

# The basics of mesh processing in neuroimaging

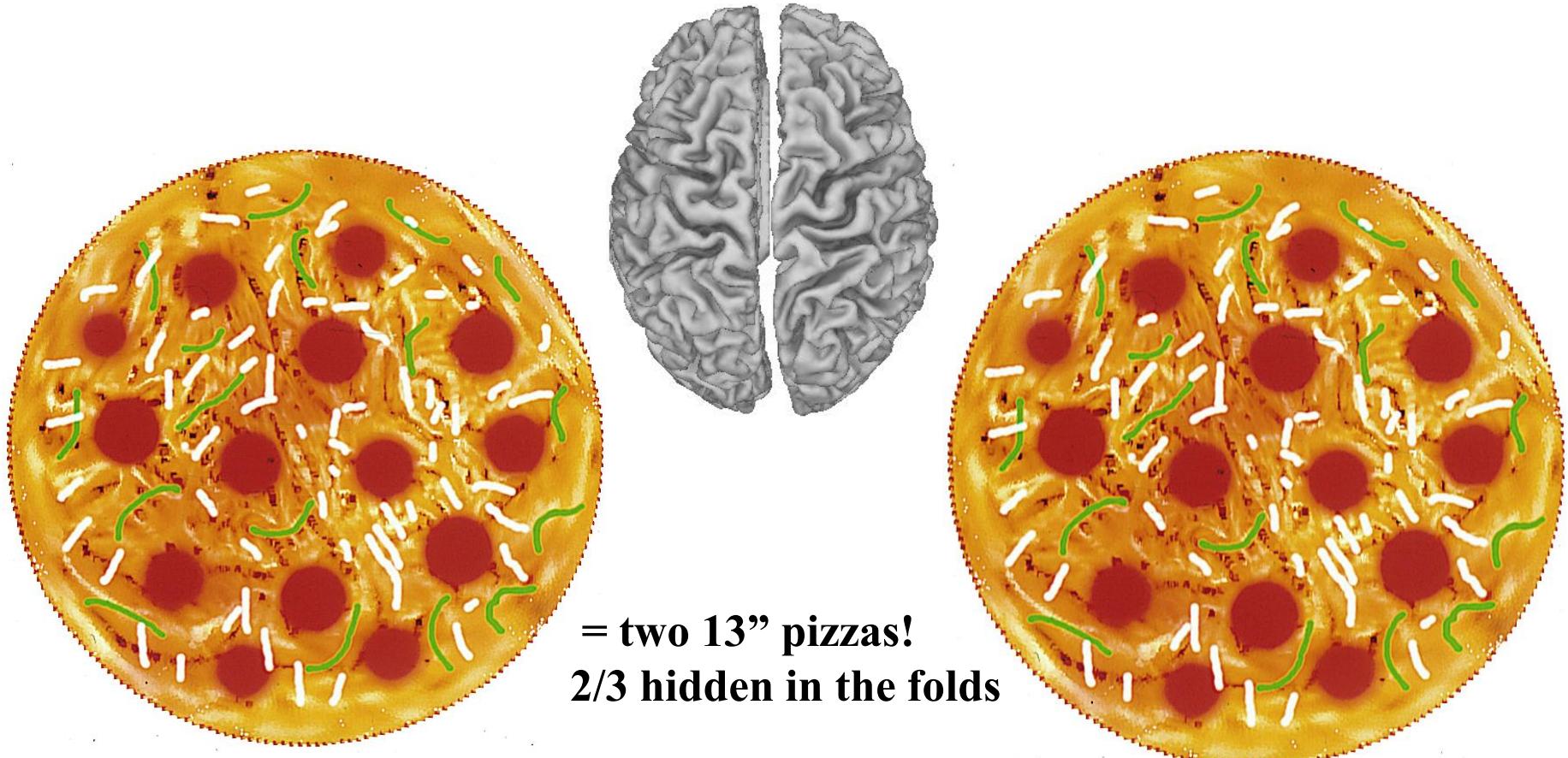
## Successive steps in a classical pipeline

Guillaume Auzias

2022-02-24  
RMN

# The essentials of cortical surface analysis: Each brain is unique and complex

Average surface area = 960 cm sq. (~1900 cm sq. for two hemispheres)

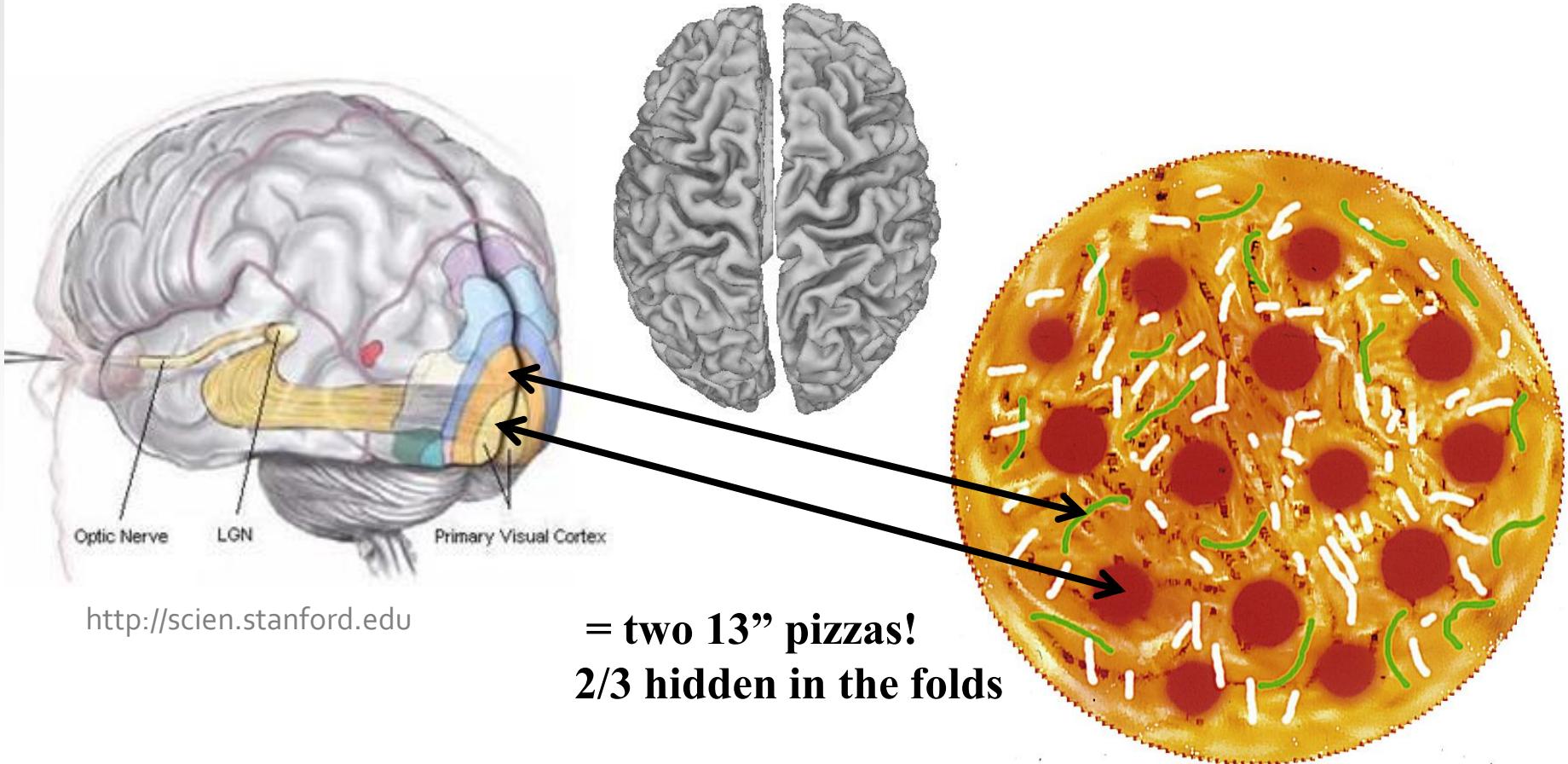


150 ~more than 250 areas

Each cortical area ~ one 3 cm pepperoni!

# The essentials of cortical surface analysis: Each brain is unique and complex

Average surface area = 960 cm sq. (~1900 cm sq. for two hemispheres)



<http://scien.stanford.edu>

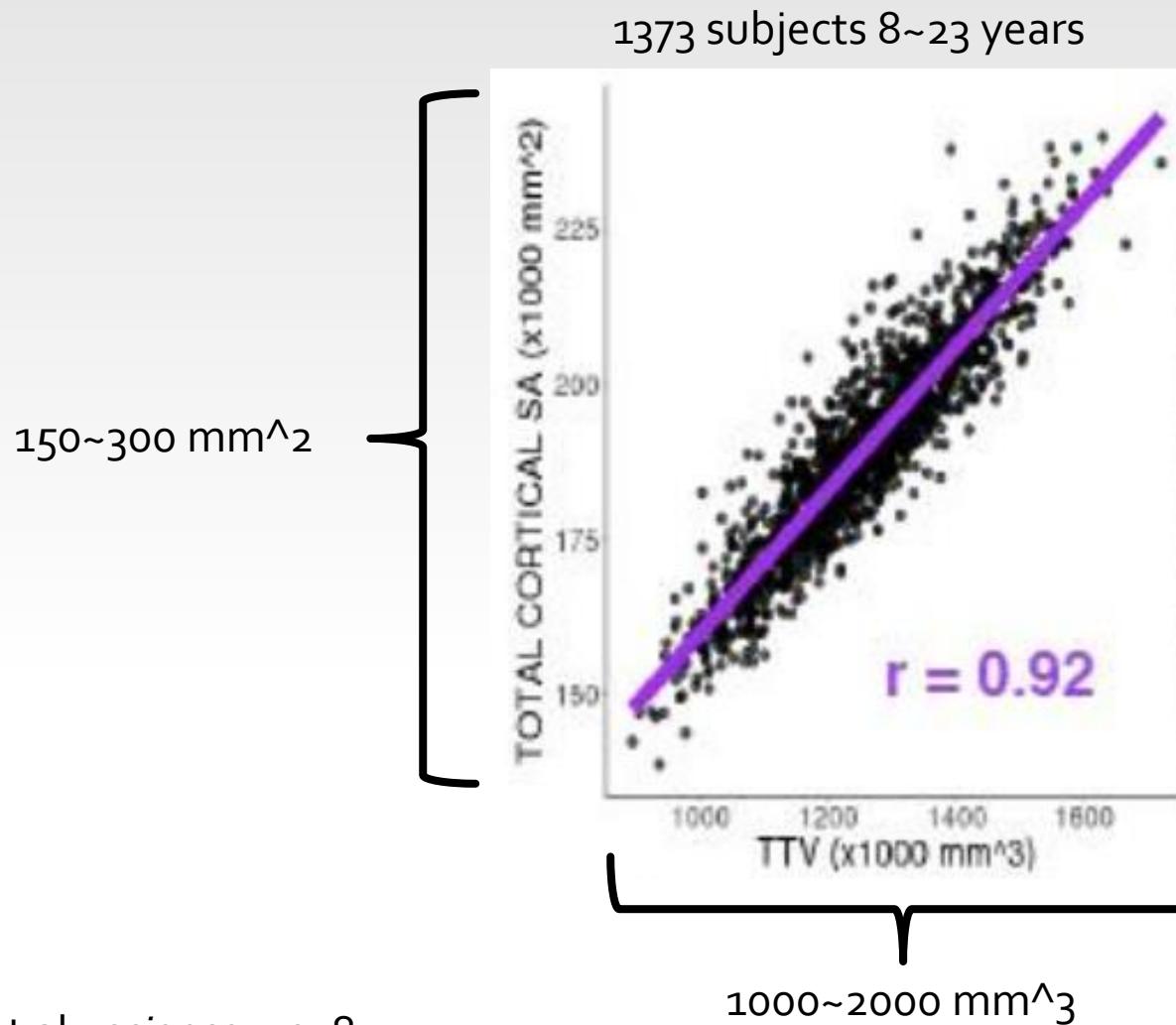
= two 13" pizzas!

2/3 hidden in the folds

150 ~more than 250 areas

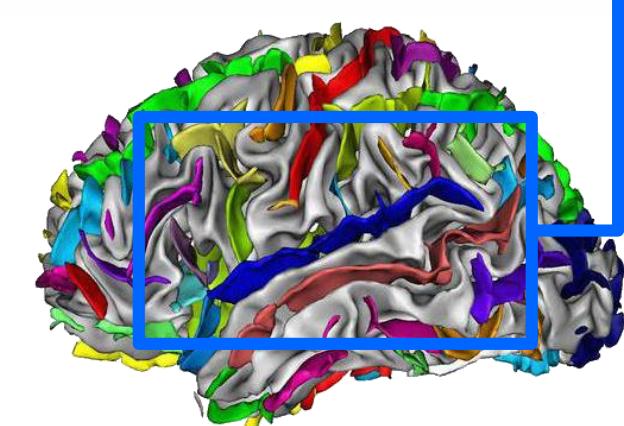
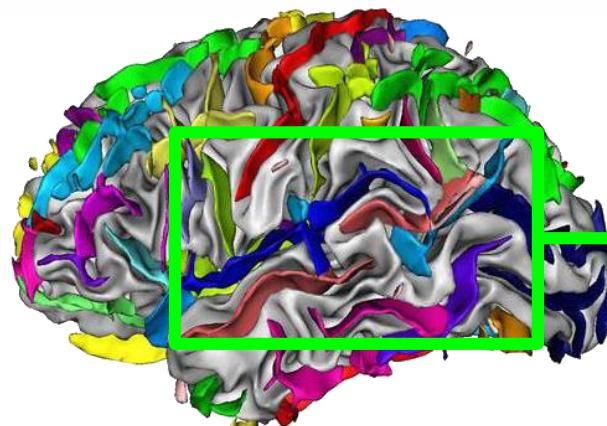
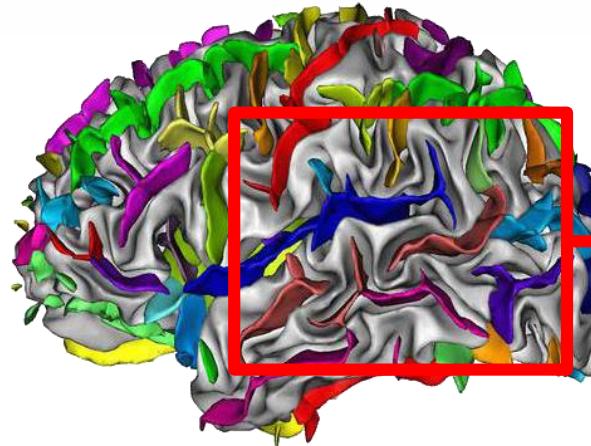
Each cortical area ~ one 3 cm pepperoni!

# The essentials of cortical surface analysis: variations across individuals: 2 folds magnitude!

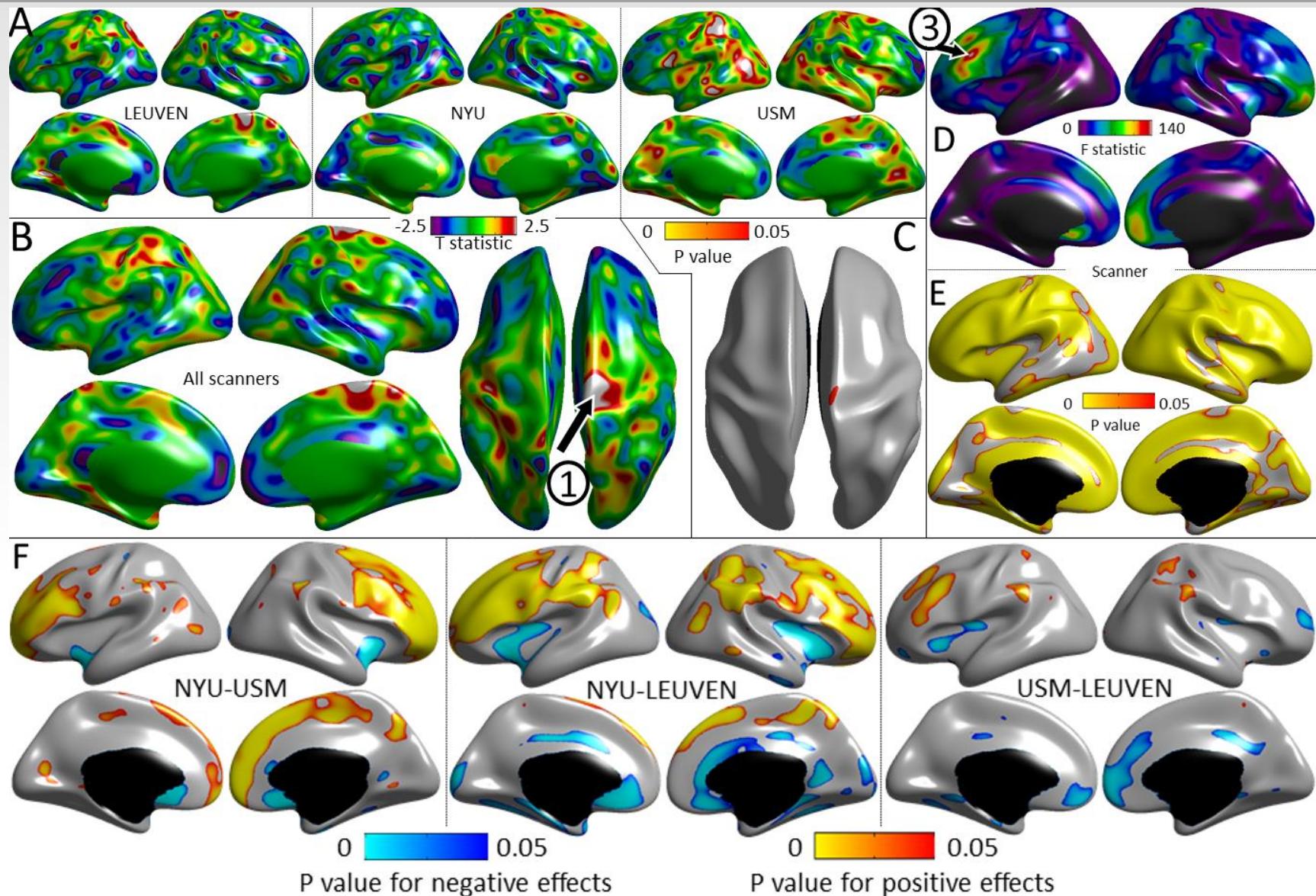


# The essentials of cortical surface analysis: Cortical geometry is complex and variable

- Defining correspondences across brains:
  - remains an open issue
  - multiple approaches/softwares



# Neuroimaging pipelines enable surface-based statistical analysis



# Successive steps in a classical pipeline

- Segmentation of the white mesh
- Topology correction
- Mesh deformation to get the pial mesh
- Mapping onto a sphere
- Spherical registration
- Remeshing / interpolation across meshes
- Volume to mesh interpolation
- Smoothing on the surface
- Computing statistics across meshes



# Successive steps in a classical pipeline

- **Segmentation of the white mesh**
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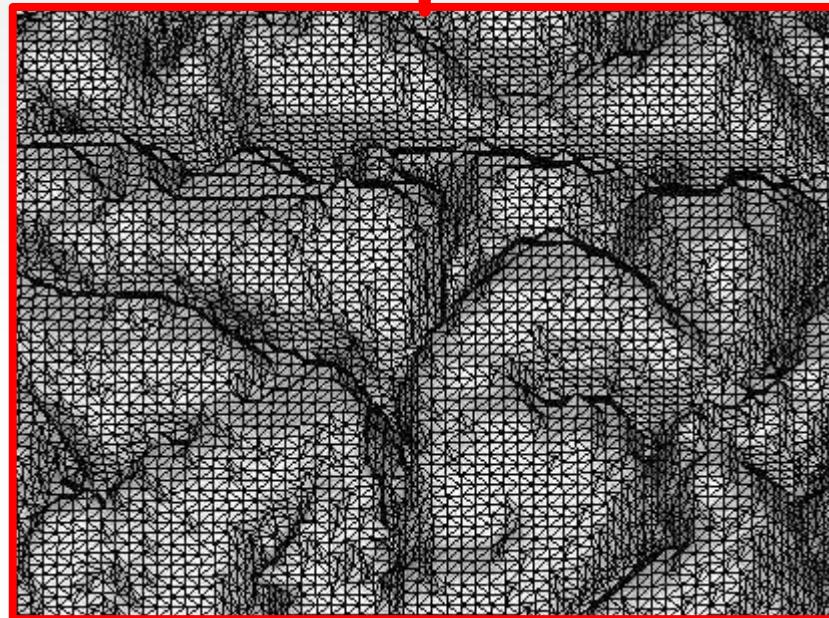
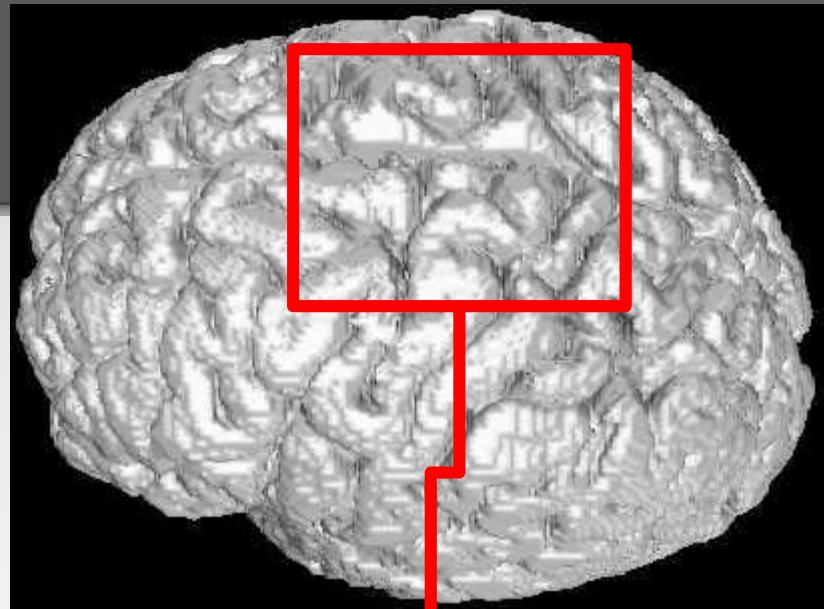
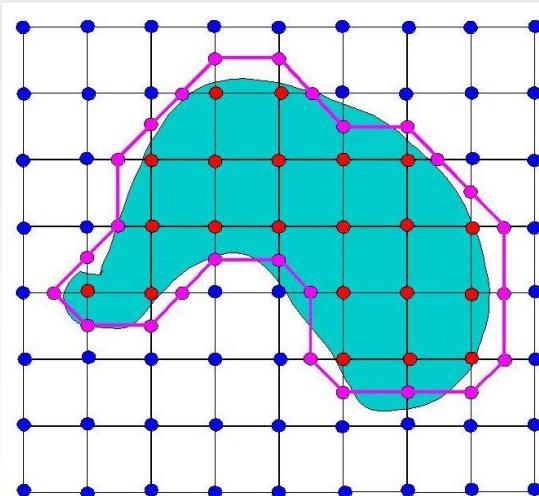
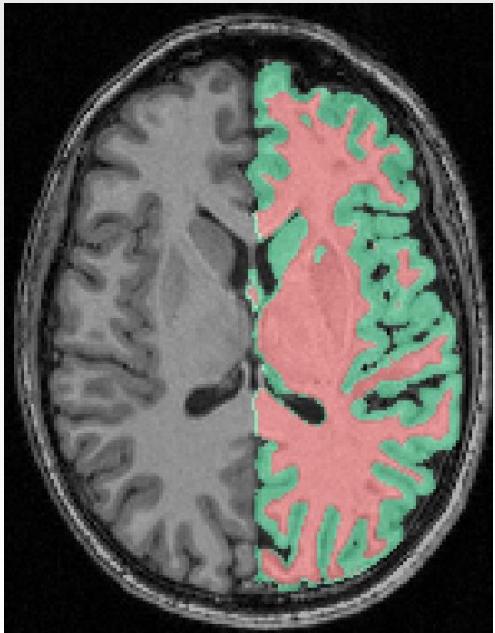


# Segmentation of the *white* (G/W) surface mesh

- Aim: extract a triangular mesh (2D surface) corresponding to an iso-intensity value in the 3D volume
- Get a surface representation of the interface **between grey and white tissues**
  - ?h.white surface in freesurfer / HCP

# volume to mesh

- Marching cubes



No constraint on the **topology**

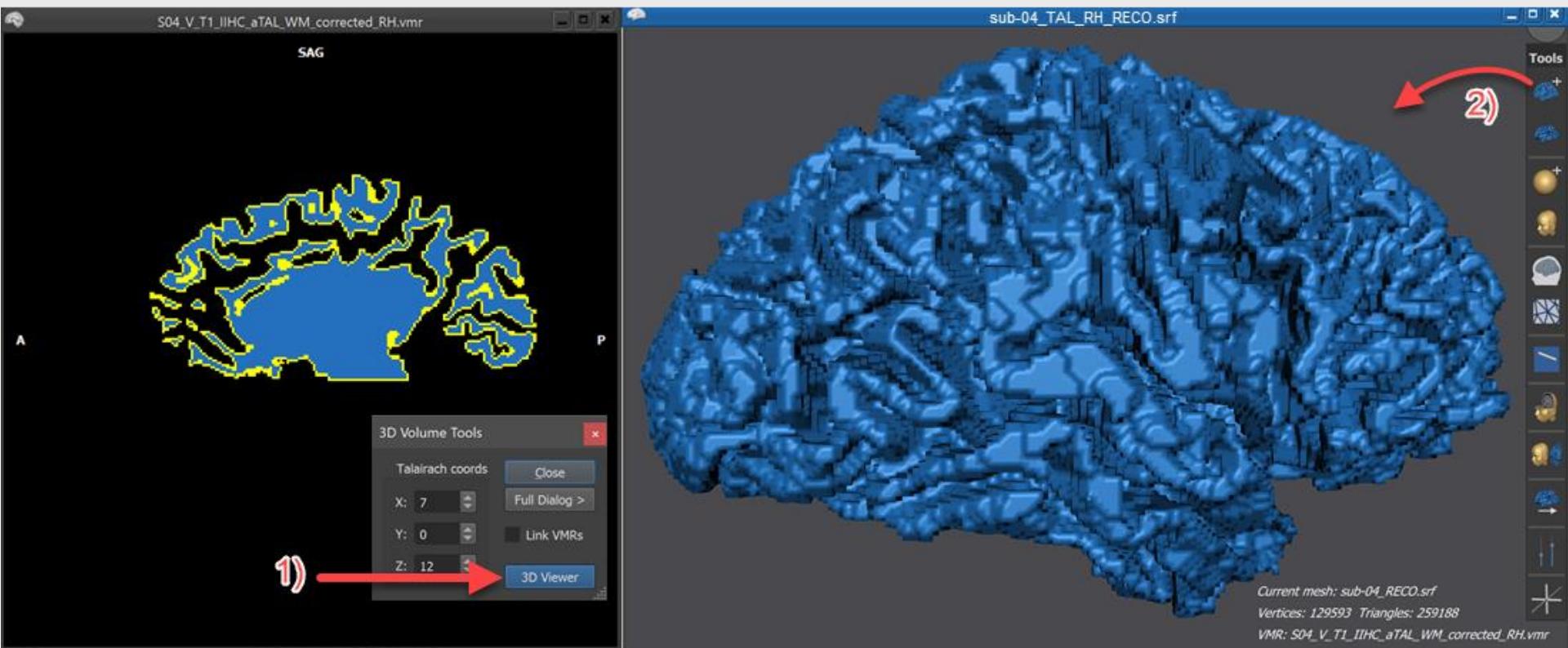
Not well suited for the pial (cortex/CSF) surface

**Works well for white surface**

A bit of smoothing required...

# volume to mesh

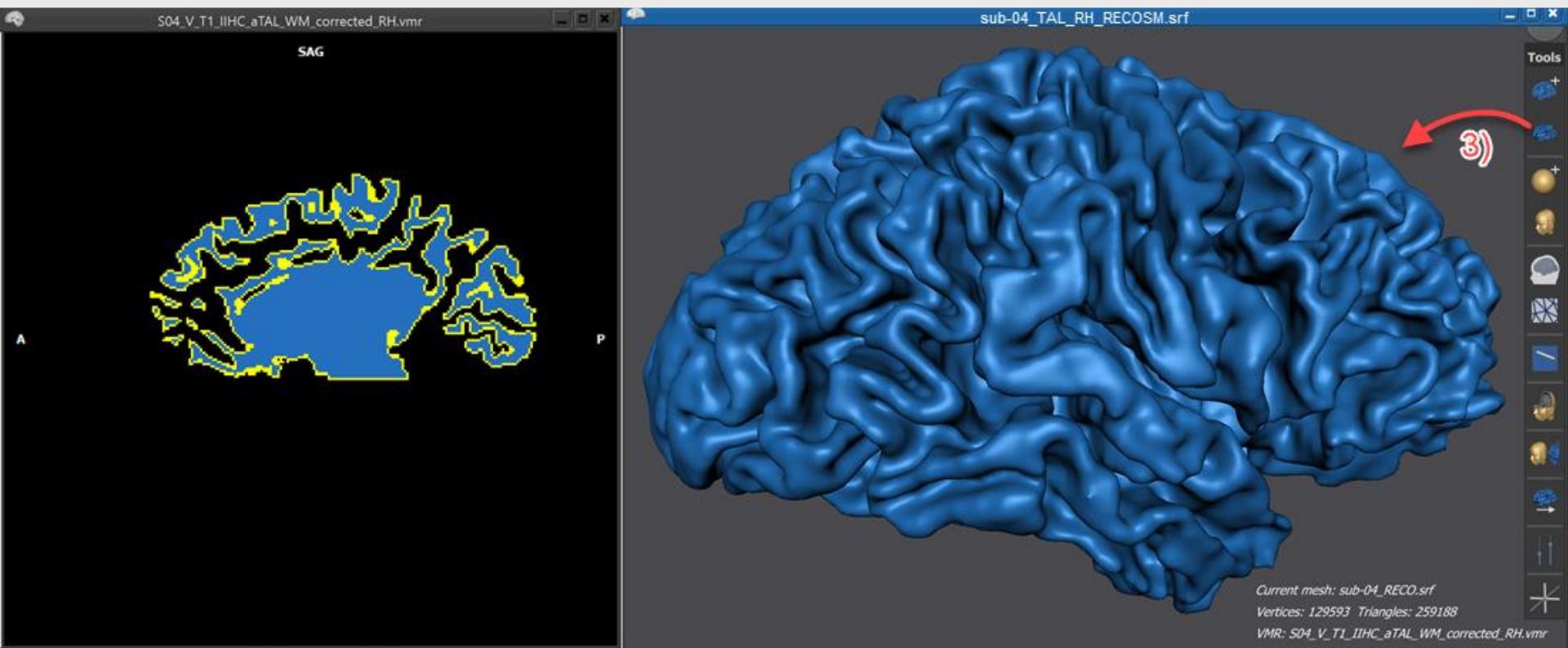
- Marching cubes



<https://download.brainvoyager.com/bv/doc/UsersGuide/CortexBasedAlignment/PreparingAMeshForCBA.html>

# volume to mesh

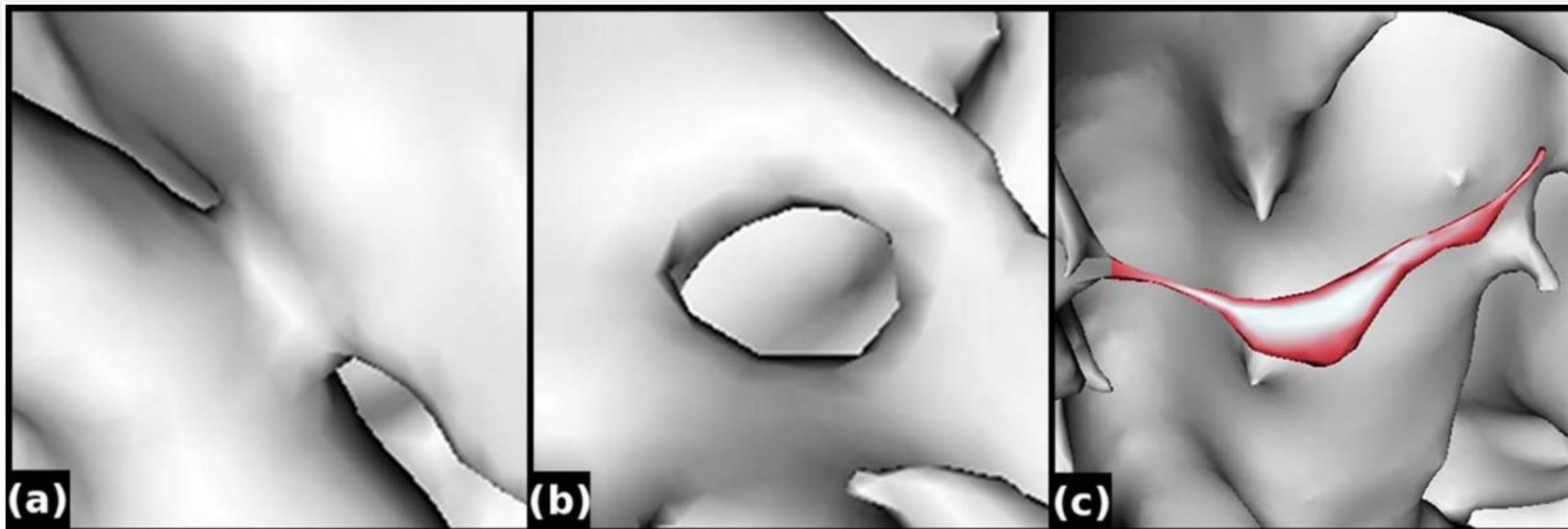
- Marching cubes + smoothing



<https://download.brainvoyager.com/bv/doc/UsersGuide/CortexBasedAlignment/PreparingAMeshForCBA.html>

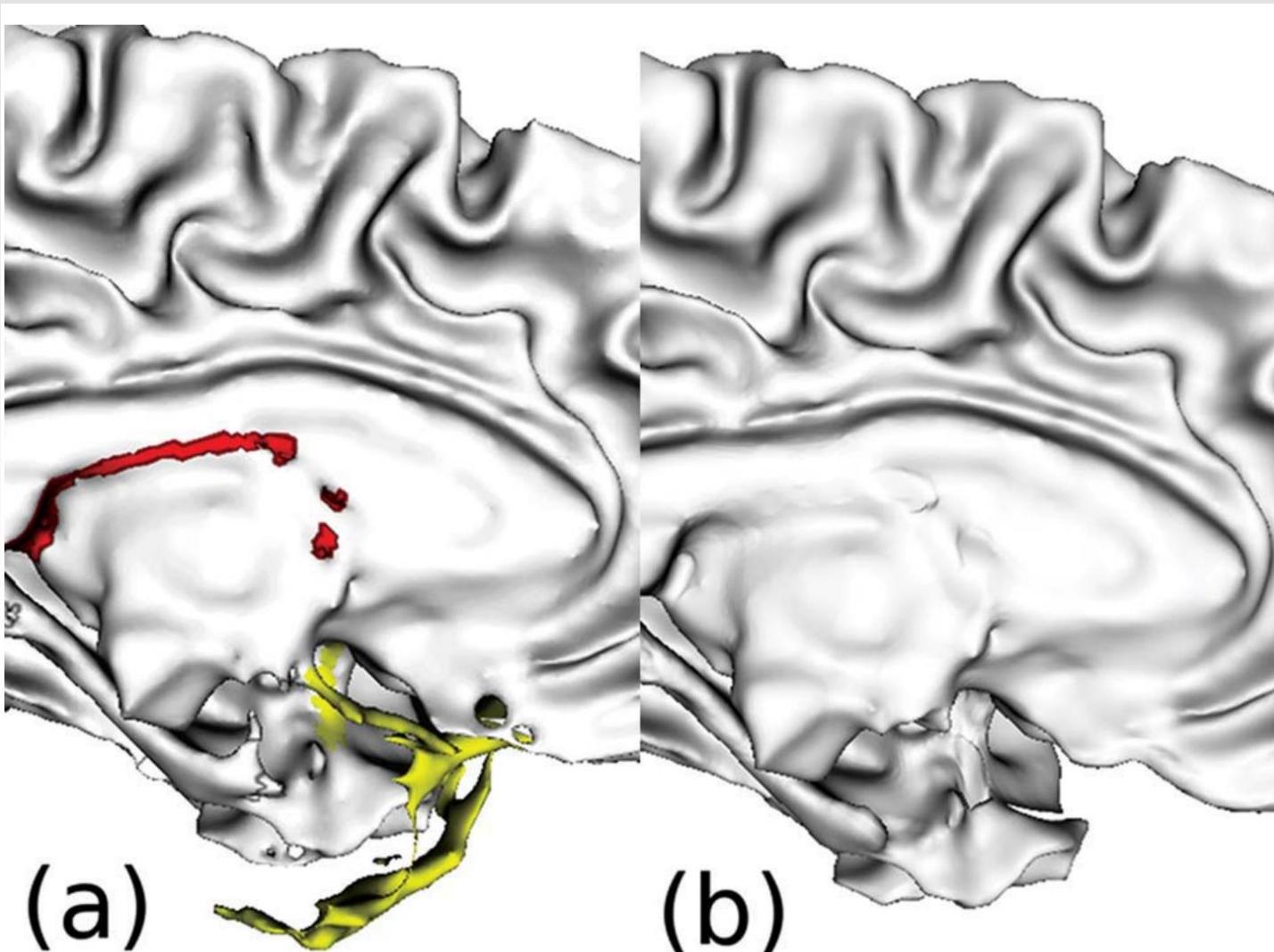
# Topology correction

- Correct topological defects so that the mesh can be mapped onto a sphere without any flipped triangle / hole / handle



- Defects correspond to segmentation errors, i.e. geometry is not biologically plausible

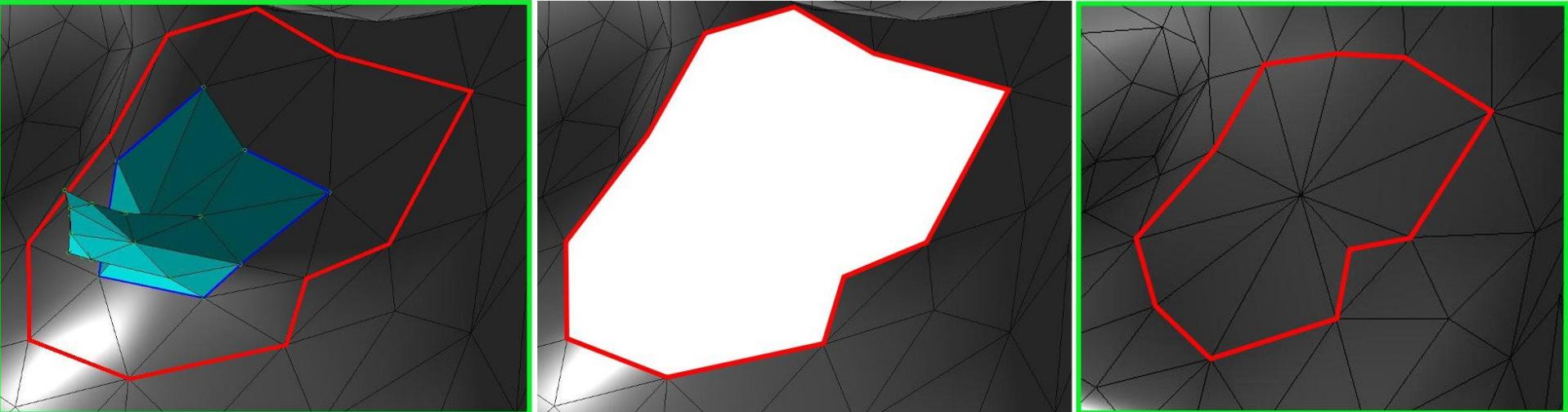
# Topology correction



Yotter et al., Human Brain Mapping, 2010

Implemented in the python package SLAM

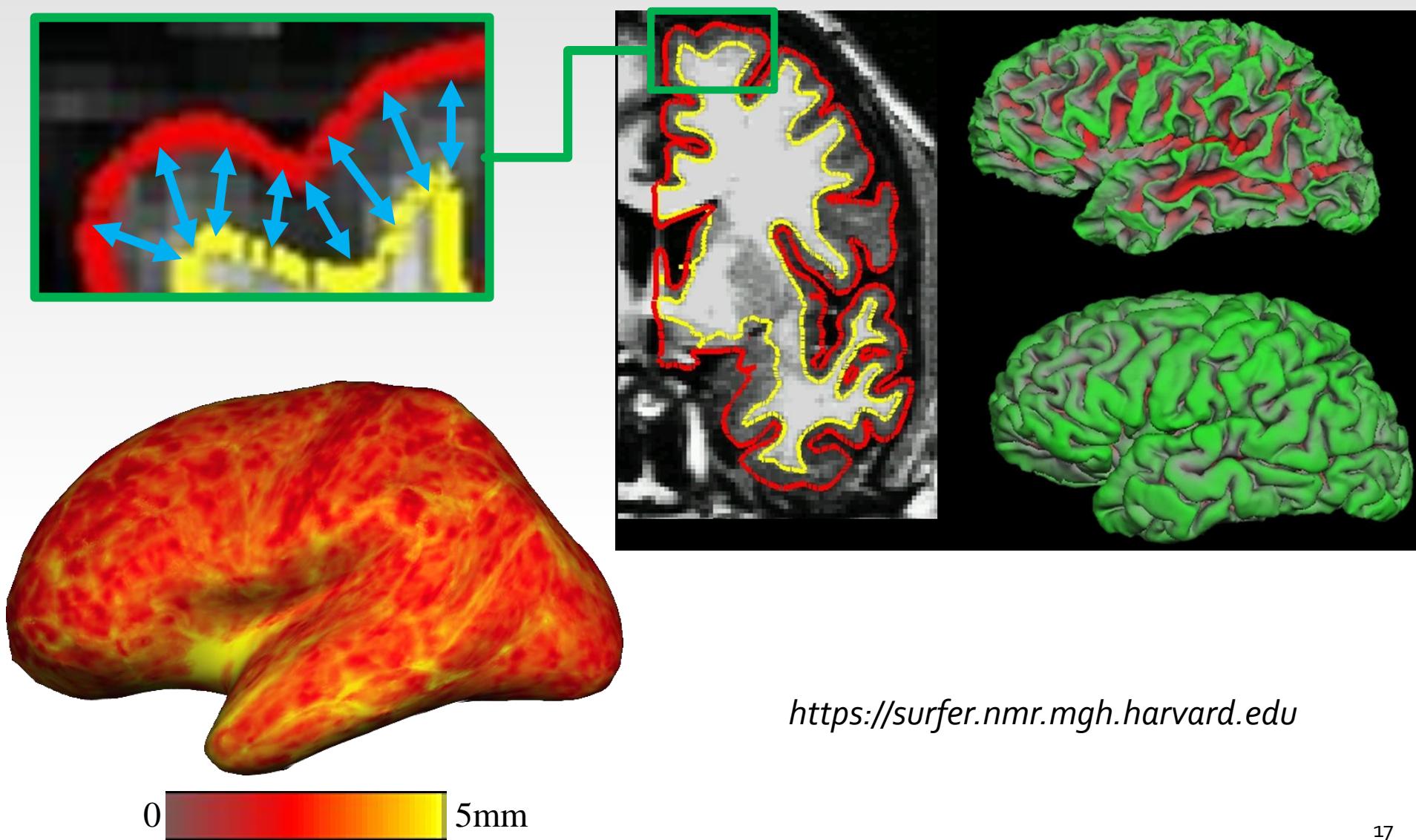
- Curvature-based defect detection
- Mapping-based defect detection
- Mesh surgery (cut and close)



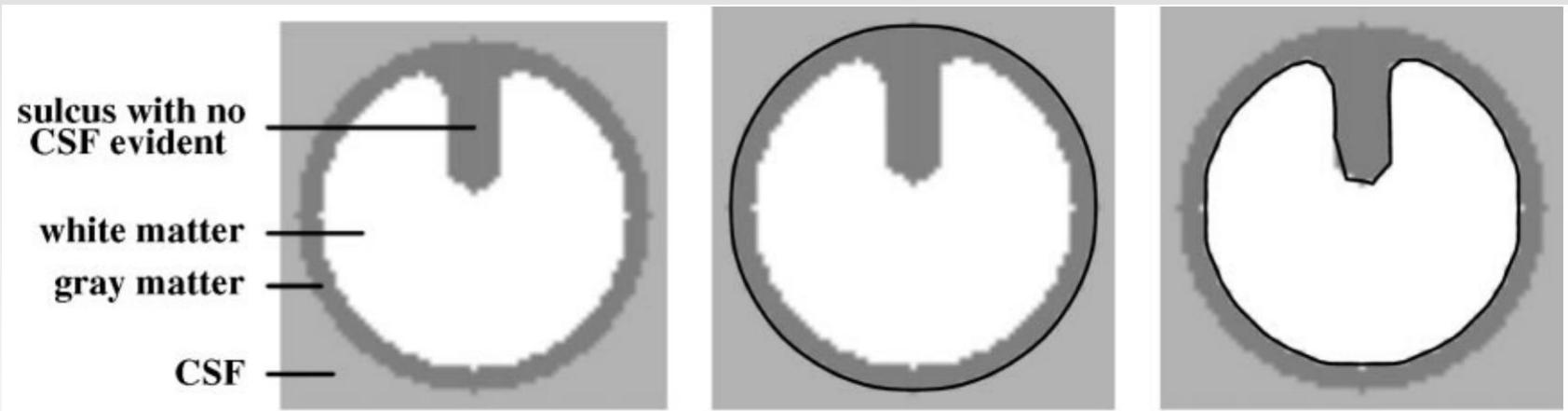
# Surface deformation

- Get a topologically correct pial surface
- Vertex correspondence between white and pial surfaces  
→ estimation of cortical thickness

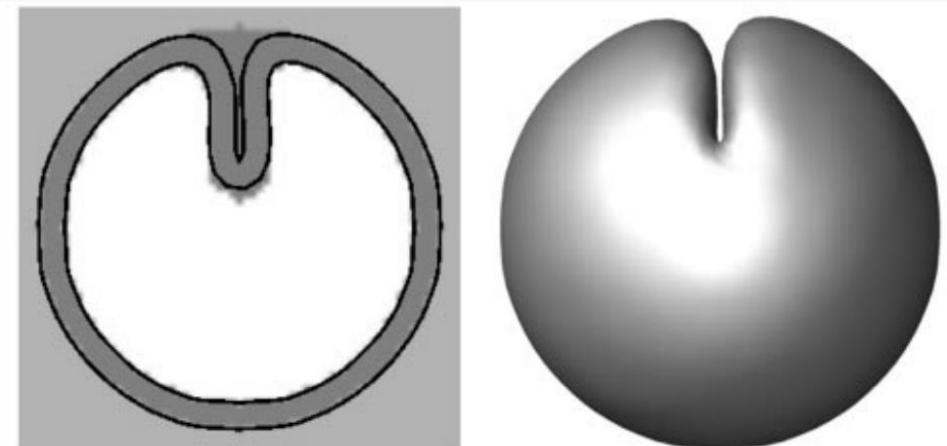
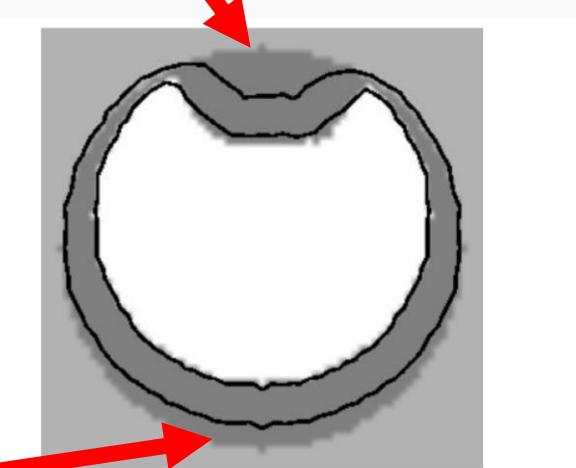
# Surface deformation



# Surface deformation



- Internal & tangential forces + self-intersections



**FIG. 5.** Response of ASP to gray thickness outside normal range. Here the phantom's cortical thickness varied from 1 to 15 mm, i.e., far beyond normal values. The algorithm constrained the thickness to between 2 and 6 mm.

# Successive steps in a classical pipeline

- Segmentation of the white mesh
- Topology correction
- Mesh deformation to get the pial mesh
- **Mapping onto a sphere**
- **Spherical registration**
- **Remeshing / interpolation across meshes**
- Volume to mesh interpolation
- Smoothing on the surface
- Computing statistics across meshes



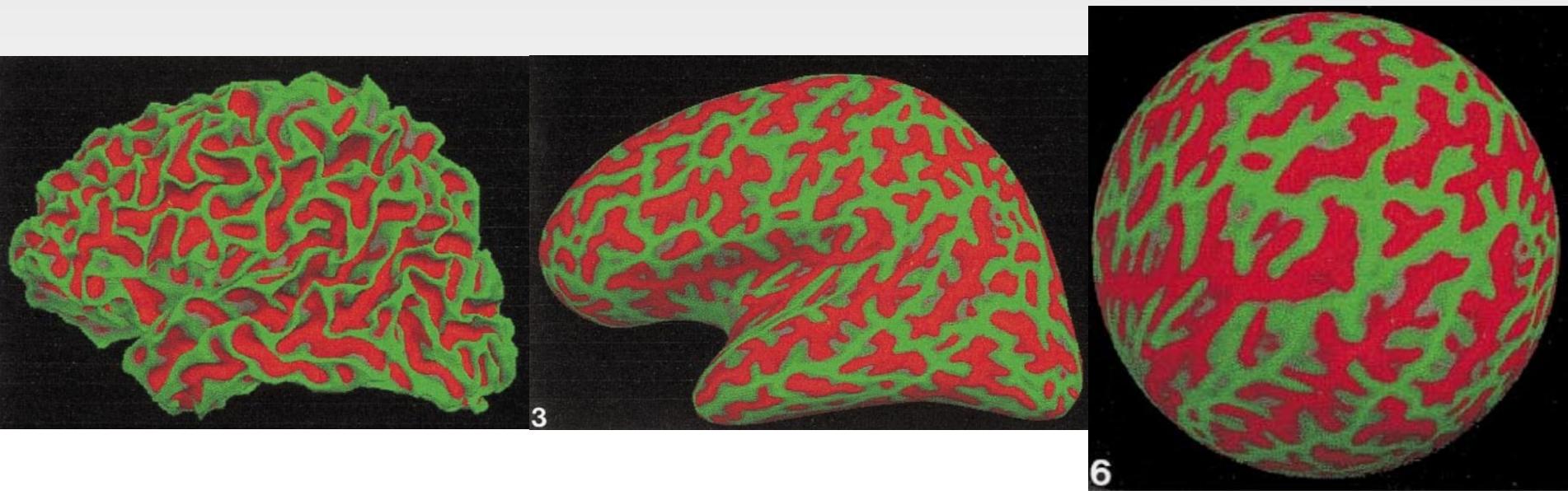
# Mapping onto a sphere

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- Map onto a canonical space common to all surfaces (i.e. subjects)
- Parameterization (latitudes/longitudes)

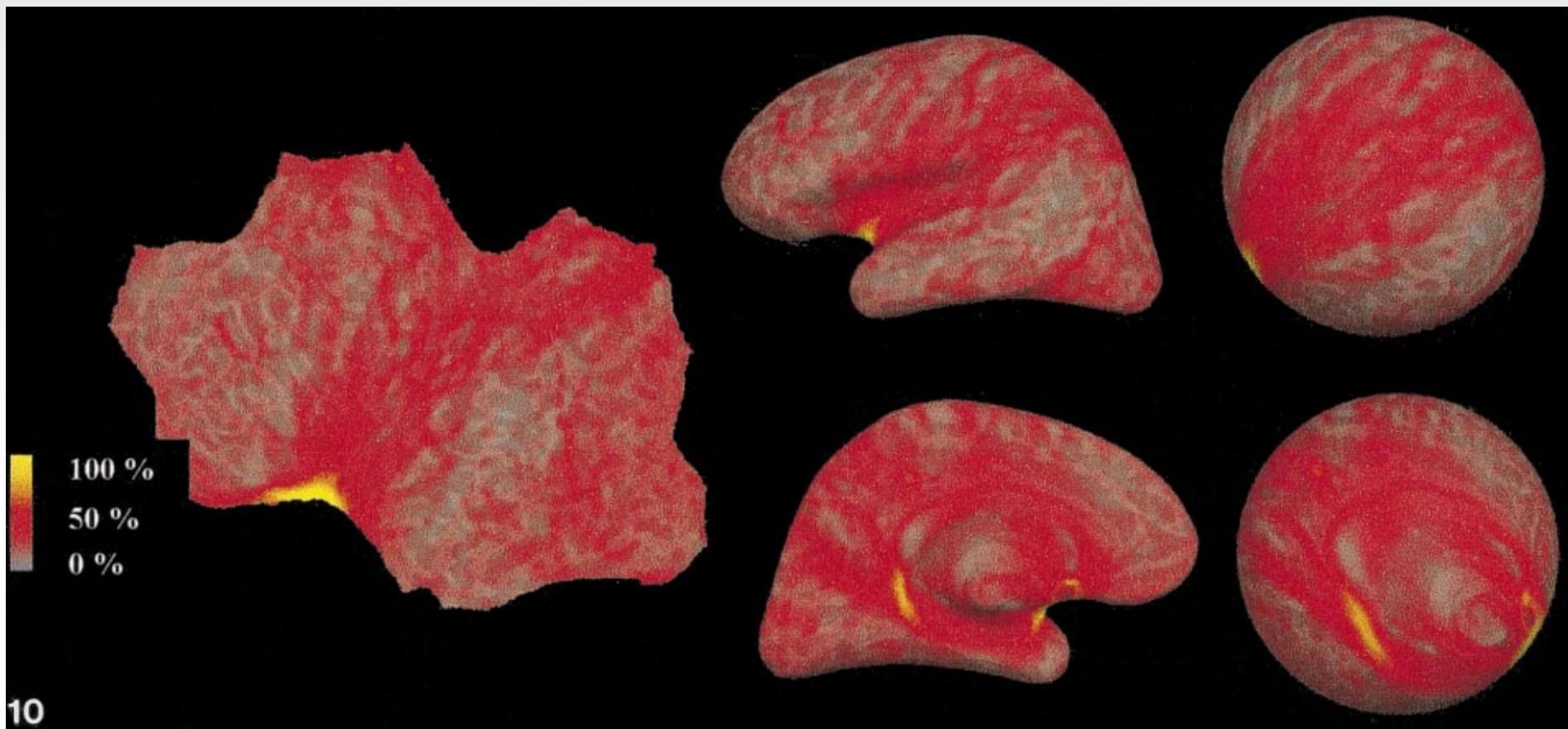
# Mapping onto a sphere

- Freesurfer : inflation + projection



# Mapping onto a sphere

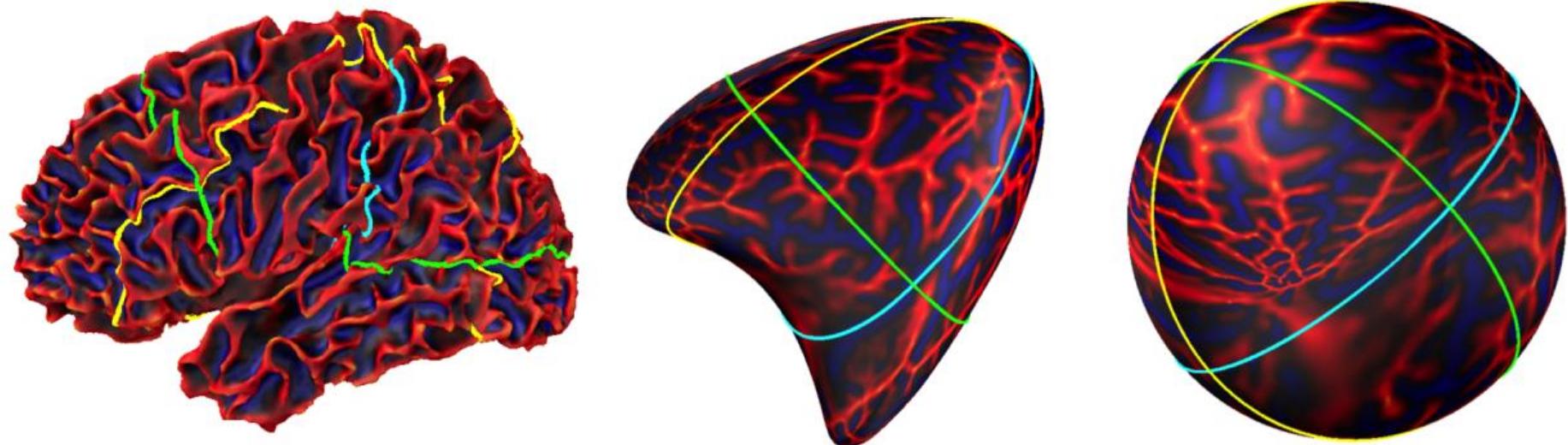
- Freesurfer : inflation + projection → **distortions!**



Fischl et al., *NeuroImage*, 1999

# Mapping onto a sphere

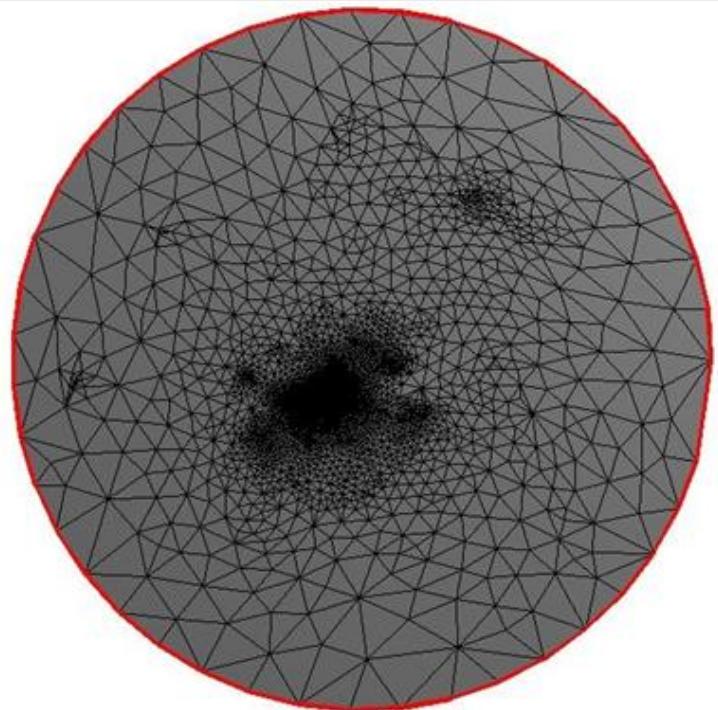
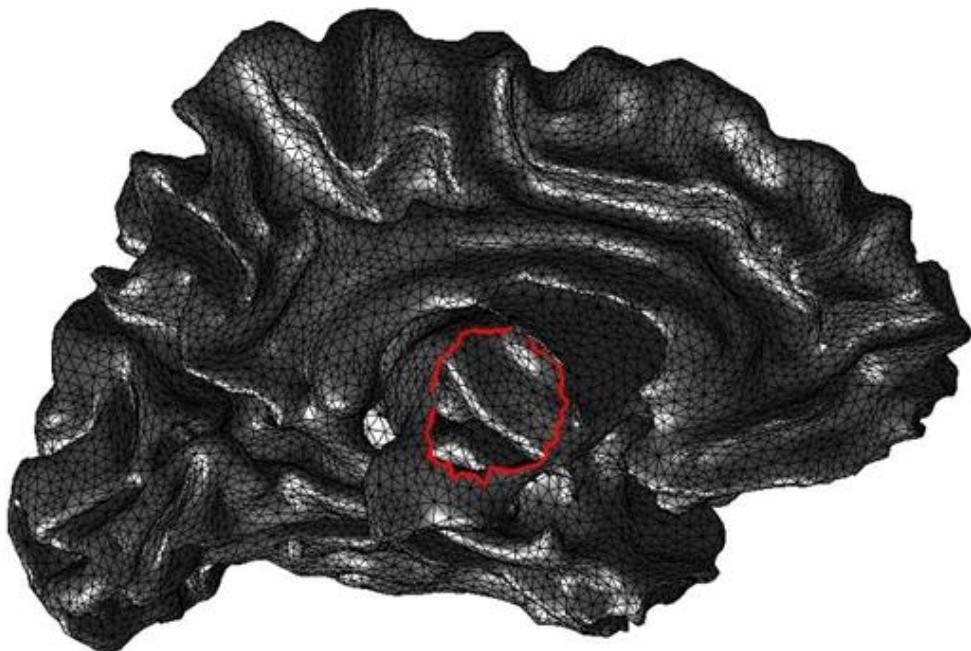
- Based on spectral decomposition



$$\begin{array}{ccc} \mathcal{M} & \longrightarrow & \mathbb{R}^3 \\ p & \longmapsto & (\Phi_1(p), \Phi_2(p), \Phi_3(p)) \end{array} \quad \begin{array}{c} \longrightarrow \\ \longmapsto \end{array} \quad \begin{array}{c} \mathbb{S}^2 \\ \frac{(\Phi_1(p), \Phi_2(p), \Phi_3(p))}{\sqrt{\Phi_1(p)^2 + \Phi_2(p)^2 + \Phi_3(p)^2}} \end{array}$$

# Mapping onto a sphere

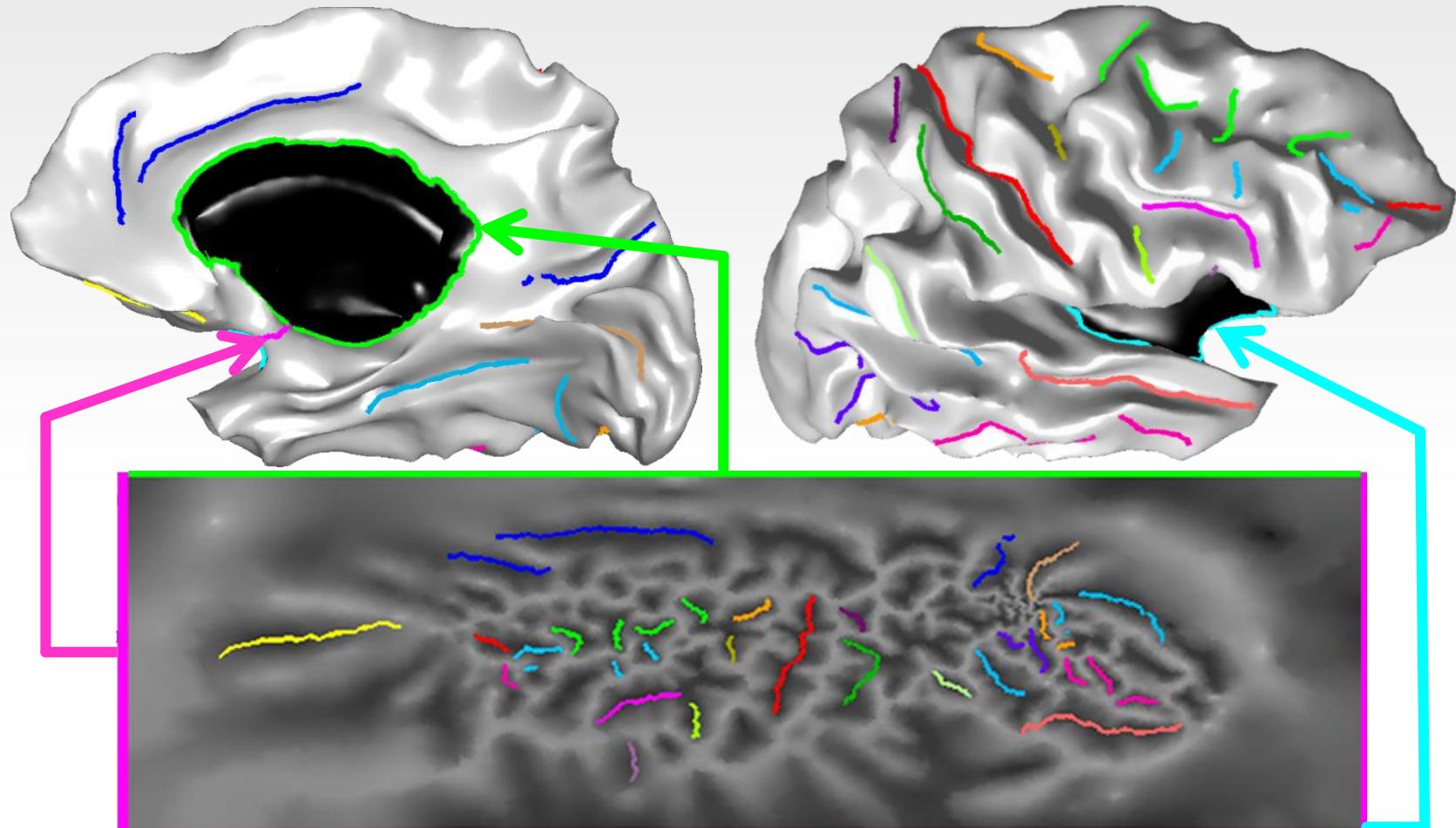
- Alternative options: disk



Keywords: conformal mapping

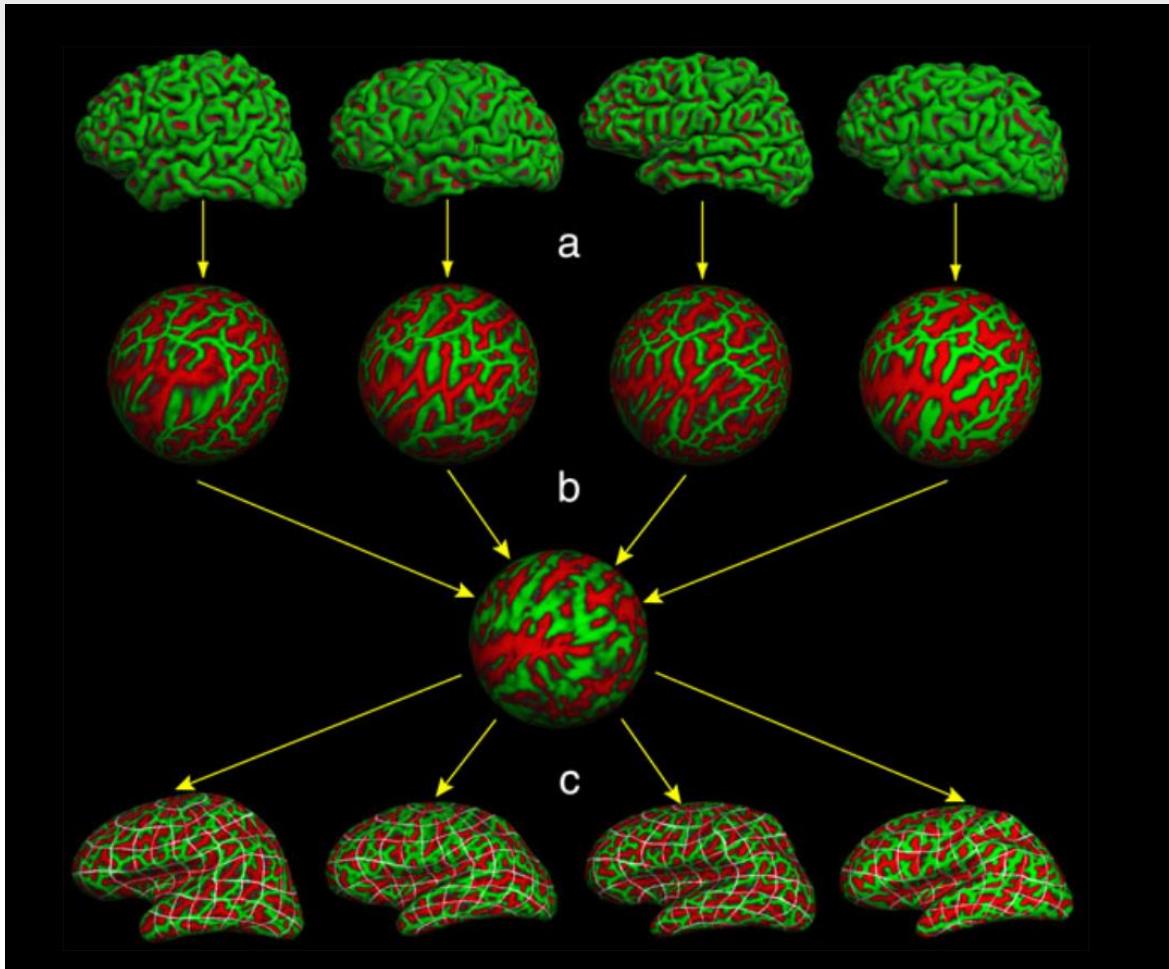
# Mapping onto a sphere

- Alternative options: rectangle (HIPHOP)

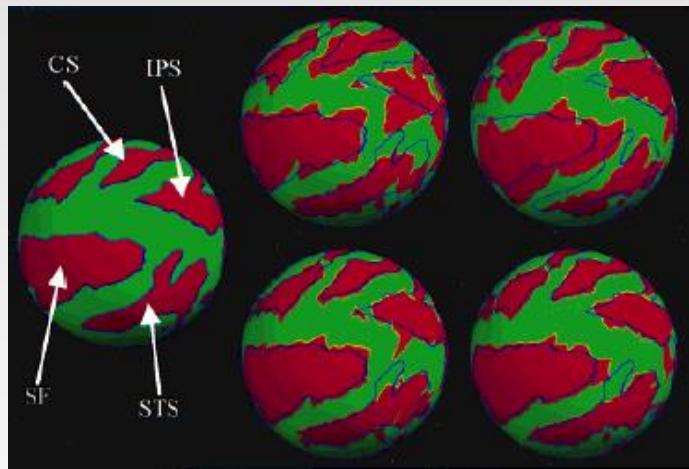


# Spherical registration

- Align anatomical / functional / ... features
- Vertex-to-vertex correspondence across surfaces

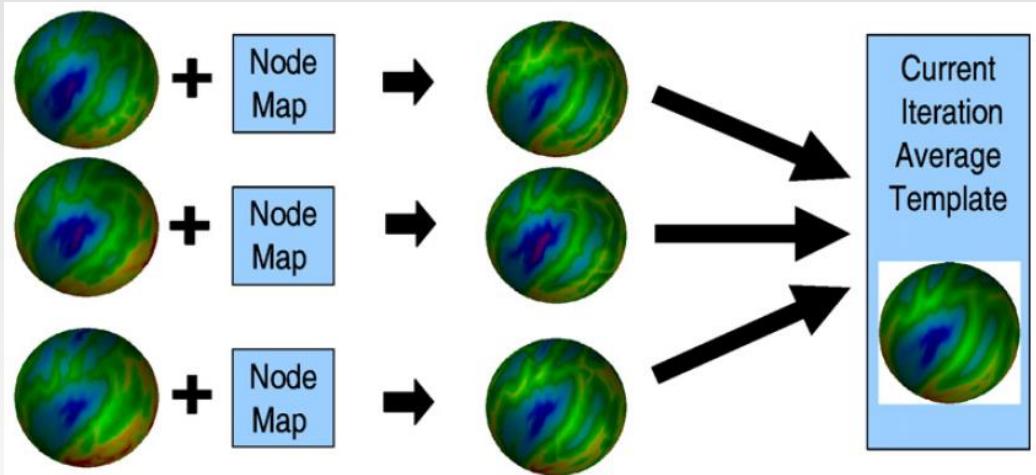


# Brain registration is a very active field

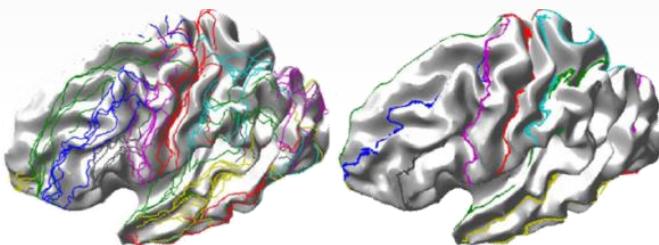
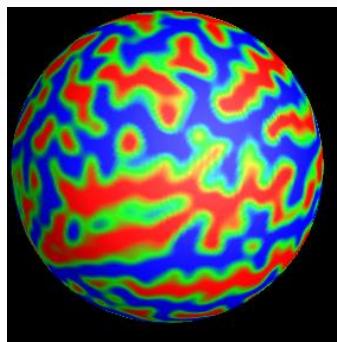


FREESURFER

Fischl et al, *Hum Brain Mapp*, 1999



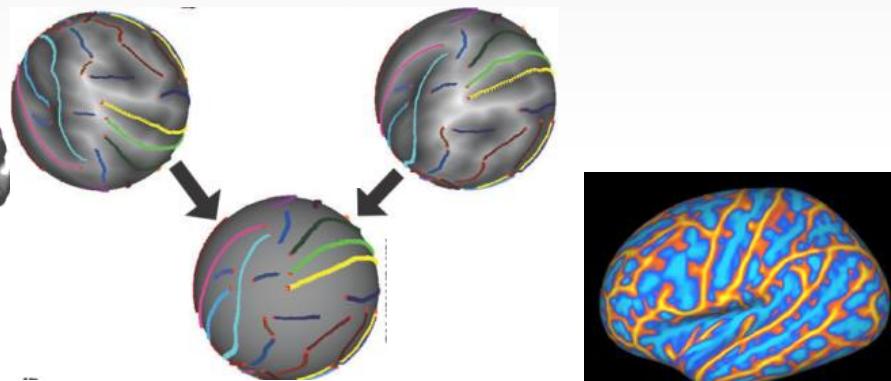
Lyttelton et al, *NeuroImage*, 2007



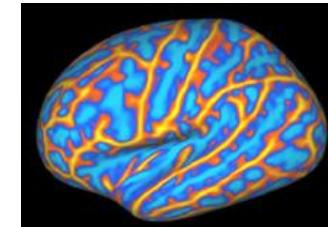
Joshi et al,  
IEEE TMI, 2007

Yeo et al.,  
IEEE TMI, 2010

See also Auzias et al., IEEE TMI, 2011 & 2013 😎



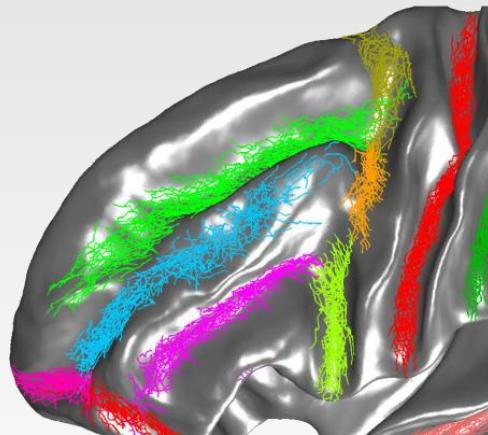
CARET, Van Essen,  
NeuroImage, 2005



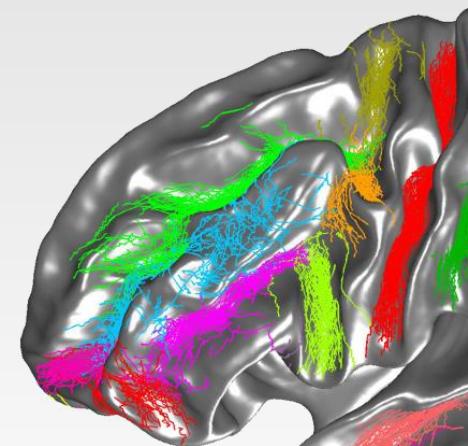
Robinson et al,  
NeuroImage, 2014

# Differences between methods outcome

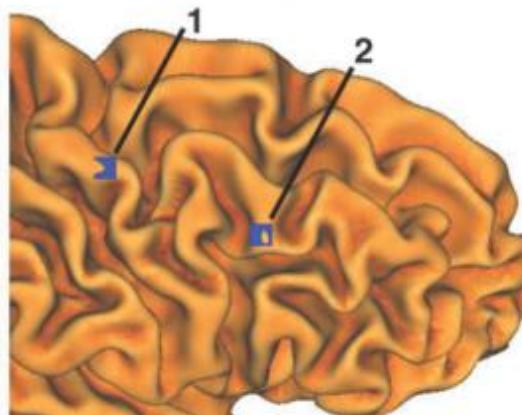
HIP-HOP



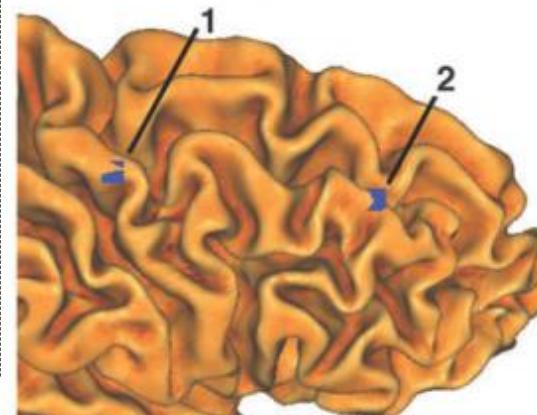
Freesurfer



A Individual registered via PALS-B12



B Individual registered via fs\_R



CARET

Freesurfer

# Differences between methods outcome

Freesurfer : alignment driven by sulcal depth and curvature

curvature



labelled sulci



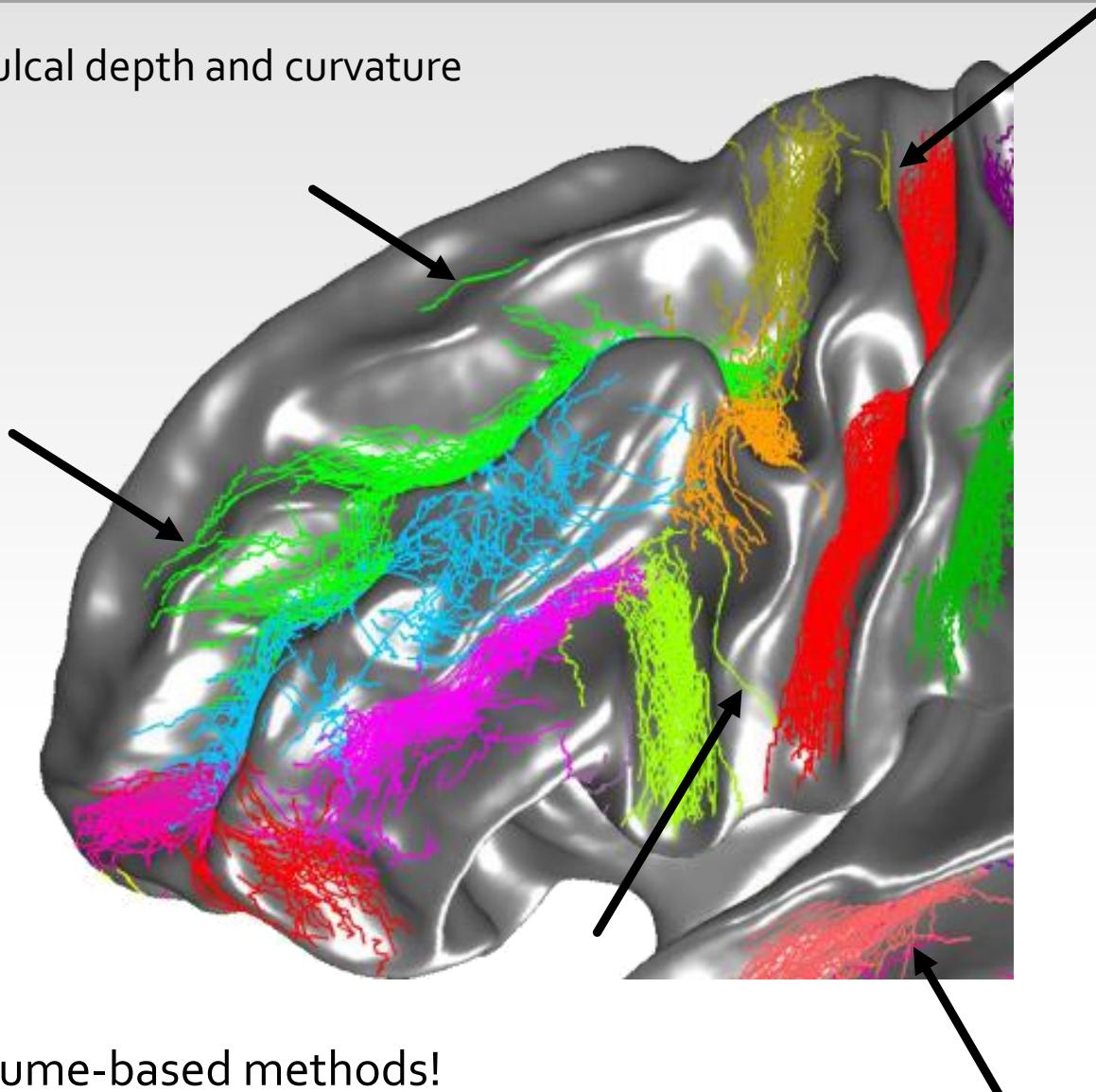
myelin



functional areas or  
activations



sulcal depth

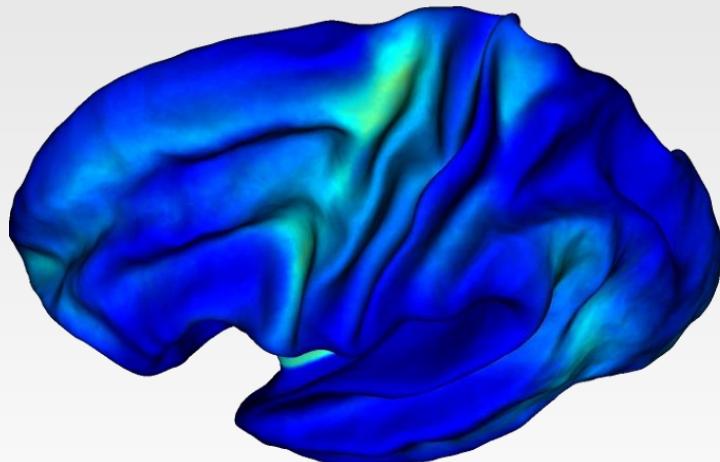


Also true for volume-based methods!

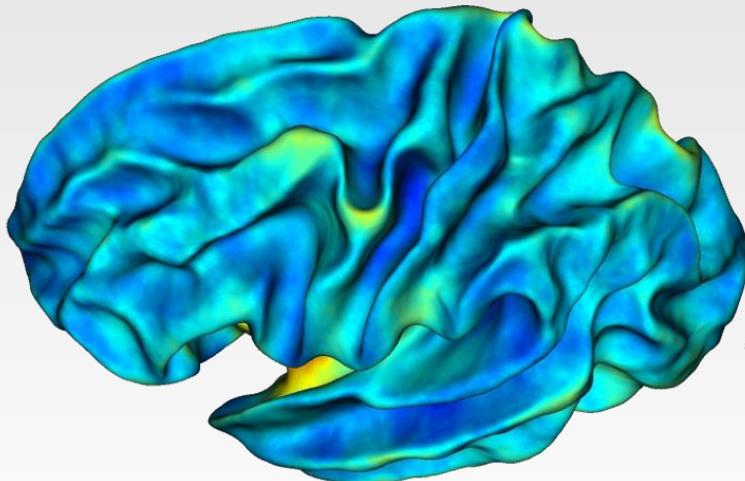
# Registration = distortions

Angular

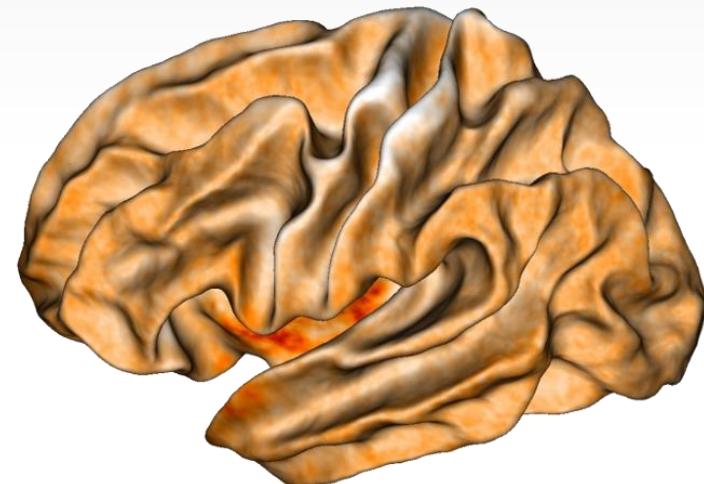
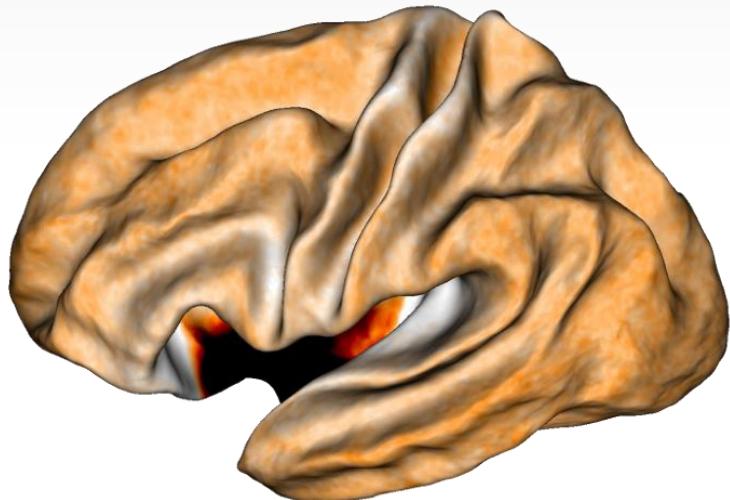
HIP-HOP



Freesurfer

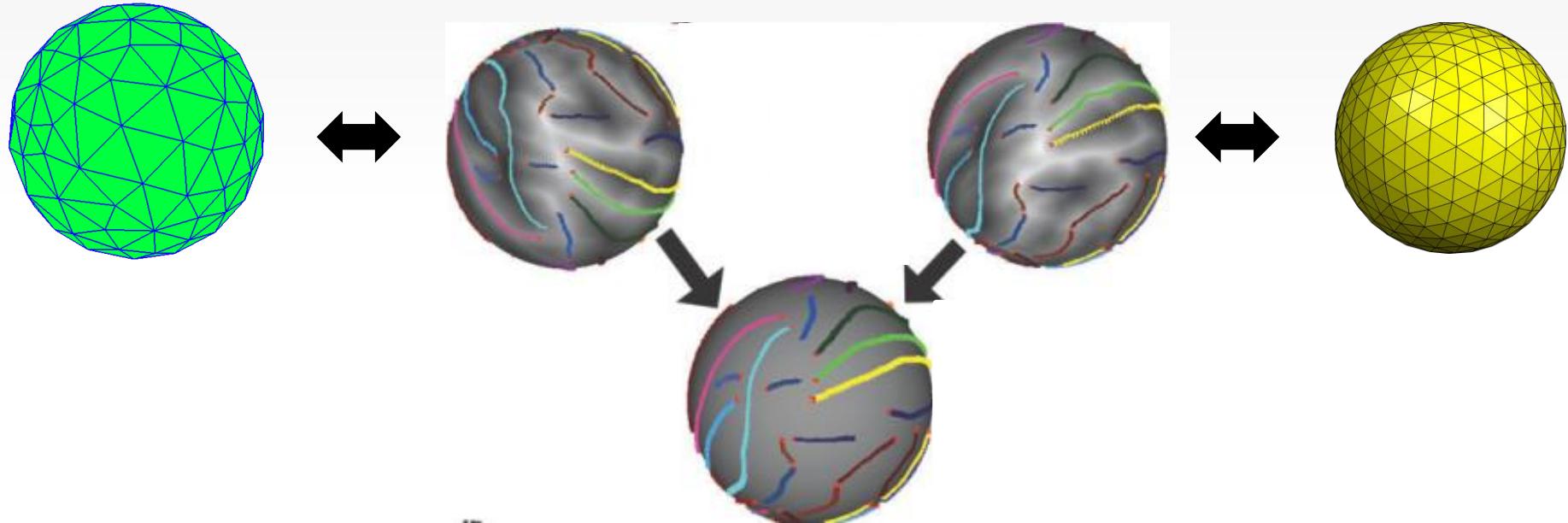


Areal

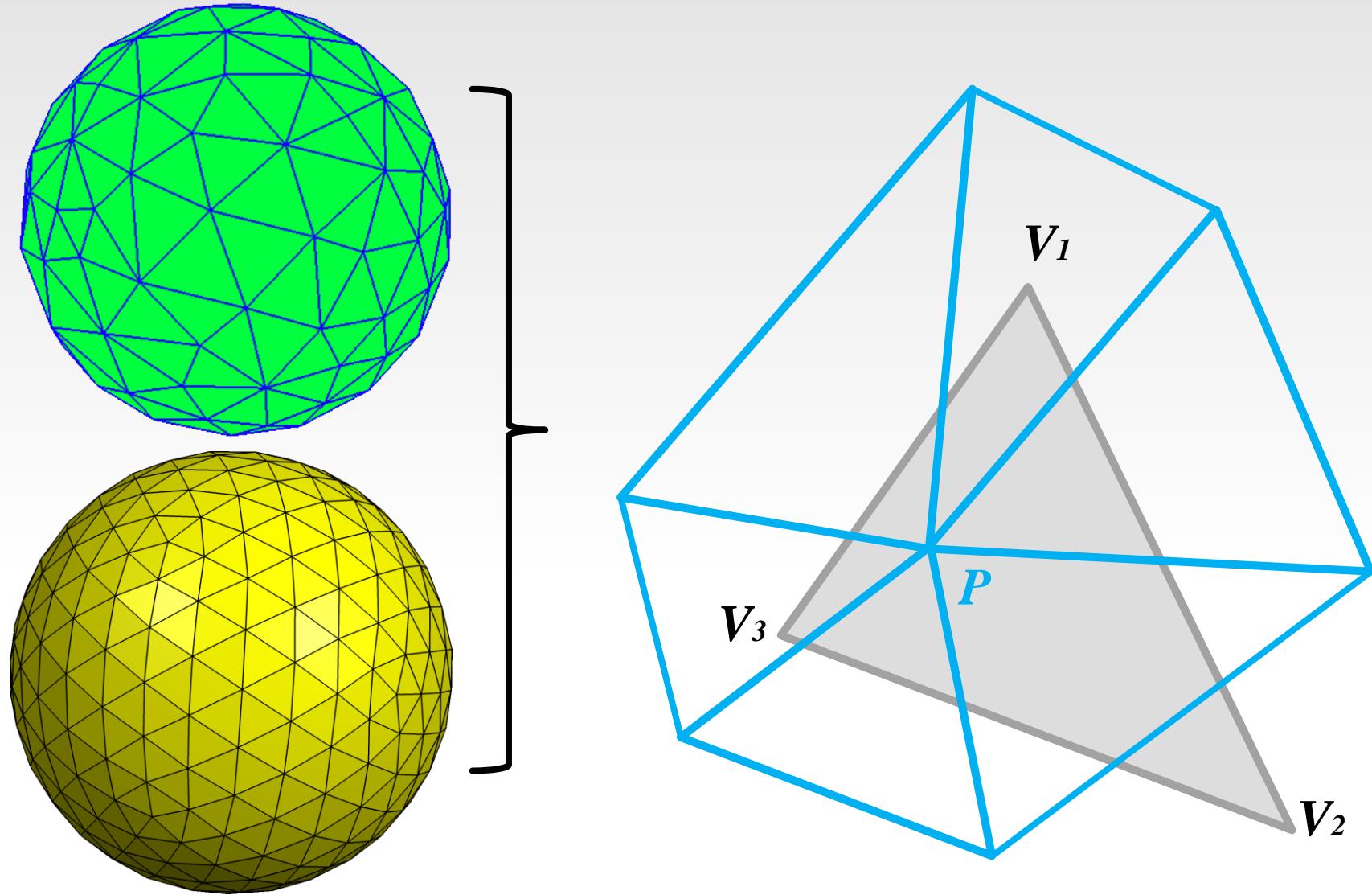


# Remeshing = interpolation across meshes

- Transfer information across meshes to a common domain
- Change the spatial resolution
- Compute an average surface

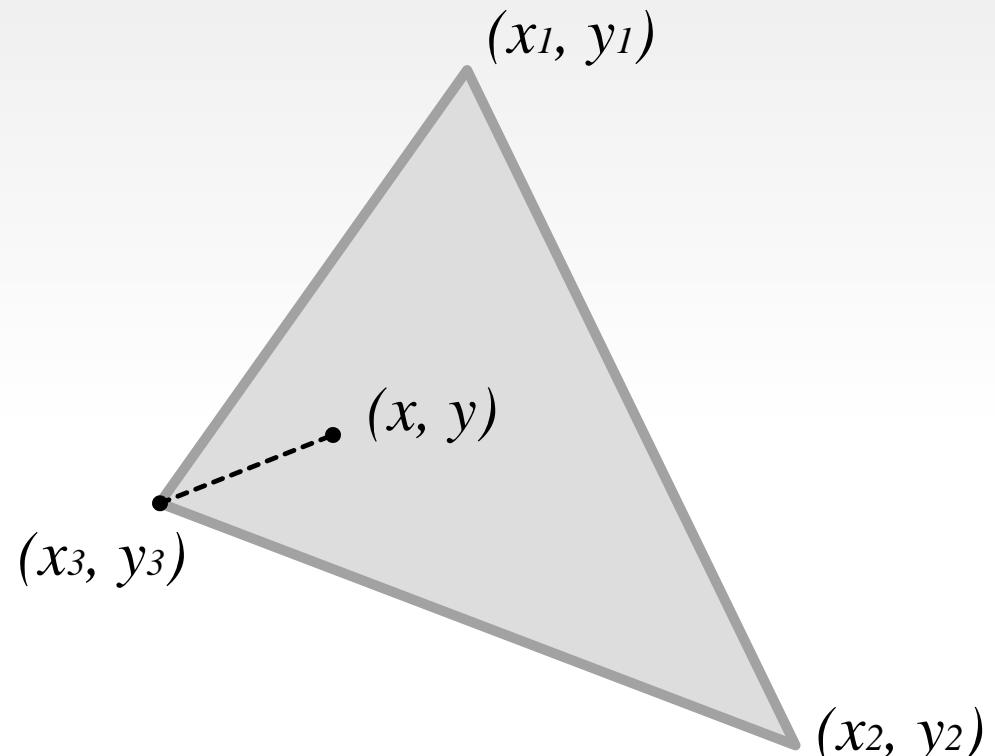


# Remeshing = interpolation across meshes



# Remeshing = interpolation across meshes

- Nearest neighbor interpolation:
- Associate the value of the closest point

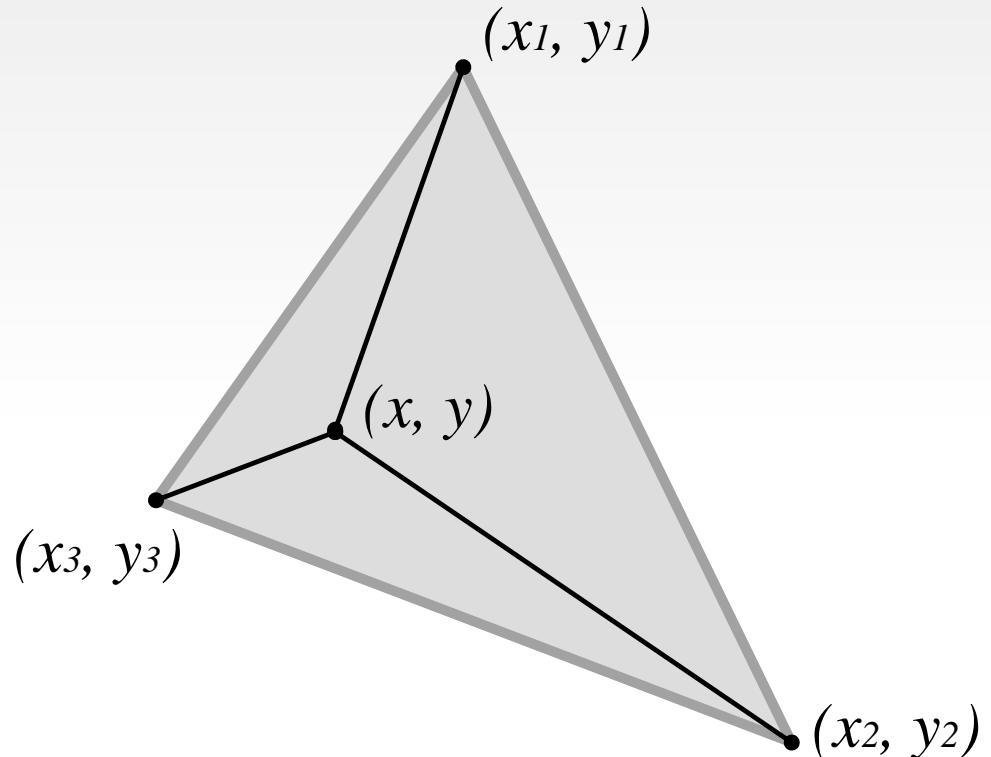


# Remeshing = interpolation across meshes

- Linear interpolation:
- Barycentric coordinates

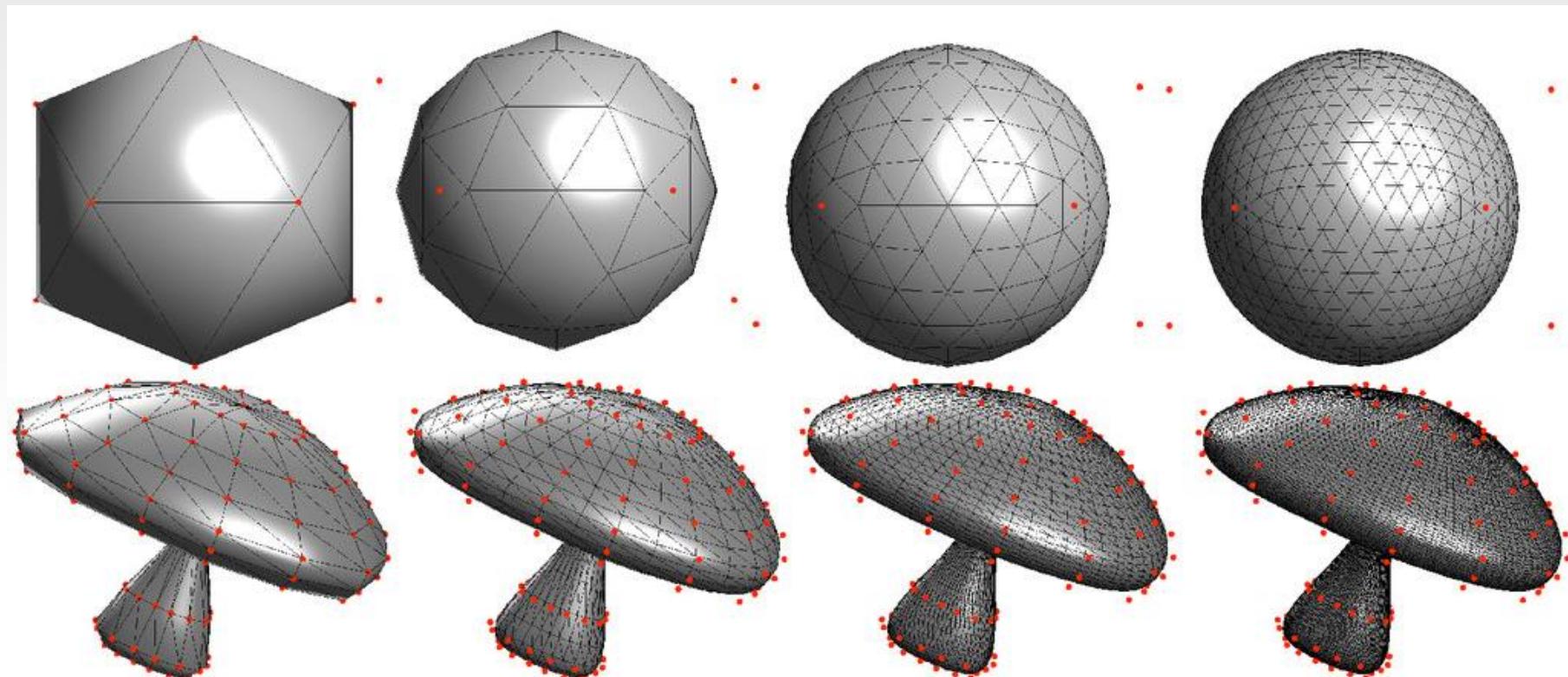
$$x = \lambda_1 x_1 + \lambda_2 x_2 + \lambda_3 x_3$$

$$y = \lambda_1 y_1 + \lambda_2 y_2 + \lambda_3 y_3$$

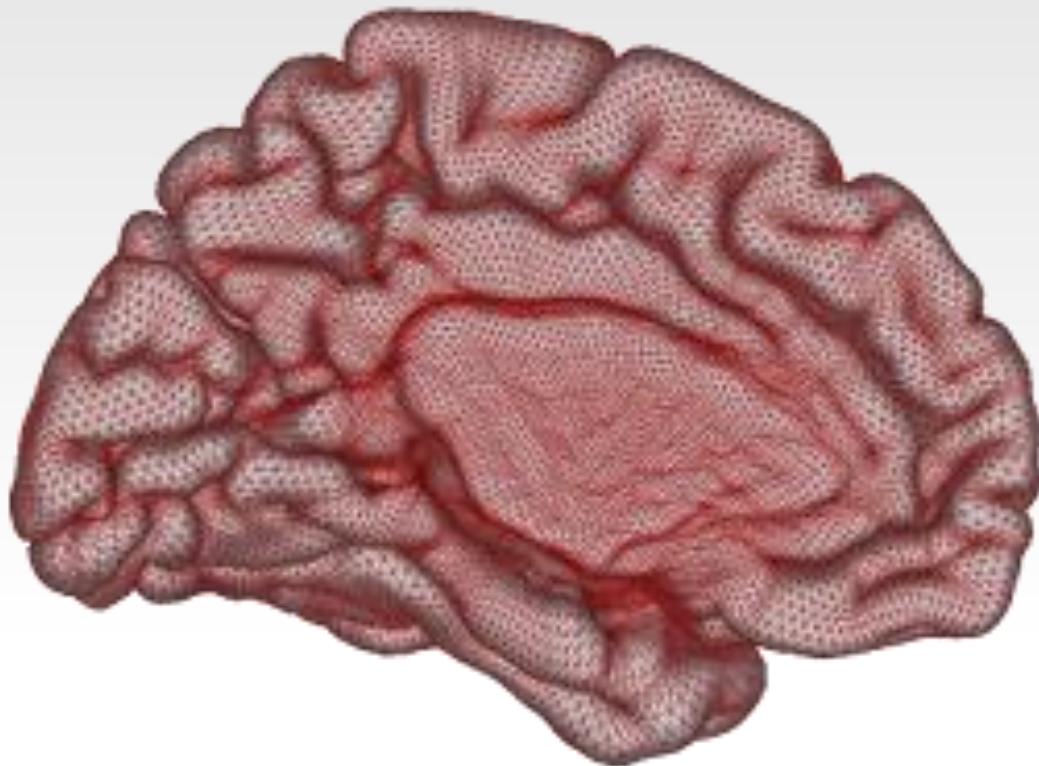


# Remeshing = interpolation across meshes

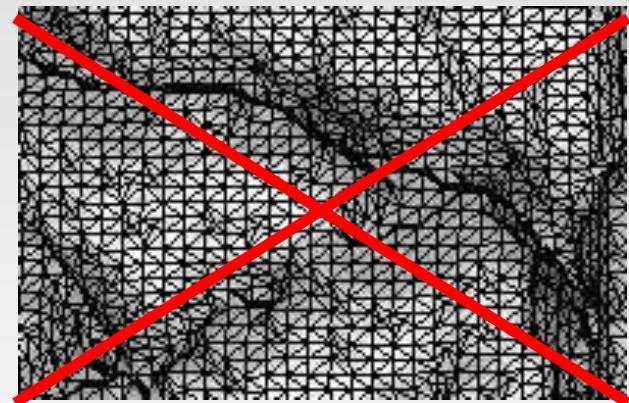
- Change the spatial resolution



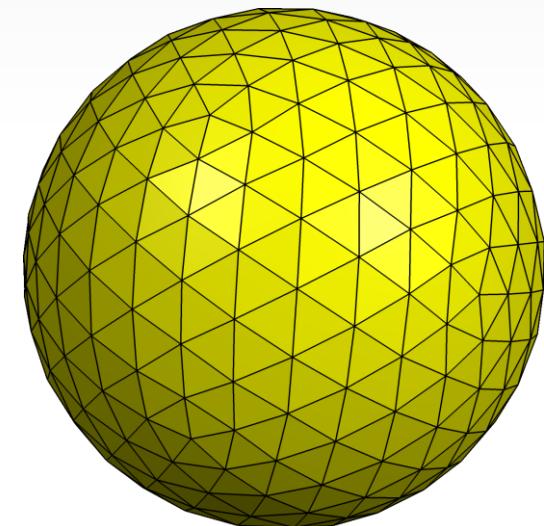
# Remeshing = interpolation across meshes



<https://mcin.ca/technology/civet/>

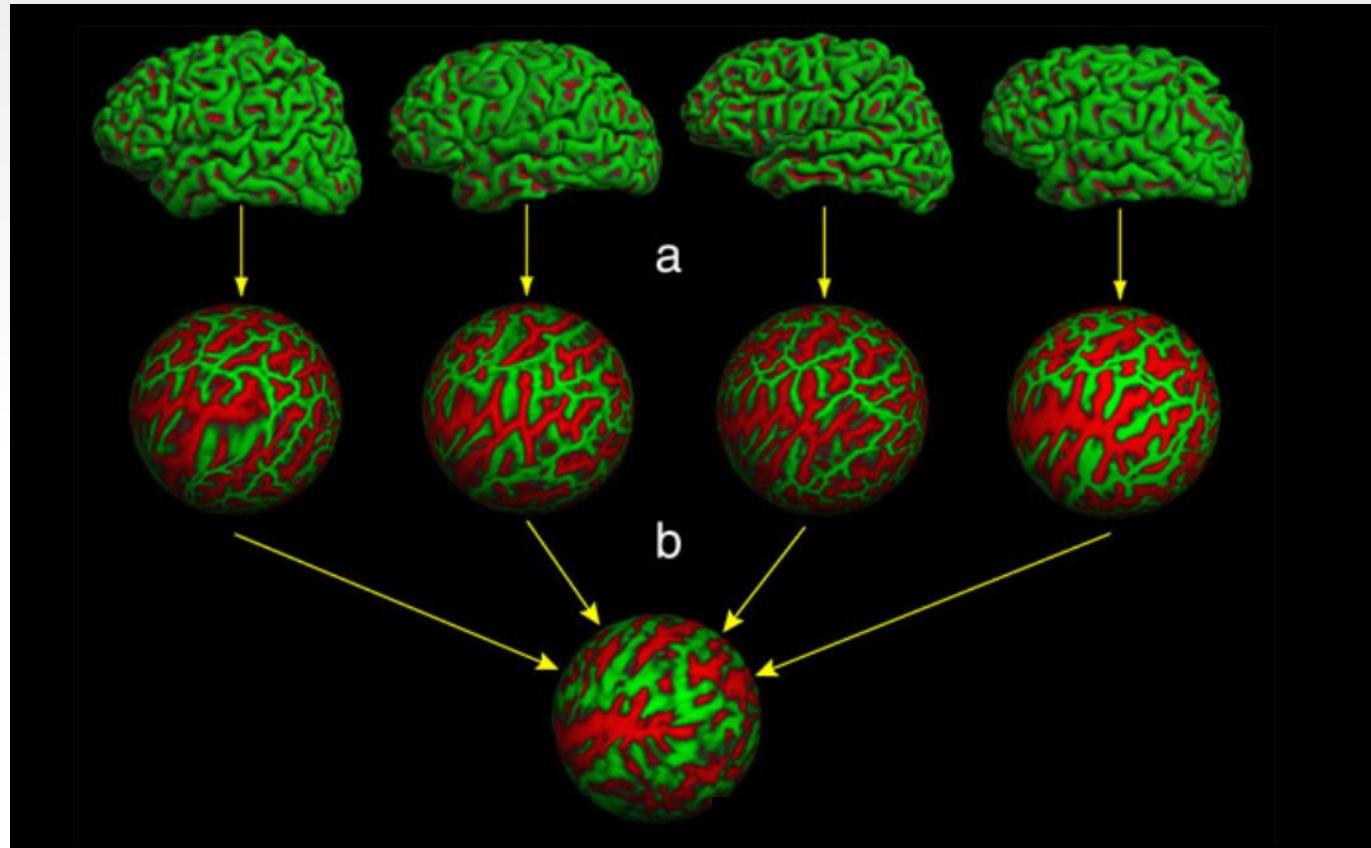


- Too regular for a marching cubes
- Heterogeneous triangle size
- > Remeshed using an icosahedron



# Computing statistics across meshes

- Compare features across meshes
- E.g. 2 groups of subjects



# Successive steps in a classical pipeline

- Segmentation of the white mesh
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- **Volume to mesh interpolation**
- **Smoothing on the surface**
- **Computing statistics across meshes**



# Volume to mesh interpolation/projection

Operto et al., *Neuroimage*, 2008

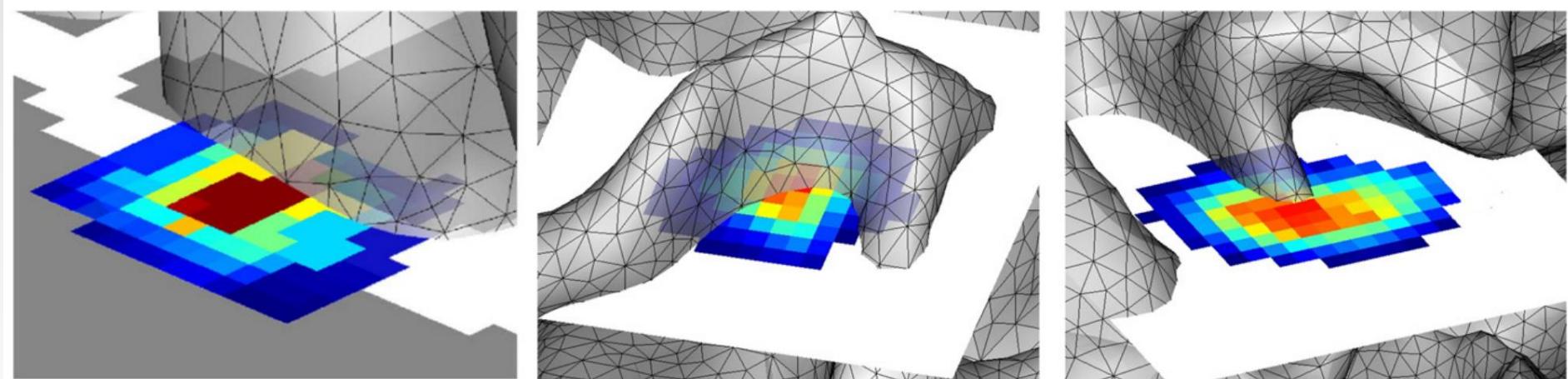
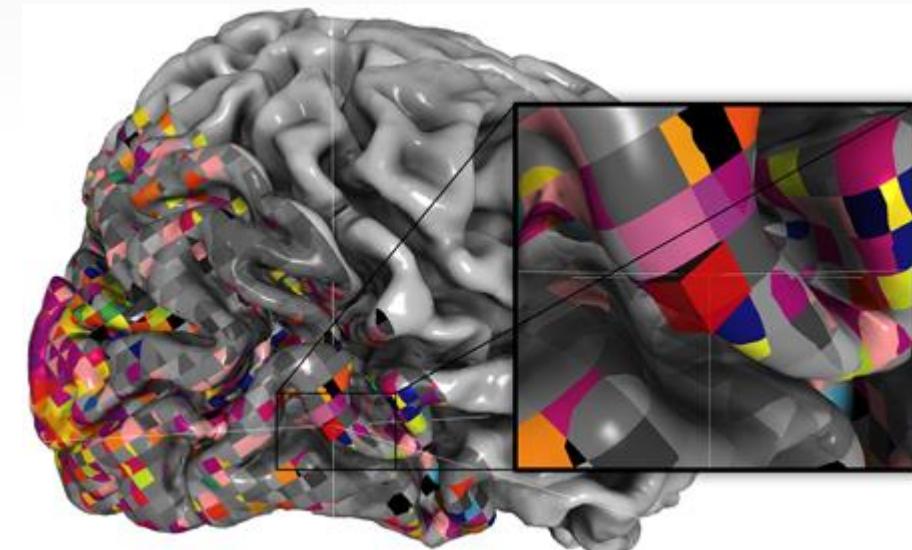


Fig. 6. Convolution kernels obtained for nodes on real cortical meshes. The kernel on the left shows a superimposed cortical mask.



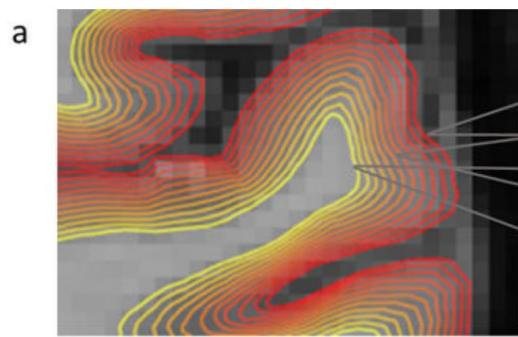
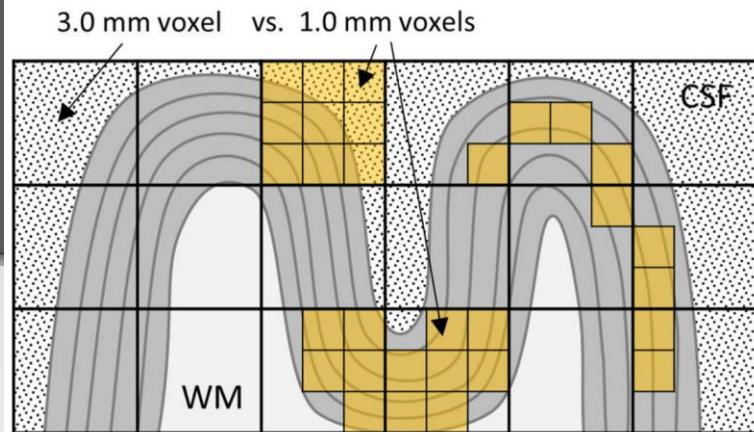
Gao et al., *Front. NeuroInf.*, 2015

Pycortex

<https://gallantlab.github.io/pycortex/index.html>

# Smoothing on the surface

AI Blazejewska et al., *Neuroimage*, 2019

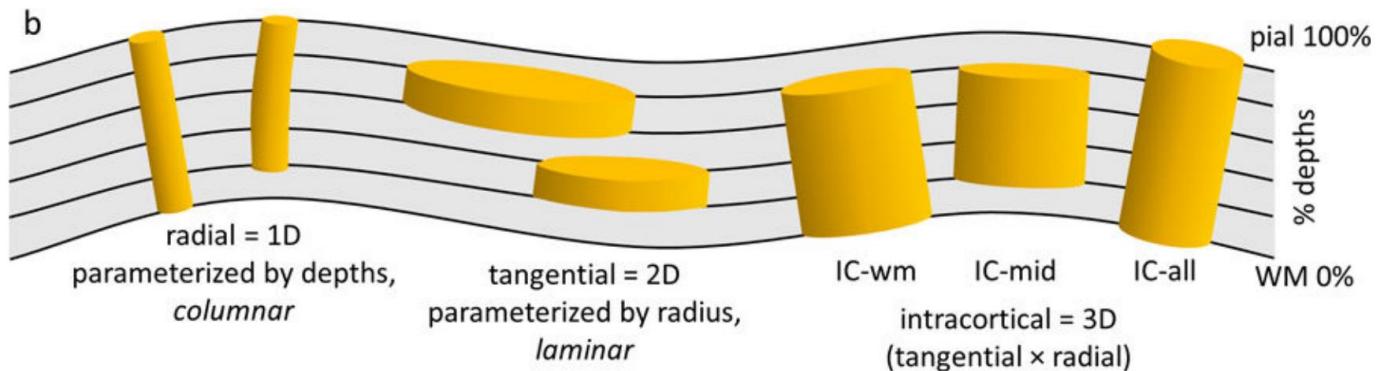


a: large voxel

|     |     |     |
|-----|-----|-----|
| 1.0 | 1.0 | 1.0 |
| 1.0 | 1.0 | 1.0 |
| 1.0 | 1.0 | 1.0 |

b: redistributed, weighted small voxels

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| 0.7 | 0.8 |     | 0.8 | 0.7 |
| 0.5 | 0.9 | 1.0 | 0.9 | 0.5 |
|     | 0.7 | 0.8 | 0.7 |     |
|     |     |     |     |     |



# Computing statistics on meshes

- Available tools
  - Freesurfer tksurfer
  - Surfstat (matlab)
  - CAT 12
  - Nilearn?

**Control False positives  
Multiple comparisons**

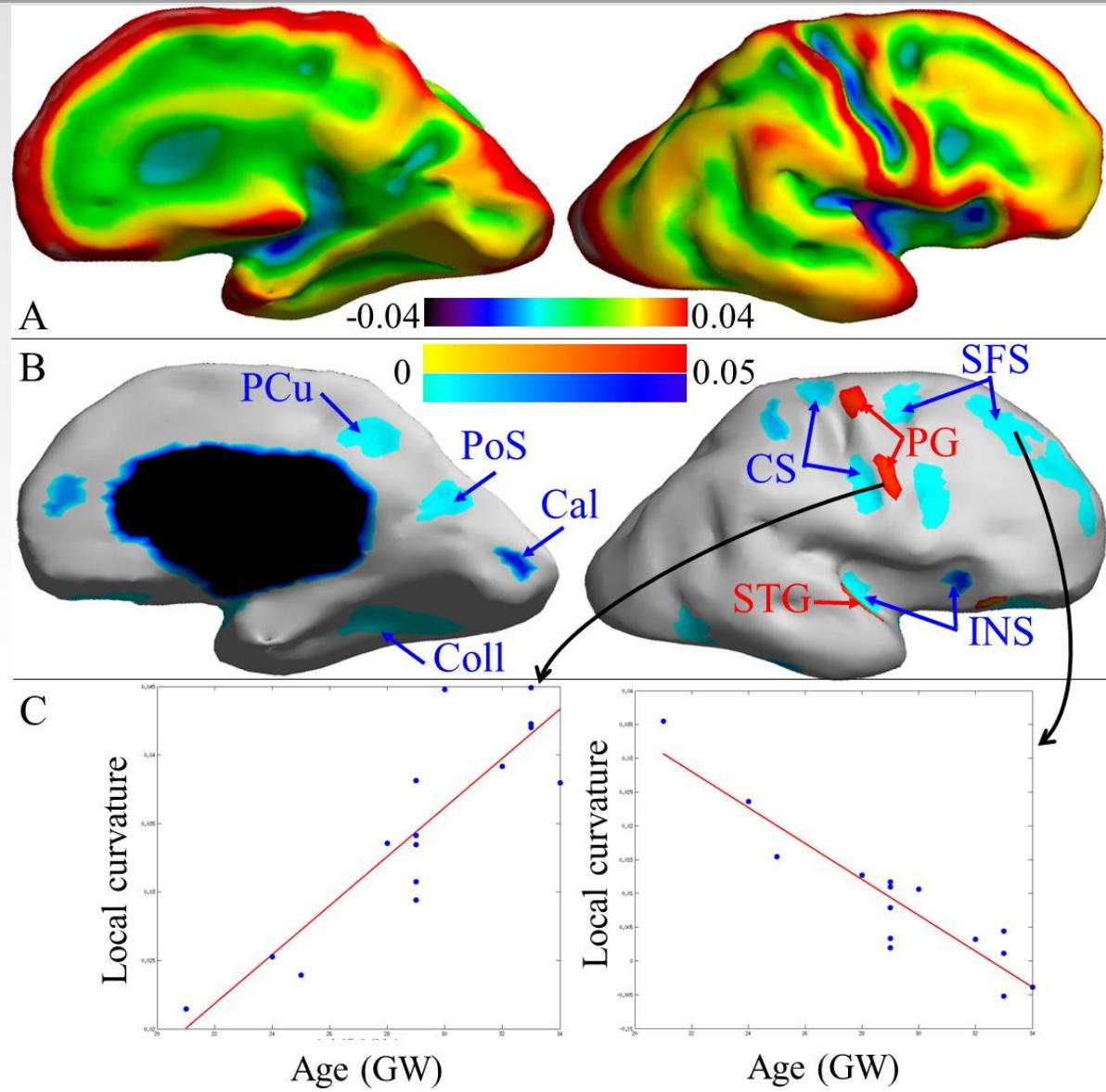
Greve et al., *Neuroimage*, 2018

Andy W. K. Yeung, *Frontiers in Human Neuroscience*, 2018

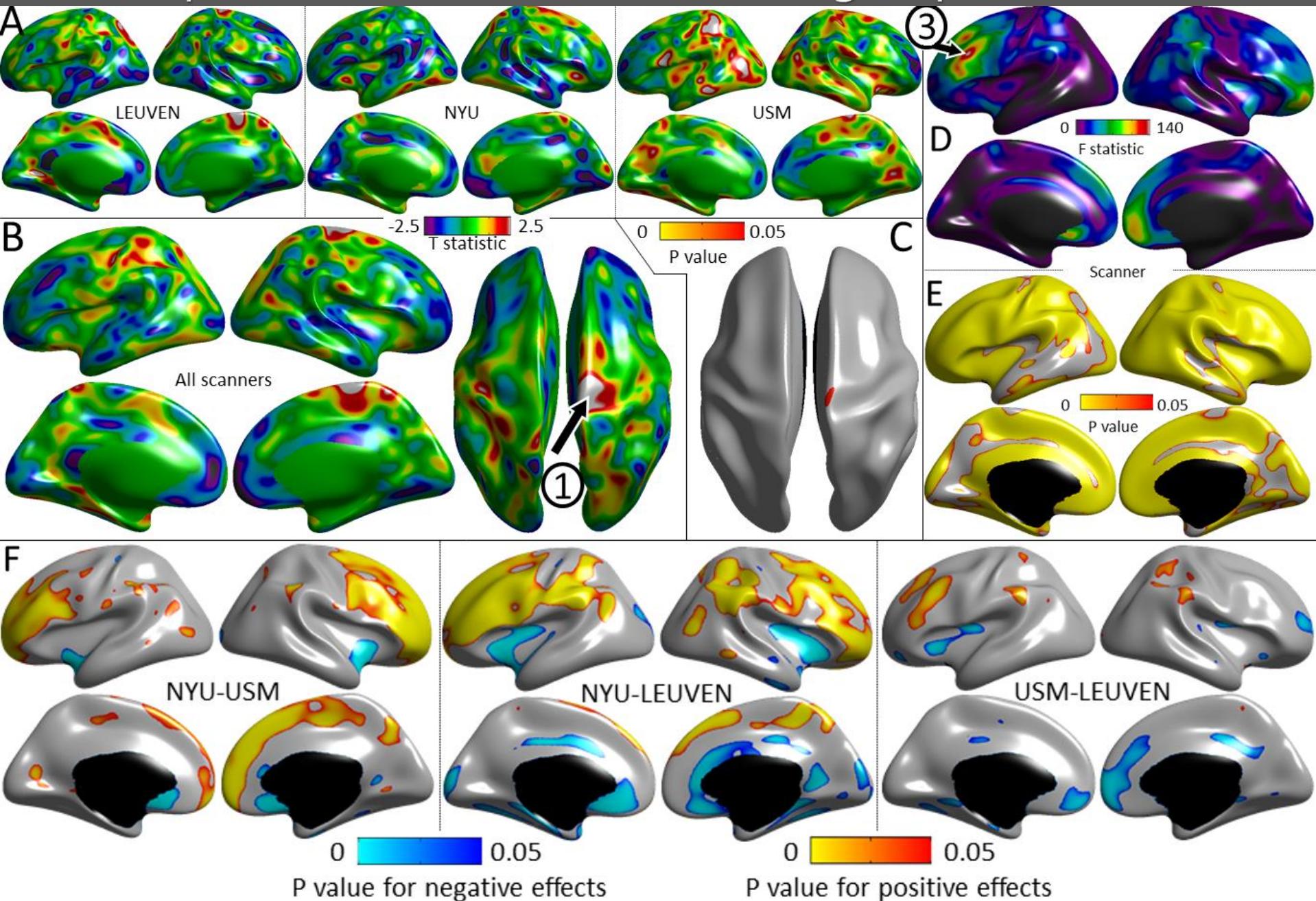
# Evolution of Cortical folding with GA

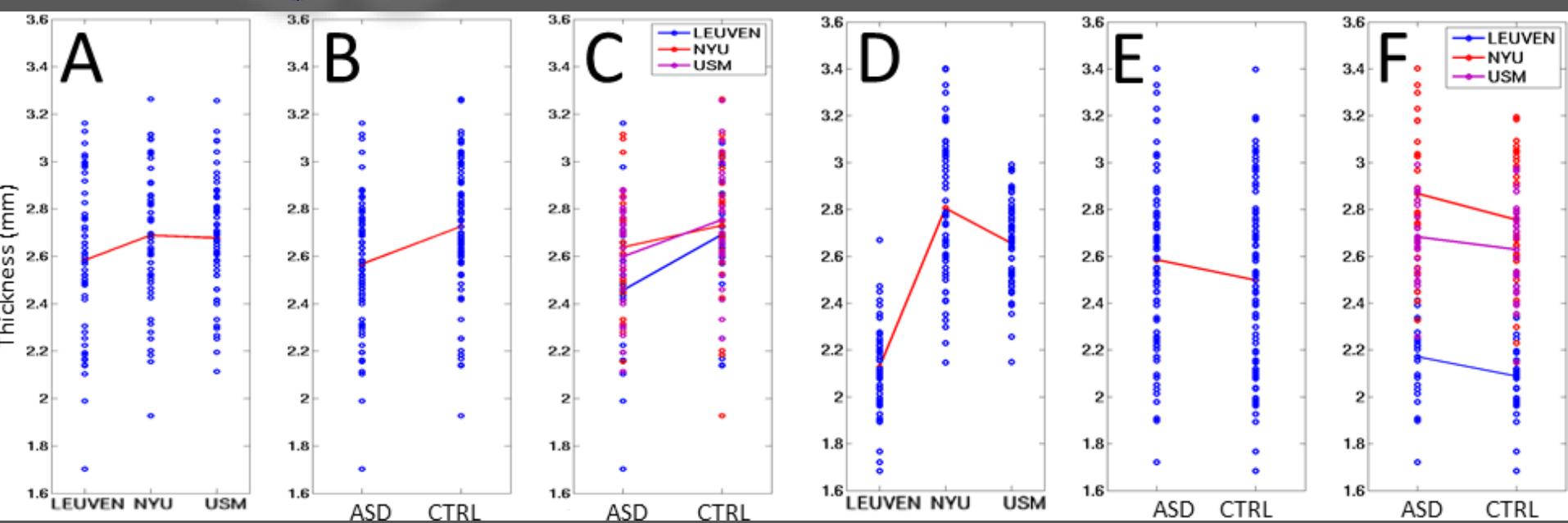
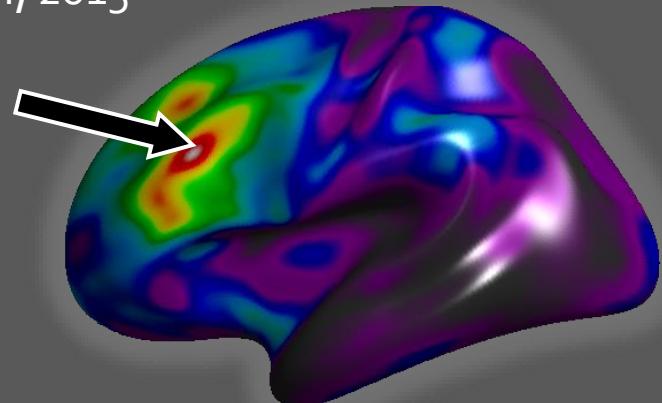
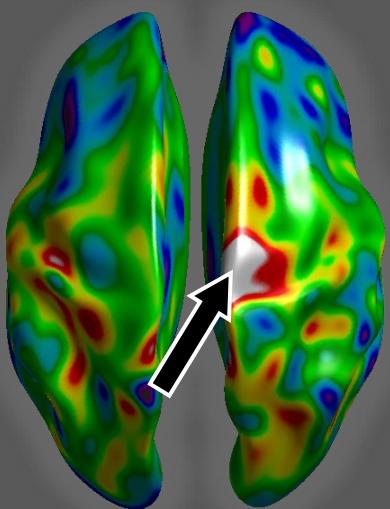
15 Fetuses  
21-34 wk GA

Auzias et al., *IEEE ISBI*, 2015



# Compare cortical thickness across groups and scanners





Diagnostic group:  $\eta^2=0.35$ ,  $p<0.0001$   
 scanner :  $\eta^2=0.07$ ,  $p=0.14$   
 Age:  $\eta^2=0.49$ ,  $p<0.0001$   
 age-by-scanner  $\eta^2=0.08$ ,  $p=0.12$

Diagnostic group:  $\eta^2=0.01$ ,  $p=0.0284$   
 Scanner:  $\eta^2=0.77$ ,  $p<0.0001$   
 Age:  $\eta^2=0.15$ ,  $p<0.0001$   
 age-by-scanner:  $\eta^2=0.05$ ,  $p<0.0001$

# Recap

## Successive steps in a classical pipeline

- Segmentation of the white mesh } **Imprecisions**
- Topology correction
- Mesh deformation to get the pial mesh      **Distortions**
- Mapping onto a sphere      **Distortions**
- Spherical registration      **Distortions / Bias**      **Interpolation**
- Remeshing / interpolation across meshes      **errors**
- Volume to mesh interpolation      **Interpolation**  
   **errors**
- Smoothing on the surface      **Interpretation**
- Computing statistics across meshes

