generative models for alignment of shape data: + applications to diffusion tractography

shantanu h. joshi

Ahmanson — Lovelace Brain Mapping Center Departments of Neurology & Bioengineering & The Program of Computational & Systems Biology **Bioinformatics IDP** University of California Los Angeles









with Andrew Lizarraga, David Lee, Elvis Nunez, and Katherine Narr









data with shapes of functions, sequences, and signals





$\{\beta\}|\beta:[0,1]\to\mathbb{R}^3$

need for geometric signal processing tools

- Biological data is subtle large variation in normative population
- Linear Models do not capture the variation in anatomy well
- Importantly Linear Models do not exploit the underlying geometry of the signals
- "Often, we are interested in comparing the deformations of the objects, rather than a precise definition of the object itself" †
- Above idea naturally translates to the mathematical modeling of transformation groups that are non-linear manifolds

†Thompson DW (1917) On Growth and Form, Cambridge University Press.



diffusion-weighted imaging





Diffusion Orientation Estimation



Diffusion Property Estimation



Diffusion Tractography

diffusion-weighted imaging

Fractional anisotropy (FA) diffusion measure — voxelwise analysis

- Measure of anisotropy
- Alterations in white matter fiber axon density, myelination, etc.



Perez-Iglesia et al., 2010





MCI AD Zhang et al., 2014



Raz et al., 2010





diffusion-weighted imaging (tractometry) measuring FA along the course of fiber tracts

Inferior Longitudinal Fasciculus









FA

0.3



main challenges

- Geometry of white matter tracts are highly heterogeneous
- Direct tract-correspondence across populations remains challenging
- Preserving geometric information is difficult
- Want to regard streamlines as an entire collection as opposed to an average:

however typically this requires pairwise comparisons of streamlines
If no pairwise comparisons, forms of dimension reduction are usually required



related methods: robust efficient linear registration

- Requires Pairwise comparisons of streamlines
- Streamlines are represented in \mathbb{R}^3
- Apply affine transformations to register tracts
- Local differences in the bundle may remain unregistered

Garyfallidis et al. NeuroImage (2015)



related methods: currents

- Tends to capture local geometry



20 mm

20 mm

• Can characterize the bundle via its response to 'exciting' vector fields • Can represent a tract using a small number of currents (dim-reduction)





Durrleman et al. NeuroImage (2011)



bundle representation

We characterize a set of streamlines as a pair:

An intrinsic shape mean β_{μ}

The rest of the fibers are represented by a low-dimensional tangent vector representation



collection of curves representation

• Coordinates of a white matter fiber bundles are represented as a collection of functions in a Hilbert space:

$$\mathcal{F} \equiv \{(f_1, f_2, \dots, f_N) \mid f_i \in \mathbb{L}^2([0])\}$$

- constraints, and translation constraints
- We don't impose such constraints on the original space of curves



• Note: One could add additional constraints, such as scaling invariance, rotation

mean fiber srvf

- For each fiber, we take the SRVF representation
- SRVF's form a subset of the unit Hilbert Sphere

Given:

$$f_i : [0, 1] \to \mathbb{R}^3$$
$$q_i := \frac{\dot{f}_i}{\sqrt{||\dot{f}_i||}}$$



Joshi SH et al. (2007 IEEE CVPR, EMMCVPR), Srivastava et al. (2011 IEEE PAMI)



mean fiber srvf

- Our representation is invariant under scaling and translation
- Fisher-Rao distance on the unit Hilbert sphere is given by:

$$\arg\min_{\gamma\in\Gamma}||q_1 - (q_2\circ\gamma)\sqrt{\dot{\gamma}}||^2$$

- Traversing a geodesic between two points in this shape space corresponds to the registration of curves in the original space
- Pairwise comparisons have a large cost if implemented among a large population shapes



projections on the tangent space space of SRVFs

- Subset of a Hilbert Sphere
- Define the Karcher Mean and project to Tangent Plane

Karcher mean $\beta_{\mu} = \underset{q}{\operatorname{argmin}} \frac{1}{N} \sum_{i=1}^{N} \underset{O,\gamma}{\operatorname{argmin}} \left\| q - \sqrt{\dot{\gamma}} \mathcal{O}q_{i}(\gamma) \right\|^{2}$

> where $\mathcal{O} \in SO(3)$ and $\gamma : [0,1] \rightarrow [0,1]$ is a reparameterization function we project the q_i to the Tangent space centered at β_{μ} via exponential maps







distributions of streamlines low-dimensional representation

- Fourier basis is chosen for $T_{\mu}(S)$ denoted by g_k
- The Fourier basis has the advantage that the coefficient of the tangent vectors capture shape variability in the tract
- We take the coefficient matrix as the representation of the tract, give by $\mathcal{A} = \langle vi, g_k \rangle, i, k = 1, ..., N$





joint alignment: means + tangent vectors metric between bundles

Compares Means Obtains registration of core fiber (means) $\gamma: [0,1] \to [0,1]$



joint alignment: means + tangent vectors parallel transport





Andrew Lizarraga

Algorithm 1: Parallel Transport of $\{v_i^2\}$ for the reconstruction of \mathcal{A}^2 along a geodesic from β_{μ}^2 to β_{μ}^1 denoted by $\Psi(\{v_i\}, \beta_{\mu}^2; \beta_{\mu}^1)$

Input: $(\beta_{\mu}^{1}, \{v_{i}^{1}\}, i = 1, ..., N), (\beta_{\mu}^{2}, \{v_{i}^{1}\}, i = 1, ..., N)$ **Output:** Transported tangent vectors $\{\tilde{v}_{i}^{2}\}, i = 1, ..., N)$ 1 Compute a tangent vector w such that $\exp_{\beta_{\mu}^2}(w) = \beta_{\mu}^1$ 2 Let $l_w = \sqrt{\langle w, w \rangle}$ **3** Define a step size k. 4 for $\tau \leftarrow 2$ to k - 1 do

5
$$q_{\tau} = \exp_{\beta_{\mu}}(\frac{w}{k})$$

6 $\tilde{v}_{i} = v_{i} - \langle v_{i}, q_{\tau} \rangle q_{\tau}, i = 1, \dots, N$
7 $\tilde{v}_{i} = \tilde{v}_{i} \frac{l_{w}}{\|\tilde{v}_{i}\|}, i = 1, \dots, N$
8 end

S

 \mathcal{W}



bundle optimization problem subject to subject bundle assignment

- Comparing bundles from one subject to a template subject requires many distance computations on the low-dimensional projections
- This reduces to the following alternating optimization problem, which allows us to find a permutation and rotation assignment indicating which bundle should be registered from the source subject to the template subject:

$$(\hat{\Gamma}, \hat{\mathcal{P}}) = \underset{\Gamma, \mathcal{P}}{\operatorname{argmin}} \left\| (\mathcal{B}^{1}_{\mu}, \mathcal{A}^{1}) - \Gamma \cdot \mathcal{P} \cdot (\mathcal{B}^{2}_{\mu}, \tilde{\mathcal{A}}^{2}) \right\|$$

• Here, Γ is an action by rotation, and \mathcal{P} is an action by assignment (permutation)

results: subject to template alignment



results: subject to template alignment

Bundle	LTh	R Th	L	R	L	R	L	R	CC F	CC F	L	R	L	R	L	R	L	R
	Rad	Rad	CST	CST	CnCn	CnCn	CnHp	CnHp	Maj	Min	ILF	ILF	SLF	SLF	Unc	Unc	Arc	Arc
T-stat	43.27	33.75	9.88	22.6	18.5	19.8	3.72	11.9	4.07	1.79	8.72	15.33	18.73	11.52	9.14	8.49	33.23	33.75
P-value	p < 1e-5	р < 1е-5	0.0748	р < 1е-5	р < 1е-5	р < 1е-5	р< 1е-5	р < 1е-5	р < 1е-5	р < 1е-5	р< 1е-5							

- We compute the bidirectional Hausdorff distance before and after alignment
- Computed for each tract for N = 43 subjects and was shown to be significantly less after soft alignment (FDR corrected)
- (Except for the CC F Min (p = 0.0748) after correcting for multiple comparisons using FDR)

but did not survive FDR

- The average Hausdorff distance for CC F Min was still lower for the soft alignment method





- registration process
- Similar looking tracts appear to carry similar FA values

• After population is aligned to template, FA profiles are resampled

Profiles appear to be aligning even without explicitly using FA in the

Lizarraga et al. In prep (2024)





- registration process
- Similar looking tracts appear to carry similar FA values

• After population is aligned to template, FA profiles are resampled

Profiles appear to be aligning even without explicitly using FA in the

Lizarraga et al. In prep (2024)





- After population is aligned to template, FA profiles are resampled
- Profiles appear to be aligning even without explicitly using FA in the registration process
- Similar looking tracts appear to carry similar FA values



Andrew Lizarraga

Lizarraga et al. In prep (2024)





discussion

- A framework for soft registration of white matter fiber tracts using a lowdimensional representation that encodes shape deformations
- The mechanism of parallel transport and product metric enables an effective computation of tract differences while simultaneously allowing the alignment of tracts
- From within-tract fiber-to-mean registration results, we see that the shape alignment of geometrically similar fibers may enhance the features of diffusion measures sampled along their lengths even though the measure (FA) was not explicitly accounted for in the deformation process
- This framework is general and will potentially allow statistical shape analysis of general collections of streamlines