

Statistical shape analysis of large datasets using diffeomorphic iterative centroids

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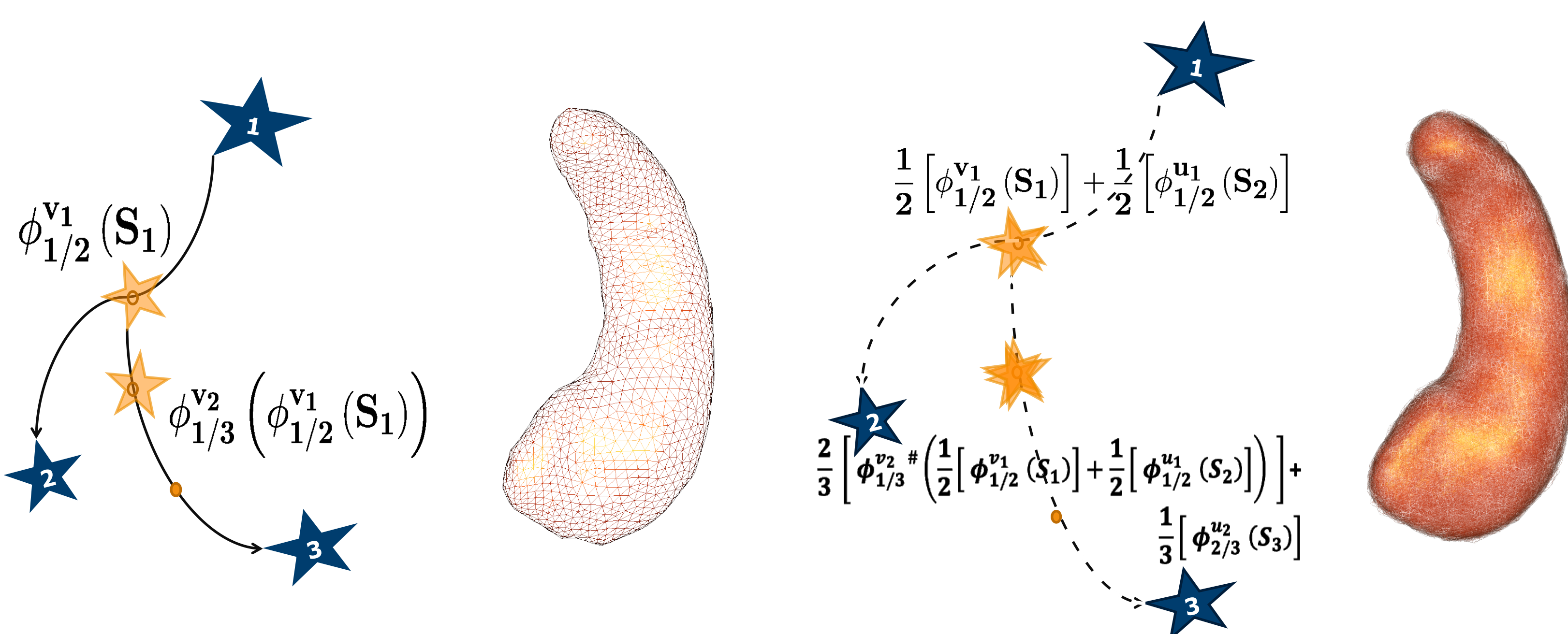
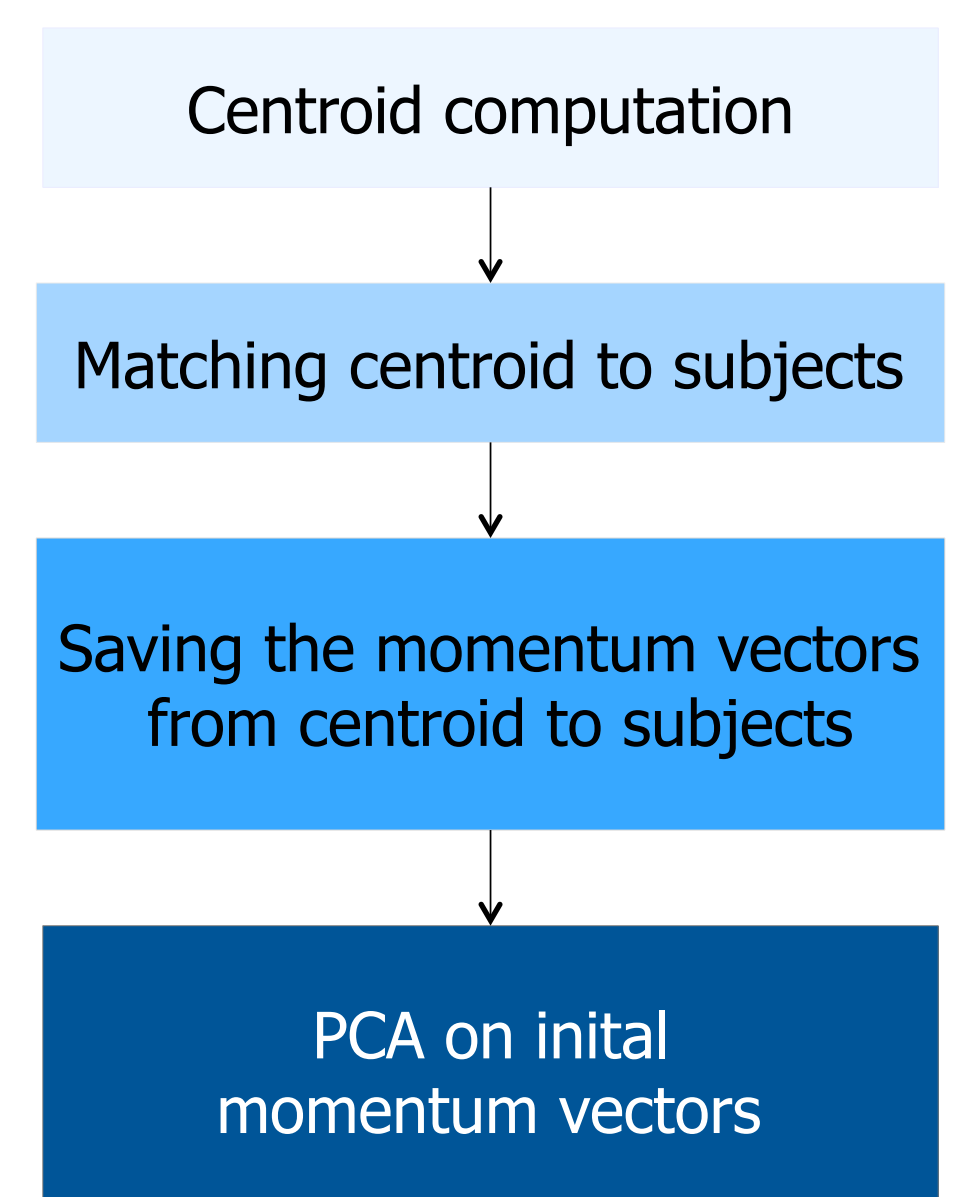
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INTRODUCTION

Statistical shape analysis methods are increasingly used in neuroscience. A challenge: performing statistical analysis on large databases. A common approach: analyzing the deformations that map individuals to a template of the population (Ashburner 1998; Vaillant 2004).

The Large Deformation Diffeomorphic Metric Mapping (LDDMM) framework provides a natural setting for quantifying deformations between anatomical shapes: the diffeomorphic deformations preserve the topology and provides a metric between shapes. We used **the framework of currents** to represent our surfaces, avoiding point to point correspondence issue and providing metric robust to different sampling and taking into account local orientation of the shapes (Vaillant 2005). Various methods have been proposed to estimate a template using the LDDMM framework (Durrleman 2008; Glaunès 2006), they are computationally expensive due to the complexity of the deformation model.

We propose an approach using a **diffeomorphic iterative centroid** using the LDDMM and the current frameworks (Cury 2014) as a template shape for a statistical shape analysis.



METHODS

→ 3 datasets composed by hippocampal meshes: **SD50** is 50 synthetic meshes build around a hippocampal mesh (the exact centre); **RD50** 50 hippocampal meshes computed from the segmentation of T1 MRI of the IMAGEN database (Schumann 2010); **RD1000** by 1000 hippocampi from IMAGEN.

→ **Diffeomorphic Iterative Centroid** : updating the centroid by transporting the actual centroid along the geodesic flow and stopped depending on the iteration number

3 different algorithms **IC1**, **IC2** and **PW**. We compared this approach to an to an estimated template computed (Glaunès et al. 2006).

RESULTS

→ Computation times (min)

		Centroid	T(centroid)	Total
SD50	IC1/PW	31	81	112
	IC2	85	87	172
RD50	IC1/PW	75	188	263
	IC2	174	252	426

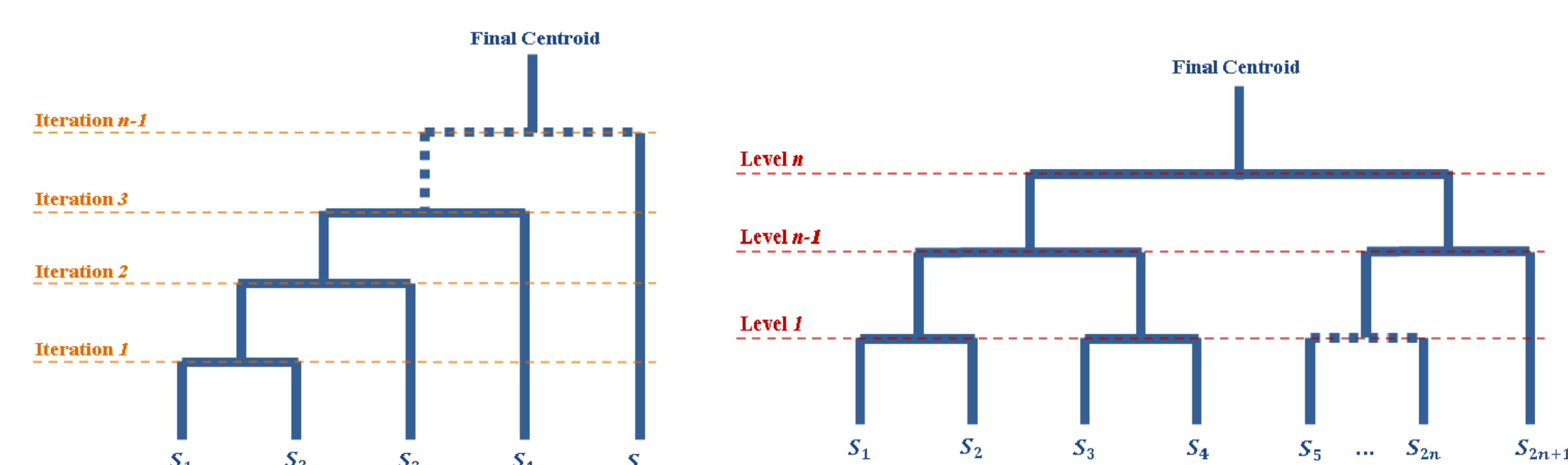
For RD1000: 832 min for IC1

→ Centering of the templates: Ratio R

$$R = \frac{\frac{1}{N} \sum_{i=1}^N v^i(\cdot, 0) \|_V}{\frac{1}{N} \sum_{i=1}^N \|v^i(\cdot, 0)\|_V}$$

		Centroid	T(centroid)
SD50	IC1/PW	0.05	0.04
	IC2	0.03	0.04
RD50	IC1/PW	0.30	0.21
	IC2	0.33	0.31

For RD1000: R = 0.10

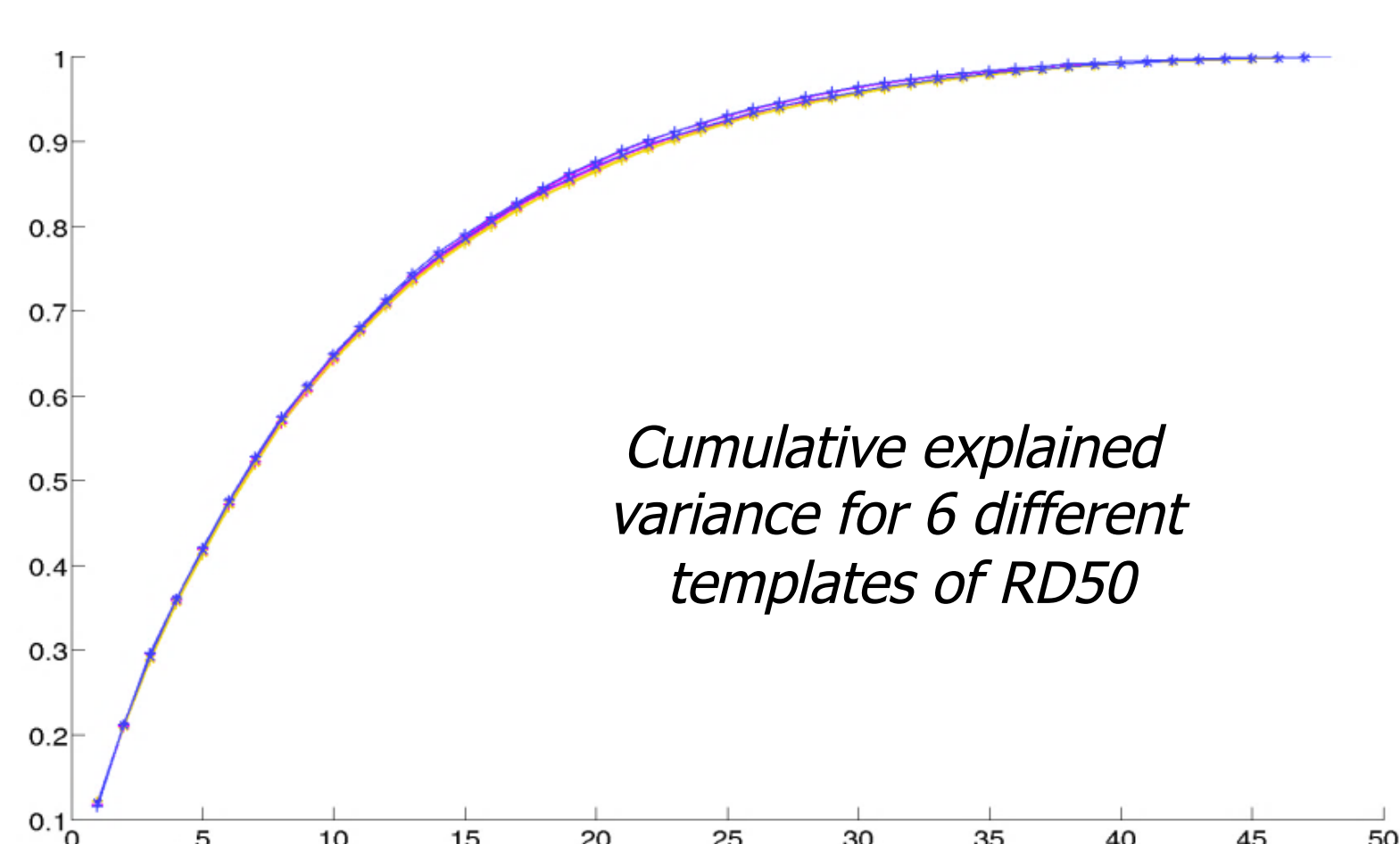


CONCLUSIONS

We proposed a fast approach for template-based shape analysis of large datasets. When applied to hippocampal shapes of young healthy subjects, the approach adequately captured the variability of the population with a reasonable number of dimensions.

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→ Results of the PCA

For SD dataset, PCA results from the different templates are very similar to the analysis make from the exact center. As for RD50 (see figure on left).

→ For **RD1000** PCA shows that 50 components are enough to explain the main (97%) anatomical variability of young normal hippocampi.

