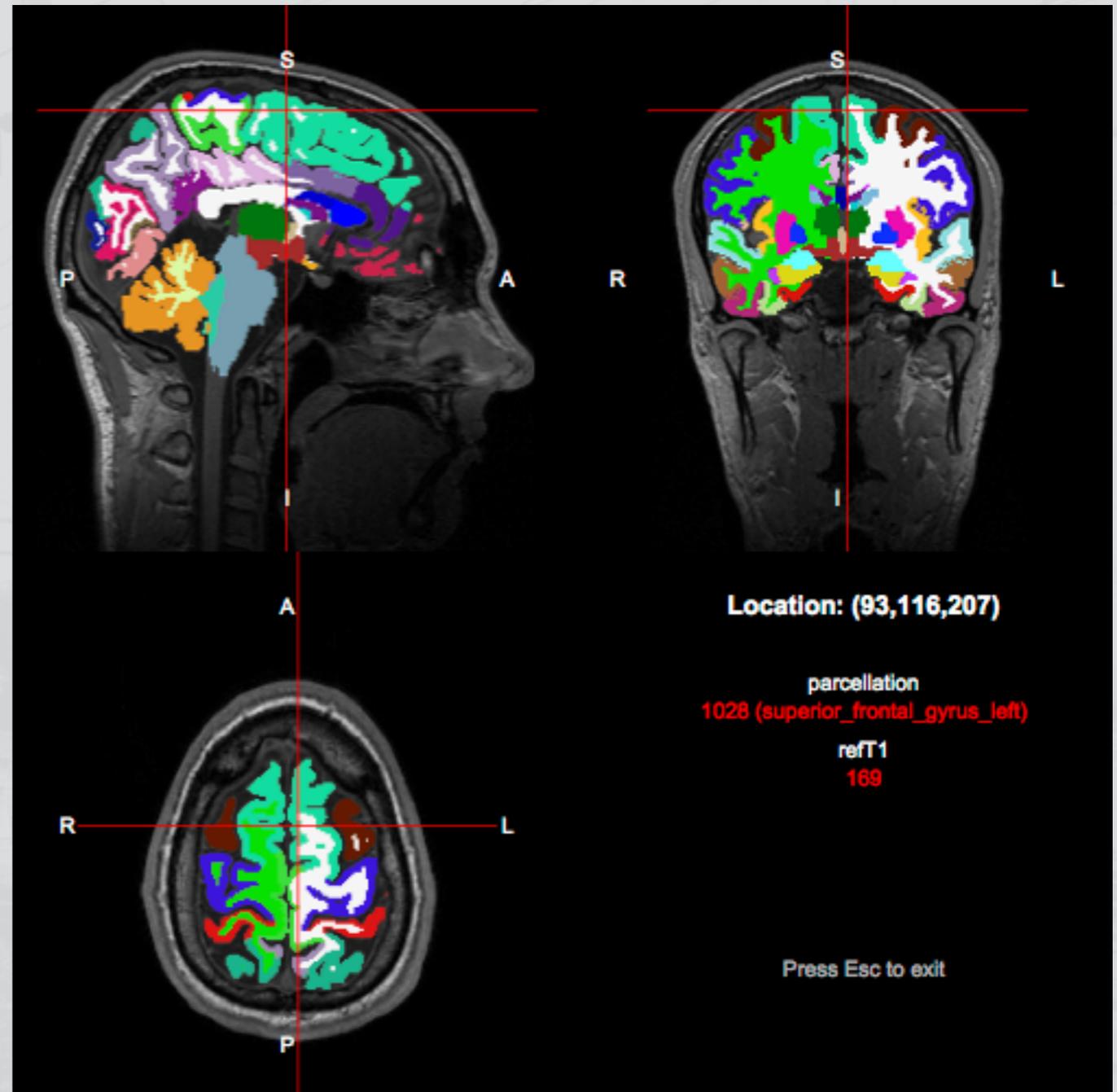


Interactive viewer

- Parcellation labels are shown where applicable

```
#sh> tractor view refT1 parcellation
```

- Other image viewers include **fslview** (FSL), **freeview** (FreeSurfer), **mrview** (MRtrix), **micron**

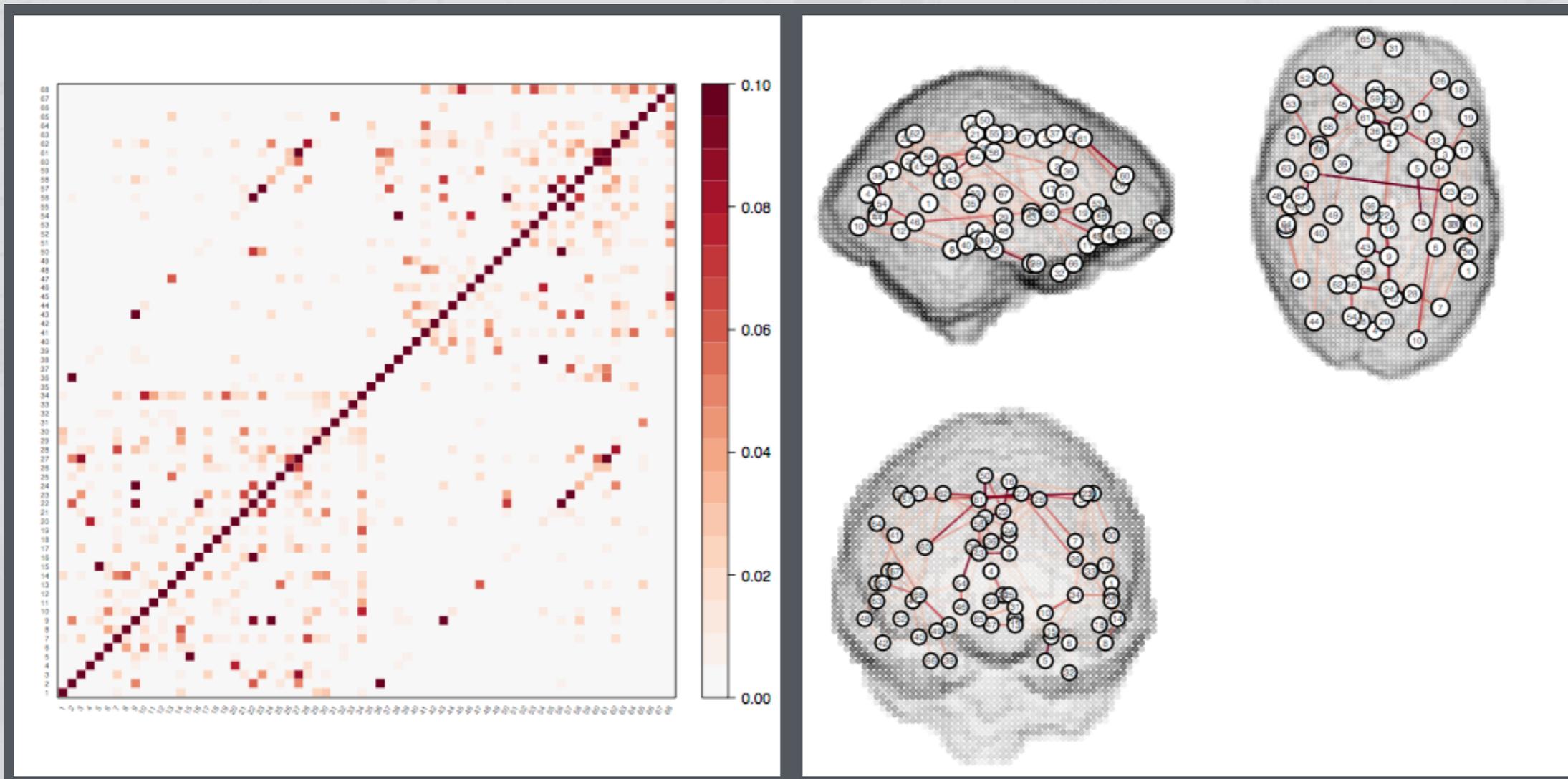


Neighbourhood tractography

- Methods for finding specified tracts in individuals
- Scripts relating to the older, simpler **heuristic neighbourhood tractography** method start with *hnt-*
- Those relating to the newer, more complex but more reliable **probabilistic** method start with *pnt-*
- Either way, a **reference tract** is required, and these are provided with TractoR for: forceps minor (CC genu), forceps major (CC splenium), arcuate and uncinate fasciculi, ILFs, ATRs, CSTs, and dorsal and ventral parts of the cingulum bundles
- **Tutorials** are available on the web site

Graph analysis

- **Structural** and **functional** connectivity analysis can be performed
- Subnetworks may be extracted using the **principal networks** approach



R and MRI

- The **medical imaging task view** is mainly focussed on MRI applications (diffusion, perfusion, functional)
- I/O between R and various imaging file formats (**Analyze, NIfTI, DICOM**) is well covered
- For example, using TractoR:

```
> library(tractor.base)
> i <- readImageFile("dti_FA.nii.gz")
> i
  Image source : /Users/jon/dti_FA
Image dimensions : 96 x 96 x 60 voxels
Voxel dimensions : 2.5 x 2.5 x 2.5 mm
Coordinate origin : (49.81,39.07,23.02)
  Additional tags : 0
  Sparseness : 79.28% (dense storage)
> class(i$getData()) # Get the voxel values
[1] "array"
```

Image manipulation in R

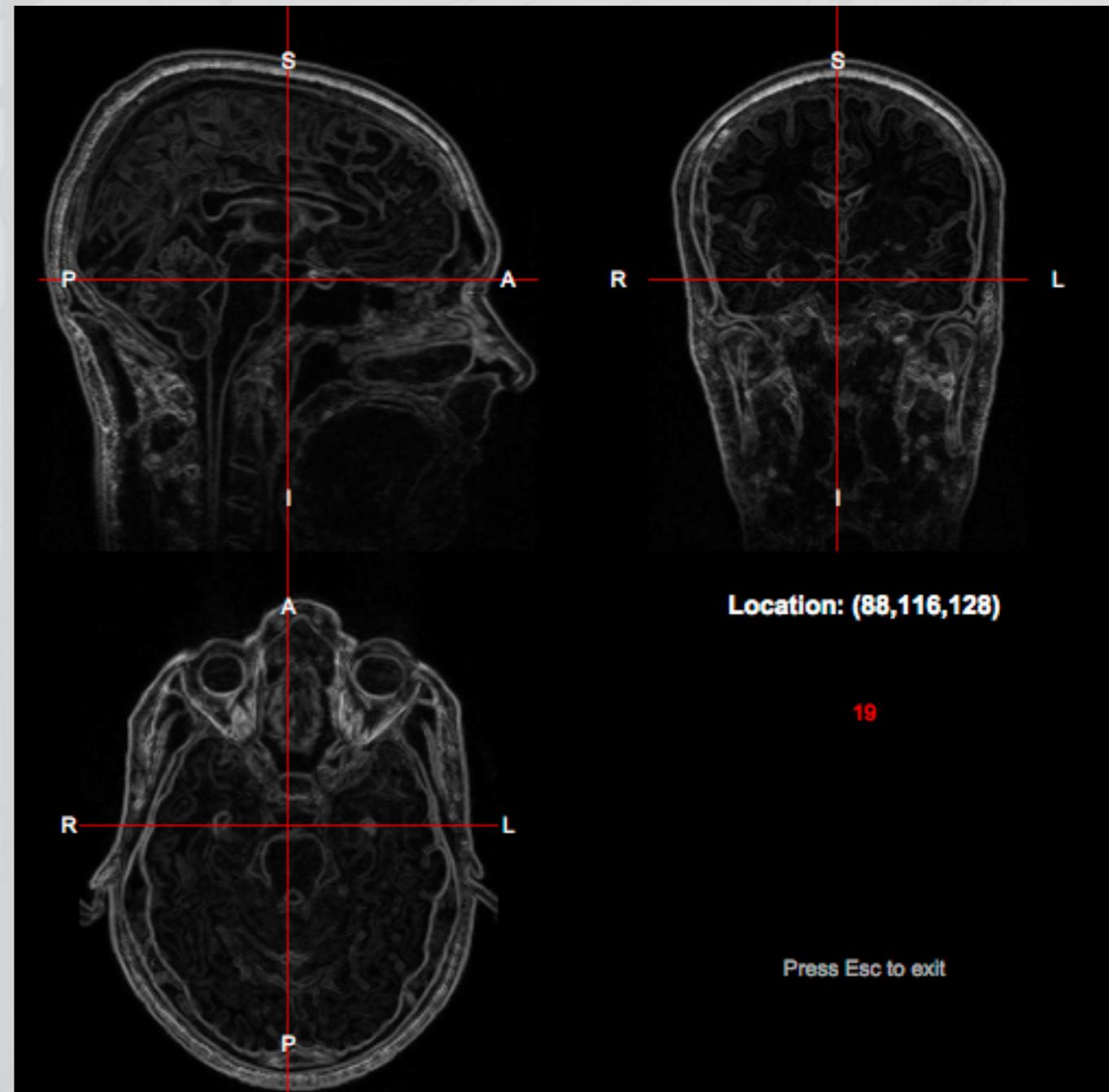
```
#R> t1 <- readImageFile("refT1")

#R> k <- shapeKernel(c(3,3,3),
  type="diamond")

#R> grad <- t1$copy()

#R> grad$map(function(x) dilate(x,k)
  - erode(x,k))

#R> showImagesInViewer(grad)
```



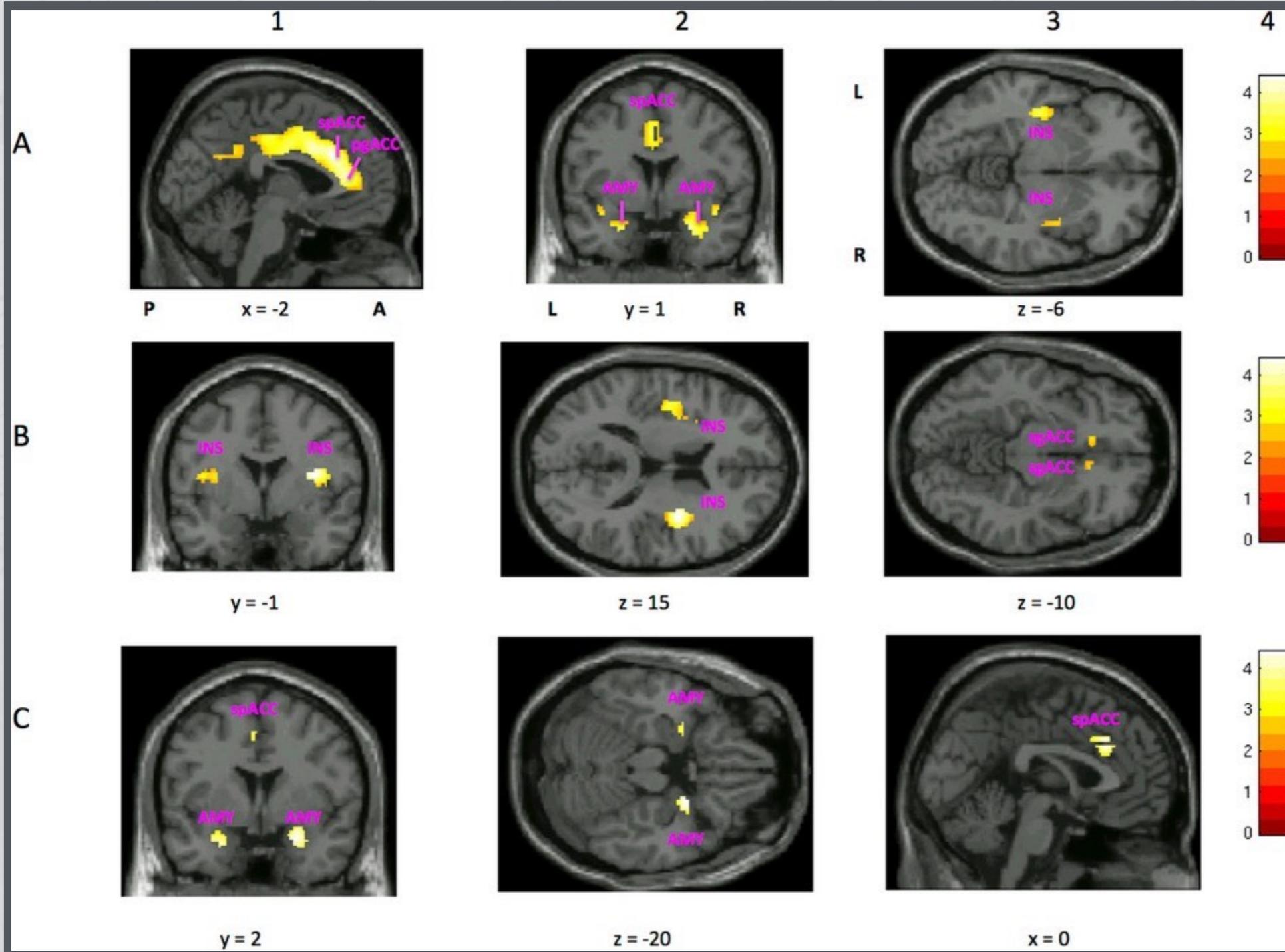
The R package landscape

Package	Repository	External Deps	Read and Write	Display	>2D Images	Key Operations
base, stats, graphics				single channel	Y	core operations (e.g. arithmetic), FFT
adimpro	CRAN	ImageMagick, dcraw	JPEG, PNG, TIFF, GIF, RAW, etc.	Y		adaptive smoothing, colour space conversion
EBImage	BioC			Y		morphology, segmentation, feature extraction
imager	CRAN	fftw3		Y	Y	edge detection, transformation, integration with plyr & ggplot2
jpeg, png, tiff	CRAN	libjpeg, libpng, libtiff	JPEG, PNG, TIFF			image read/write
magick	CRAN	ImageMagick	JPEG, PNG, TIFF, etc.	Y	Y	many
mmand	CRAN			Y	Y	morphology, resampling, connected components
OpenImageR	CRAN			Y		image recognition, transformation, filtering
ripa	CRAN	BWidget, Tktable, lmg, libjpeg	LAN, AVIRIS	Y		filtering, FFT, graphical interface
RNiftyReg	CRAN		NIFTI-1		Y	transformation, registration, image similarity

Other software packages

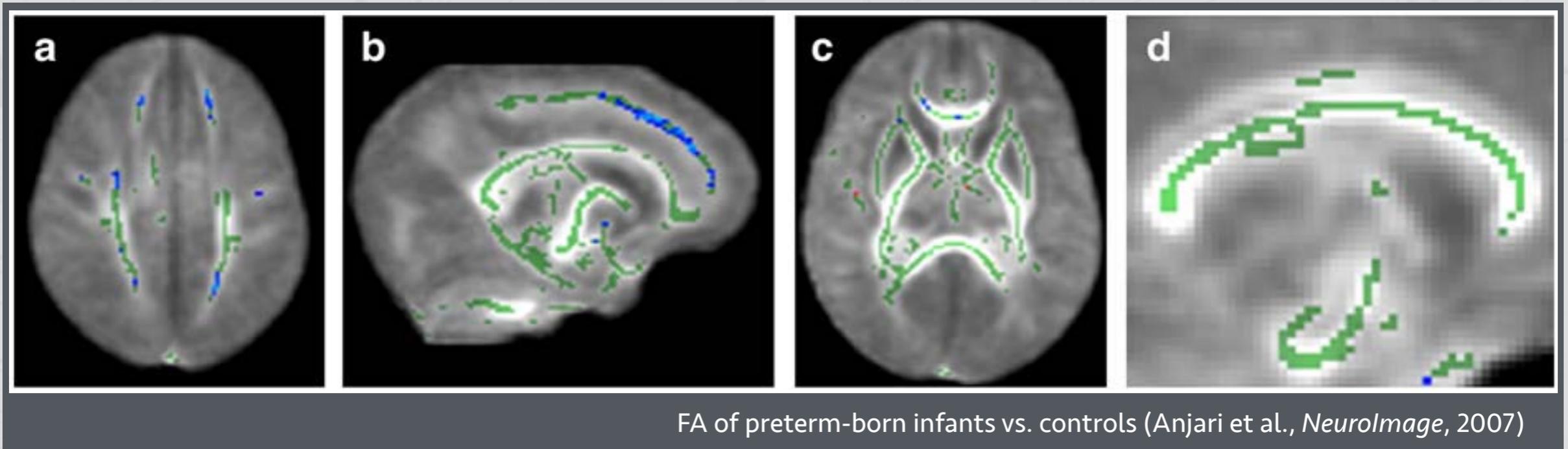
- **SPM** (FIL, UCL): task and resting fMRI analysis; effective connectivity; EEG, MEG, PET, SPECT; grey and white matter volumes
- **FSL** (FMRIB, Oxford): task and resting fMRI analysis; probabilistic tractography; voxel-based white matter analysis
- **FreeSurfer** (MGH): cortical parcellation; longitudinal processing; visualisation
- **CONN** (MIT) for functional connectivity; **Brain Connectivity Toolbox** (Cambridge and Indiana) for graph analysis
- For diffusion, Camino (CMIC, UCL); NifTK (CMIC, UCL); MRtrix (Melbourne and elsewhere); DTI Studio/MRI Studio (JHU); Explore DTI (Utrecht); Diffusion Toolkit/TrackVis (MGH)
- 3D Slicer (Harvard); MedInria (Inria, France); etc.

SPM

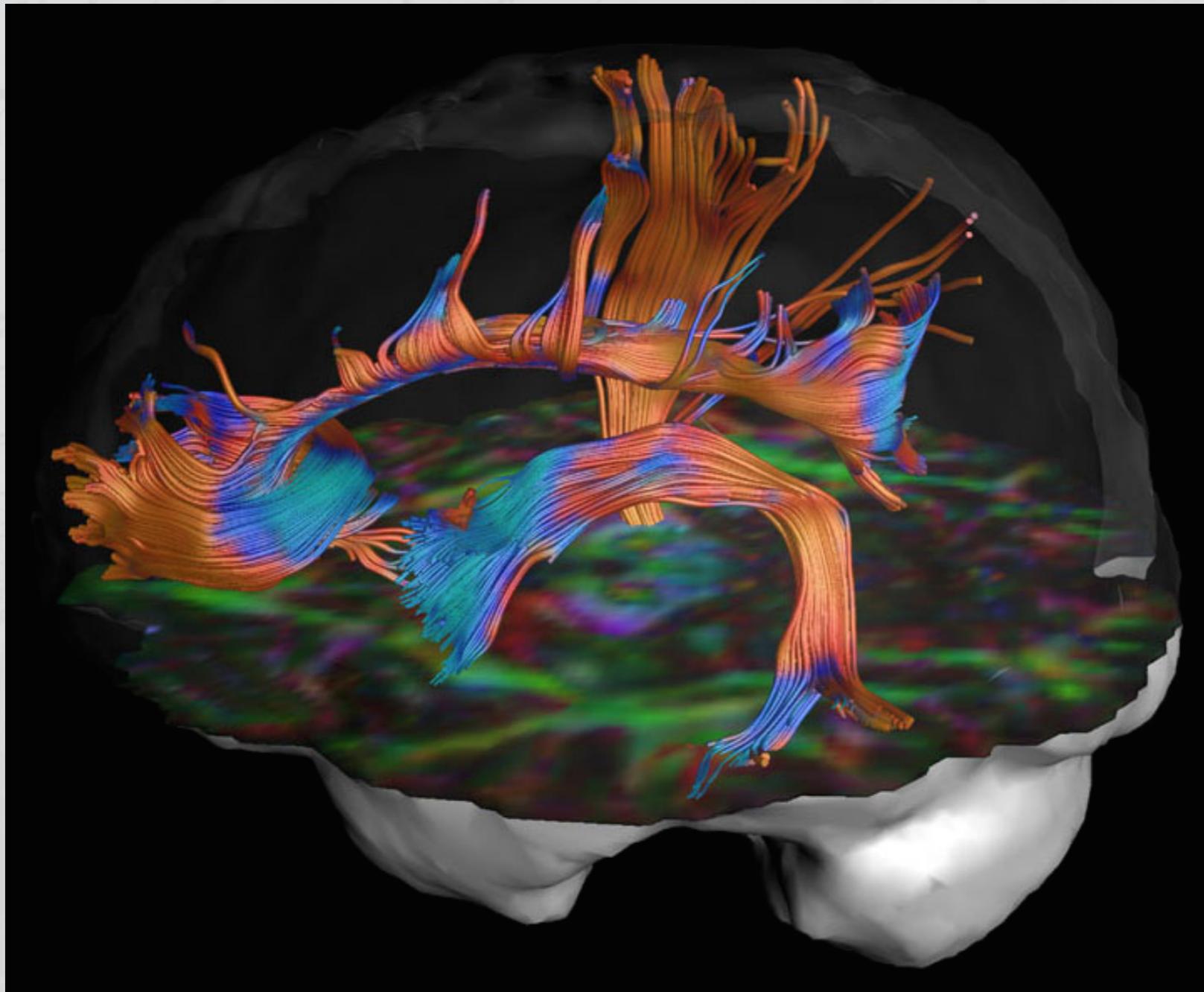


Savitz et al., *Sci Reports*, 2012

TBSS



Visualisation of DTI metrics along tracts (Explore DTI)



Recommended tools

- Brain extraction: BET (FSL)
- Cortical parcellation: FreeSurfer or NiftySeg, with manual checking
- Deep grey matter parcellation: As above, or FIRST (FSL)
- Gross tissue segmentation: As above, or FAST (FSL)
- Diffusion modelling: BEDPOSTX (FSL) or CSD (MRtrix)
- Tractography: TractoR or MRtrix
- Registration: SPM, FSL or NiftyReg

Links

- TractoR: <http://www.tractor-mri.org.uk>
- SPM: <http://www.fil.ion.ucl.ac.uk/spm/>
- FSL: <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/>
- FreeSurfer: <http://surfer.nmr.mgh.harvard.edu>
- CONN: <http://www.nitrc.org/projects/conn/>
- Brain Connectivity Toolbox: <https://sites.google.com/site/bctnet/>
- Camino: <http://www.camino.org.uk>
- NifTK: <http://cmictig.cs.ucl.ac.uk/research/software>
- MRtrix: <http://www.mrtrix.org>
- DTI Studio/MRI Studio: <https://www.mristudio.org>
- Explore DTI: <http://www.exploredti.com>
- Diffusion Toolkit/TrackVis: <http://www.trackvis.org>
- 3D Slicer: <http://www.slicer.org>
- MedInria: <http://med.inria.fr>