Statistical Shape Analysis for Population Studies via Level-set based Shape Morphing

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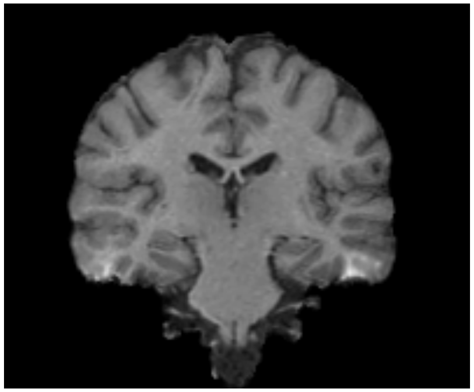
Motivation

NC



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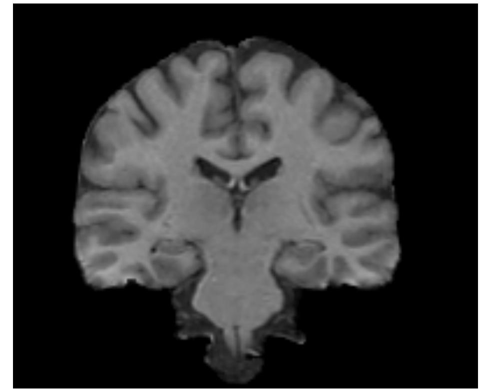
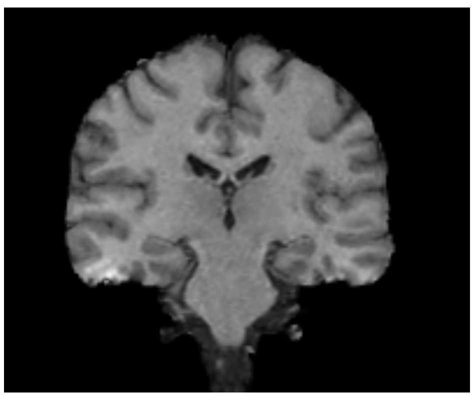


SZ



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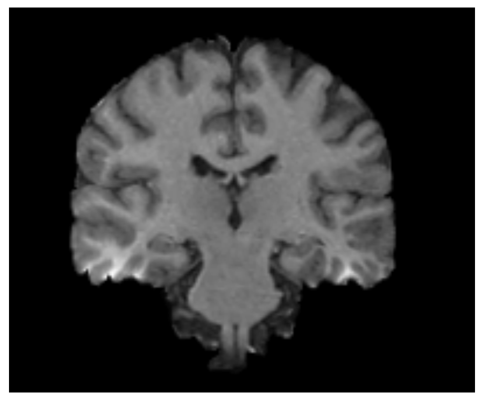

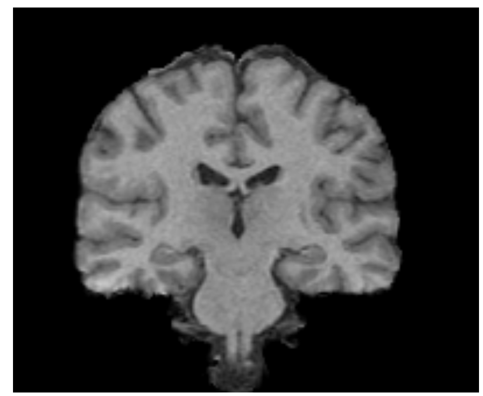

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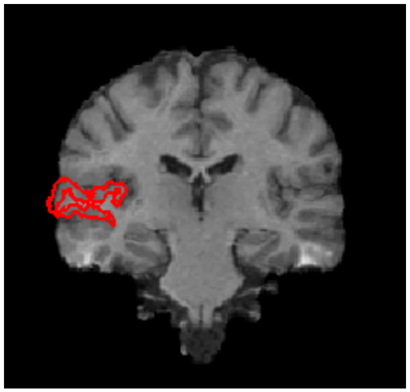

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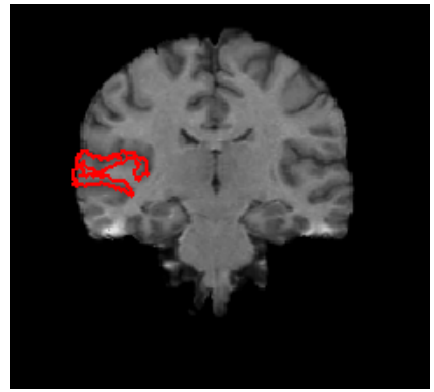

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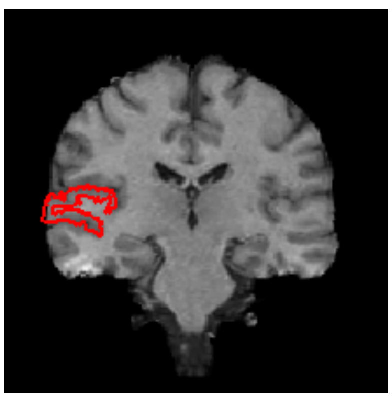

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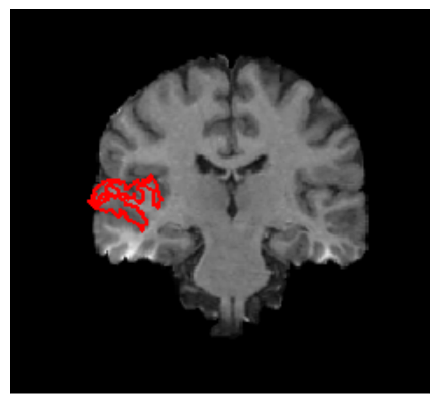
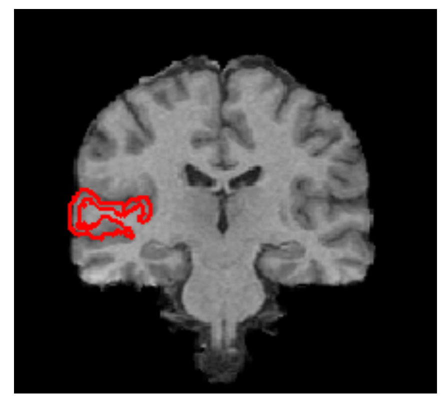
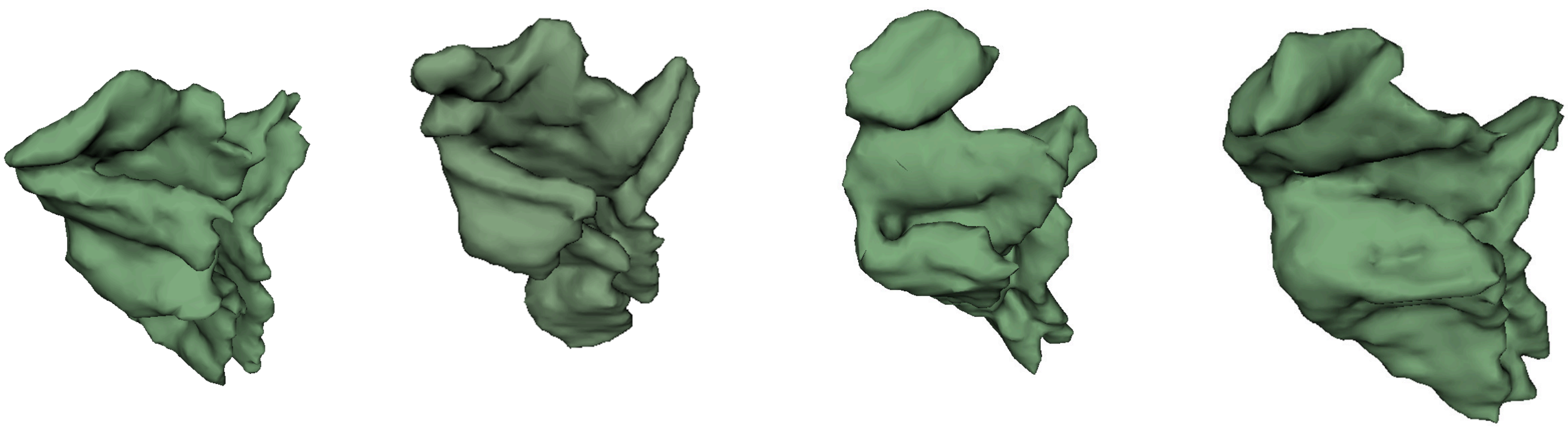




STG of First Episode Schizophrenics



Objective

- Detect, Locate and Quantify spatial morphological differences between two shape populations (e.g. healthy controls and patients).

Shape Representations and Related Methods

- Surface representation: methods such as SPHARM-PDM. Require one-to-one correspondences. [Styner 2004]
- Medial representation: more compact. Similar challenges. [Bouix 2005]
- Feature vectors: Robust but not intuitive.

[Reuter 2006 (Shape DNA), Niethammer 2007]

Method Outlines

- Surface representation: Signed Distance Transform
- Shape metric: modified Hausdorff distance ->
  does not require point-to-point correspondence.
- Shape Alignment: Align shape using 12-affine transformation by minimizing shape distances.
- Shape morphing: construct mean shape via level-set framework by minimizing shape distances.
- Shape statistics: Find statistically significant differences by calculating the signed distances to the mean shape.

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- Shape statistics: Find statistically significant differences by calculating the signed distances to the mean shape.

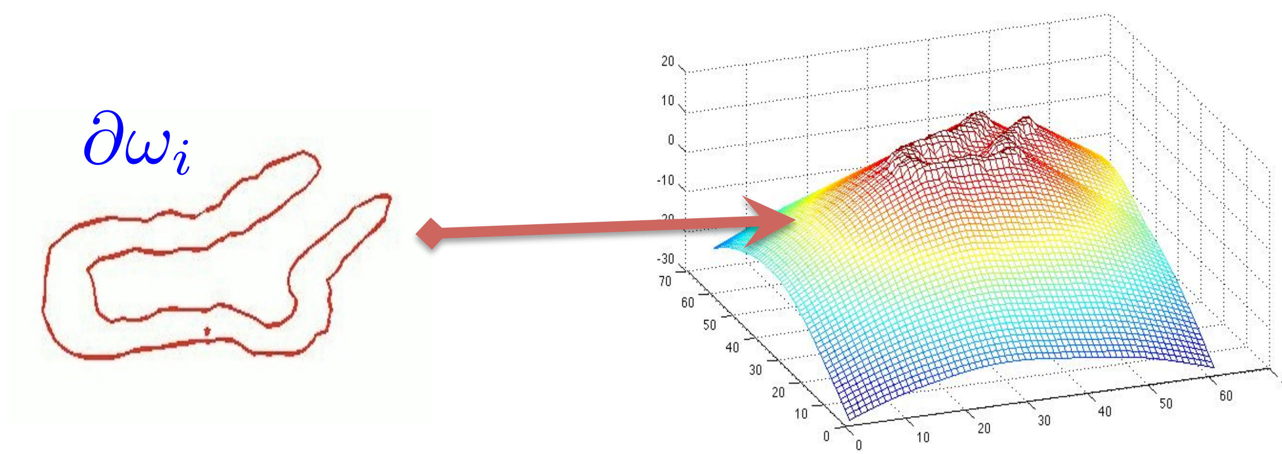
Shape Representation

A shape S_i is defined by the image region $\omega_i \in \Omega$ that corresponds to the structure of interest.

S_i is represented by its signed distance function (SDF) :

$$\phi_{S_i} : \Omega \to \mathbb{R}$$

such that the Eikonal equation $|\nabla \phi_{S_i}| = 1$ holds.



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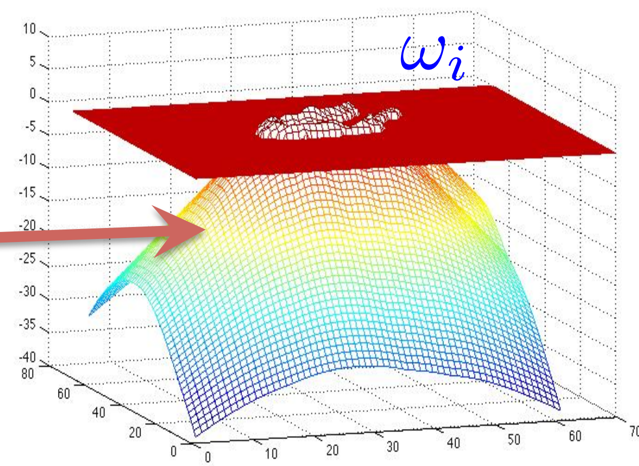
$$\partial \omega_i = \{\mathbf{x} | \phi_{S_i}(\mathbf{x}) = 0\}$$



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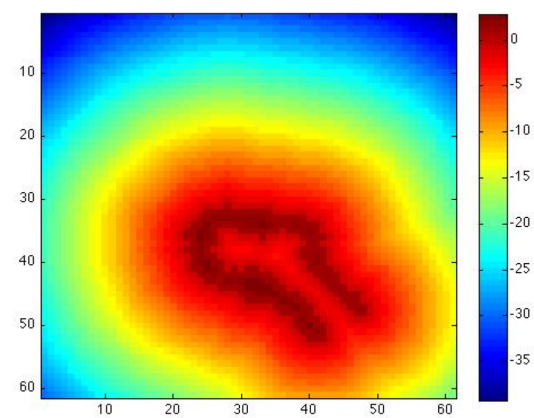

Distance Between Shapes

We define the distance between S_i and S_j by the modified symmetrical Hausdorff distance between their boundaries:

$$\mathbf{dist}(S_i, S_j) = \int_{\partial\omega_i} |\phi_{S_j}| d\mathbf{x} + \int_{\partial\omega_j} |\phi_{S_i}| d\mathbf{x}$$

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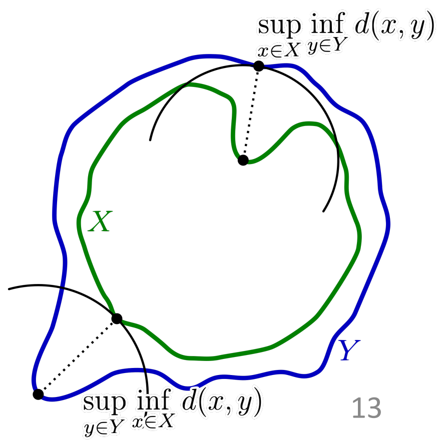

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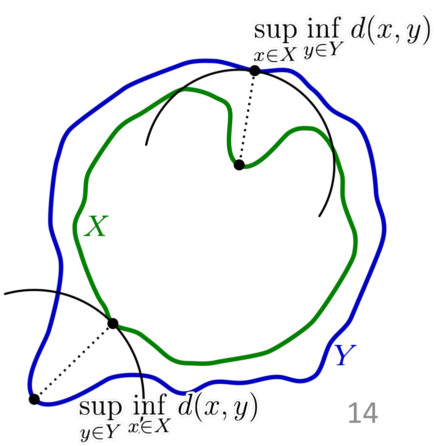

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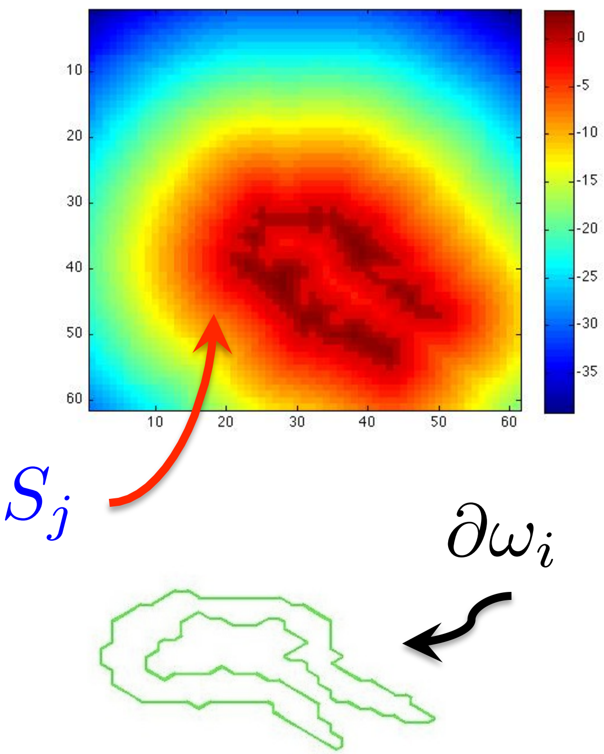

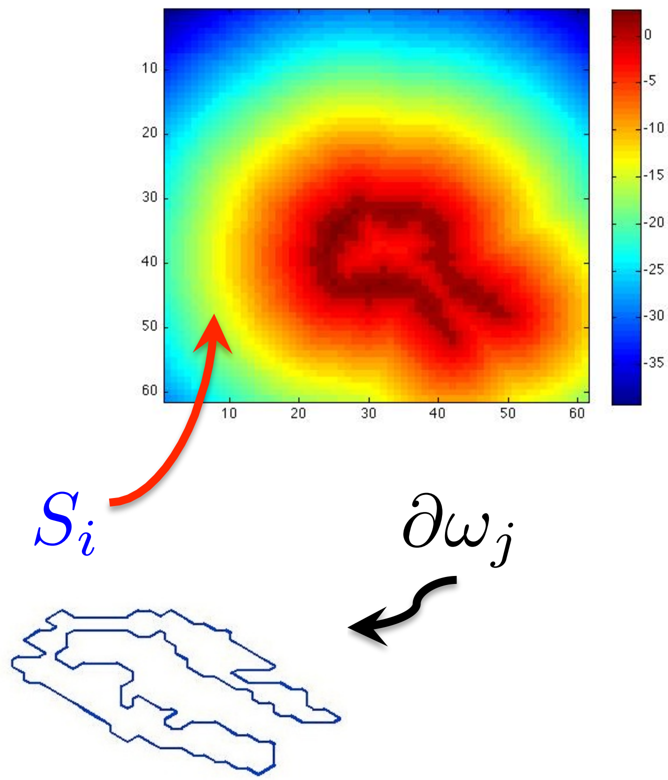

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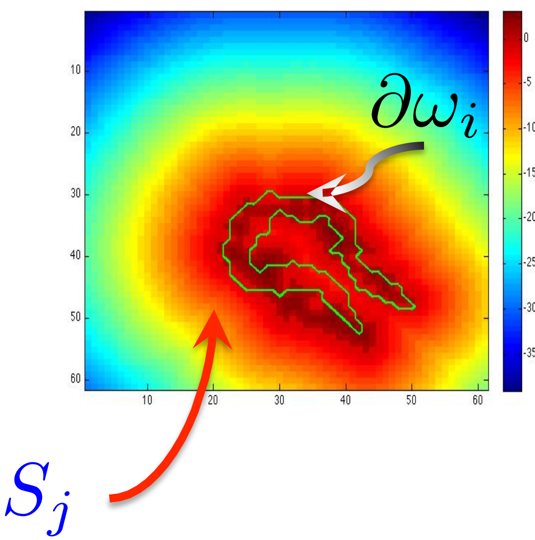
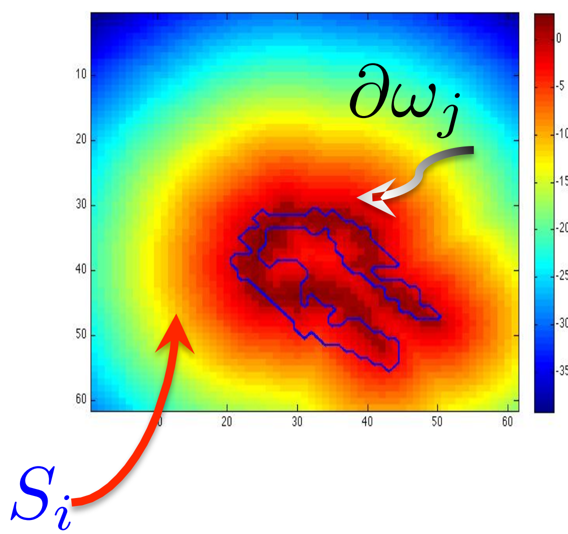




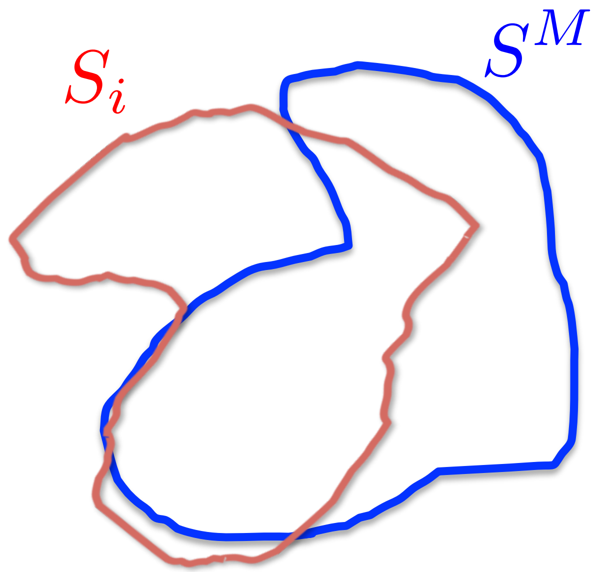
Mean Shape

We define the mean S^M of a shape ensemble $\{S_1 \ldots S_N\}$ as the shape that minimizes the sum of the distances from all the shapes in the set:

$$\hat{S}^M = \arg\min_{S^M} \sum_{i=1}^{N} \mathbf{dist}(S_i \circ \hat{T}_{i,M}, S^M),$$

where $T_{i,M}$ is the estimated affine (12 parameters) transform that aligns a shape S_i to the mean shape.

Alignment of shapes



$$\hat{T}_{i,M} = \arg\min_{T_{i,M}} \mathbf{dist}(S_i \circ T_{i,M}, \hat{S}^M).$$

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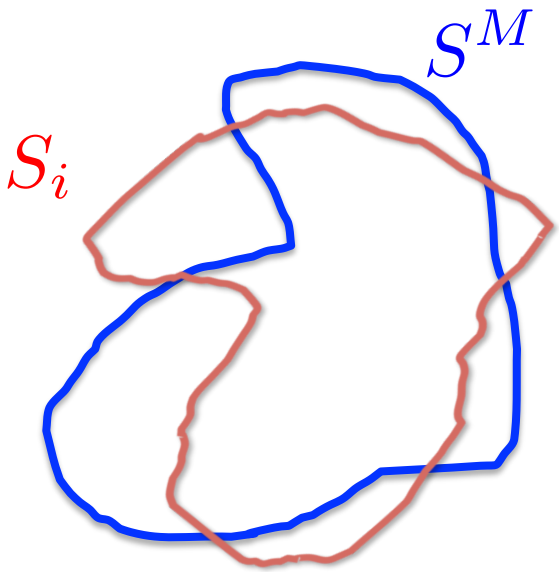

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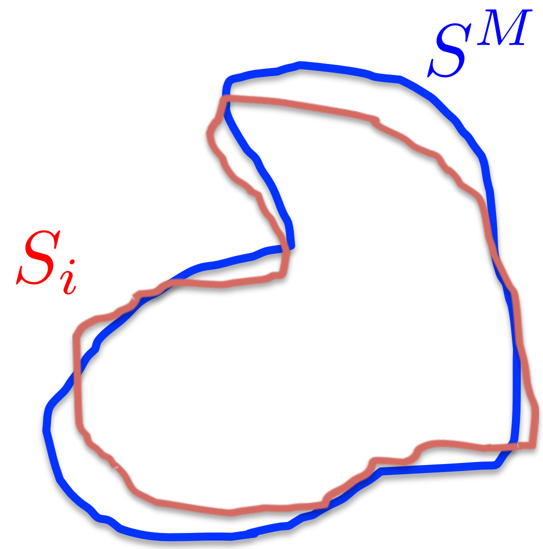

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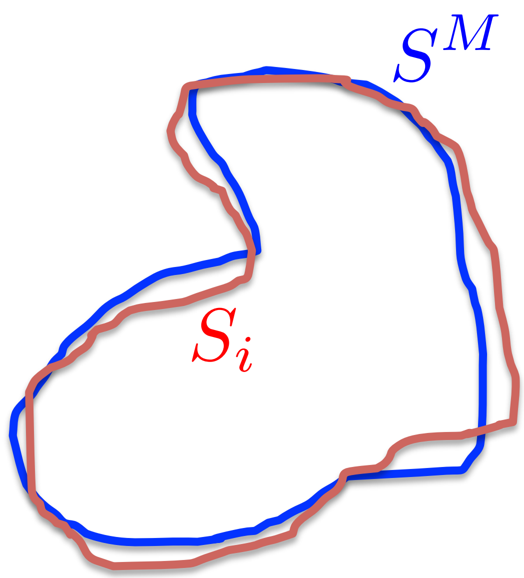

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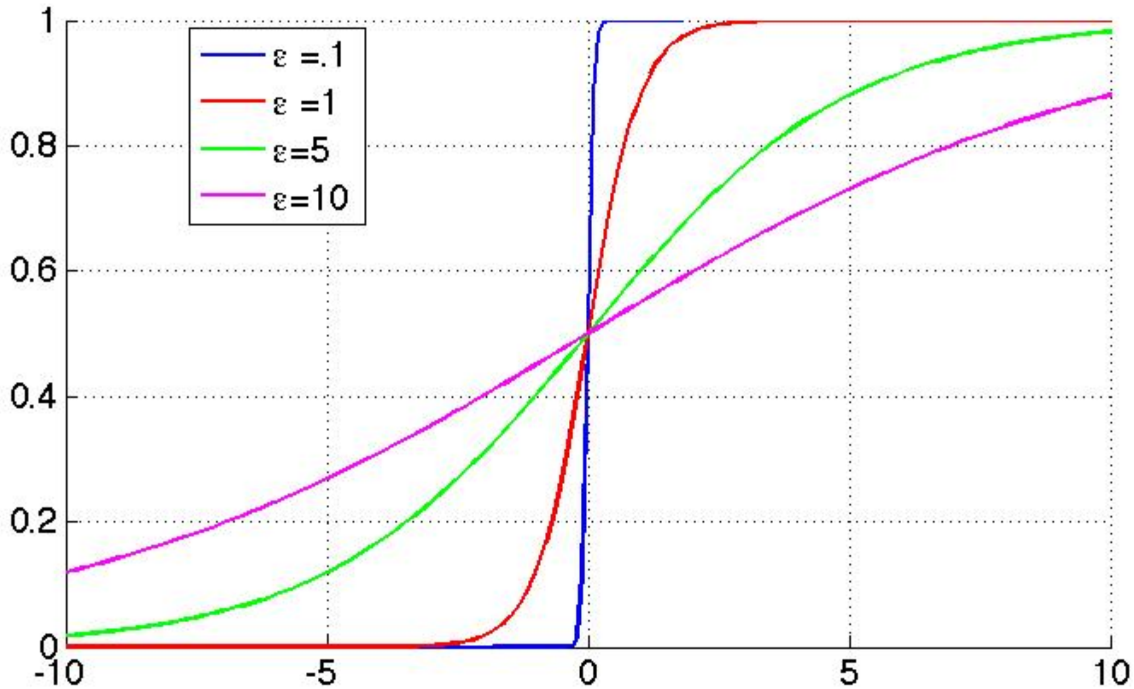
Smoothed Heaviside function



$$H_\epsilon(\phi) = \frac{1}{2}\left(1 + \tanh\left(\frac{\phi}{2\epsilon}\right)\right) = \frac{1}{1 + e^{-\phi/\epsilon}}$$

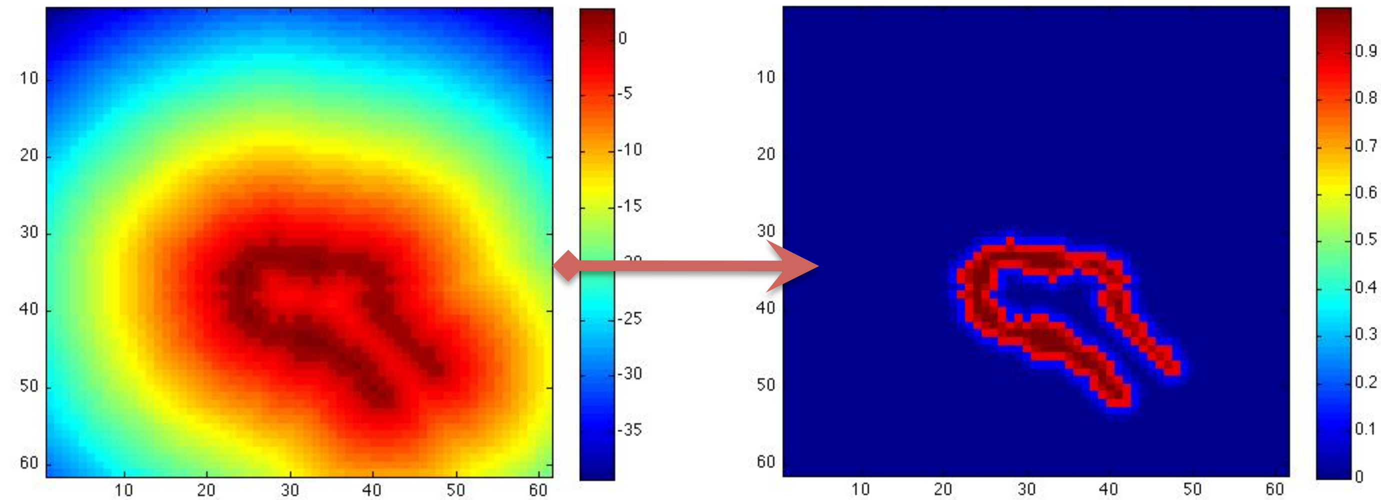
Level set Framework

$$\int_{\partial\omega_i} \rightarrow \int_{\Omega} |\nabla H_\epsilon(\phi_{S_i})|$$

$$\mathbf{dist}(S_i, S_j) = \int_{\partial\omega_i} |\phi_{S_j}| d\mathbf{x} + \int_{\partial\omega_j} |\phi_{S_i}| d\mathbf{x}$$

$$\mathbf{dist}(S_i, S_j) = \int_{\Omega} [|\nabla H_\epsilon(\phi_{S_i})||\phi_{S_j}| + |\nabla H_\epsilon(\phi_{S_j})||\phi_{S_i}|] d\mathbf{x}$$

From SDT to Probability Map



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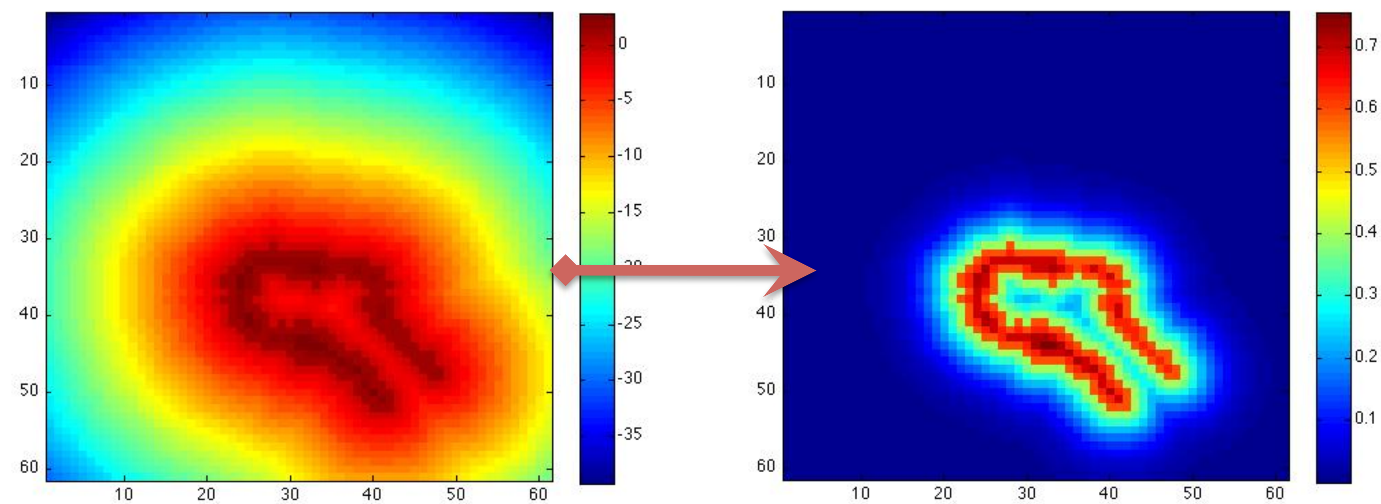

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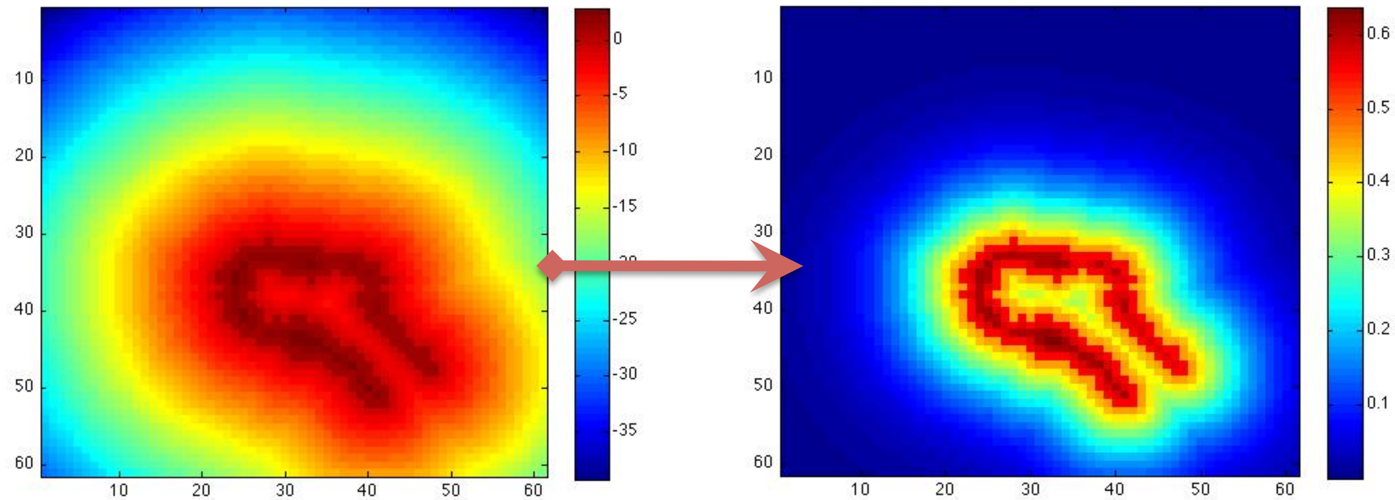

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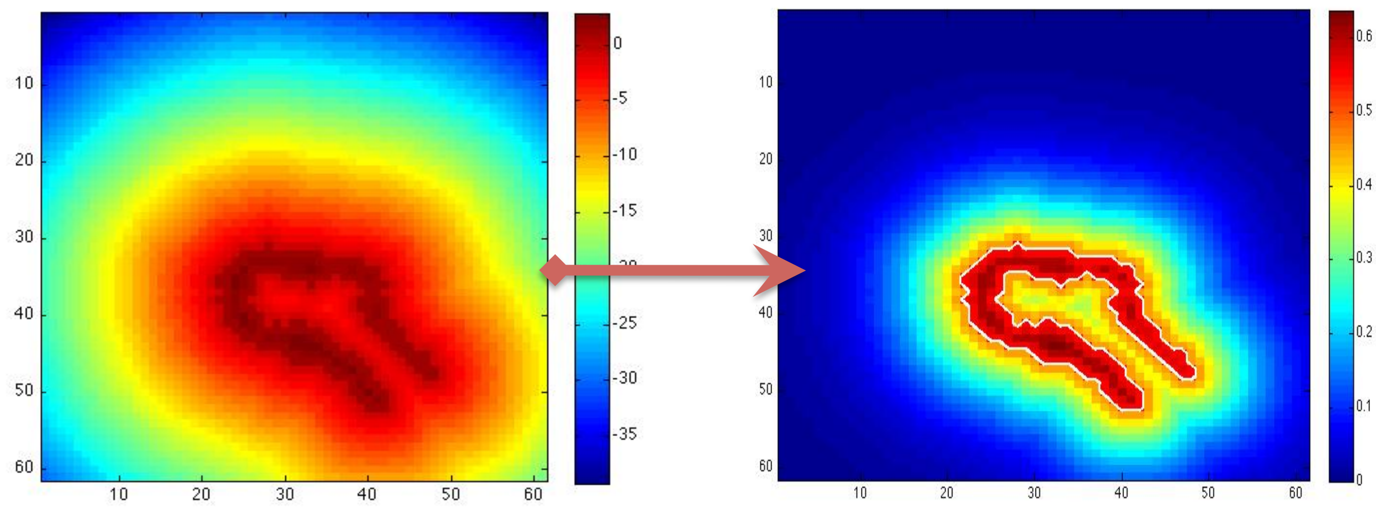

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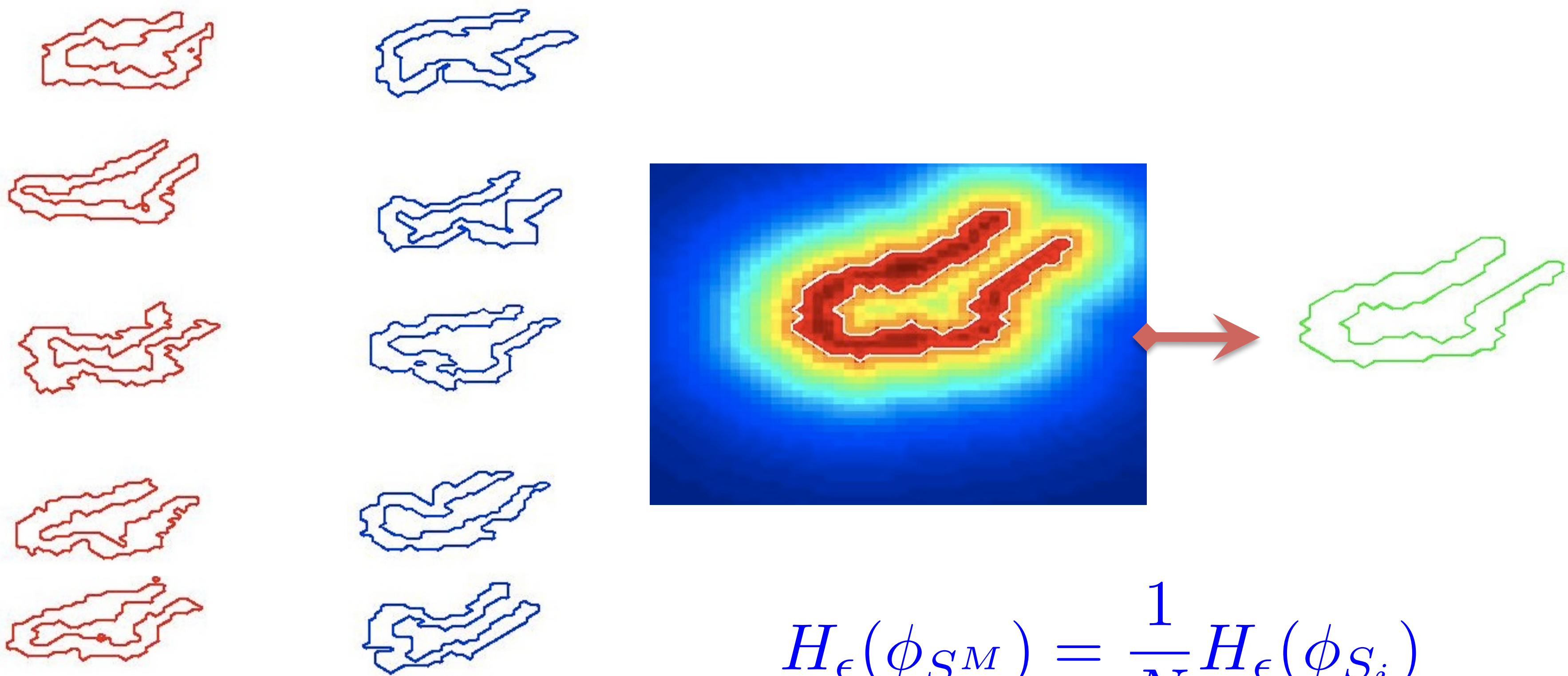
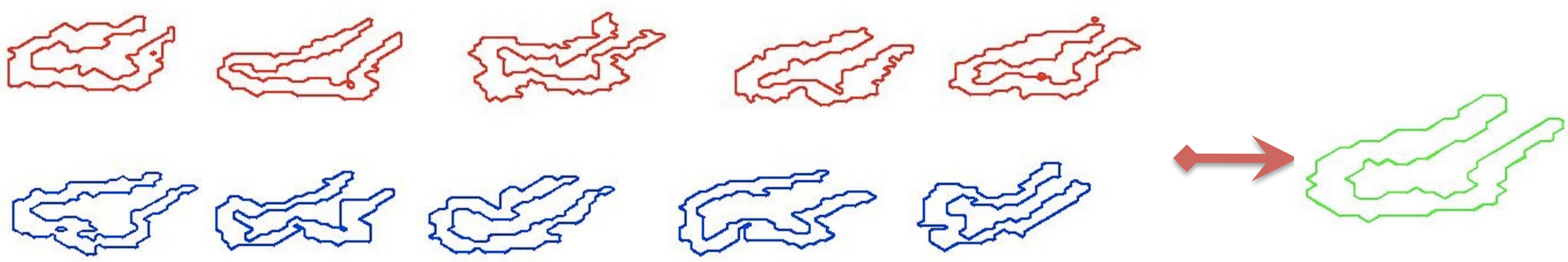
Mean Shape Initialization



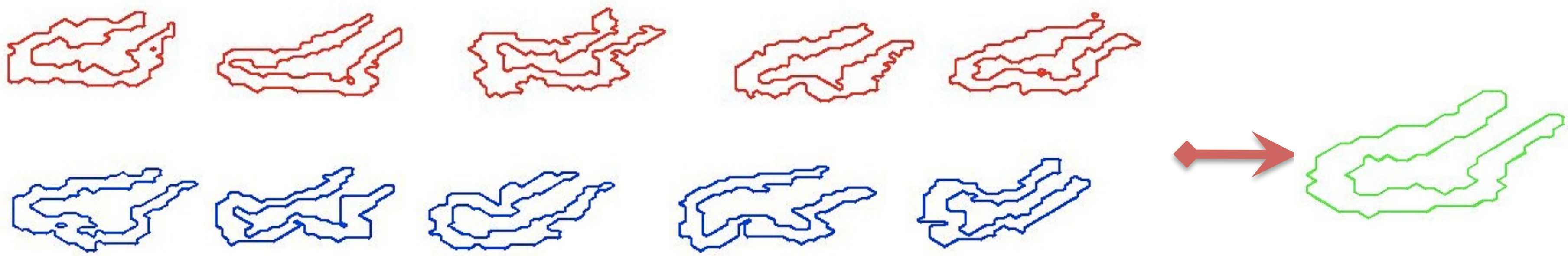
$$H_\epsilon(\phi_{S^M}) = \frac{1}{N} H_\epsilon(\phi_{S_i})$$

Mean Shape Morphing



$$D(S^M, \{S_i\}) = \sum_i \int_\Omega \left[|\phi_{S^M}| |\nabla H_\epsilon(\phi_{S_i})| + |\phi_{S_i}| |\nabla H_\epsilon(\phi_{S^M})| \right] d\mathbf{x}$$

Mean Shape Morphing



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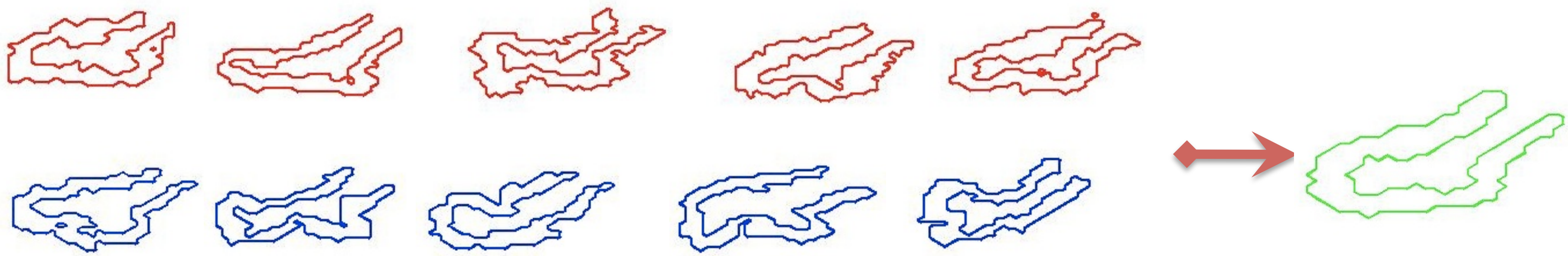
$$\hat{\phi}_{S^M} = \arg\min_{\phi_{S_M}} D(S^M, \{S_i\})$$

Mean Shape Morphing



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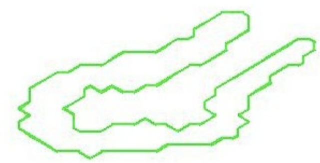
$$\phi_t^M = \sum_i \left[\mathrm{sign}(\phi_{S^M}) |\nabla H_\epsilon(\phi_{S_i})| + \delta_\epsilon(\phi_{S^M}) \mathrm{div} \left(\frac{\nabla \phi_{S^M}}{|\nabla \phi_{S^M}|} |\phi_{S_i}| \right) \right]$$

Localization of shape differences between populations

Population 1: $\phi^{\mathrm{sz}}_{S_1}, \ldots, \phi^{\mathrm{sz}}_{S_{N^{\mathrm{sz}}}}$

Population 2: $\phi^{\mathrm{nc}}_{S_1}, \ldots, \phi^{\mathrm{nc}}_{S_{N^{\mathrm{nc}}}}$



For each voxel on the boundary of the mean shape calculate:

$$\vec{d}^{\mathrm{sz}}(\mathbf{x}) = \{d(\mathbf{x} \in \partial\omega^M, \partial\omega_1^{\mathrm{sz}}), \ldots, d(\mathbf{x} \in \partial\omega^M, \partial\omega_N^{\mathrm{sz}})\}$$

$$\vec{d}^{\mathrm{nc}}(\mathbf{x}) = \{d(\mathbf{x} \in \partial\omega^M, \partial\omega_1^{\mathrm{nc}}), \ldots, d(\mathbf{x} \in \partial\omega^M, \partial\omega_N^{\mathrm{nc}})\}$$

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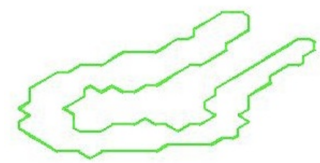

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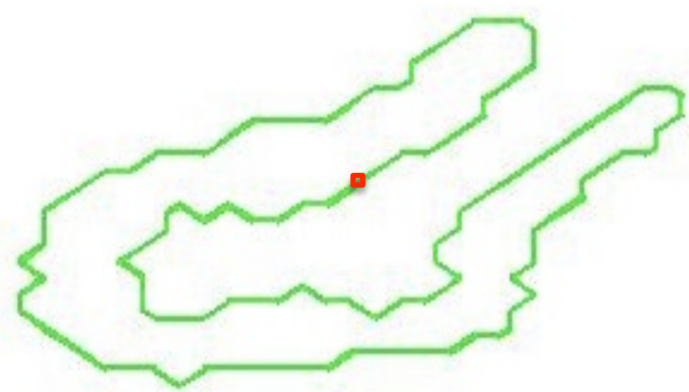
Localization of shape differences between populations

For each voxel on the boundary of the mean shape apply the

two-sample t-test on $\vec{d}^{\mathrm{sz}}(\mathbf{x})$ and $\vec{d}^{\mathrm{nc}}(\mathbf{x})$.

The p-value threshold is determined by using

False Discovery Rate (FDR) to correct for multiple comparisons



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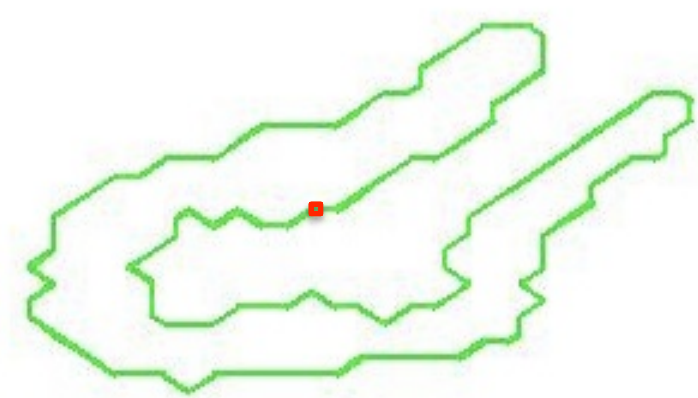

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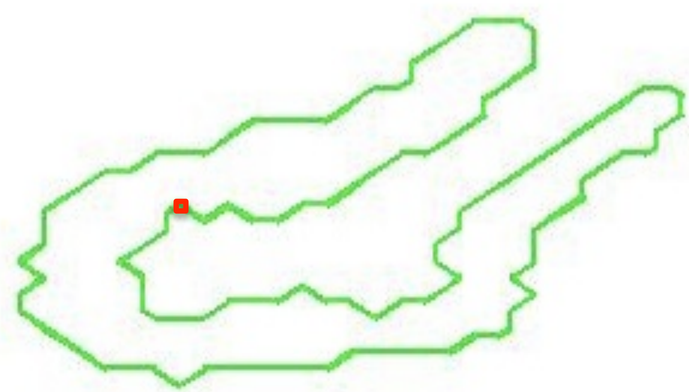

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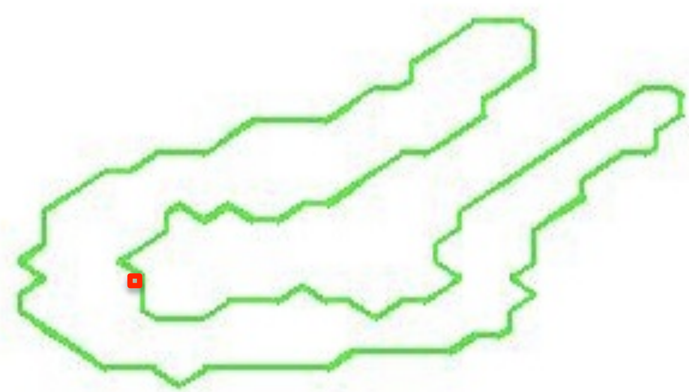


Shape Analysis Algorithm

Input: two populations of shapes (e.g. brain structures).

Algorithm:

1. Use probability maps of the SDTs to initialize the mean shape

2. Iterate

a. Align the shapes represented by their SDTs by minimizing the modified Hausdorff distances (mHDs).

b. Morph the mean shape to minimize the mHDs to the shape ensemble.

3. Calculate the signed distances between the mean shape surface to each shape in the two populations.

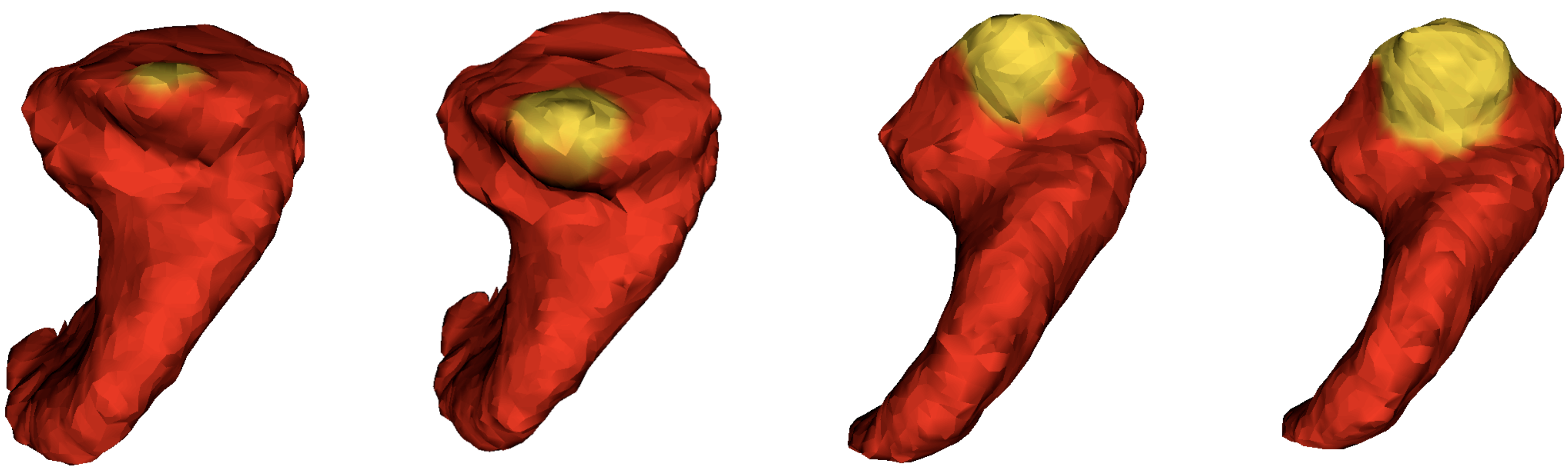
4. Use two-sample t-test to find statistically significant differences between the two populations.

- Use False Discovery Rate (FDR) to correct for multiple comparisons.

Output: Highlighted regions on the mean shape surface for which statistically significant differences were found.

Results: Synthetic Amygdala-Hippocampus Complexes

Bump databases



3 Voxels   4 Voxels   5 Voxels   6 Voxels

Results: Synthetic Amygdala-Hippocampus Complexes

Dimple databases

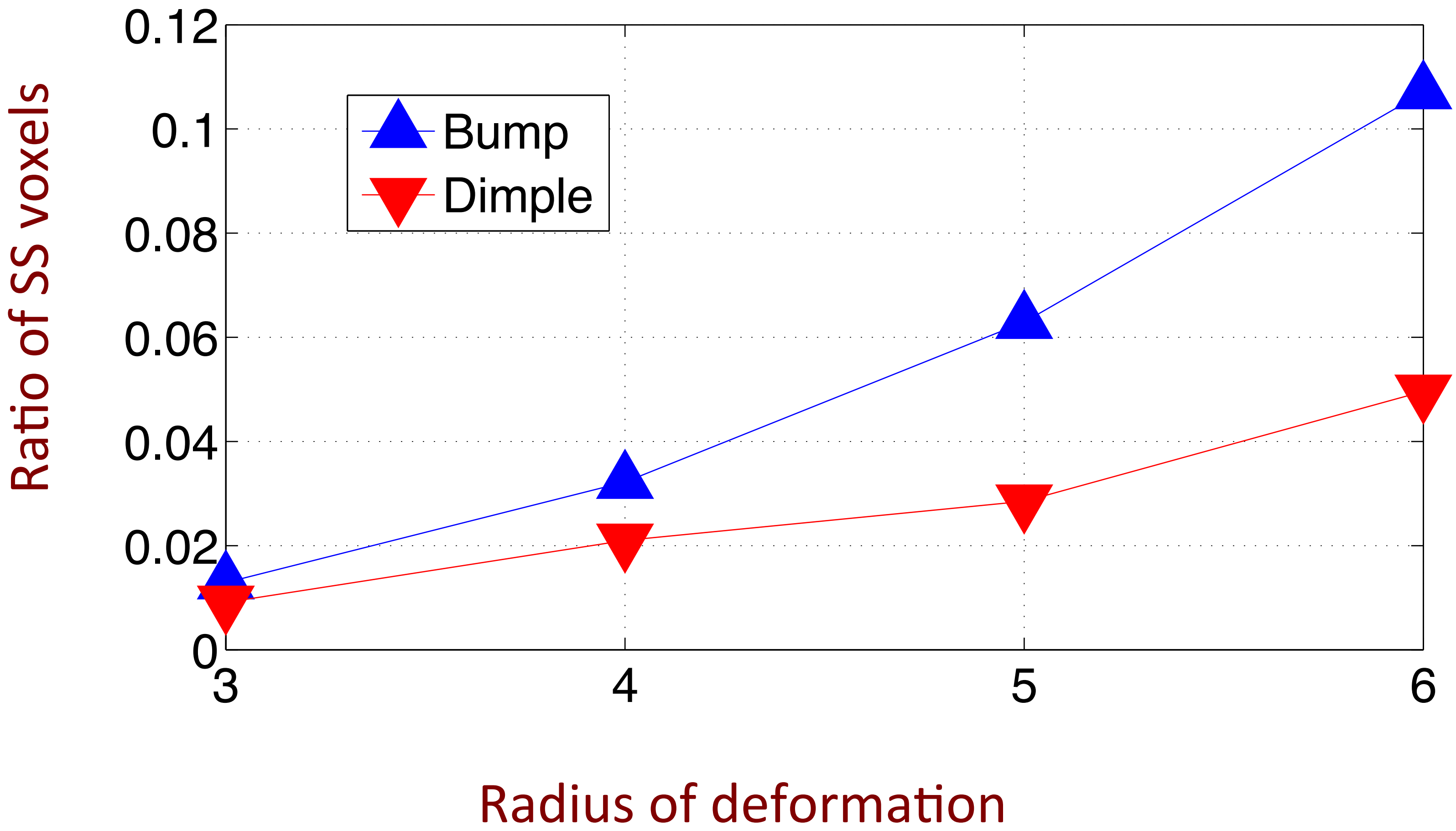
3 Voxels

4 Voxels

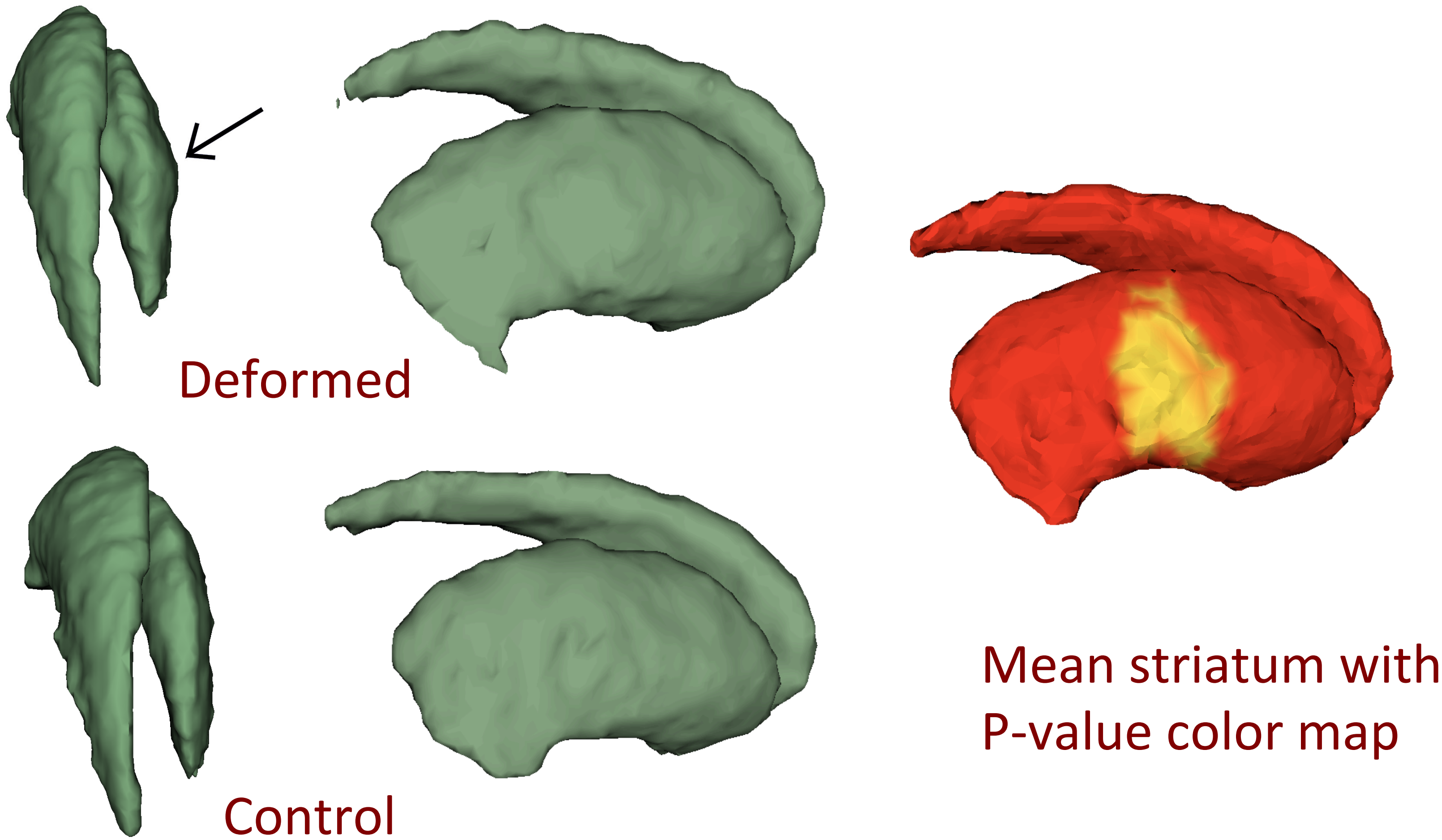
5 Voxels

6 Voxels

Results: Synthetic Amygdala-Hippocampus Complexes

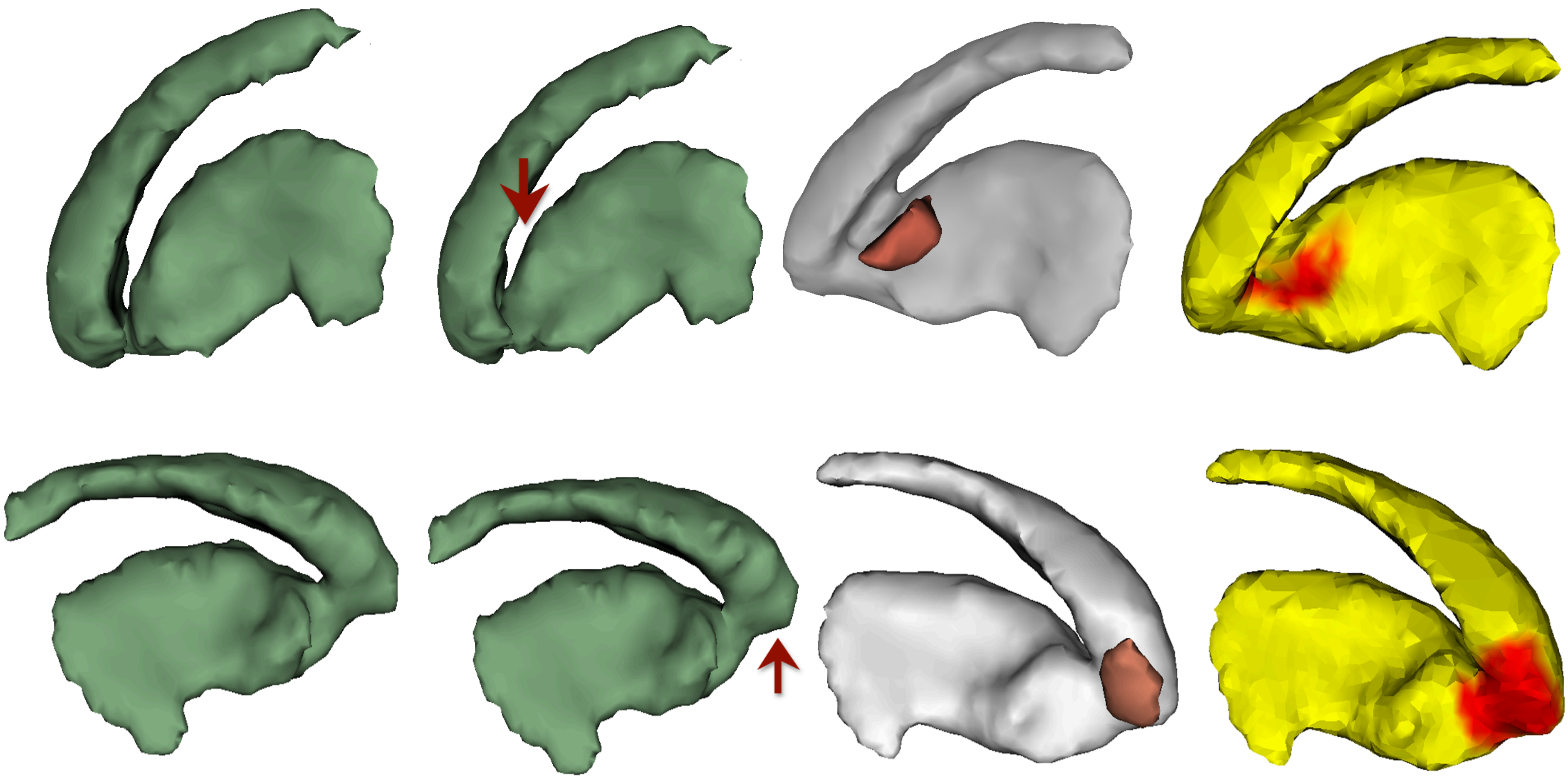


Results: Synthetic Striatum



Gao, Y., Bouix, S., October 2012. Synthesis of realistic subcortical anatomy with known surface deformations. In: MICCAI Workshop on Mesh Processing in Medical Image Analysis.

Results: Synthetic Striatum



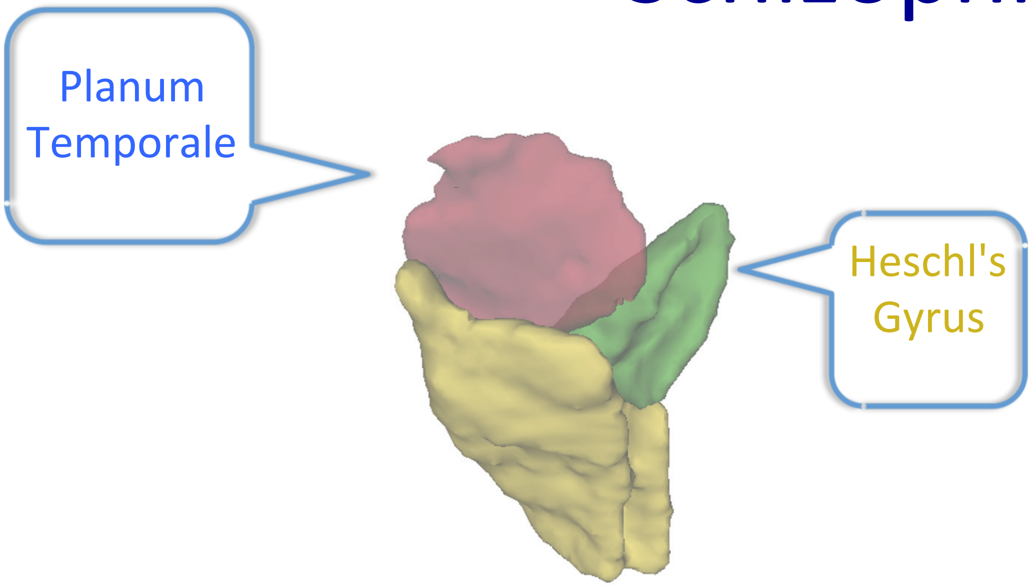
Shape Analysis of First-episode Schizophrenics

- **Lower left temporal lobe MRI volumes in patients with first-episode schizophrenia compared with psychotic patients with first-episode affective disorder and normal subjects** Y. Hirayasu *et. al.* Am J Psychiatry 1998

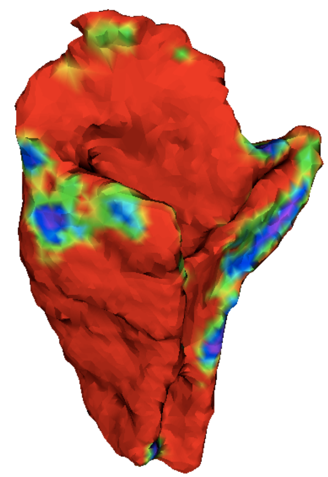
- **Planum temporale and heschl's gyrus volume reduction in schizophrenia: A MRI study of first-episode patients** Y. Hirayasu *et. al.* Arch Gen Psychiatry 2000

- **Hippocampus and superior temporal gyrus volume in first-episode schizophrenia** Y. Hirayasu *et. al.* Arch Gen Psychiatry 2000

Results: Left STG of First Episode Schizophrenics

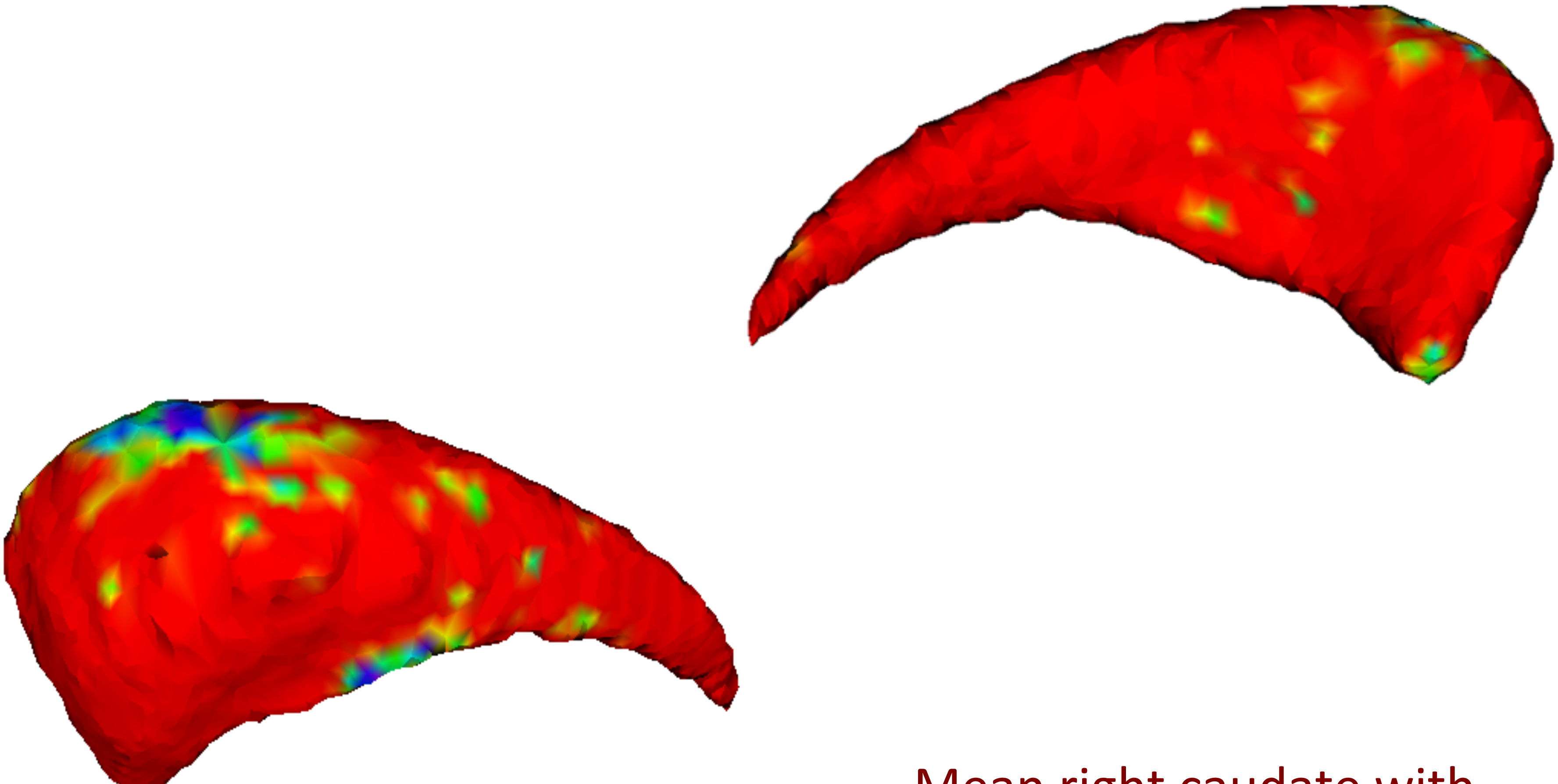


Mean left STG



Mean left STG with p-values color map

Results: Caudate of Schizotypal Personality Disorder (SPD) Subjects



Mean right caudate with p-values color map

Summary and Future Work

Detection, localization and quantification of shape
Deformations for population studies.
One-to-one point correspondences are not require!
-> Low computational complexity; robustness
Intuitive output
Handles shapes with complicated morphology
Does not require pre-processing such as smoothing.
Next step:
Incorporate the concept of boundary/surface uncertainty within the analysis.

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Thank you!