Diffusion MRI: advanced tractography

Outline

Line-propagation tracking

- Deterministic (previous lecture)
- Probabilistic: extension to allow uncertainty in the tracking

Geodesic tracking

- Principle of *shortest path* between two ROIs
- ► Fast marching, graph based

Global inverse problem: bottom-up

- Reconstruct all fibers at once by *fitting fiber models* to the data
- ► GIBBS tracker

Global inverse problem: top-down

- ► First reconstruct a *superset of fibers* and then *filter* them
- BlueMatter and SIFT/SIFT2

2

Deterministic tracking [Conturo et al., 1999; Mori et al., 1999; ...]

$$\frac{\mathrm{d}\mathbf{f}(t)}{\mathrm{d}t} = \mathbf{d}\big(\mathbf{f}(t)\big) \quad \text{with} \quad \begin{cases} 0 \le t \le 1\\ \mathbf{f}(0) = \mathbf{f}_0 \end{cases}$$

- ▶ $f(\cdot)$: fiber trajectory ()
- ► d(·) : main diffusion direction estimated in each voxel ()
- ▶ **f**₀ : seed/starting point (●)
- ► *t* : step size

Notes

- ► ~ few minutes/brain
- Deterministic = the same trajectories are reconstructed from same seed points
 - Random seeding is still considered deterministic



seed

point

#3

3



seed

point

#1



(1/4)

























principal diffusion

direction

Probabilistic tracking [Parker et al., 2003; Behrens et al., 2003; ...]

$$\frac{\mathrm{d}\mathbf{f}(t)}{\mathrm{d}t} = \mathbf{d}\big(\mathbf{f}(t)\big) \quad \text{with} \quad \begin{cases} 0 \le t \le 1\\ \mathbf{f}(0) = \mathbf{f}_0 \end{cases}$$



possible

propagating directions



- Next direction drawn from distribution (uncertainty in the tracking)
- Seed a *large number of fibers* (probability of connection)

Notes

- ► ≃ 1 day/brain
- Adds confidence levels to tracts
- Probabilities maps are difficult to interpret [Jones, 2010; Jbabdi et al., 2011; Jones et al., 2013]





R

5

Δt

























Geodesic tracking

Intrinsic issues of previous local formulations

- Line-propagation suffers from local inaccuracies along the path
 - e.g. wrong fODF estimated due to high noise
- While tracking, algorithm has no information about the region it will end up in

Possible improvement

- **Optimize a <u>global</u> criterion** while reconstructing
- Global = information not only from the voxel



It's shorter to pass through the incorrect voxel rather than passing around it (in case of Euclidean distance)

Basic hypothesis used in geodesic tracking

- Fiber tracts between two gray-matter regions can be interpreted as minimal distance paths (geodesics) for a metric derived from dMRI data
- ▶ NB: the *shortest path* is <u>intended with respect to a given metric</u>

Geodesic tracking

Front-evolution algorithms [Parker et al., 2002; Jbabdi et al., 2008]

- Model the evolution over time of an interface (or front) from a seed point
- Local diffusion profiles (e.g. tensors) are the speed function controlling the propagation
 - ⁻ different variants proposed in the literature
 - $\bar{}$ e.g. coherence between front normals (n) and the field ($\boldsymbol{\epsilon}_1)$
- As front propagates, different regions will be reached with a different arrival time
- Path with minimal arrival time between two regions interpreted as the globally optimal fiber tract

- using gradient descent through time-of-arrival map



Local diffusion information



Time-of-arrival map



Optimal paths from S



Geodesic tracking

Graph-based algorithms [Zalesky et al., 2008]

- Pose tractography as computing minimal paths in a weighted graph
 - <u>Vertices</u>: center of the *voxels*
 - Edges: cost of transition from one voxel to its neighbor
- Lower costs are assigned to edges that are aligned with fiber trajectories in their close proximity
- Shortest paths between regions can be found using classical algorithms, e.g. Dijkstra
- NB: the terms shortest path or minimal cost path are always intended w.r.t a given metric

NB: this approach is similar to previous one

- It uses a direct formulation of the problem as a graph
- More intuitive but also usually more efficient







 \mathbf{x}_4

Biomedical Image Processing

Global inverse problem

Basic ideas

- 1. Tractography is an inverse problem
- 2. Use forward-models to associate a contribution to each fiber
- 3. Fit to the data to estimate these contributions

General formulation

$$\mathcal{F} = \operatorname{argmax} \ \mathcal{E}\Big(S, \hat{S}(\mathcal{F})\Big)$$

- \mathcal{F} : *fiber tracts* to be estimated
- $\blacktriangleright S$ and $\hat{S}(\mathcal{F})$: acquired and predicted diffusion data
- $\blacktriangleright \ \mathcal{E}(\cdot, \cdot)$: similarity function to drive optimization
- ► All fibers *simultaneously estimated*

Two major strategies: "bottom-up" and "top-down"





Bottom-up strategy [Kreher et al., 2008; Fillard et al., 2009]

 $\mathcal{F} = \operatorname{argmax} \ \mathcal{E}\Big(S, \hat{S}(\mathcal{F})\Big)$

- Fiber trajectories *F* parametrized as collection of segments
 - Defined by position, orientation and length
 - *Contribute to the dMRI signal* in corresponding voxels according to a *given model*
- $\mathcal{E}(\cdot, \cdot)$ consists of **two terms**:
 - data fitting, e.g. $||S \hat{S}(\mathcal{F})||_2$
 - regularization, e.g. segments should join and form long chains





optimal configuration

Different reconstruction paradigm from before

- ► Fiber tracts are not "tracked one-by-one", e.g. following local diffusion directions
- They are "built piece-by-piece" all together
- Driven by how well a configuration of segments explain the measured dMRI data

GIBBS Tracker algorithm [Kreher et al., 2008]

Basic principle:

- 1. Creation of an *initial configuration of segments*
- 2. Calculation of the *corresponding dMRI signal*
- 3. Adjustment of the segments to explain better the measured dMRI data

Segments are modified using a combination of:

- Monte Carlo Markov Chain (MCMC) sampler
 - Randomly changes the current configuration of segments

Target Density

ωb

Temp.

 $\ln(T)$

 $P_{i}(0 | \mathbf{S})$

- A proposal can be either accepted or rejected
- Simulated Annealing (SA) → to make small changes while converging

12

(2/5)







 $\overrightarrow{\mathbf{\omega}}$ c

Main elements

- Segments (cylinders with position, orientation, length...)
- Attraction and connection areas
- Elementary random proposals
 - Create new segment (birth) or remove an existing one (death)
 - Move/rotate segment
 - Connect two close segments





data energy interaction energy



How well the current configuration explains the measured dMRI data



Favors the formation of the cylinders into chains

13



~ 1 month/brain

Algorithm overv

- Higher quality of reconstructions, but...
- ...huge complexity leaves many open problems <

Billions of segments For each: position, orientation, length etc... Constraints for joining them and form chains

14

Example: problems for connectivity estimation

▶ Partial fibers: <u>do not form</u> a full trajectory/fiber







• **Orphan fibers**: <u>do not reach</u> the gray matter



Global inverse problem: top-down

Top-down strategy [Sherbondy et al., 2009]

$$\mathcal{F} = \operatorname{argmax} \ \mathcal{E}\Big(S, \hat{S}(\mathcal{F})\Big)$$

- *F* is a *large* superset of fibers
 estimated combining standard methods
- ▶ Fibers **removed** from \mathcal{F} based on $\mathcal{E}(\cdot, \cdot)$

BlueMatter algorithm [Sherbondy et al., 2009]

- ► *F* consists of ~**180 billion candidate fascicles** (mixes many algorithms, e.g. deterministic and probabilistic)
- $\mathcal{E}(\cdot, \cdot)$ simultaneously accounts for:
 - how well the acquired dMRI signal is explained
 - volume occupied by fascicles in a voxel
- Optimal subset of fibers searched using a parallel stochastic hill climbing algorithm
- Requires a BlueGene/L supercomputer





Global inverse problem: top-down

NB: it represents only a proof of concept

- ▶ ~ 9 days/brain on a supercomputer (2048 cores + 500 GB ram), but...
- ...showed a <u>different perspective</u> to approach tractography

Notes

- Since then, optimized techniques have been developed
 - SIFT: ~ 15-20 hours/brain, 100M fibers, 26 GB ram [Smith et al., 2013]
 - SIFT2: ≃ few hours/brain, 10M fibers, few GB ram [Smith et al., 2015]
- Optimized tractograms are more biologically meaningful

[Smith et al., 2015; Yeh et al., 2016]







Still room for improvement (coming lecture)

e.g. adding biophysical models might give access to features like *actual density* or the *axon caliber* of each bundle

Questions?

Comments?

Suggestions?