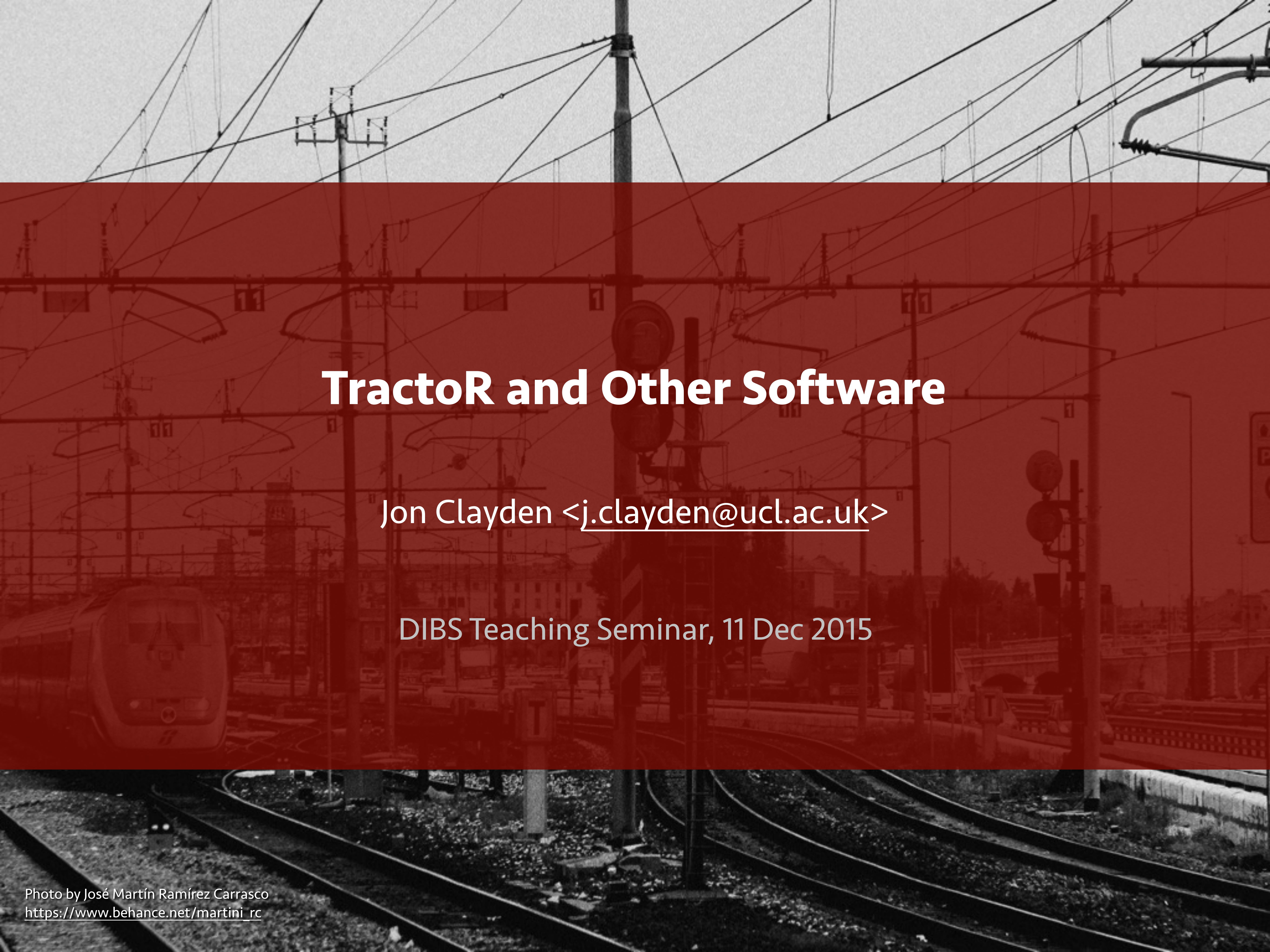

TractoR and Other Software

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Photo by José Martín Ramírez Carrasco
https://www.behance.net/martini_rc

TractoR

- A set of R packages
- Additional infrastructure to run common tasks without using R directly
- A set of self-tests and example data
- A toolset for image data analysis
- A dissemination platform for methodological work
- Home page: http://www.tractor-mri.org.uk
- *Journal of Statistical Software* **44**(8):1–18 (link from the home page)
- Interface is currently command-line only, Linux and Mac OS X supported
- R packages should work in Windows

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

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
    /fdt.track...............FSL tractography output
    /camino..................images and other files used by the Camino toolkit
    /structural..............structural (e.g. T1-weighted) images
    /freesurfer..............output from the Freesurfer pipeline
    /functional..............functional (generally T2*-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

Getting help

- How do I use the command line interface?

```
$ tractor -h
$ man tractor
```

- What scripts are available?

```
$ tractor list
```

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

```
$ tractor -o track
```

- What version of TractoR and R am I running?

```
$ tractor platform
```

Typical tasks

- Sort DICOM files and convert to NIfTI format

```
$ tractor dicomsort
$ tractor dicomread 01_3DFLASH_T1W_sag
```

- Preprocess diffusion data interactively and fit tensors

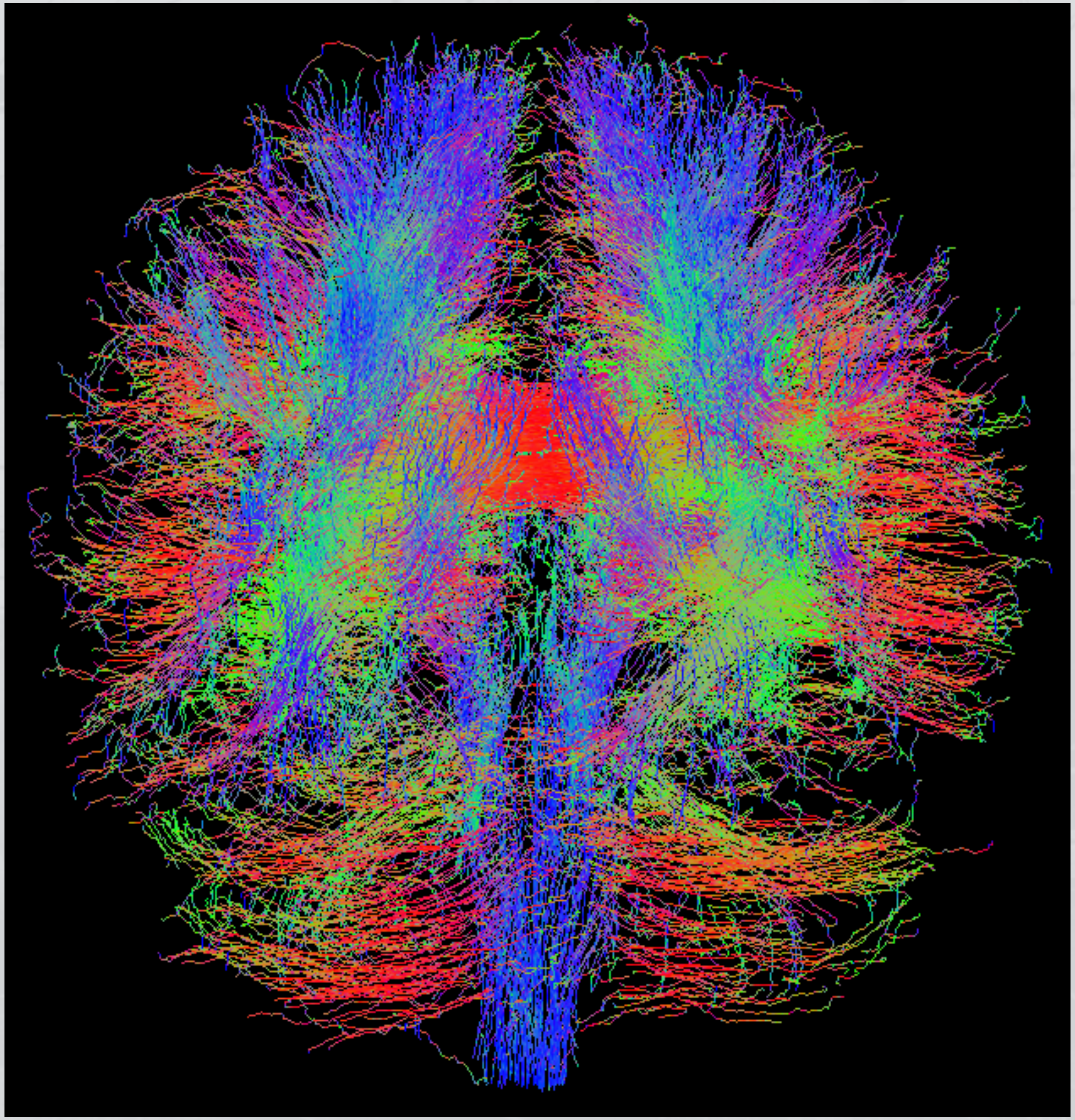
```
$ tractor dpreproc /data/subject1
$ tractor tensorfit /data/subject1
```

- Run tractography with a seed point or mask and create images of the results

```
$ tractor track /data/subject1 34,29,14 PointType:R CreateImages:true TractName:tract1

$ tractor mtrack /data/subject1 SeedMaskFile:mask.nii.gz CreateImages:true TractName:tract2
```

Streamline visualisation via TrackVis

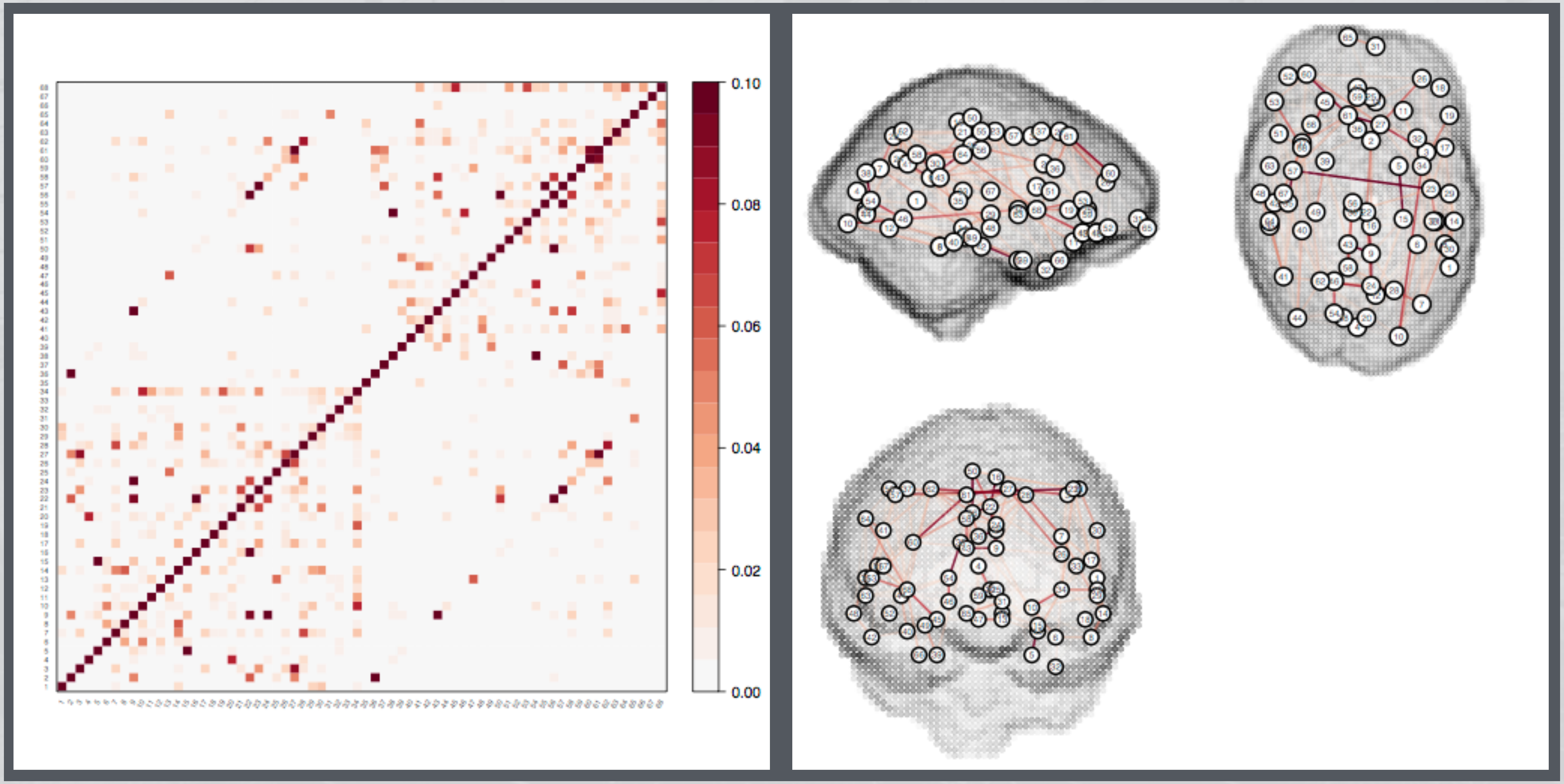


Neighbourhood tractography

- 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



Recent history

- Version 2.2: Image processing (smoothing, mathematical morphology); connectivity profiling; TrackVis compatibility (Aug 2012)
- Version 2.3: Simple interactive image viewer; better DICOM sorting; termination masks (Feb 2013)
- Version 2.4: Linear and nonlinear image registration; new command-line interface (Jul 2013)
- Version 2.5: Graph analysis methods including principal networks implementation (Mar 2014)
- Version 2.6: Functional network analysis; more efficient region-to-region tractography (Mar 2015)
- Version 3.0 coming in early 2016
- Very open to suggestions and/or help!

Roadmap

- Much better whole-brain tractography performance
- Multishell diffusion processing
- Registration checking using edge overlays
- Greater generalisation
- Interface to MRtrix constrained spherical deconvolution for tracking
- Reading Siemens DICOM ASCII header
- Functional data preprocessing
- More multimodal integration
- Whole-brain neighbourhood tractography
- More graph analysis methods

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"
```

The MriImage class

- A reference class, like many of TractoR’s main data types
- Methods can be used to retrieve information about the image
- Can be treated as a standard R array for many purposes

```
> class(i)
[1] "MriImage"
attr(,"package")
[1] “tractor.base"

> i$getFieldOfView()
[1] 240 240 150
> i$getStoredXformMatrix()
     [,1] [,2] [,3]      [,4]
[1,] -2.5  0.0  0.0 122.03390
[2,]  0.0  2.5  0.0 -95.18523
[3,]  0.0  0.0  2.5 -55.03814
[4,]  0.0  0.0  0.0   1.00000

> dim(i)
[1] 96 96 60
> i[48,48,30]
[1] 0.3071784
> range(i, na.rm=TRUE)
[1] 0.00801412 1.22474486
```

Tractography

- FSL-BEDPOSTX must be run first:

```
> s <- newSessionFromDirectory("/data/subject1")
> runBedpostWithSession(s)
```

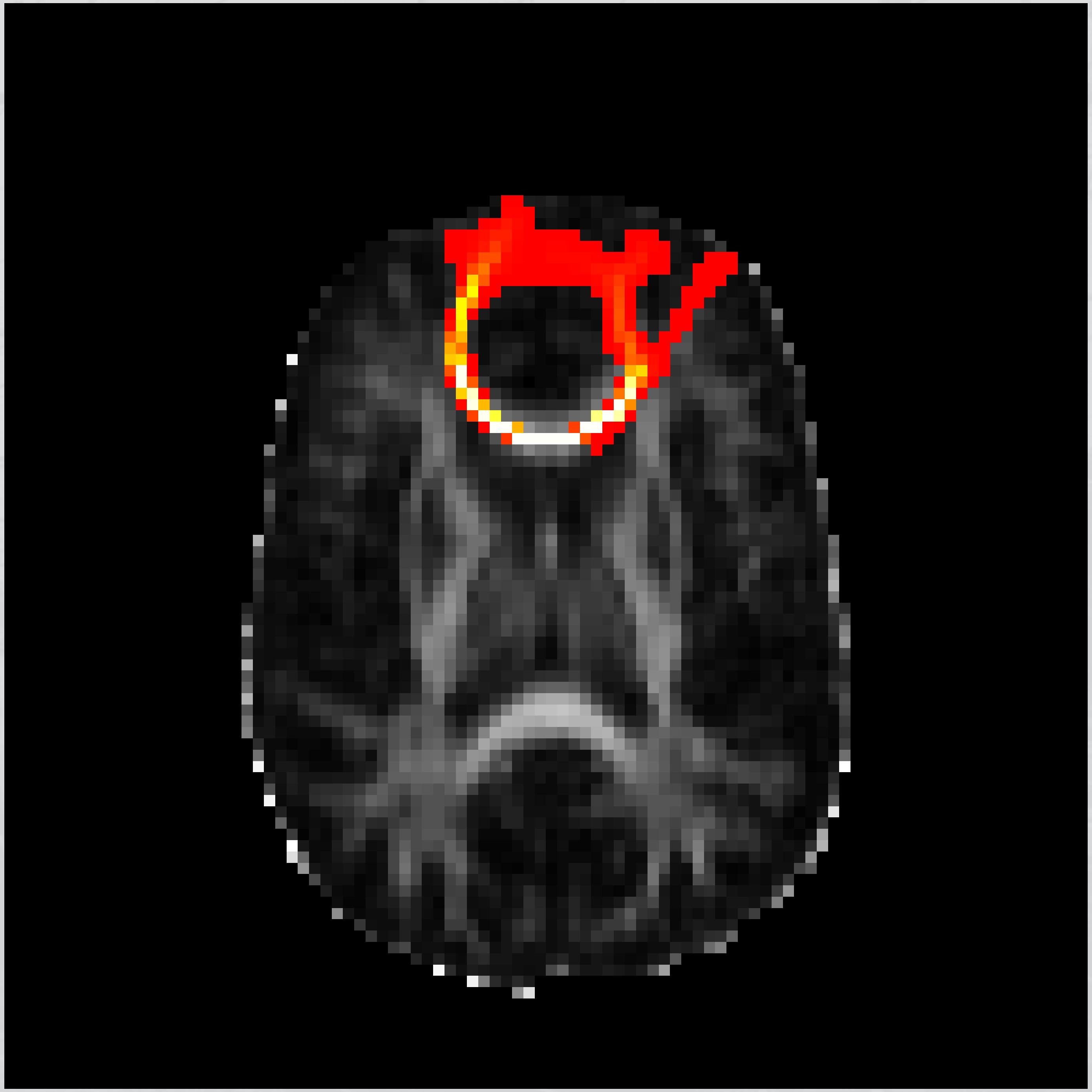
- Then we can run tractography:

```
> library(tractor.track)
> r <- trackWithSession(s, c(34,29,14), requireImage=TRUE)
```

- Now retrieve the FA map and visualise the tract on top:

```
> fa <- s$getImageByType("FA")
> createSliceGraphic(fa, z=14)
> createProjectionGraphic(r$image, 3, colourScale=2, add=TRUE)
```

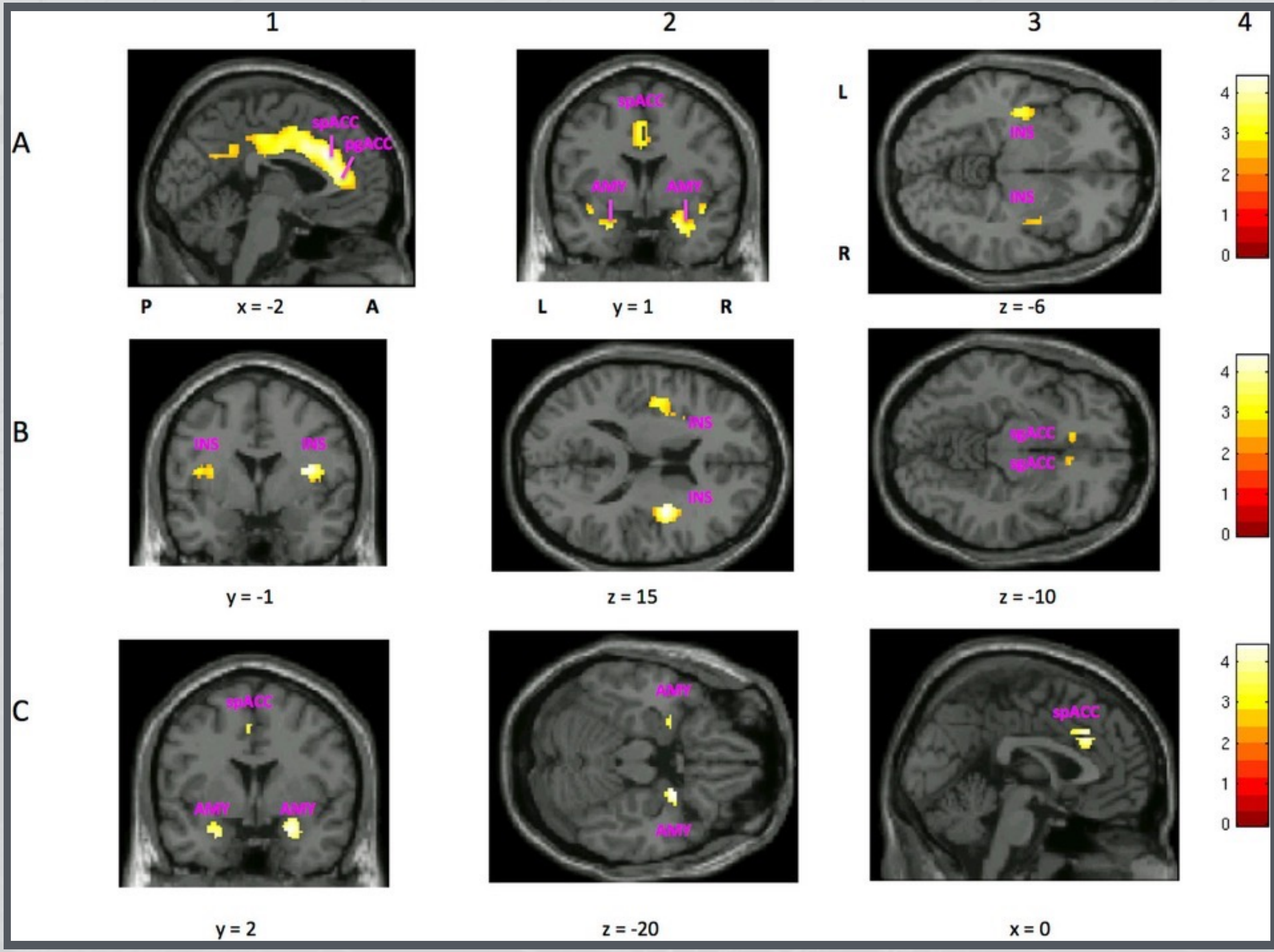
Result of the previous overlay



Other software packages

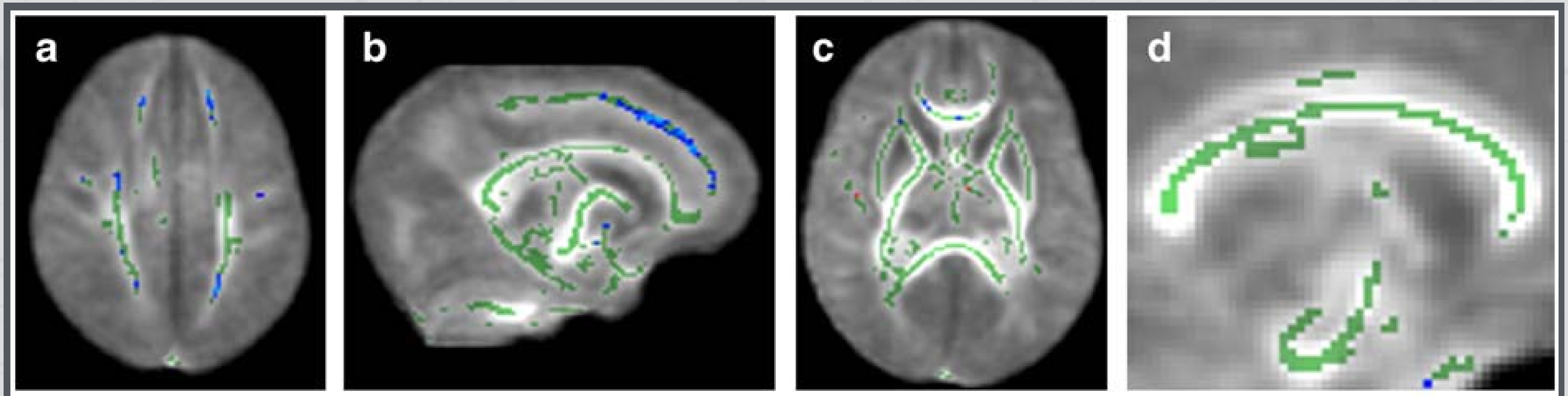
- SPM (FIL, UCL): task and resting fMRI analysis; effective connectivity; EEG, MEG, PET, SPECT; grey and white matter volumes
- FSL (FMRIB, Oxford): task and resting fMRI analysis; probabilistic tractography; voxel-based white matter analysis
- FreeSurfer (MGH, USA): cortical parcellation; longitudinal processing; visualisation
- Camino (CMIC, UCL); NifTK (CMIC, UCL); MRtrix (Melbourne, Australia and elsewhere); DTI Studio/MRI Studio (JHU, USA); Explore DTI (Utrecht, The Netherlands); Diffusion Toolkit/TrackVis (MGH, UK)
- 3D Slicer (Harvard, USA); MedInria (Inria, France); etc.

SPM



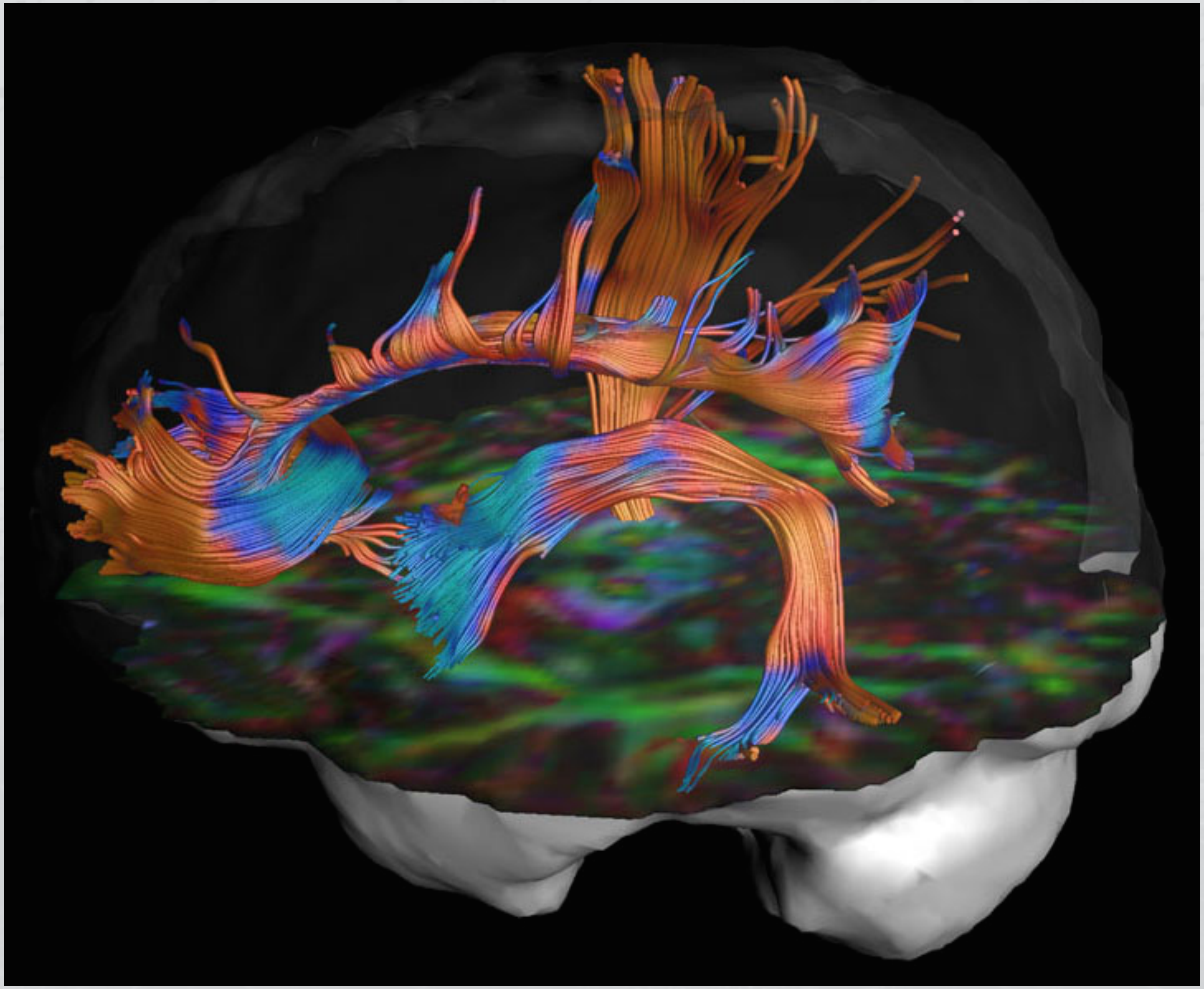
Savitz et al., *Sci Reports*, 2012

TBSS



FA of preterm-born infants vs. controls (Anjari et al., *NeuroImage*, 2007)

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
- Camino: http://www.camino.org.uk
- NifTK: http://cmictig.cs.ucl.ac.uk/research/software
- MRtrix: http://www.nitrc.org/projects/mrtrix/
- 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