

Direct native space bundle alignment for group comparisons

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Diffusion Imaging in Python

<http://dipy.org>

Sherbrooke Connectivity Imaging
Laboratory (SCIL)

<http://scil.dinf.usherbrooke.ca>

DIPY

SCIL



UNIVERSITÉ DE
SHERBROOKE

Declaration of Financial Interests or Relationships

Speaker Name: Eleftherios Garyfallidis

I have no **financial interests or relationships** to disclose with regard to the subject matter of this presentation.

Problem: We want to study bundles across populations.

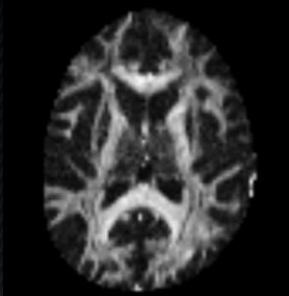


Question: What is the best way to register the bundles together so that we can calculate statistics, study their shape, etc.?

Picture: Courtesy of Flavio Dell'Acqua

Current solutions

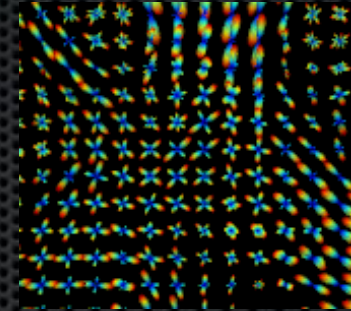
Voxel-based



Scalar e.g. FA¹



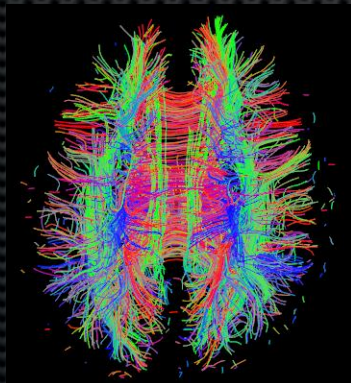
Tensors²



ODF/FOD³

Streamline-based^{4,5}

full brain



same bundle



[1] Smith et al. Neuroimage 2006, [2] Zhang et al., IEEE TMI 2007, [3] Raffaeli et al. Neuroimage 2011, [4] Durrleman et al., Neuroimage 2011, [5] Mayer et al., IEEE TMI 2011.

Bundles of interest alignment

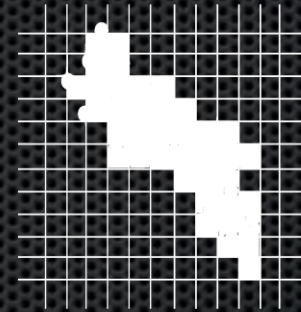
Let's assume that we have already segmented our bundles.

Image-based registration

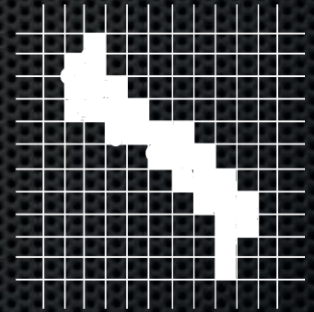
- Mean Square Differences (MSD)
- Mutual Information
- Cross Correlation



Static



Moving



Point-based registration

- Iterative Closest Point ++



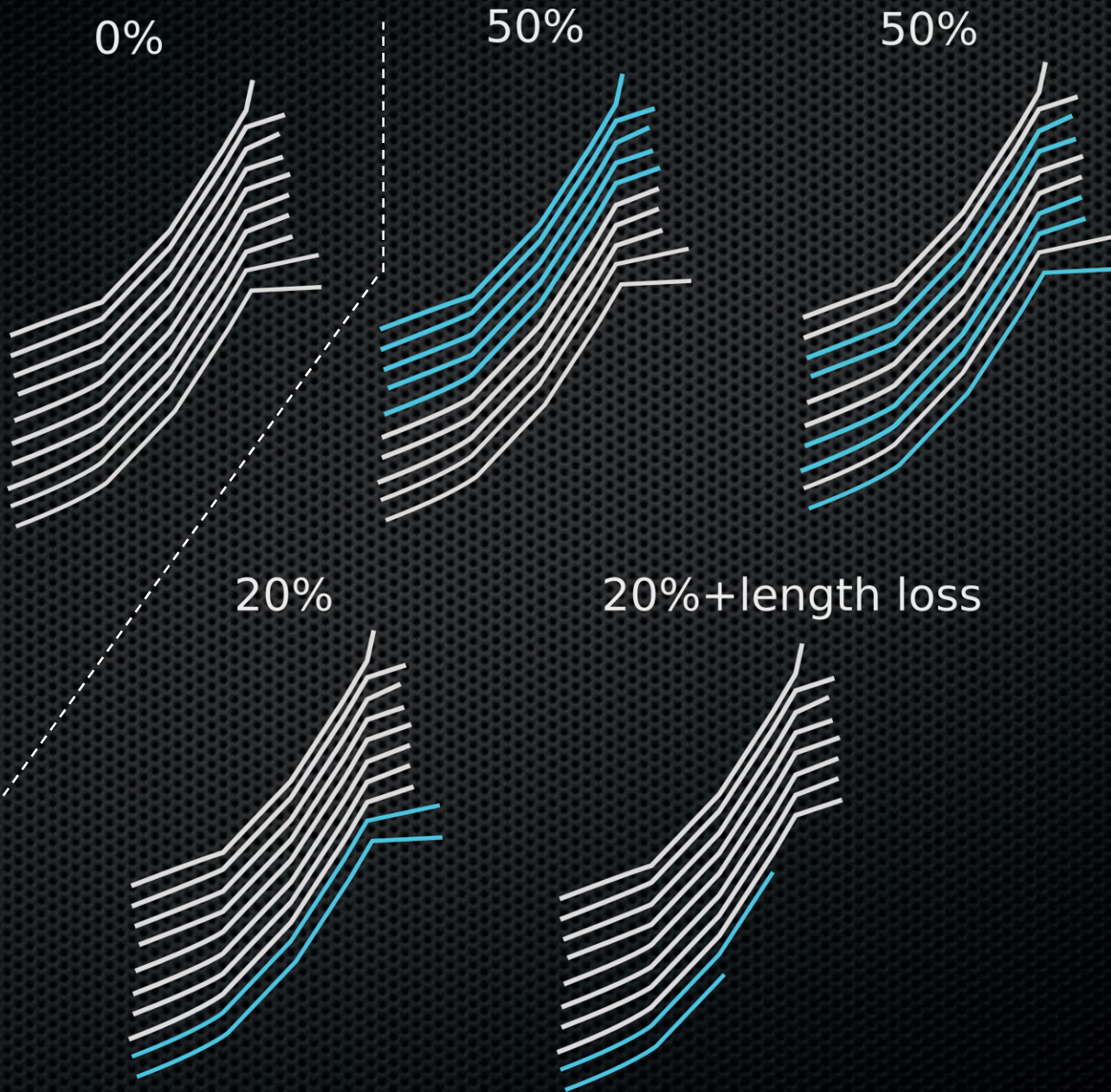
Streamline-based registration

- Which metric?
 - Shape, neighborhood, distance!

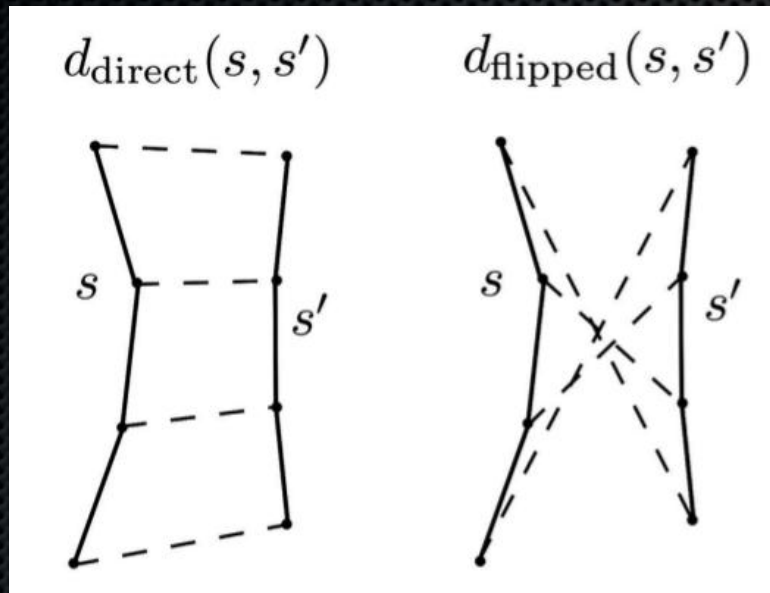


We need to resolve partial data

static



Distance metric



Minimum Direct Flipped^{1,2} (MDF)

$\min(d_{\text{direct}}, d_{\text{flipped}})$

- Fast
- Symmetric
- Proper distance metric²

Cost function

The squared sum of minimums along the rows and the columns of a distance matrix (D) created by the pairwise MDF distances.

Bundle Minimum distance (BMD)

$$\text{BMD}(S_a, S_b) \rightarrow \frac{1}{4} \left(\frac{1}{A} \sum_i \min_j D(i, j) + \frac{1}{B} \sum_j \min_i D(i, j) \right)^2$$

Optimization method:

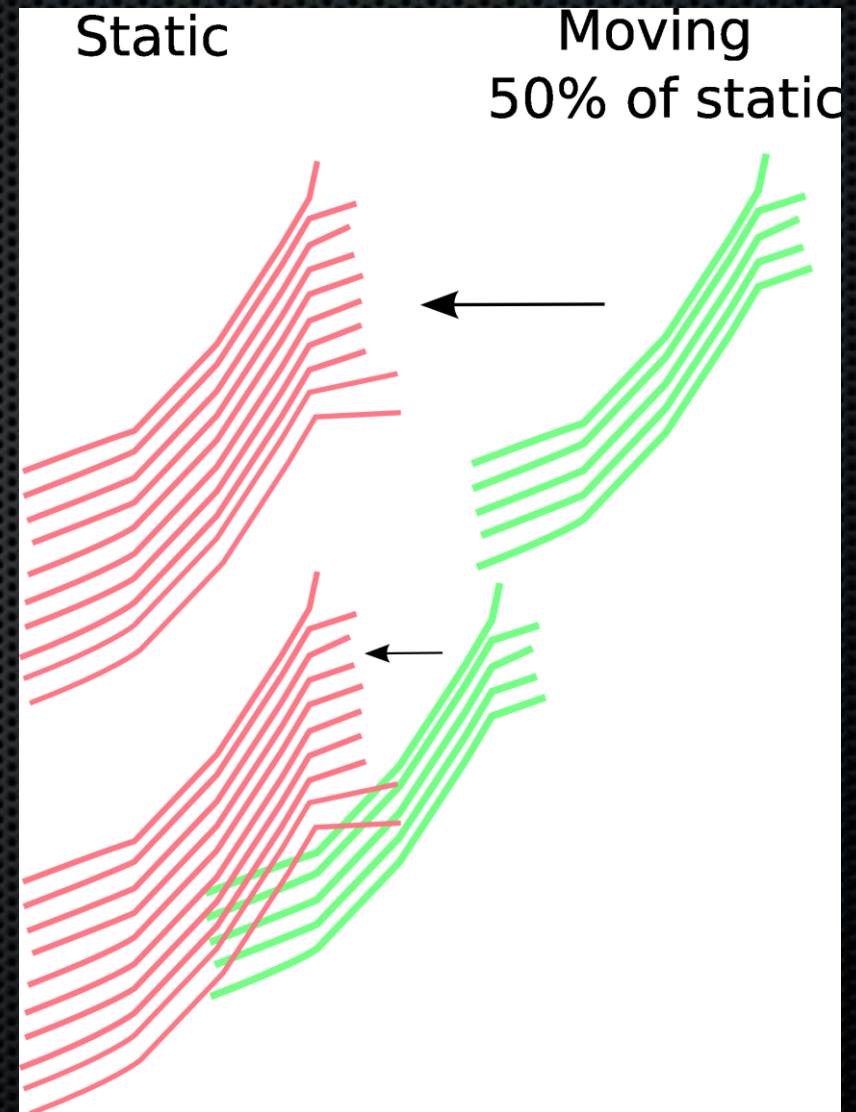
Streamline-based Linear Registration (SLR)

Cost function:	Bundle Min Distance (BMD)
Rigid :	6 parameters
Affine :	12 parameters
Optimizer :	Powell L-BFGS-B (bounded)

Basic optimization check experiment

For the same subject:

- a) we take a bundle (static)
- b) copy and transform one part of it (moving)
- c) measure our cost function as we transform it back to its original place.

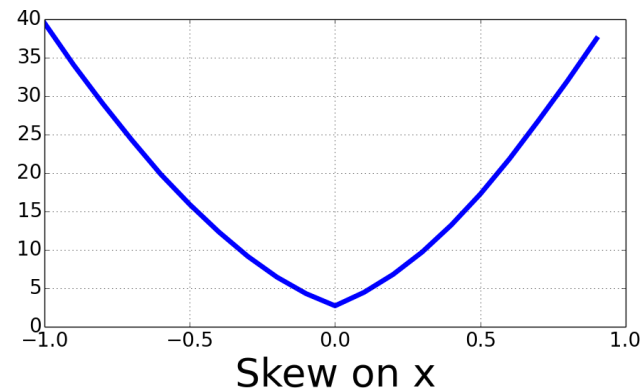
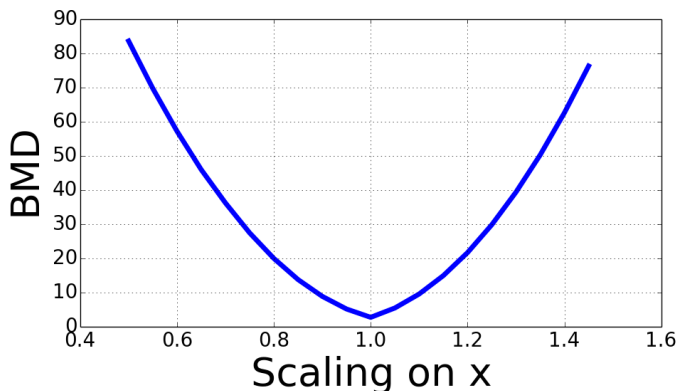
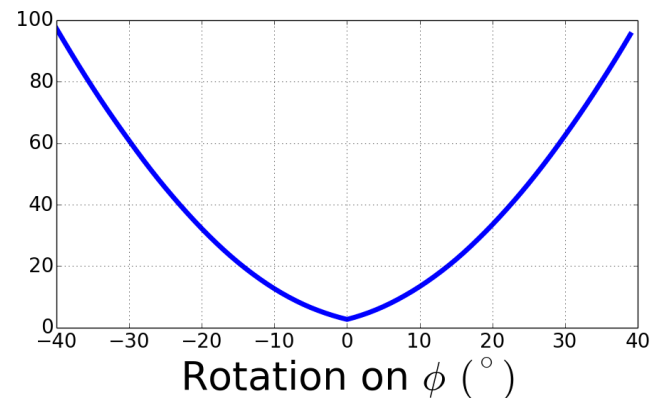
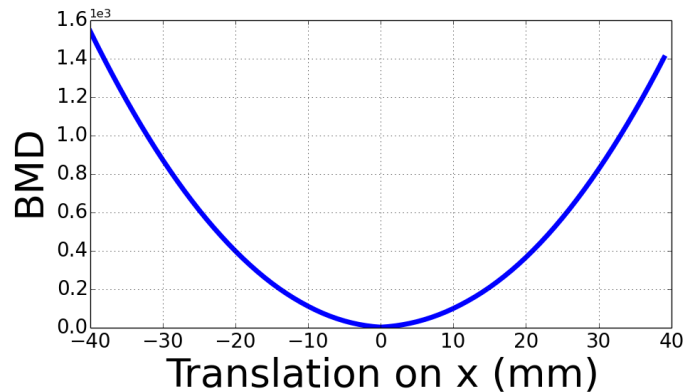


BMD is great for optimization

In this experiment we copied 33% of the **left SLF** bundle and started transforming it measuring BMD.

Our cost function is smooth and convex even with partial data!

Affine parameters



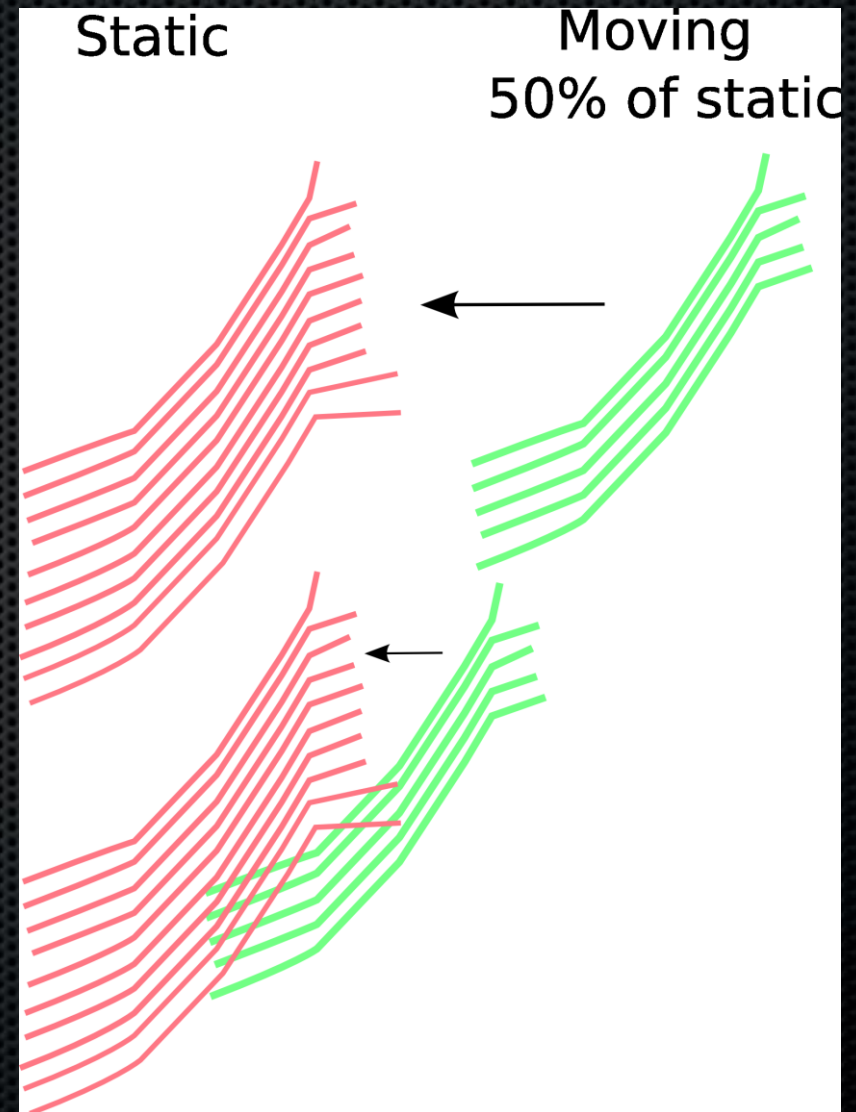
Basic validation experiment

For the same subject:

- a) we take a bundle (static)
- b) register the moving bundle
- c) discretize the registered bundles
- d) measure Jaccard Index

Jaccard index is a measure of overlap.

- 1 means perfect overlap
- 0 means no overlap



Results: Same subject comparison

Middle section of Corpus Callosum

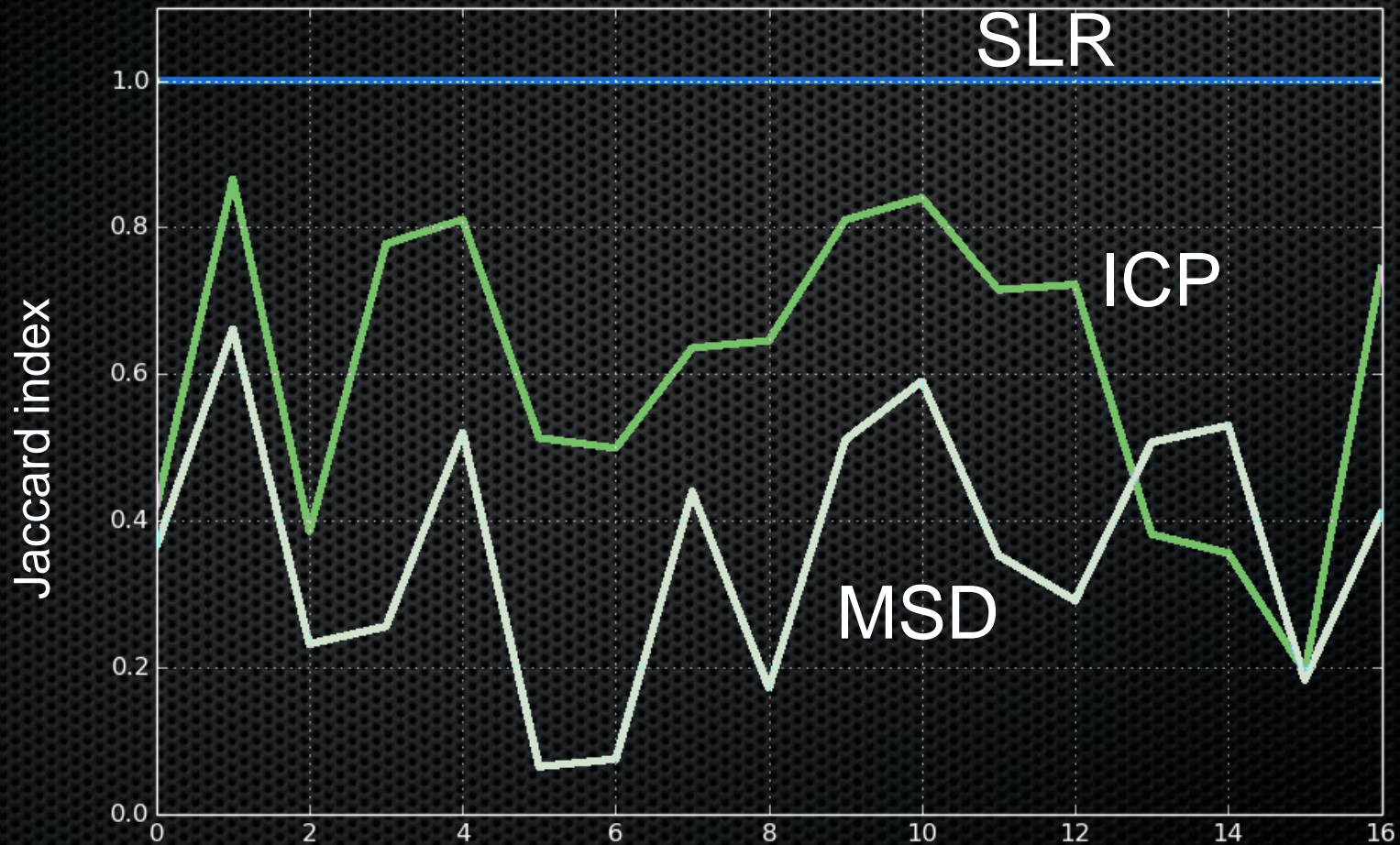
Let's compare the Jaccard indices of:

- SLR (streamlines)
- ICP (points)
- MSD (binarized bundle)

	SLR	ICP	MSD
0% missing	1.00	1.00	0.90
	SLR	ICP	MSD
50% missing	1.00	0.87	0.66

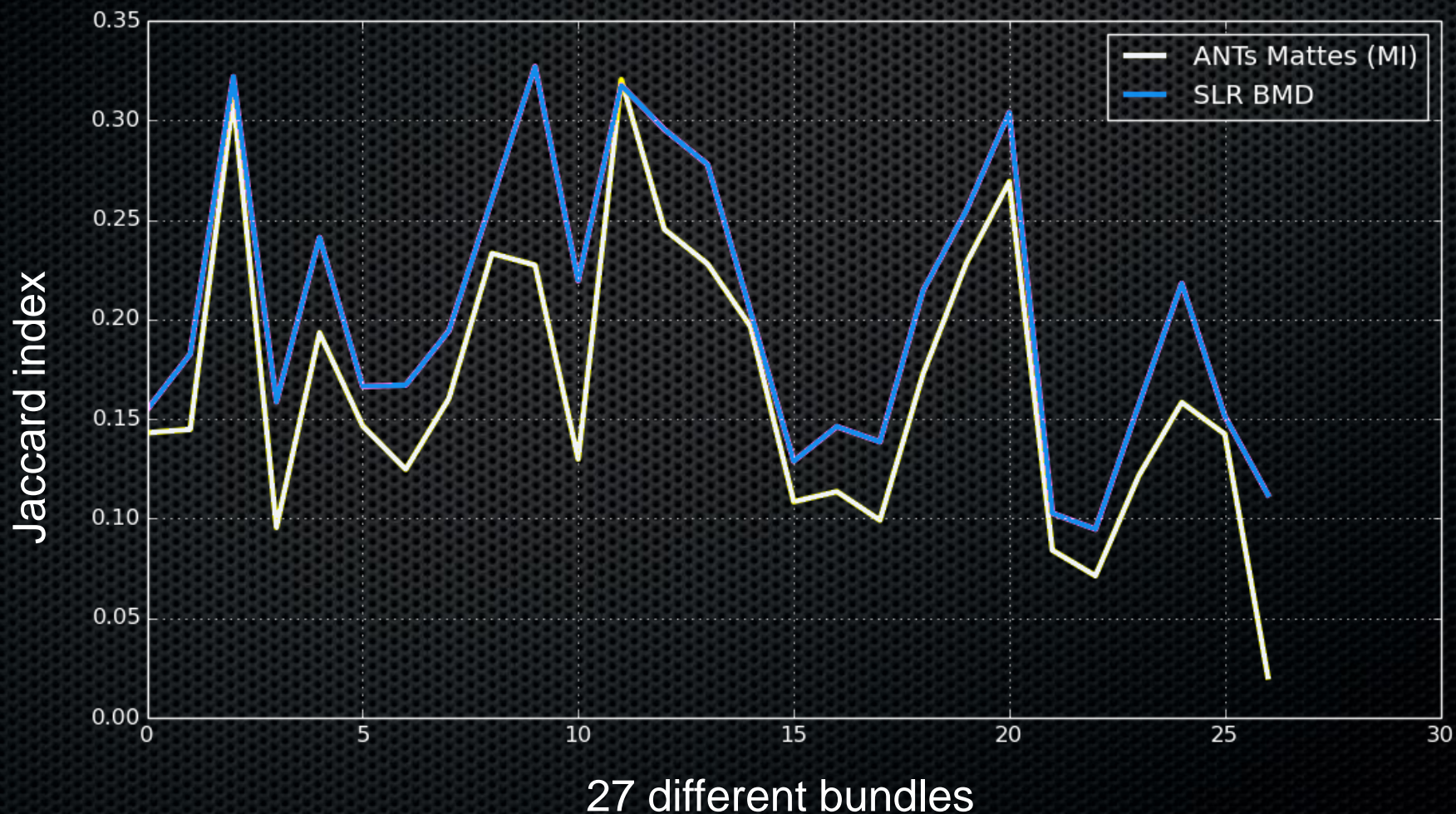
Results: Same subject comparison

17 different bundles



Results: FA-based full brain vs bundle-based SLR (2 subjects)

Rigid: Mutual Information (ANTs) vs SLR



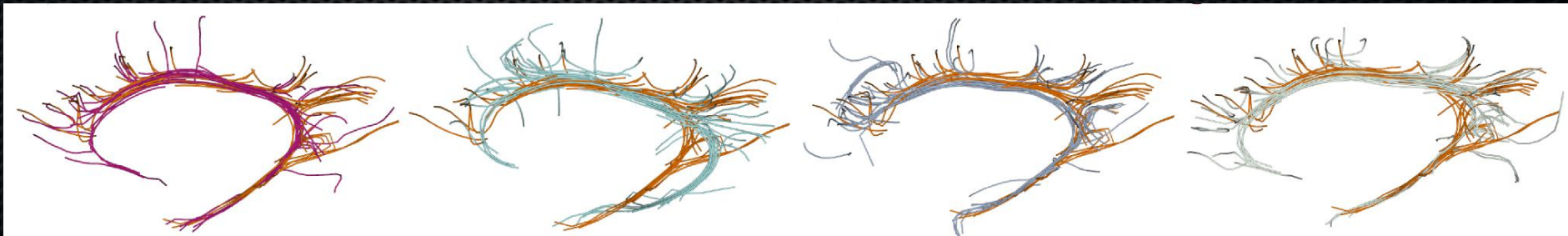
Results: Example 5 subjects' CGs



5 cingulum bundles in native space



Cluster centroids e.g.
from QuickBundles
(optional)

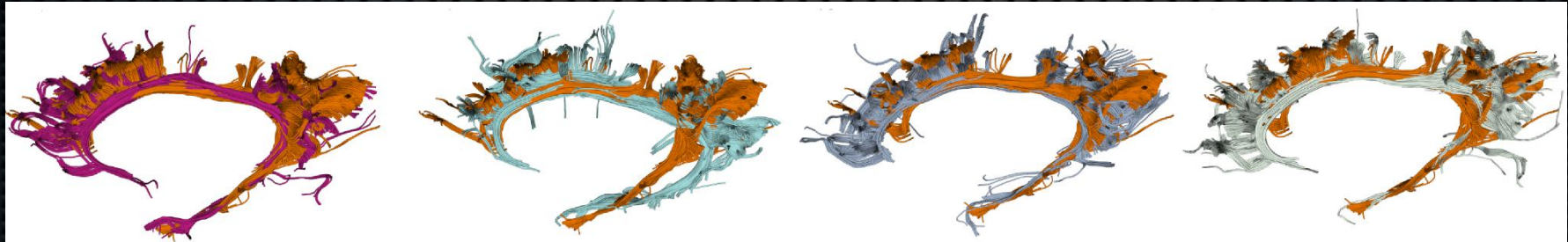


4 bundles aligned with the orange bundle (static)

Results: Example 5 subjects' CGs

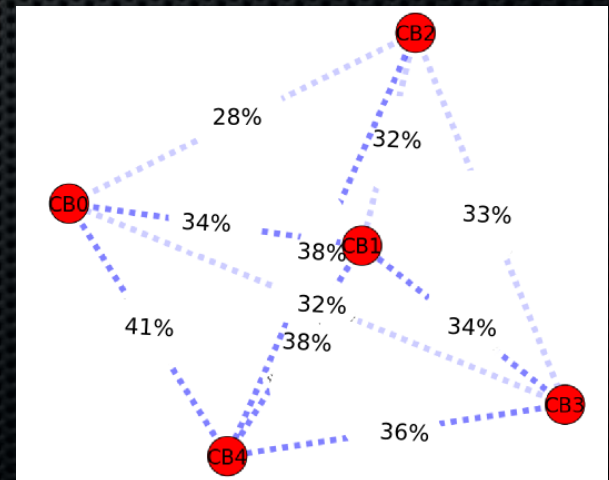


Apply the transformation matrix



Now if we repeat this procedure so that CG of every subject can be the static.

We can create a **network** showing the difference, e.g. % overlap, between **every subject's bundle** to any other subject's bundle.



Results: video

Demonstrations with rigid and affine registration.

- Same subject
- Different subjects

In the following video the **static** (reference) bundle will be always depicted with red and the **moving** will be green.

The bundles have been segmented using the **tract-querier**¹ with the white matter query language.

[1] Wassermann et al. MICCAI 2013
<http://tract-querier.readthedocs.org>

Conclusion

- The **SLR** uses streamline-only information to align bundles of interest.
- The **BMD** cost function used with the **SLR** has shown that is robust with partial and noisy real data.
- The code will be soon available in **DIPY**.
- Try it and give us feedback.

Thank you!

SCIL



<http://scil.dinf.usherbrooke.ca>



<http://tractometer.org>

DIPY

<http://dipy.org>



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