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 focused 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:

```r
> 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 MrImage 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

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

> i$getFieldOfView()
[1] 240 240 150

> i$getStoredXformMatrix()
[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:
  
  ```r
  > s <- newSessionFromDirectory("/data/subject1")
  > runBedpostWithSession(s)
  ```

- Then we can run tractography:
  
  ```r
  > library(tractor.track)
  > r <- trackWithSession(s, c(34,29,14), requireImage=TRUE)
  ```

- Now retrieve the FA map and visualise the tract on top:
  
  ```r
  > 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.
Tract-based spatial statistics (TBSS) is an automated observer-independent approach for assessing groupwise microstructural differences in the major white matter pathways of the brain (Smith et al., 2006). The aim of this study was to determine if TBSS could be implemented in the preterm population, and to test the hypothesis that preterm infants have microstructural differences in cerebral white matter compared to term-born control infants in the absence of focal abnormalities such as cystic periventricular leukomalacia (cPVL) or hemorrhagic parenchymal infarction (HPI) on conventional MR imaging.

Materials and methods

Ethical permission for MR imaging was granted by the Hammersmith Hospital Research Ethics Committee. Written parental consent was obtained prior to imaging for each subject.

Subjects

DTI data were acquired from 26 preterm infants (11 females, 15 males) imaged at term equivalent age. The median (range) gestational age of the infants at birth was 28.9 (25.7–32.6) weeks, and the median birth weight was 1084 (654–1848) g. The median post-menstrual age at the time of imaging was 41.3 (38.1–45.3) weeks. The median weight and head circumference at the time of imaging were 3200 (1980–5500) g and 36.0 (31.5–39.6) cm respectively.

In the subgroup of 11 preterm infants (4 females, 7 males) who were born at 28 weeks gestation or less, the median (range) gestational age of the infants at birth was 26.7 (25.7–28.0) weeks, and the median birth weight was 920 (714–1200) g. The median post-menstrual age at the time of imaging was 41.0 (38.1–44.0) weeks. The median weight and head circumference at the time of imaging were 3060 (2000–3685) g and 35.5 (31.5–38.7) cm respectively.

DTI was also obtained on 6 healthy, term-born control infants (2 females, 4 males). The median (range) gestational age of the infants at birth was 39.7 (39.0–40.6) weeks, and the median birth weight was 3300 (3106–4000) g. The median post-menstrual age at the time of imaging was 41.7 (41.0–46.0) weeks. The median weight and head circumference at the time of imaging were 3500 (3300–4510) g and 36 (34.0–37.8) cm respectively.

There were no significant differences in age at scanning (p = 0.24) or in gender (p = 0.53) between the preterm group and the term-born controls. There were no significant differences in age at scanning (p = 0.14) or in gender (p = 0.47) between the subset of preterm infants born ≤28 weeks gestational age and term-born control infants.

Magnetic resonance imaging

MRI was performed on a Philips 3T scanner (Philips Medical Systems, Netherlands) using a phased array head coil. 3D MPRAGE imaging and high-resolution T2-weighted fast spin echo (FSE) were obtained prior to DTI. Single shot EPI DTI was acquired in 15 non-collinear directions using the following parameters: TR 8000 ms, TE 79 ms, slice thickness 2 mm, field of view 224 mm, matrix 128 × 128 (voxel size=1.75 × 1.75 × 2 mm3), b value=750 s/mm2. The data were acquired with a SENSE factor of 2 and the scanning time for this sequence was 5 min.

Fig. 1. The effect of preterm birth on FA at term equivalent age. Mean FA skeleton overlaid on the mean FA map. Regions of the mean FA skeleton in green represent areas where there were no significant differences in FA values in the preterm infants imaged at term compared to the term-born controls. Areas in blue are regions where the FA was significantly lower in the preterm group (a–d), and can be observed in the centrum semiovale (a), frontal white matter (b) and genu of the corpus callosum (c). Those infants born ≤28 weeks gestational age (e–h) had greater regions of reduced anisotropy within the centrum semiovale (e), frontal white matter (f) and genu of the corpus callosum (g), and displayed additional reductions in FA in the posterior aspect of the posterior limb of the internal capsule (g) and the external capsule (g). These areas of FA difference were used for subsequent ROI-based analyses of TBSS-processed FA data (Tables 1 and 2).

Areas in red represent voxels where the FA was significantly higher in the preterm infants.

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