Introduction to the Geometry and Structure of the Human Brain

Neurohackademy 2020

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Outline

- Magnetic Resonance Imagine (MRI)
- Volumetric Image Data
- The Cerebral Cortex and Surface Meshes
- Intersubject Comparison

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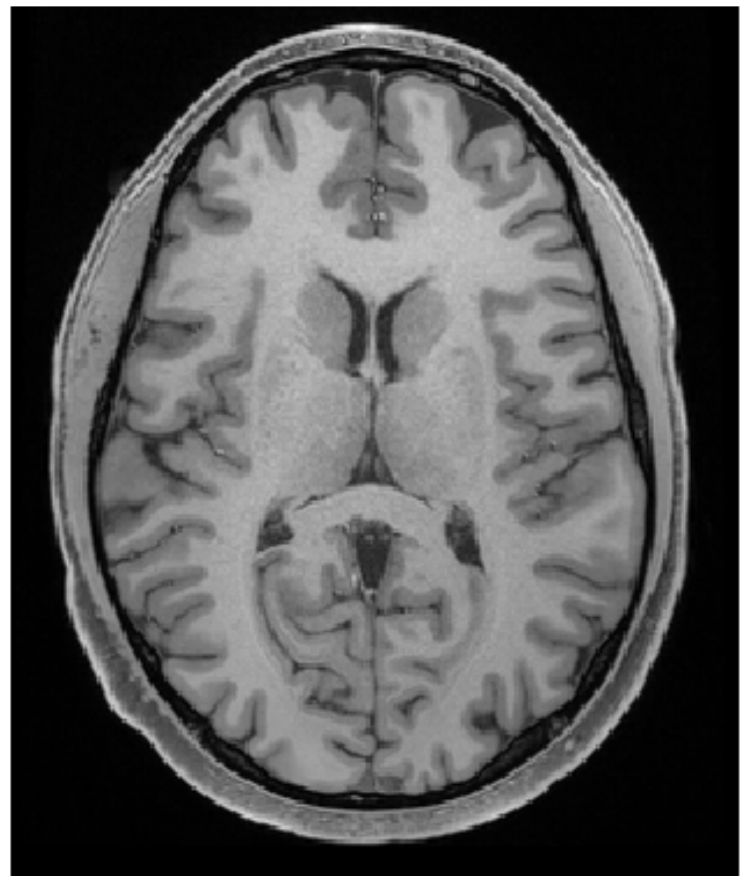
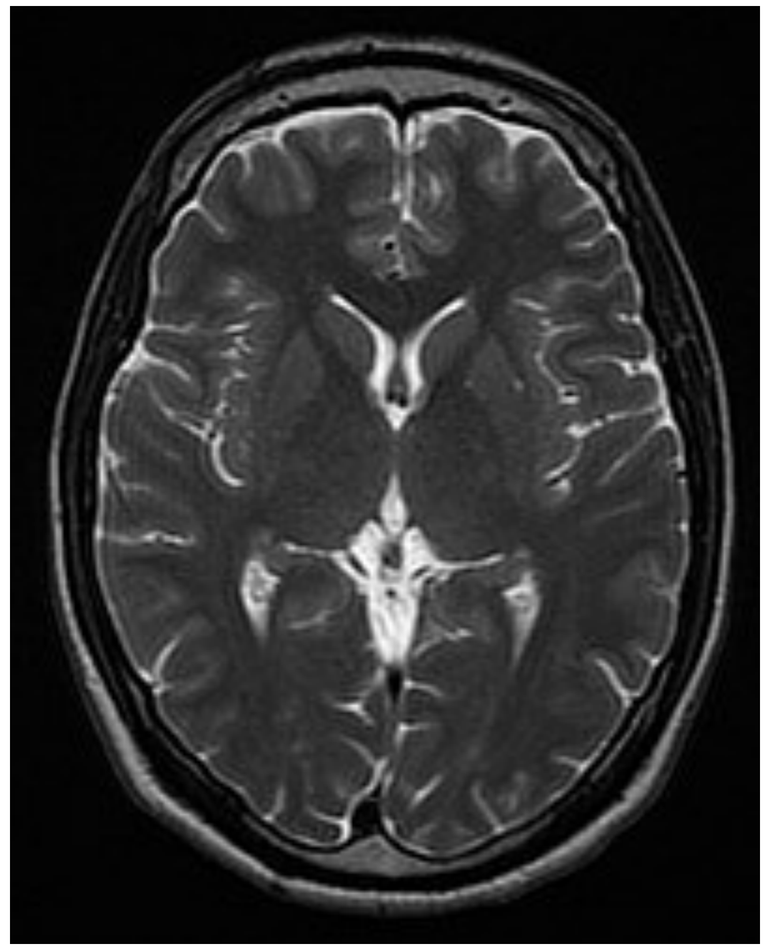
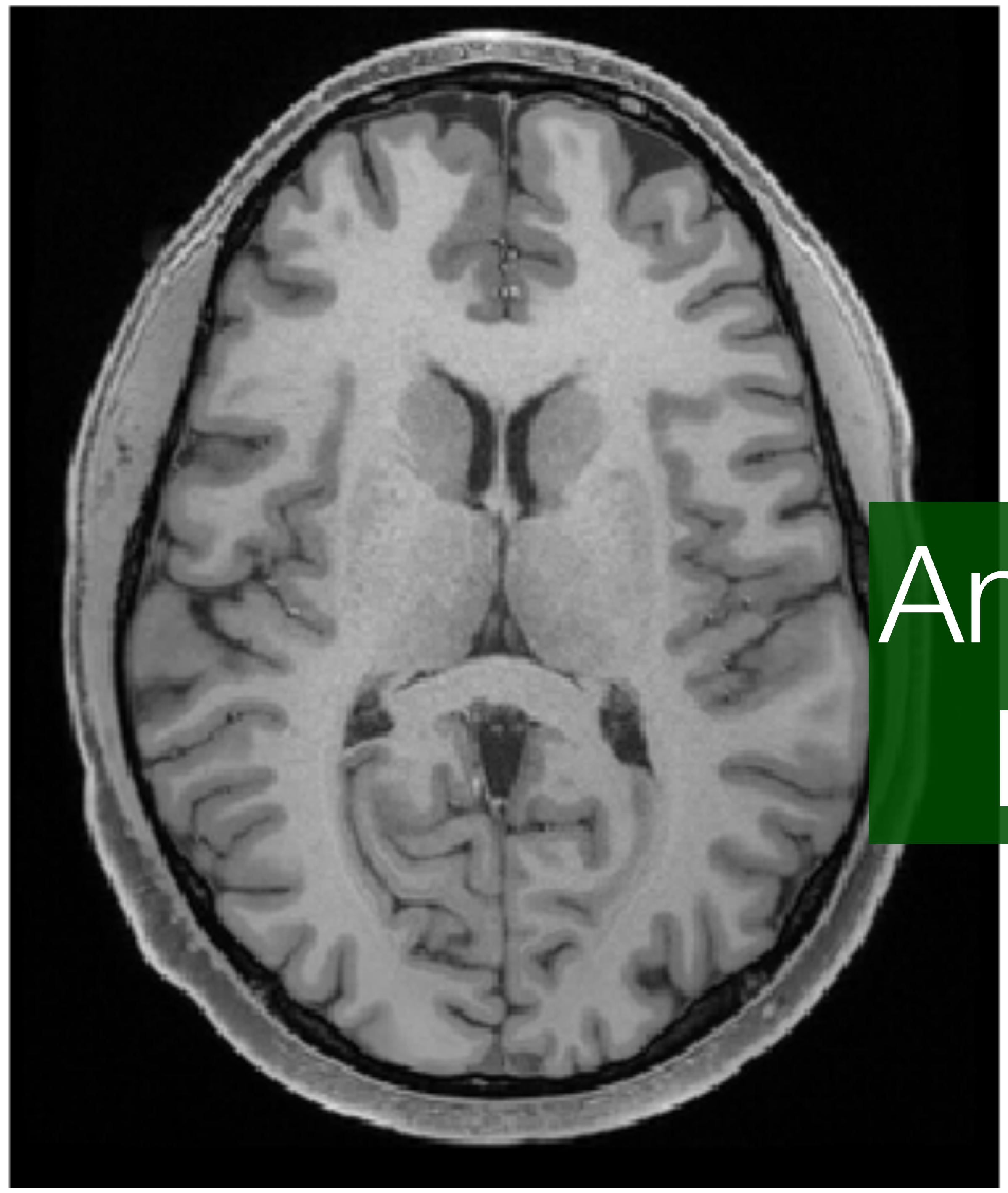
Magnetic Resonance Imaging (MRI)





There are a few kinds of MR Images

T1-weighted Image

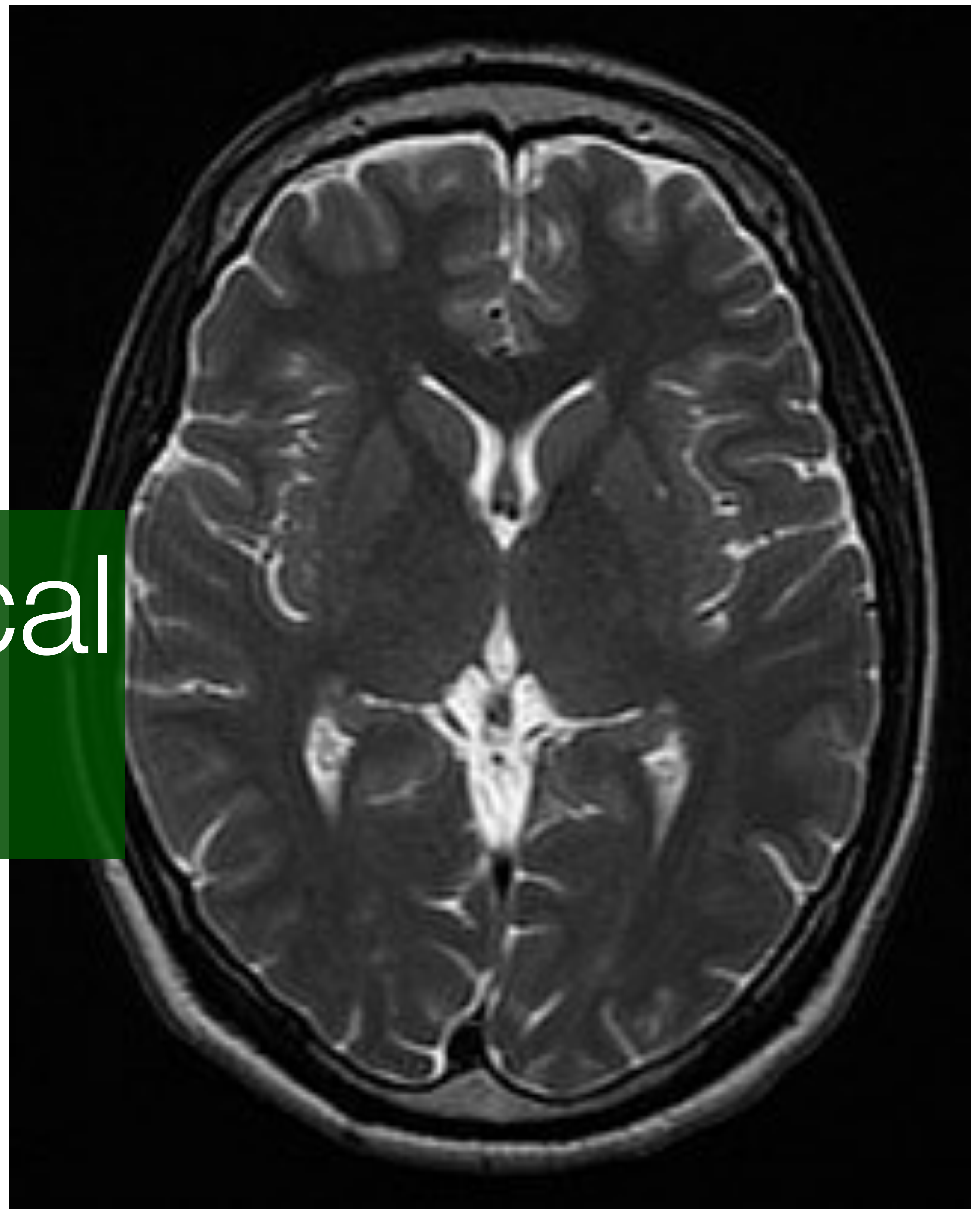


Fat is bright;
water is dark.

0.3 mm³ — 1 mm³

Anatomical
Images

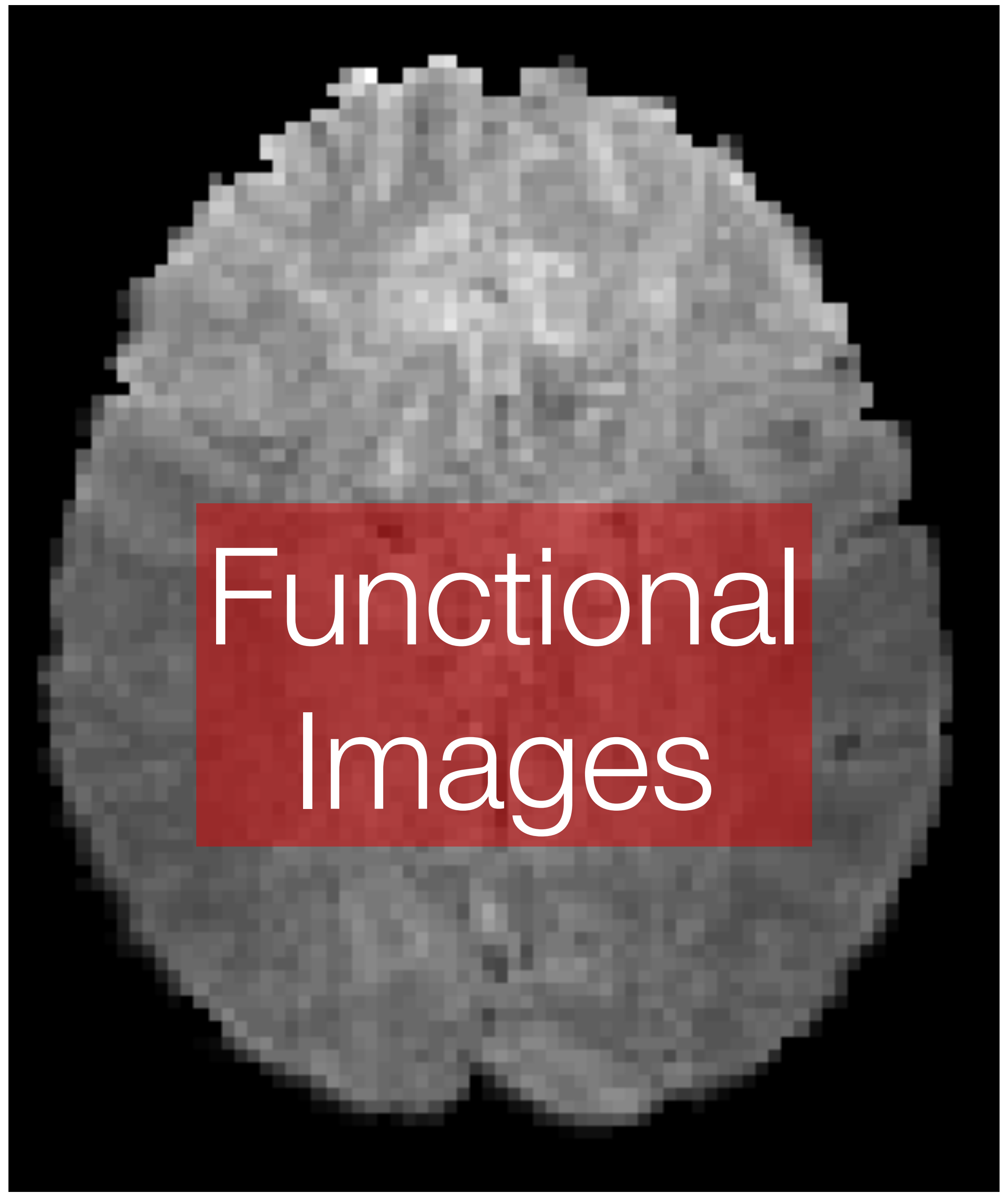
T2-weighted



Water is bright;
fat is dark.

0.3 mm³ — 1 mm³

BOLD



Oxygenated blood is light;
deoxygenated blood is dark

4 mm³ — 20 mm³

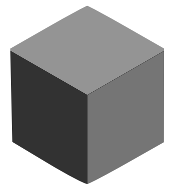
Functional measurements need structural data

- Functional MRI
  - T1-weighted images are used to identify ROIs of functional voxels
  - Motion correction often uses T1-weighted images
- ECoG (Intracranial EEG)
  - T1-weighted images used to determine cortical electrode location
- EEG and MEG
  - Source localization requires T1-weighted image data
- General
  - Visualization is usually clearest on the cortical surface
  - Inter-subject comparison usually requires anatomical data

Structural MRI: T1-weighted images

T1-weighted Image

1 Voxel

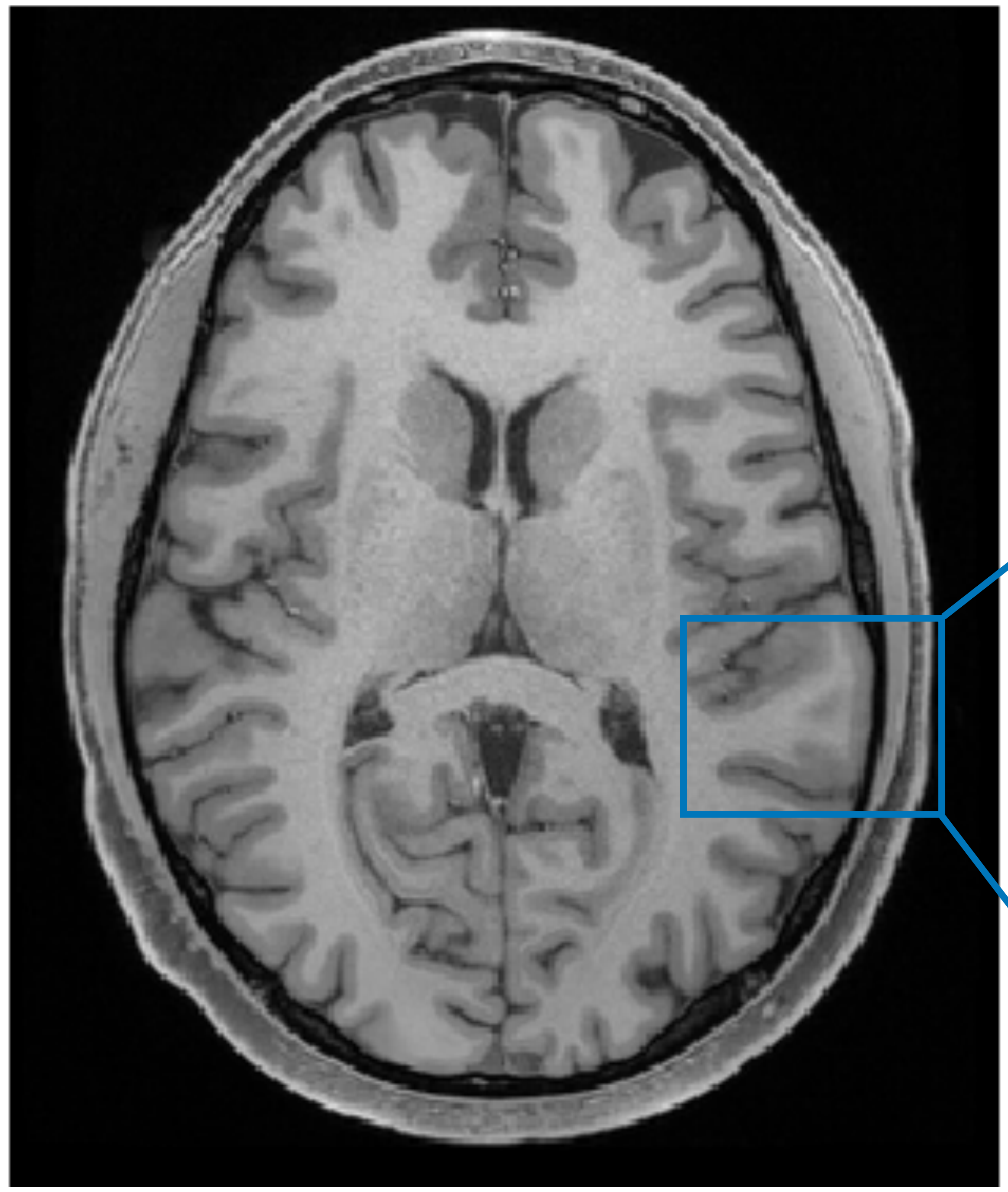


$1 \times 1 \times 1$ mm^3
~100,000 neurons

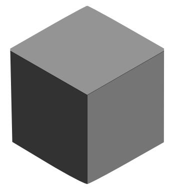
- High resolution
  - $1 \times 1 \times 1$ mm for 3T MRI
  - $0.7 \times 0.7 \times 0.7$ mm for 7T MRI
- Fairly quick to collect (few minutes)
- Gives high quality image of the anatomical structure of the brain
- Often used to complement other neuroimaging measurements due to high spatial resolution (for example in MEG and EEG source localization)

Structural MRI: T1-weighted images

T1-weighted Image



1 Voxel



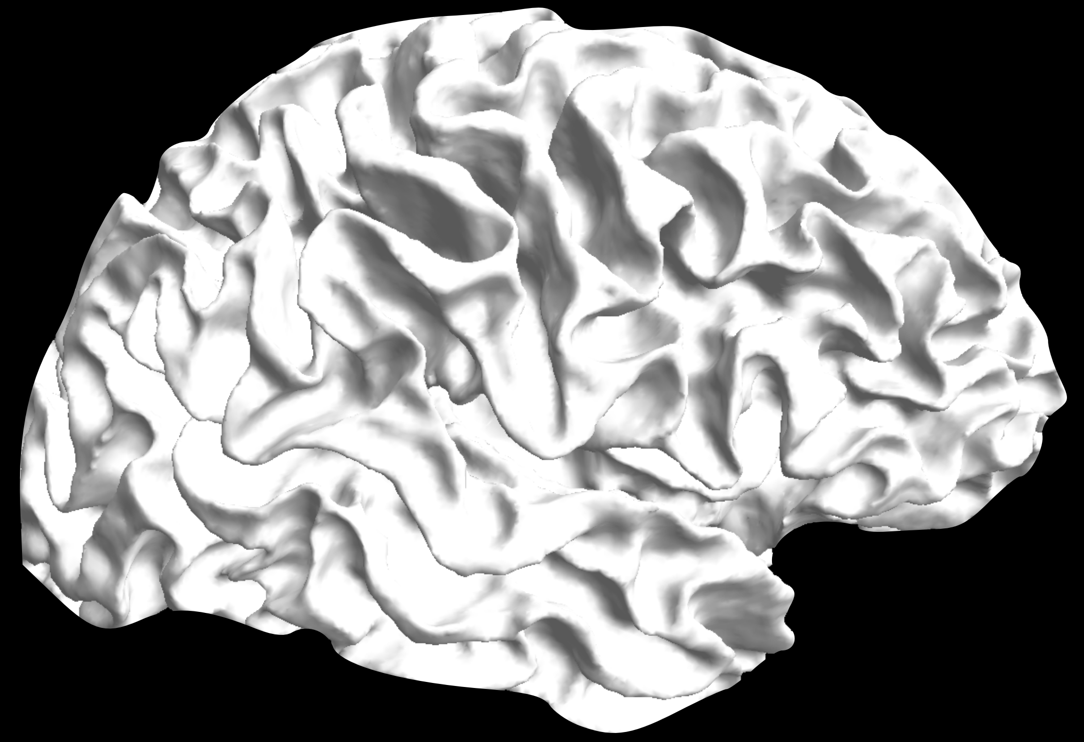
1 x 1 x 1 mm^3

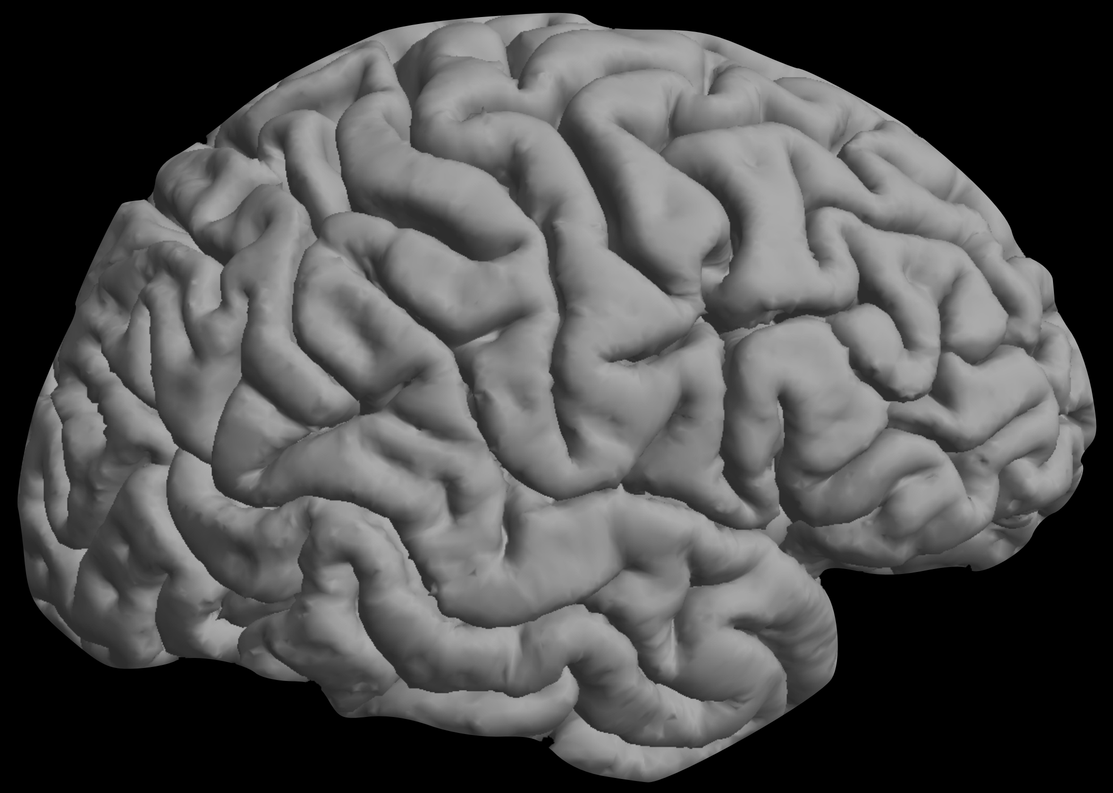
~100,000 neurons

- High resolution
  - 1
  - 0.
- Fai
- Giv ical stru
- Oft neu gh spa and EEG source localization)

Cortex is composed of gray and white matter

White-matter Surface

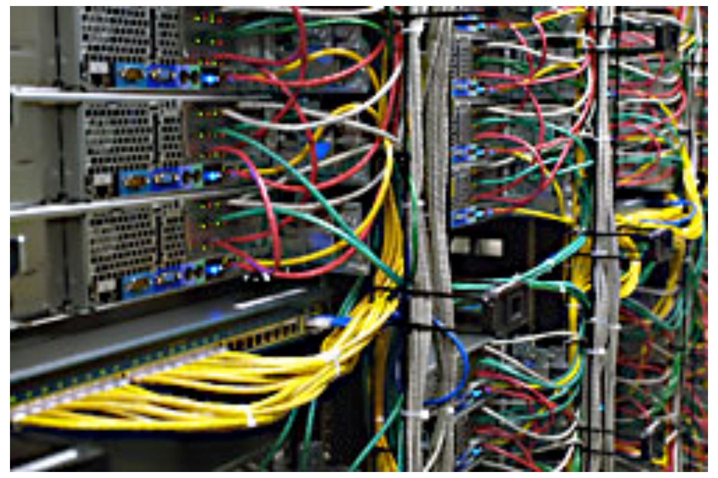


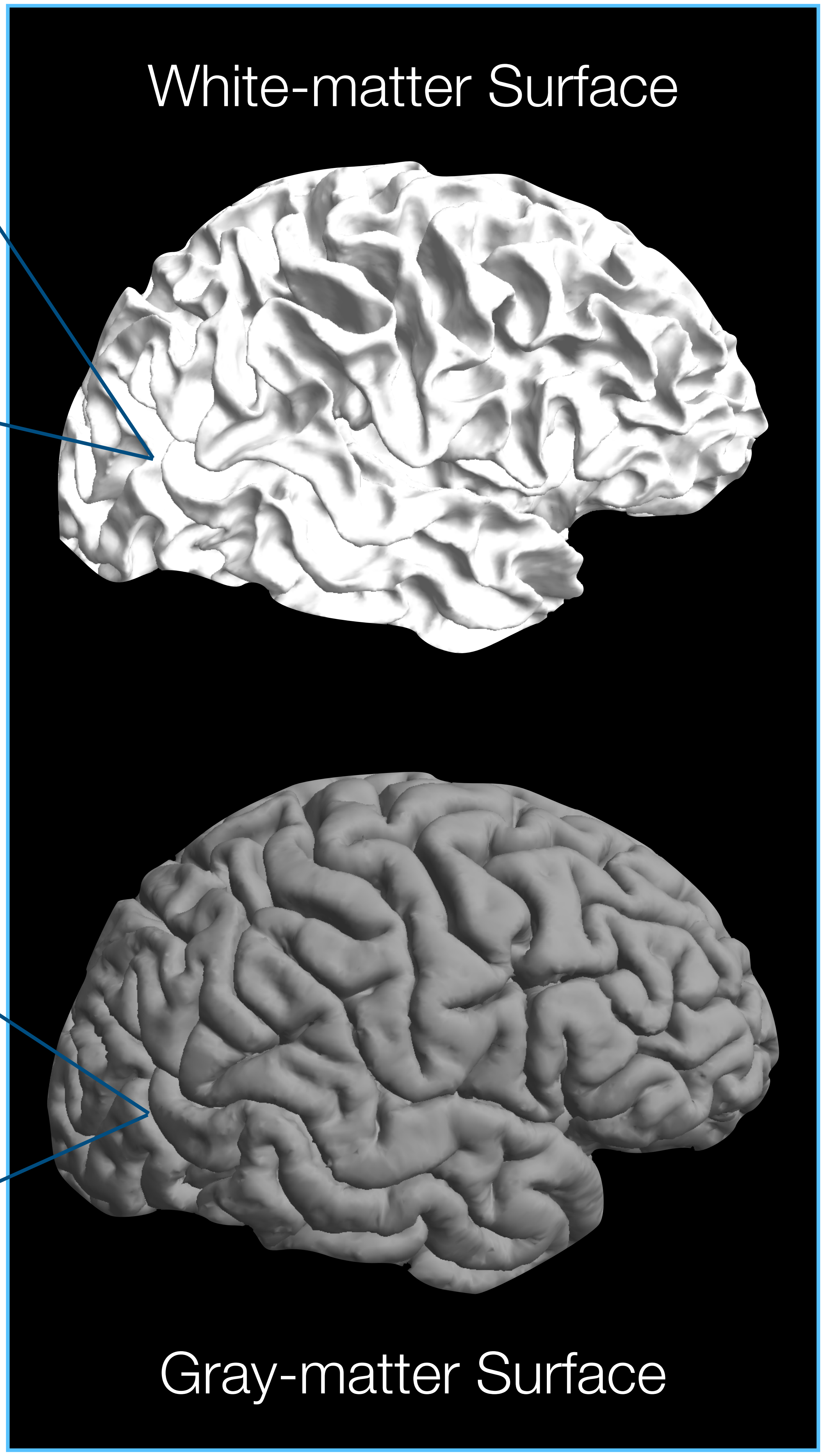


Gray-matter Surface

Cortex is like a computer

White matter:
- long-range connections
- axons / wires





Gray matter:
- processing
- neural cell bodies / CPUs

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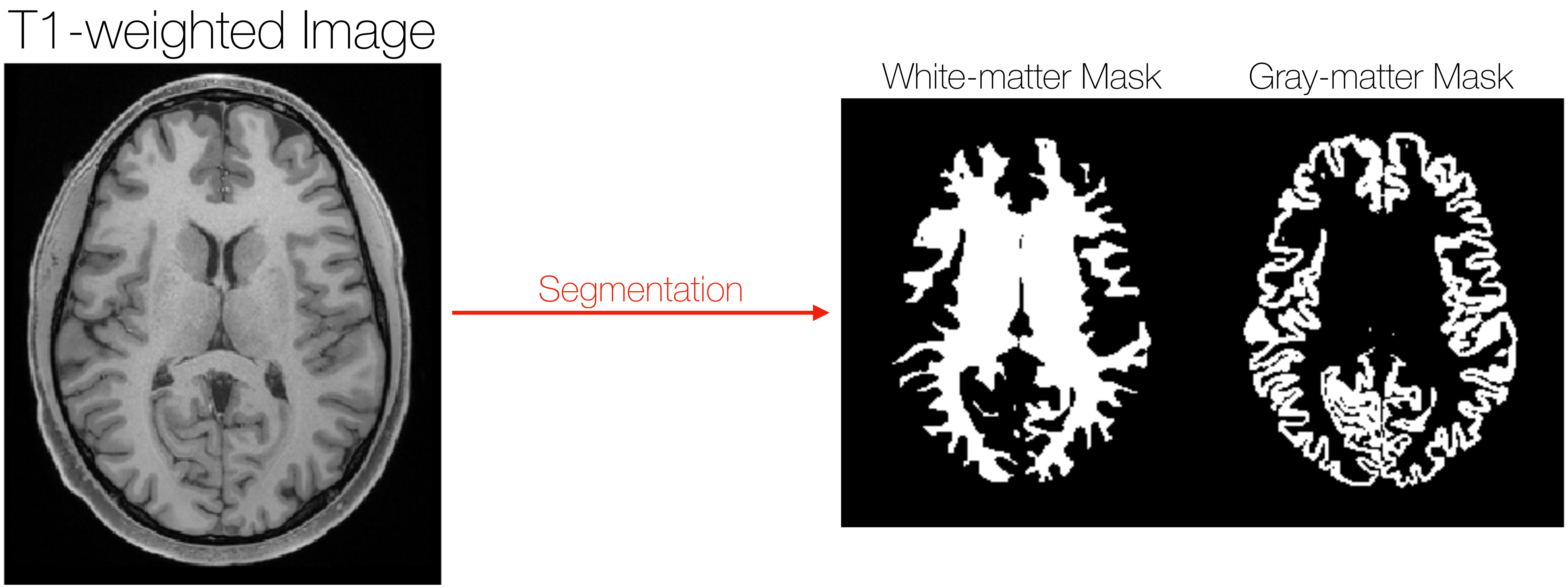
- Intersubject Comparison

MR Images are just 3D images of the brain

Segmentation: label brain voxels by type



Segmentation labels structures in the image volume:

- gray- and white-matter voxels
- hippocampus, amygdala, thalmus, cerebellum, many others

Segmentation of T1-weighted images

- Many tools to process T1w images
  - **FreeSurfer**
    https://surfer.nmr.mgh.harvard.edu/
  - **HCP Pipelines** (FreeSurfer + extras)
    https://www.humanconnectome.org/software/hcp-mr-pipelines
  - **AFNI + SUMA**
    https://afni.nimh.nih.gov/ and https://afni.nimh.nih.gov/Suma
  - **VistaSoft**
    https://github.com/vistalab/vistasoft/wiki
- Most tools allow for hand-correction of automated segmentations

MRI Volume Files

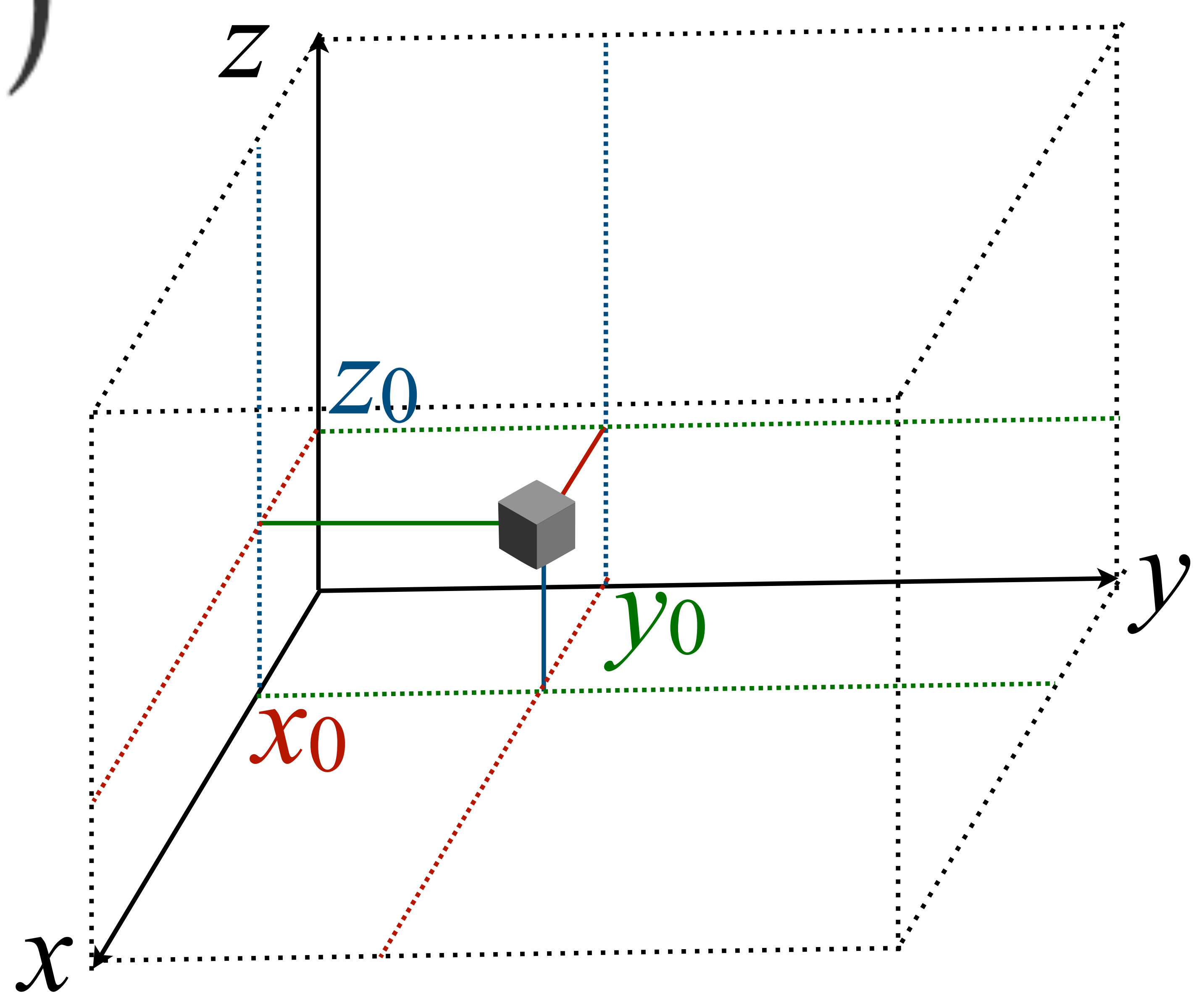
- Contents
  - A 3D or 4D array of voxels (4th dimension is usually time)
  - An affine transformation matrix
  - Additional meta-data (varies)
    - MR scan parameters
    - Units for each dimension
    - Orientation information
- File types
  - NIFTI (*.nii and *.nii.gz) is the *de facto* standard
  - FreeSurfer uses MGH (*.mgh and *.mgz), which is similar
  - Scanners usually produce DICOM files

Affine Transformations

- Usually represented as a 4×4 matrix

$$\begin{pmatrix} a & b & c & t_x \\ d & e & f & t_y \\ g & h & i & t_z \\ 0 & 0 & 0 & 1 \end{pmatrix} \cdot \begin{pmatrix} x_0 \\ y_0 \\ z_0 \\ 1 \end{pmatrix} = \begin{pmatrix} x \\ y \\ z \\ 1 \end{pmatrix}$$

- Stores volumetric…
  - Rotation
  - Resizing
  - Reflection
  - Translation
  - Any other linear transform (*e.g.*, shearing)



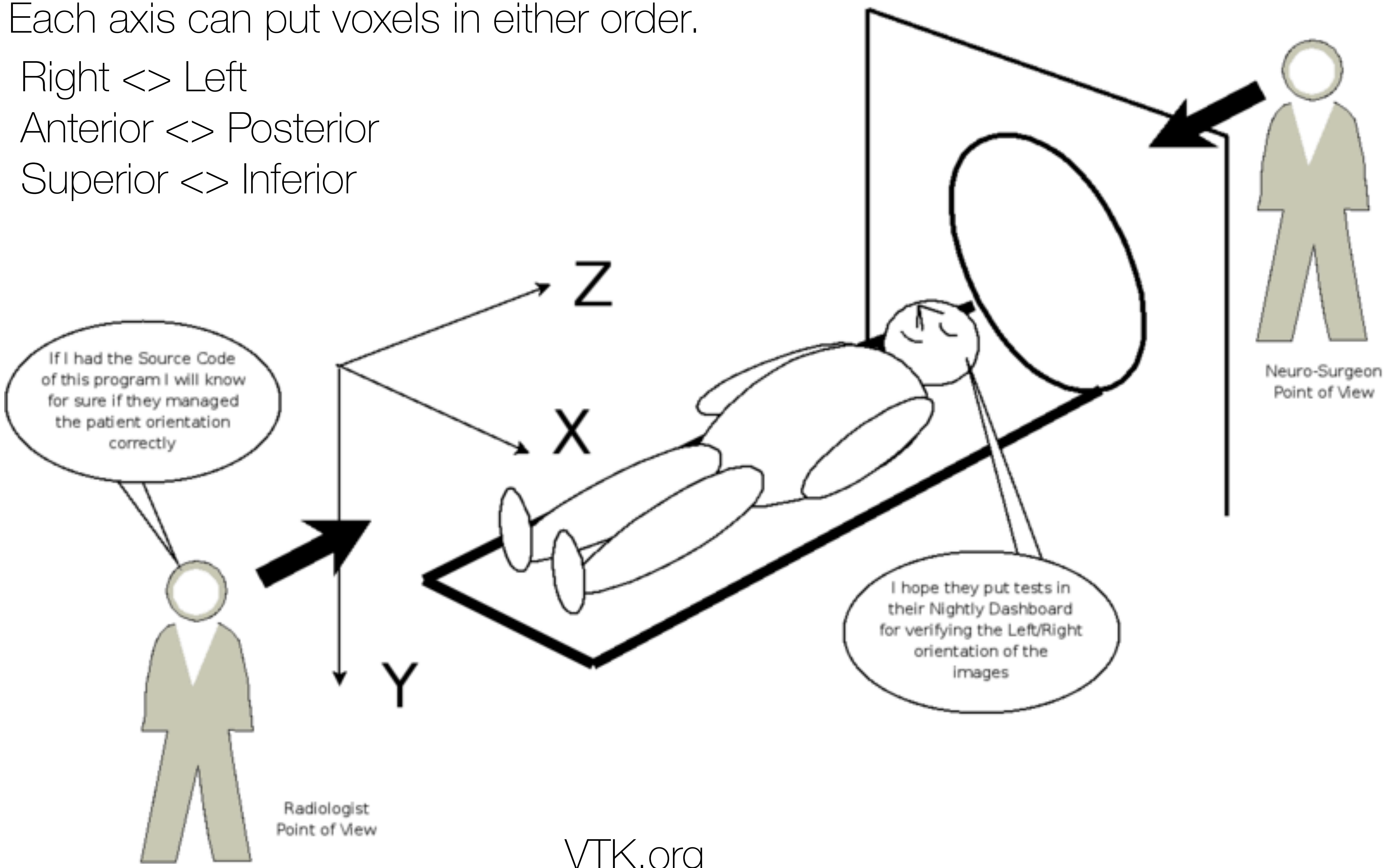
Affine Transformations

- Transforms each voxel using (*row*, *column*, *slice*) as (x_0, y_0, z_0)
- Usually, the affine is used for one of three things:
  - To align the voxels of an image with those of another image (*e.g.*, multiple scans of the same subject)
  - To align the voxels of an image with an anatomical template (*e.g.*, MNI-space)
  - To align the voxels of an image with a model of the cortical surface (e.g., FreeSurfer's `tkr_VOX2RAS` matrix)

Orientation Information

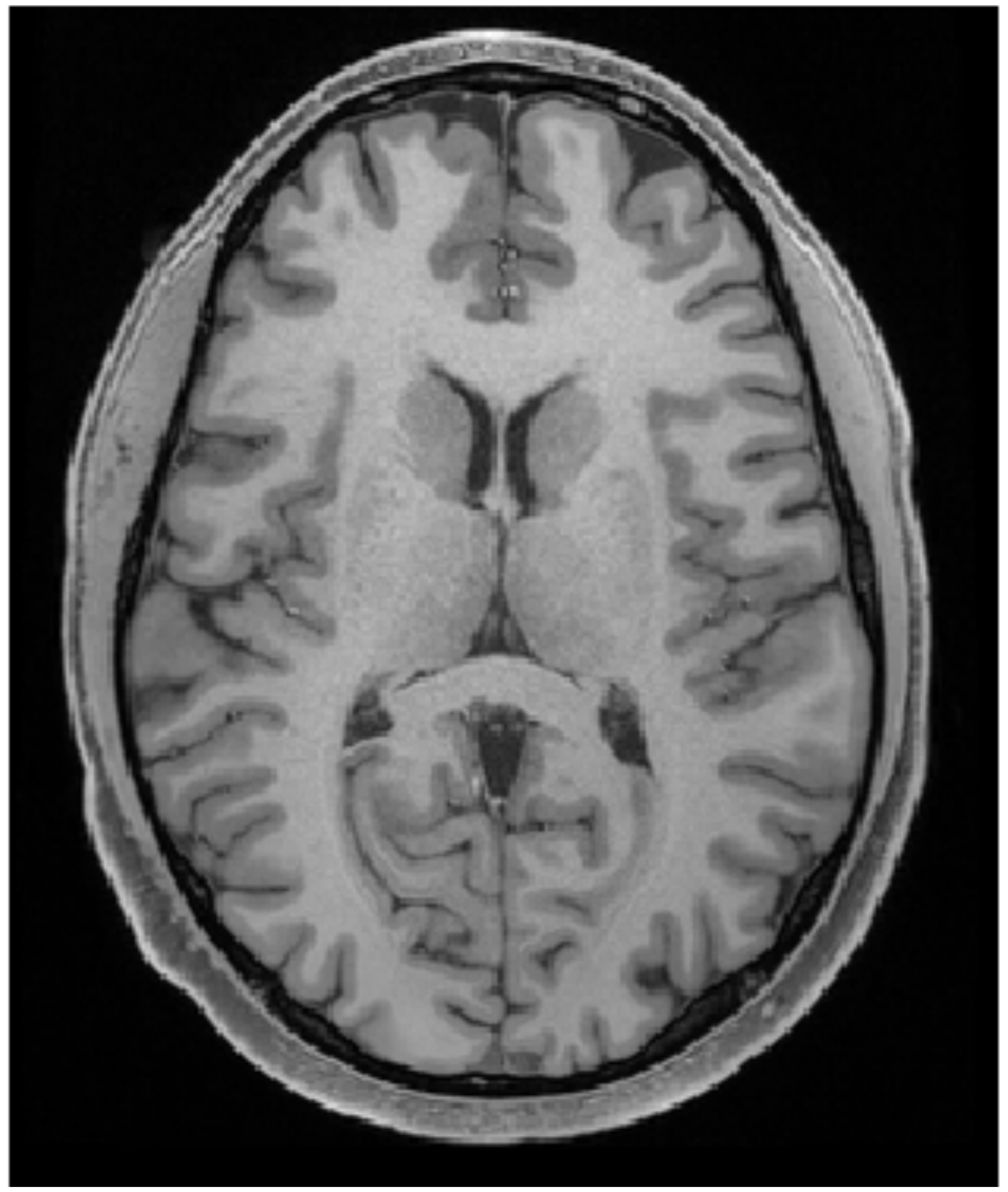
There is more than one way to store 3D Images!
Each axis can put voxels in either order.

Right <> Left
Anterior <> Posterior
Superior <> Inferior



VTK.org

T1-weighted Image

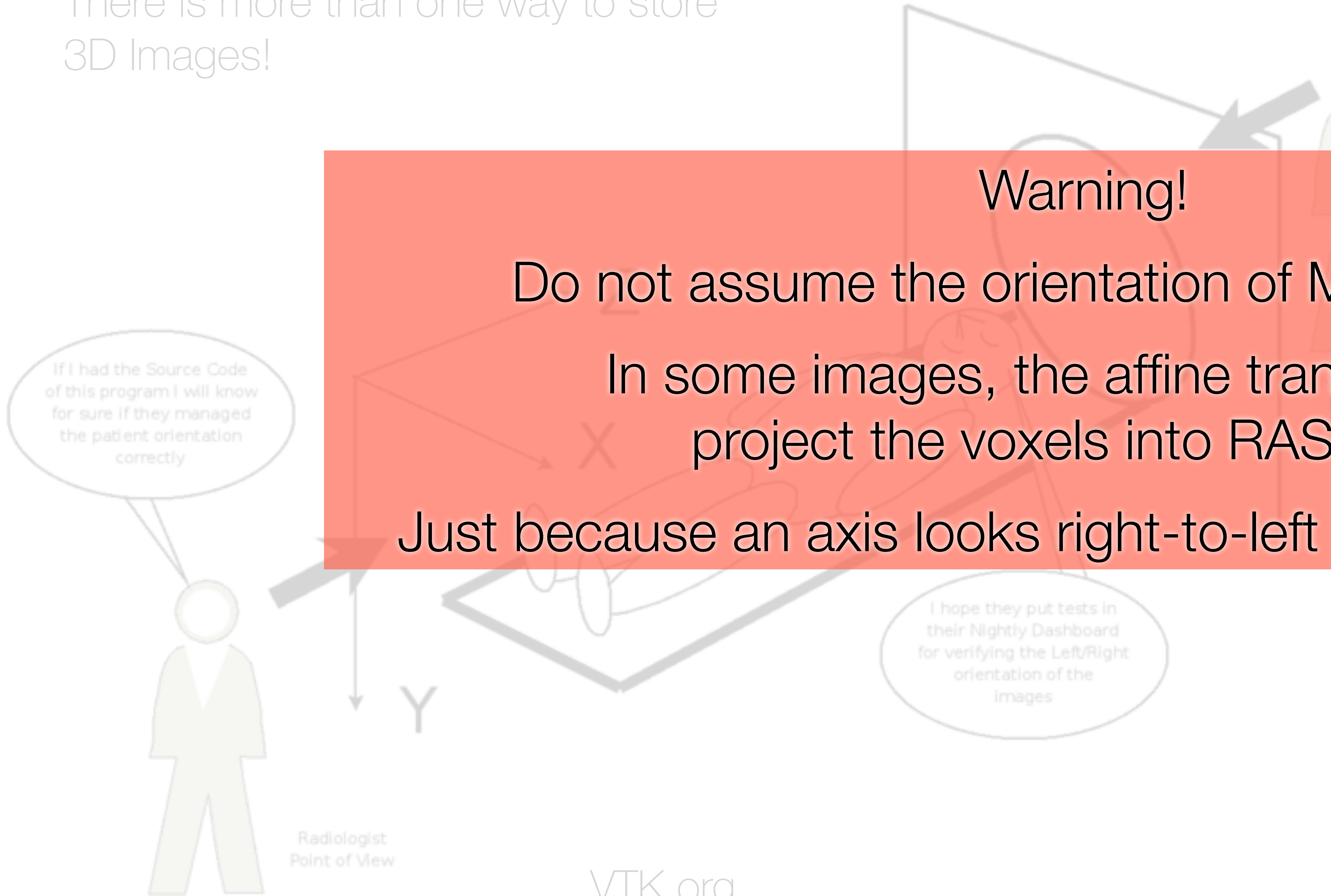


RAS
+x is **R**ight
+y is **A**nterior
+z is **S**uperior

LIA
+x is **L**eft
+y is **I**nferior
+z is **A**nterior

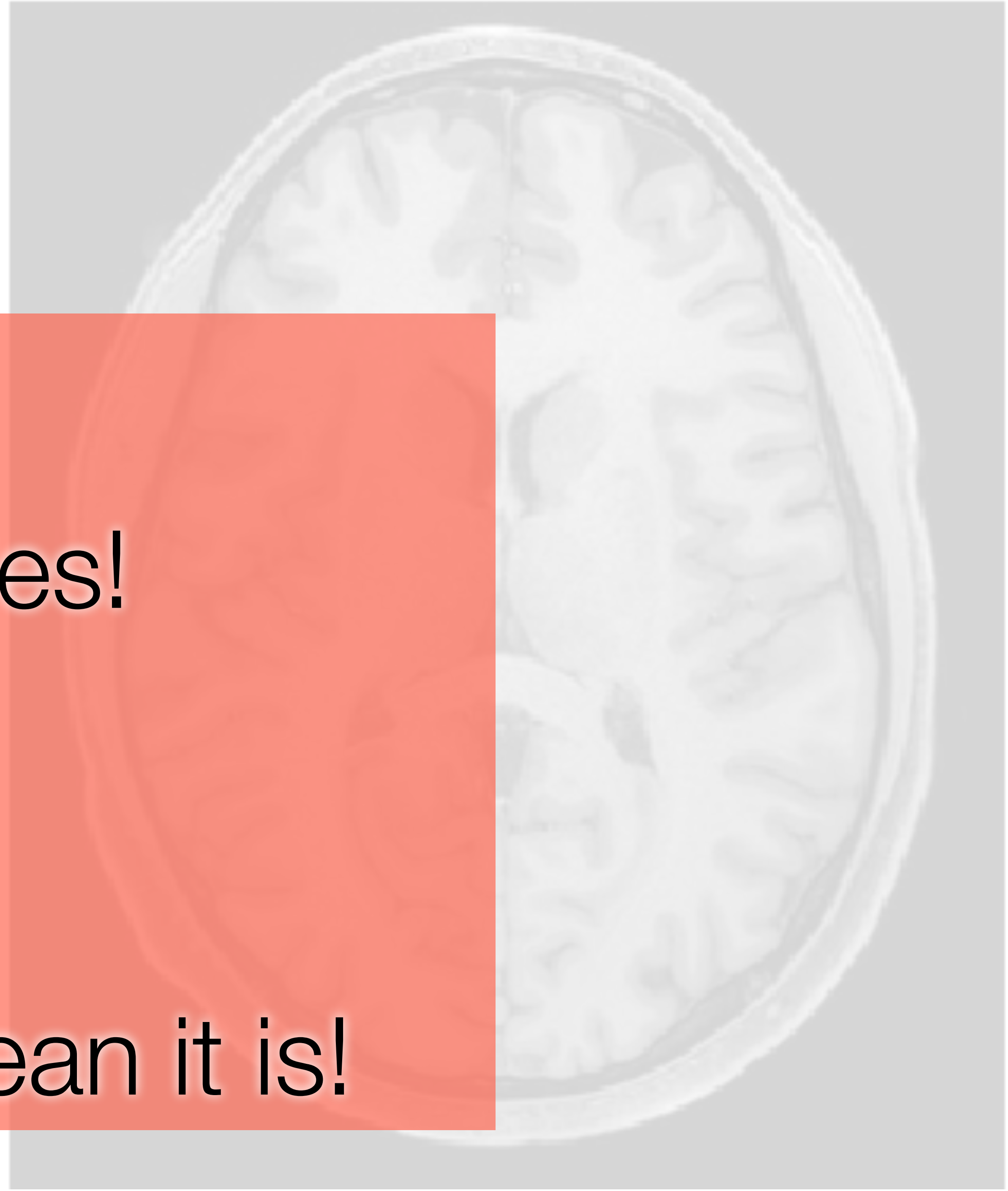
Orientation Information

There is more than one way to store 3D Images!



VTK.org

T1-weighted Image



Warning!

Do not assume the orientation of MRImage files!

In some images, the affine transform will project the voxels into RAS axes.

Just because an axis looks right-to-left doesn't mean it is!

RAS
- +x is **R**ight
- +y is **A**nterior
- +z is **S**uperior

LIA
- +x is **L**eft
- +y is **I**nferior
- +z is **A**nterior

Anatomical MRImage Processing: FreeSurfer

- https://surfer.nmr.mgh.harvard.edu/
- Open Source / Public
  (but you have to register with them)
- Performs a variety of anatomical processing steps and produces a variety of data describing the subject's anatomy:
  - various normalizations and operations (e.g., skull-stripping) are applied to the image
  - white and gray matter segmentation is performed and outputs the ribbon: LH/RH white-/gray-matter voxel labels
- To run FreeSurfer on a subejct, use the recon-all command; documentation here: https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all

Anatomical MRImage Processing: FreeSurfer

- https://surfer.nmr.mgh.harvard.edu/
- To run FreeSurfer on a subejct, use the `recon-all` command; documentation here: https://surfer.nmr.mgh.harvard.edu/fswiki/recon-all
- Running FreeSurfer on a subject creates a directory of data-files for that subject in the "FreeSurfer Subjects Directory" which is always stored in the environment variable `SUBJECTS_DIR`
- You can edit the `SUBJECTS_DIR` variable in your shell's initialization files to change where FreeSurfer stores these data
- A more technical description of what's actually happening when you run recon-all can be found here: https://surfer.nmr.mgh.harvard.edu/fswiki/ReconAllDevTable

Anatomical Processing: FreeSurfer

A typical subject's directory:

Ordinary Subjects
(bert is a builtin example subject)

```
> cd "$SUBJECTS_DIR"
> ls
S1202              bert               cvs_avg35
fsaverage          fsaverage4         fsaverage6
lh.EC_average      S11047             V1_average
fsaverage3         fsaverage5         fsaverage_sym
rh.EC_average
>
```

fsaverage is an atlas subject made from the average of many subjects' brains

The fsaverageX are lower resolution versions of the fsaverage

fsaverage_sym is an atlas subject used to compare LH and RH

Anatomical Processing: FreeSurfer

A typical subject's directory:

```
> cd "$SUBJECTS_DIR"
> ls
S1202                bert                 cvs_avg35
fsaverage            fsaverage4           fsaverage6
lh.EC_average        S11047               V1_average
fsaverage3           fsaverage5           fsaverage_sym
rh.EC_average
> cd bert
> ls
label    mri      scripts stats    surf
tmp      touch    trash   xhemi
>
```

The label directory contains Brodmann labels and various parcellations of the cortex.

The mri directory contains images such as normalized T1w images and the ribbon.

The xhemi directory stores a LH/RH inverted subject for use with the fsaverage_sym atlas subejct.

The surf directory contains files that specify the surface geometry of cortex (lh.white, rh.pial) and various anatomical properties (curvature, thickness); also contains surface-based anatomical alignments to the fsaverage atlas subject.

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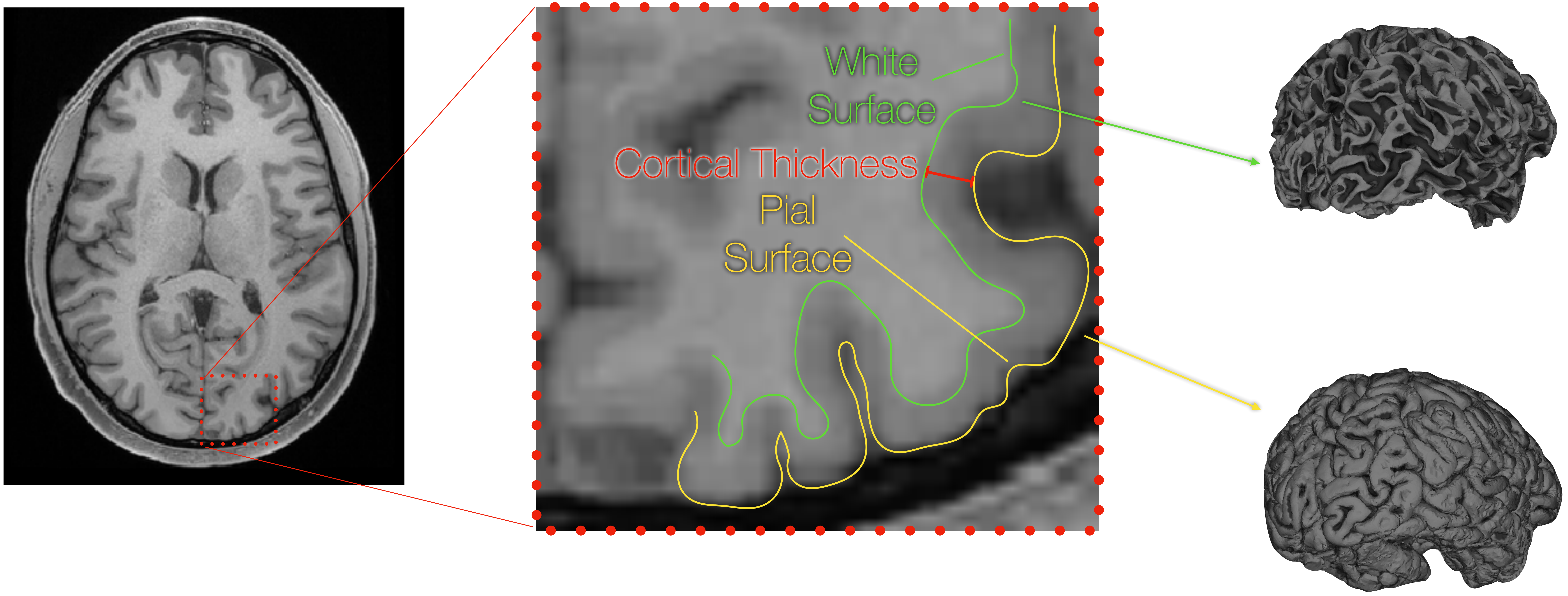
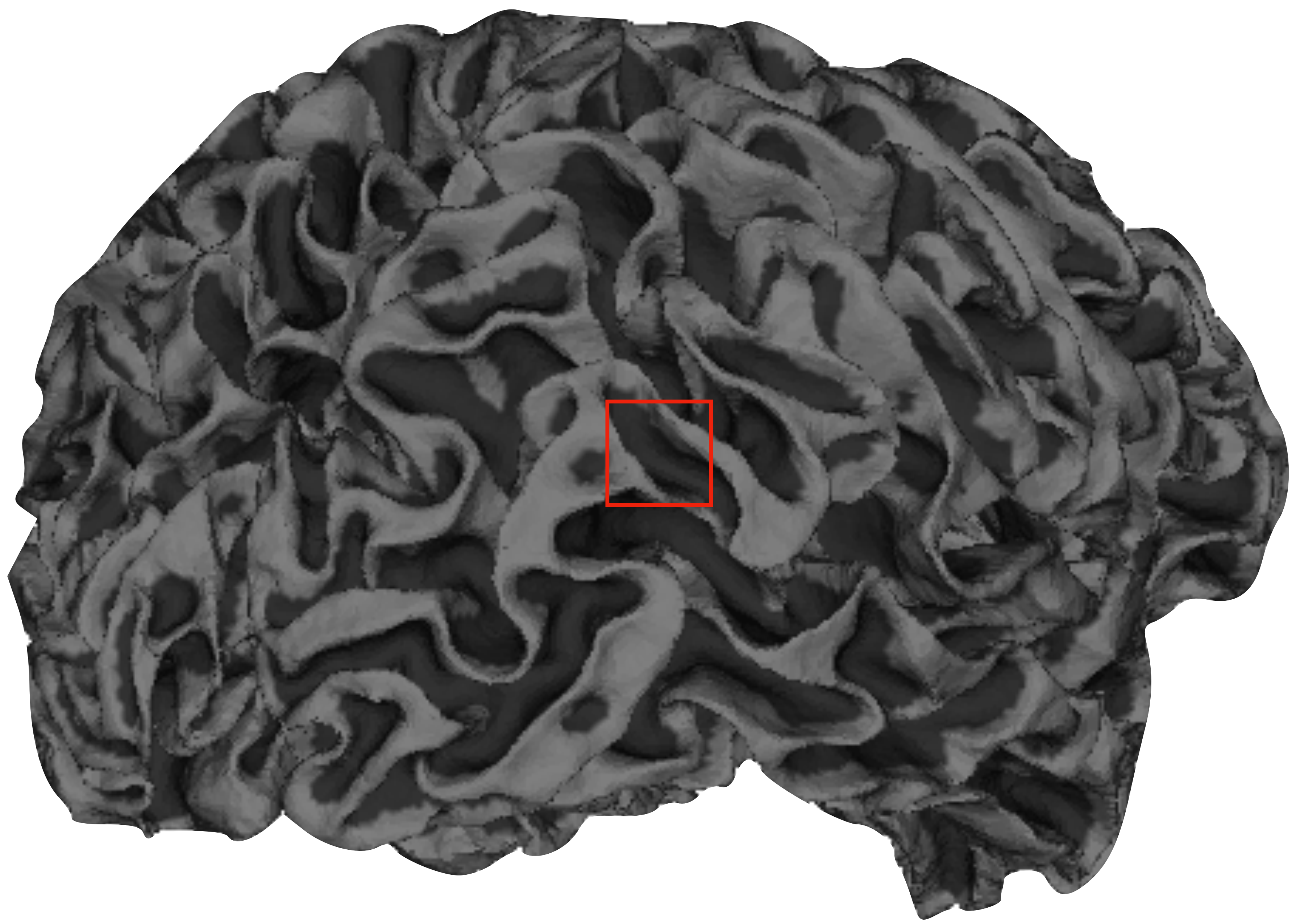
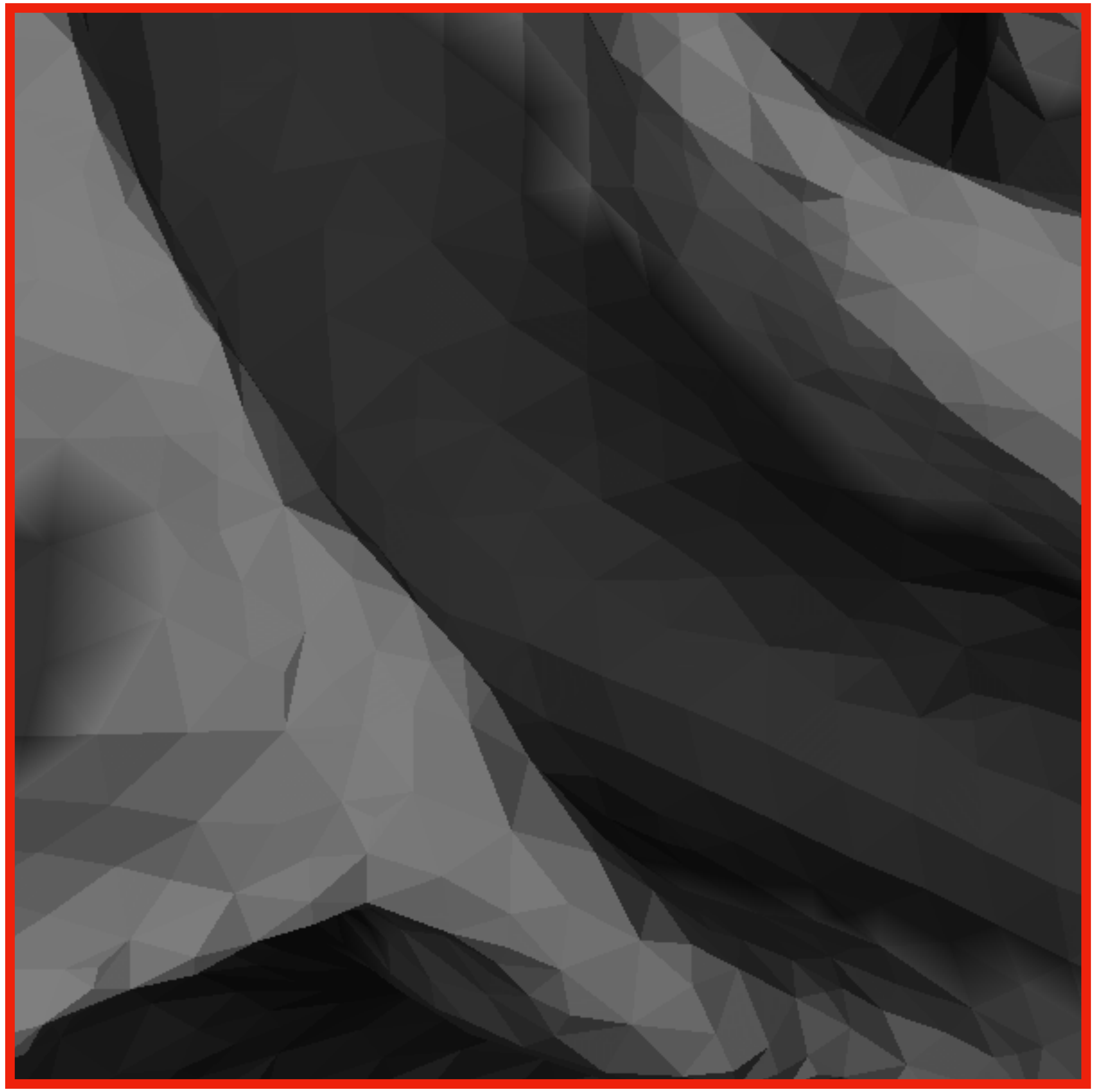
Anatomical Segments can be Modeled



Tesselation: constructing a model of the surface

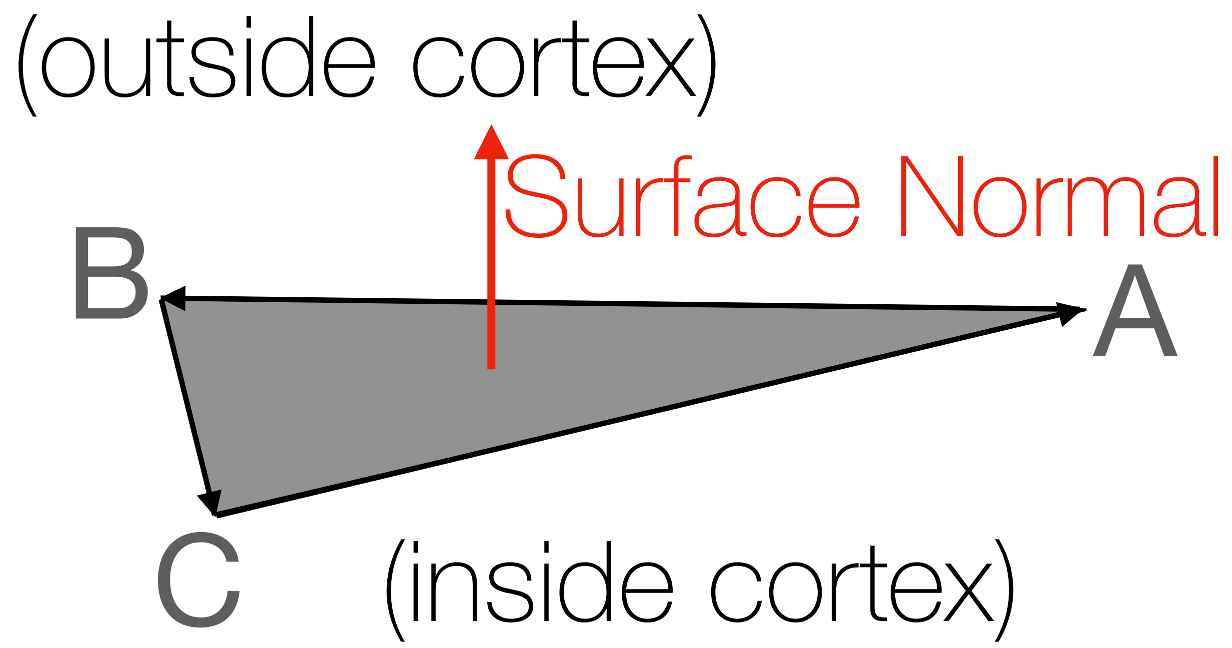


Surfaces are represented as triangle meshes



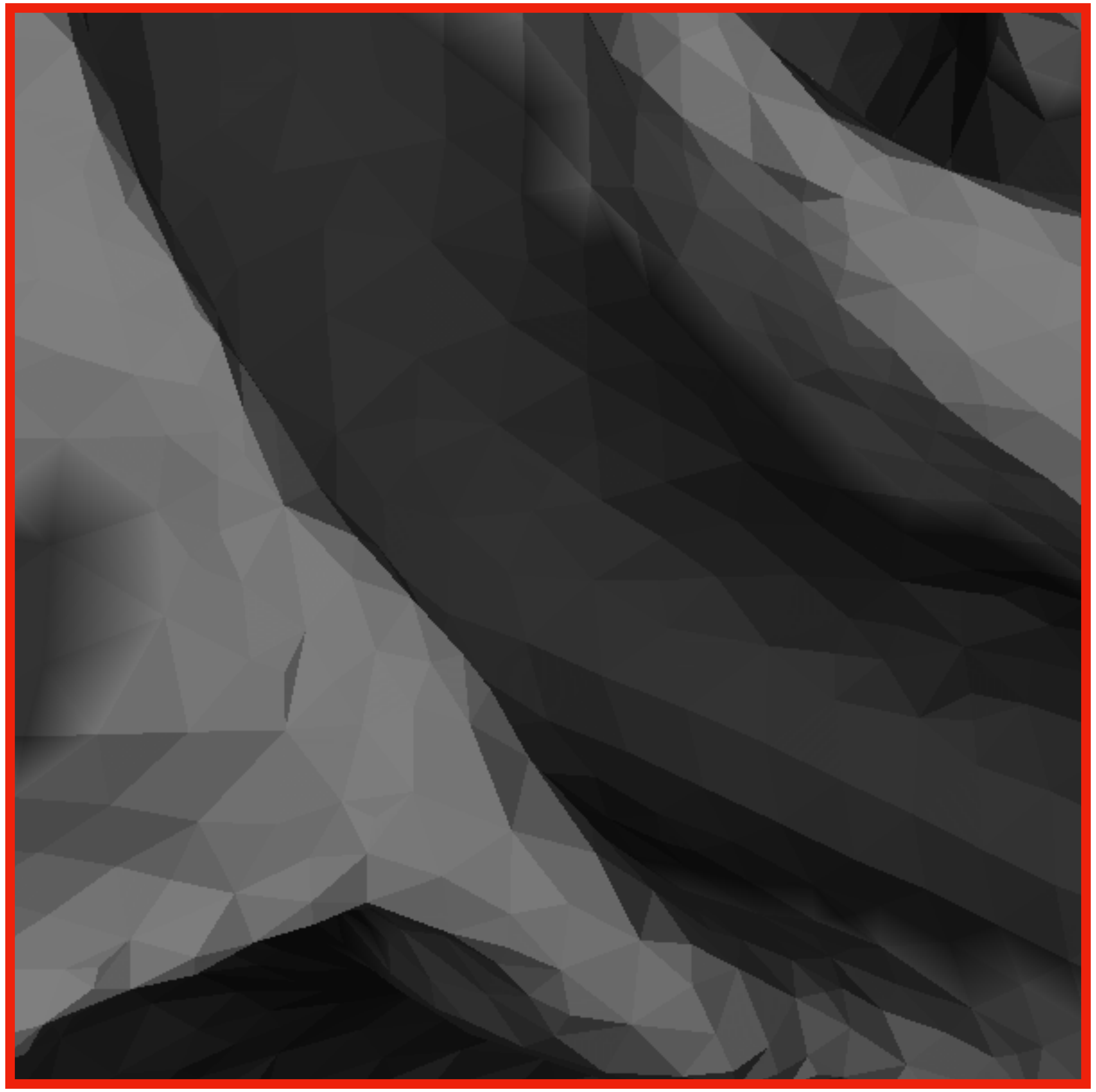
Tesselation: constructing a model of the surface

- Triangles are all specified in the counter-clockwise direction

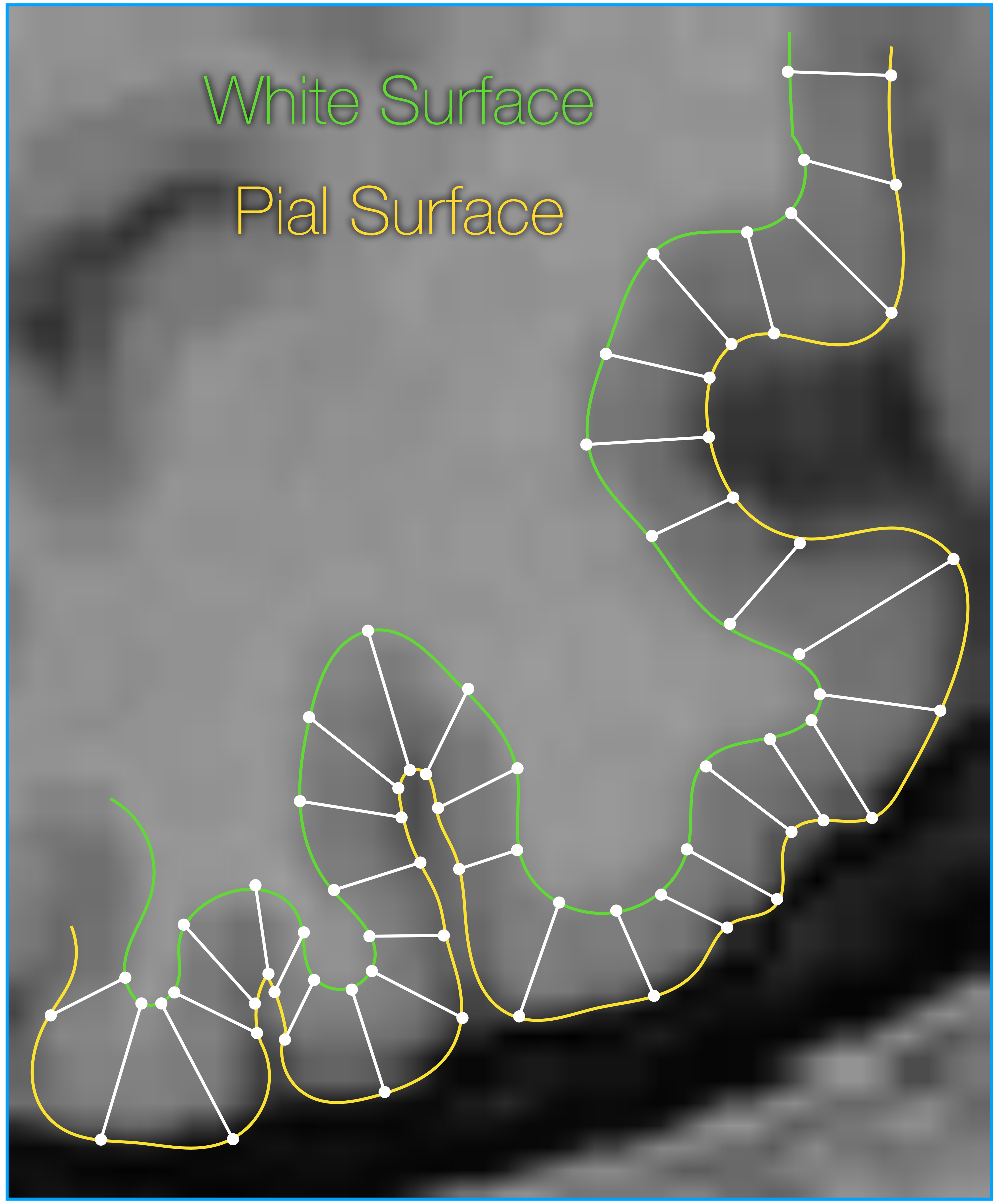


- There is no coherent ordering to the vertices on the surface
- There is no coherent ordering to the triangles on the surface

Surfaces are represented as triangle meshes

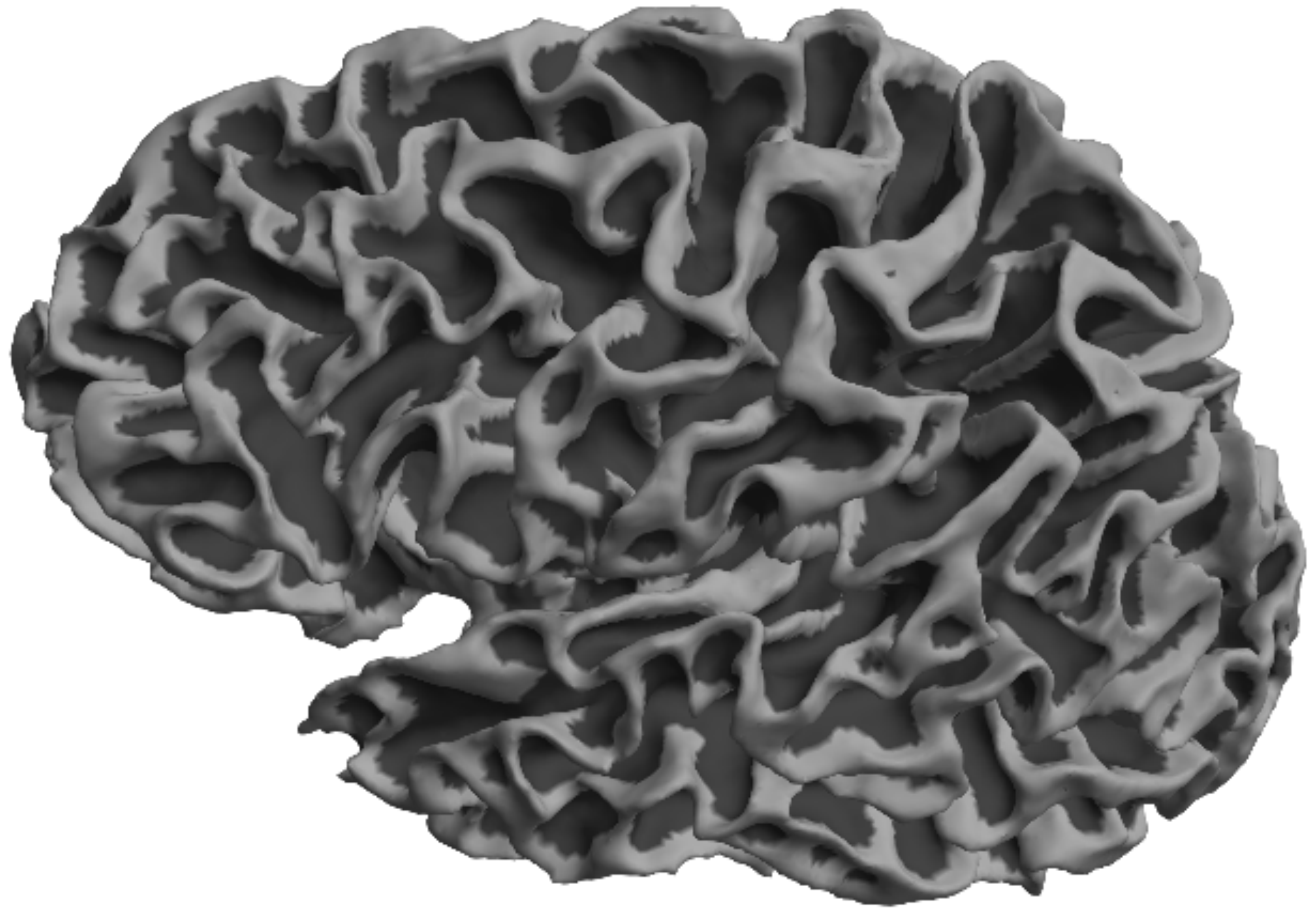


Hemispheres are different, surfaces are similar

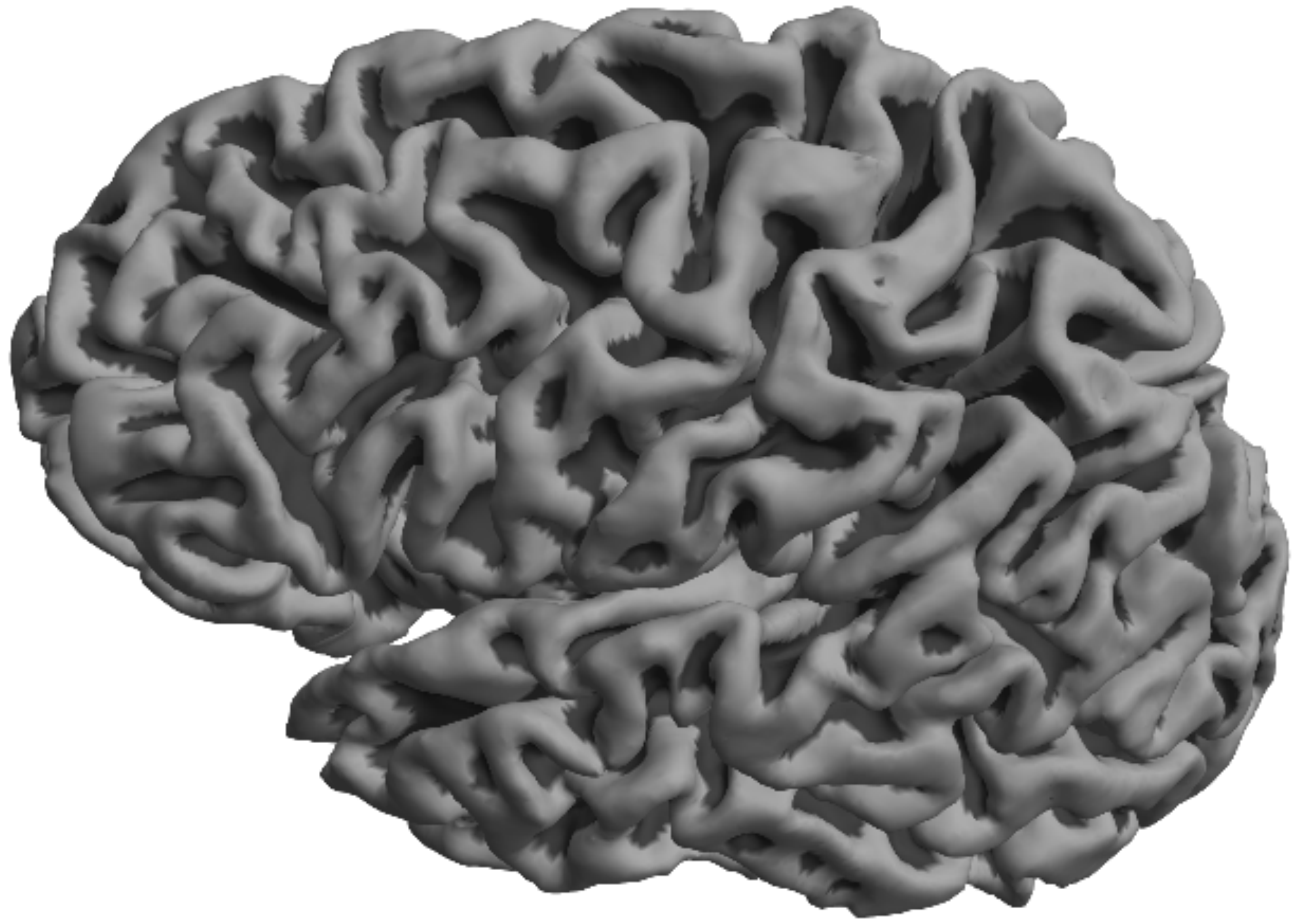


- Hemispheres are usually split at the corpus callosum: one triangle-mesh each
- For each hemisphere, many surfaces
- All surfaces of one hemisphere have the same number of vertices—in fact they are the same vertices
- This means that vertices are closer together in the *sulci* of the pial surface and the *gyri* of the white surface

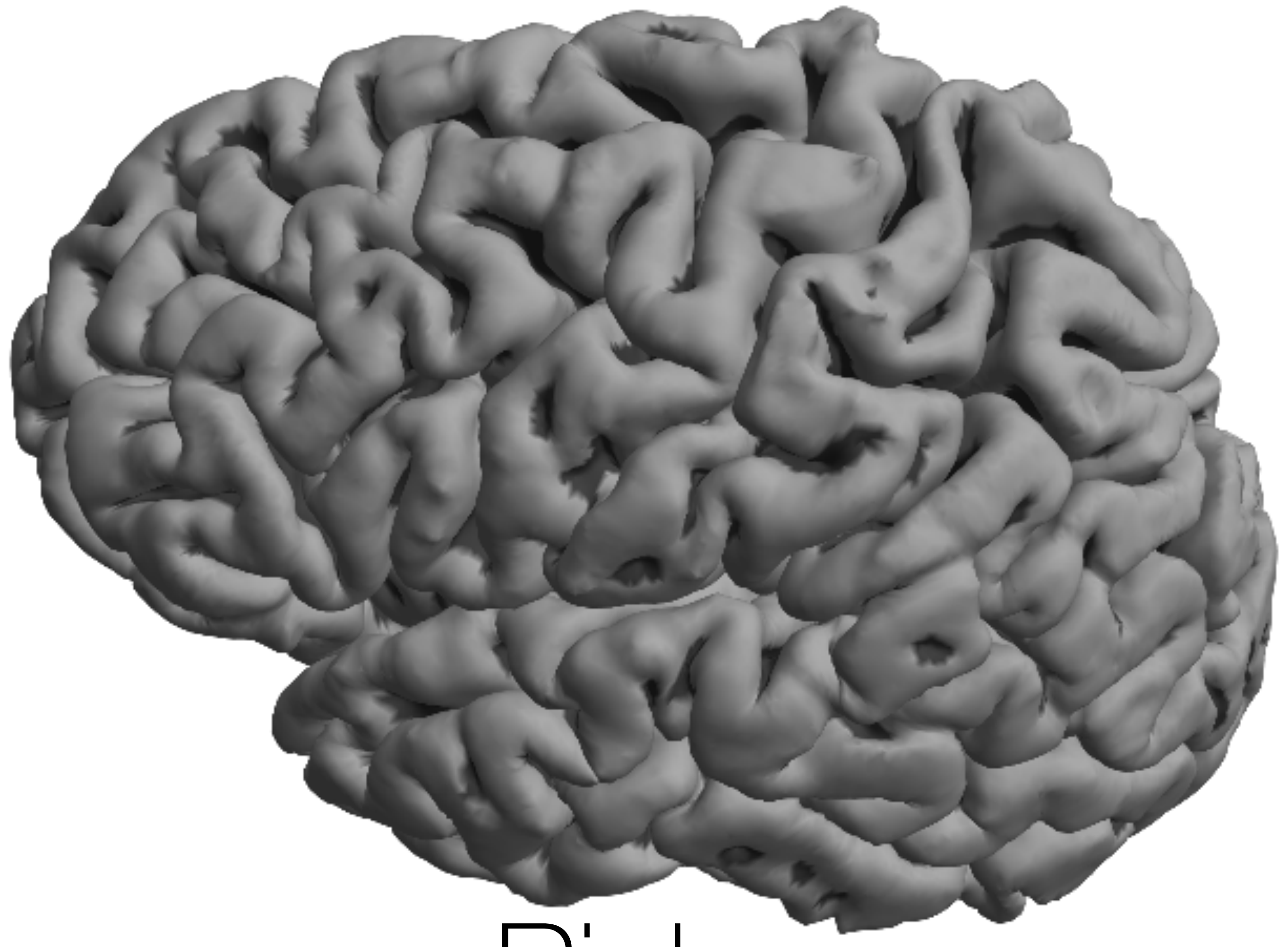
There are many surfaces for each hemisphere



White



Mid-gray



Pial

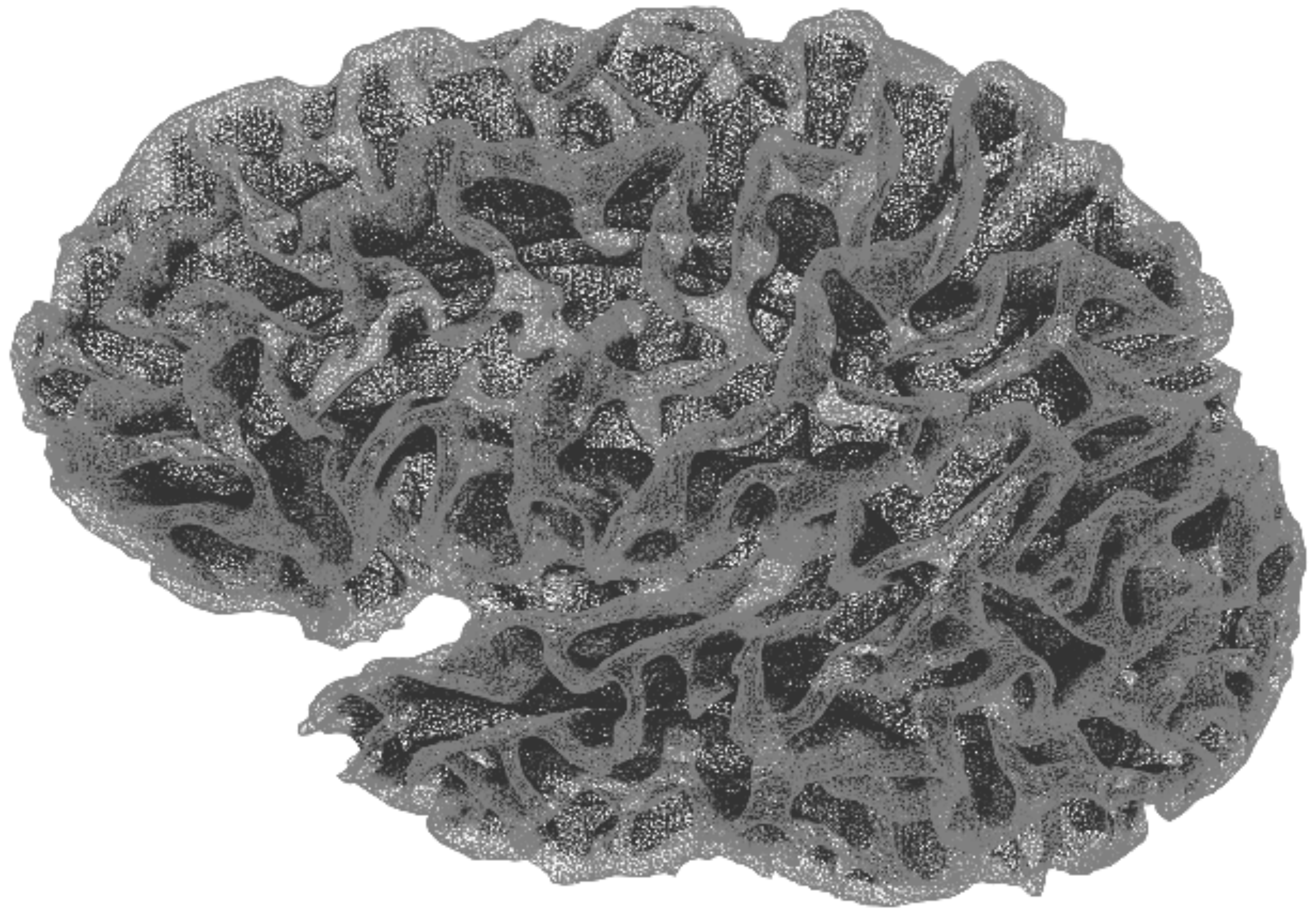
Inflated

Spherical

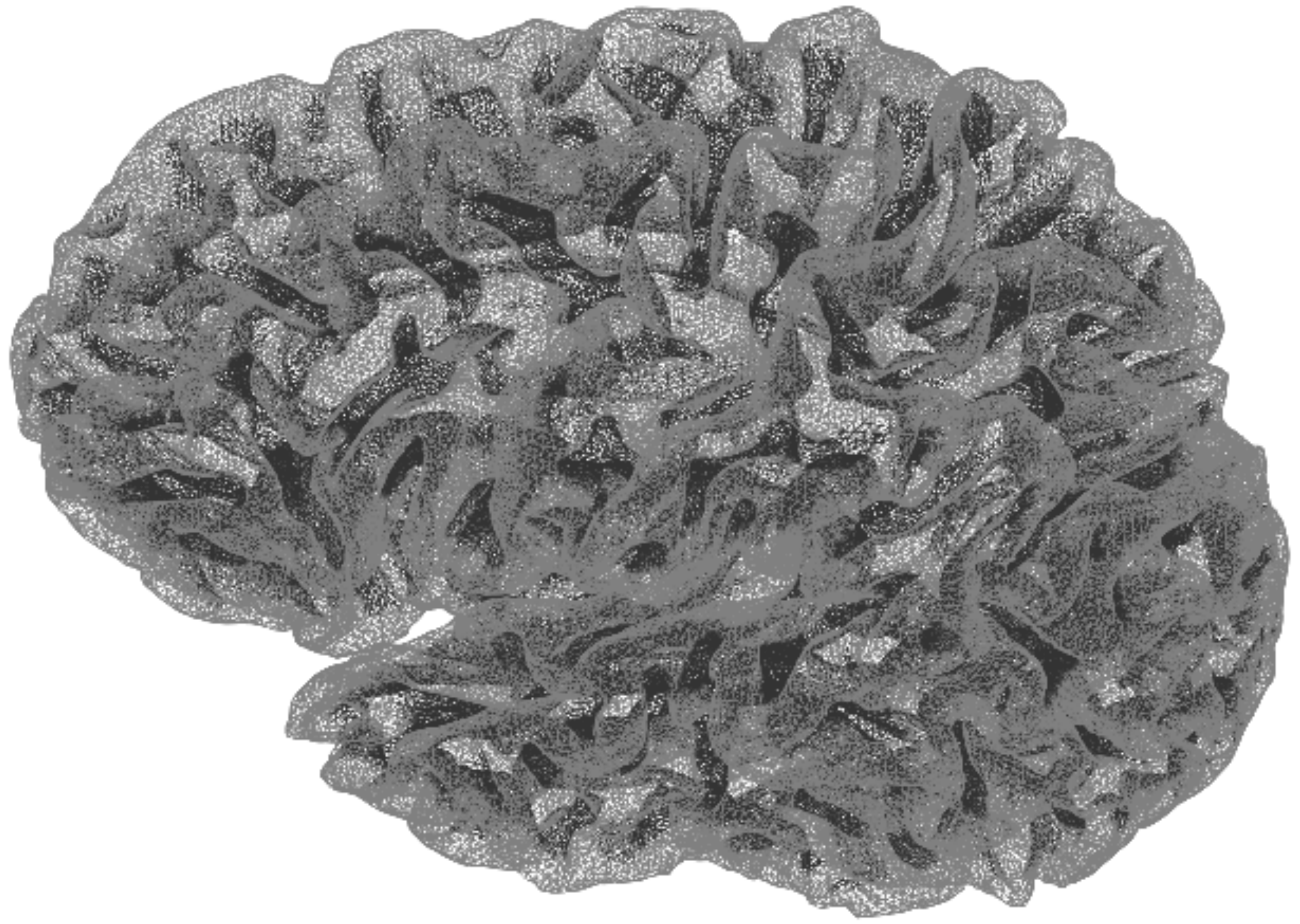
The vertices are equivalent for all surfaces of one hemisphere.

FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

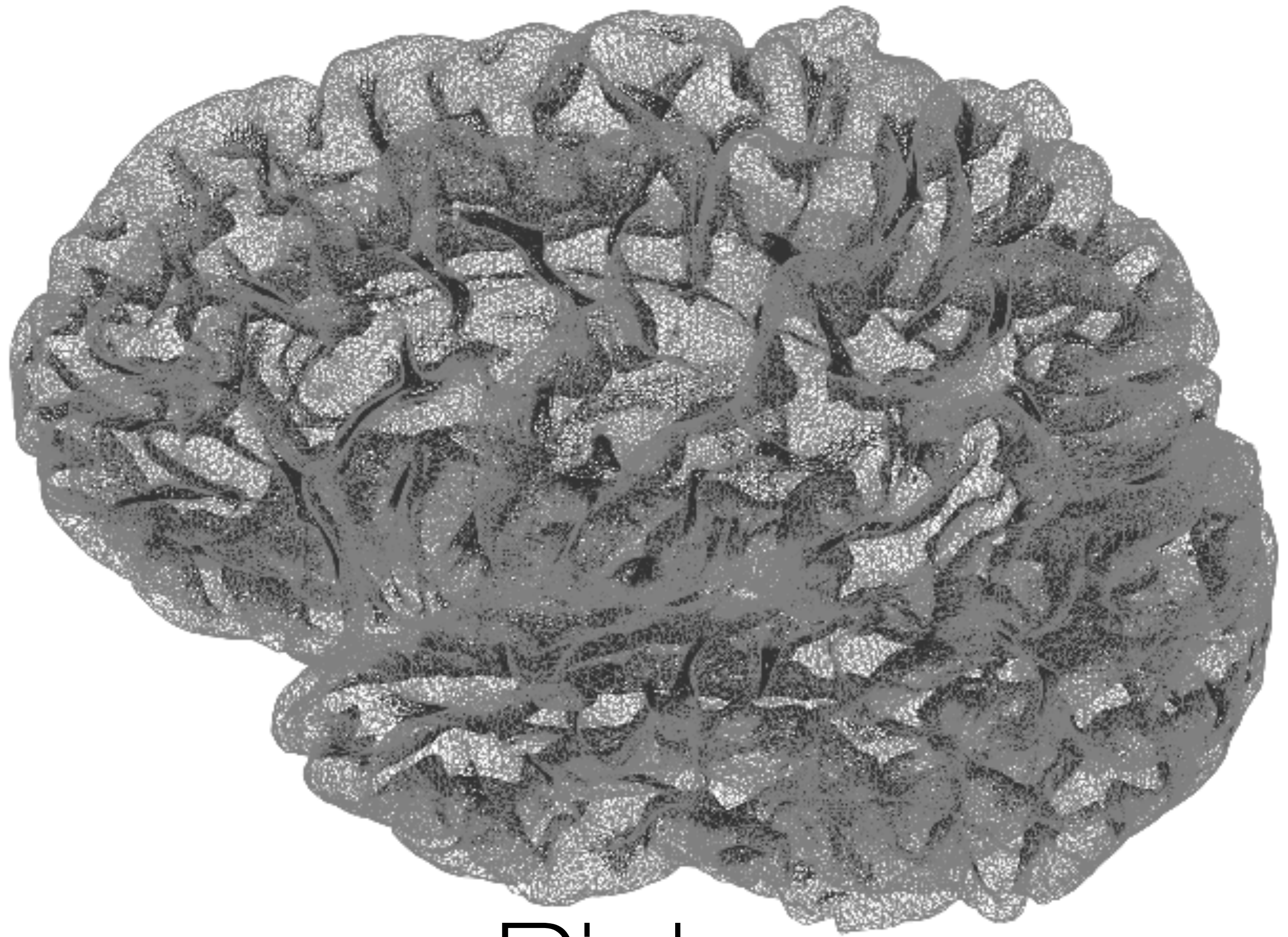
There are many surfaces for each hemisphere



White



Mid-gray



Pial

Inflated

Spherical

The vertices are equivalent for all surfaces of one hemisphere.

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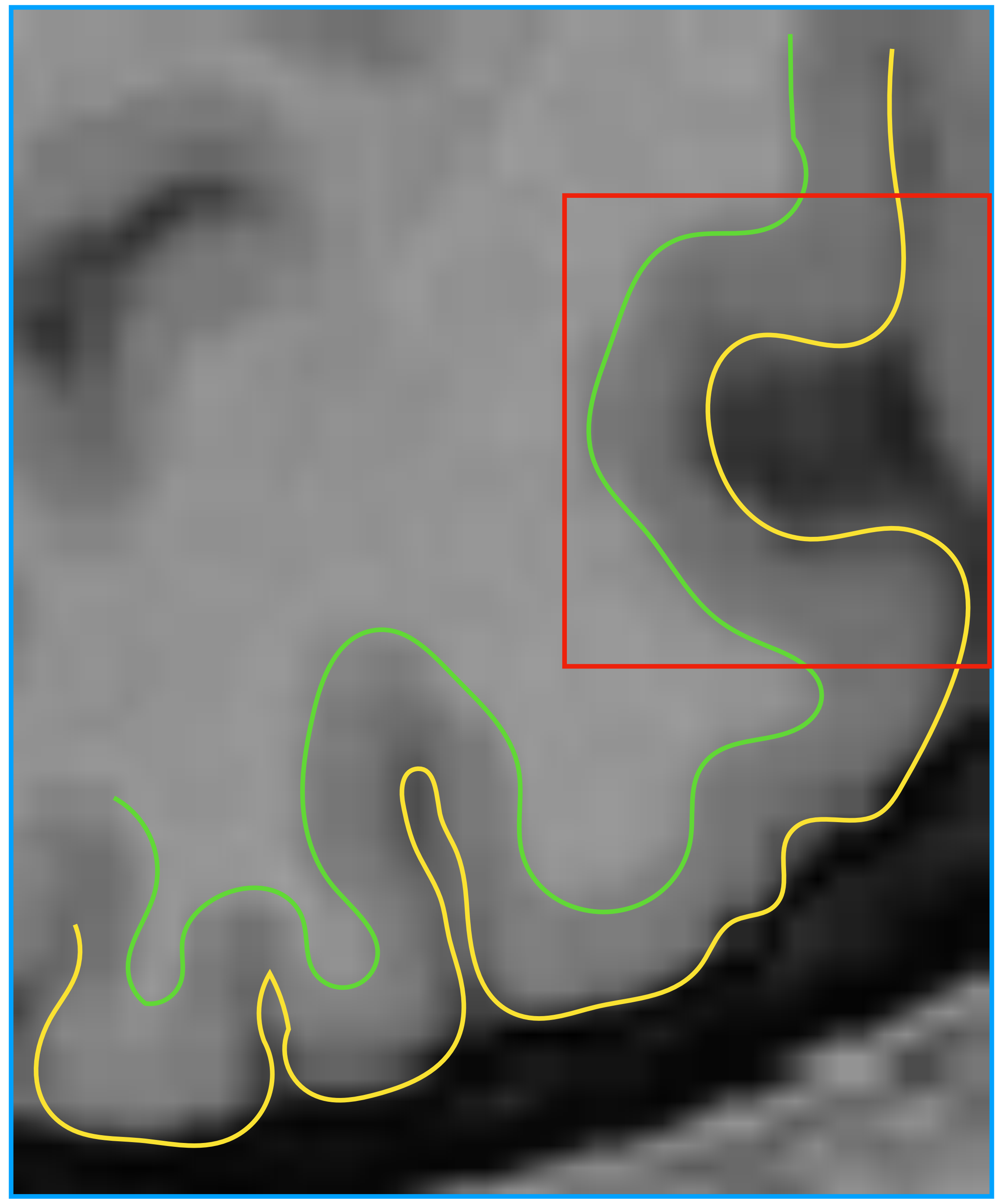
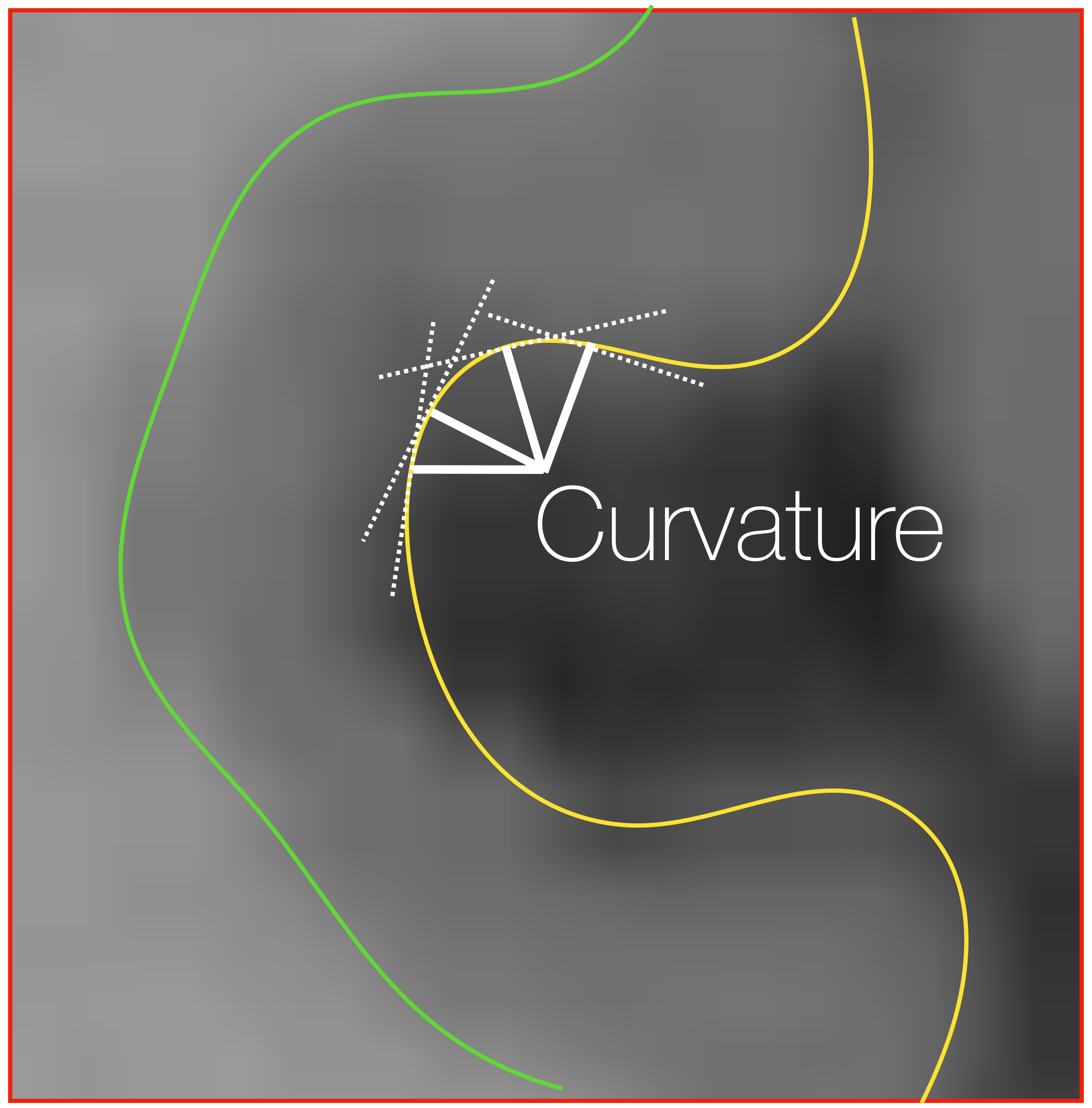
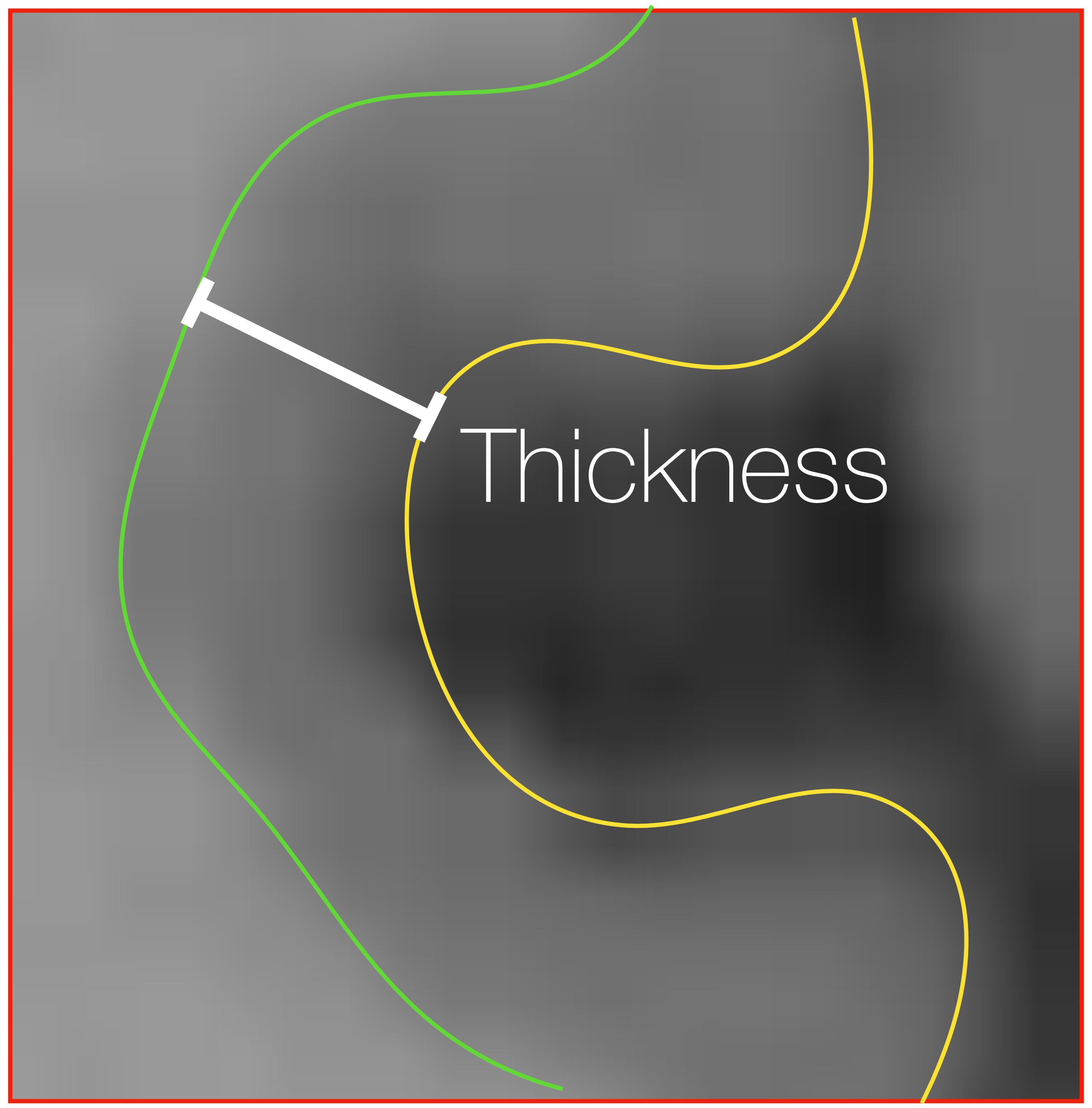
Cortical Surface Properties

- “Cortical surface properties” are just data described in terms of cortical surface vertices instead of in 3D voxels
- This is usually more efficient, but it is not always intuitive
- The ordering of vertices is arbitrary (based on the tessellation algorithm and random seed); nearby vertices are **not** necessarily near each other on the cortical surface







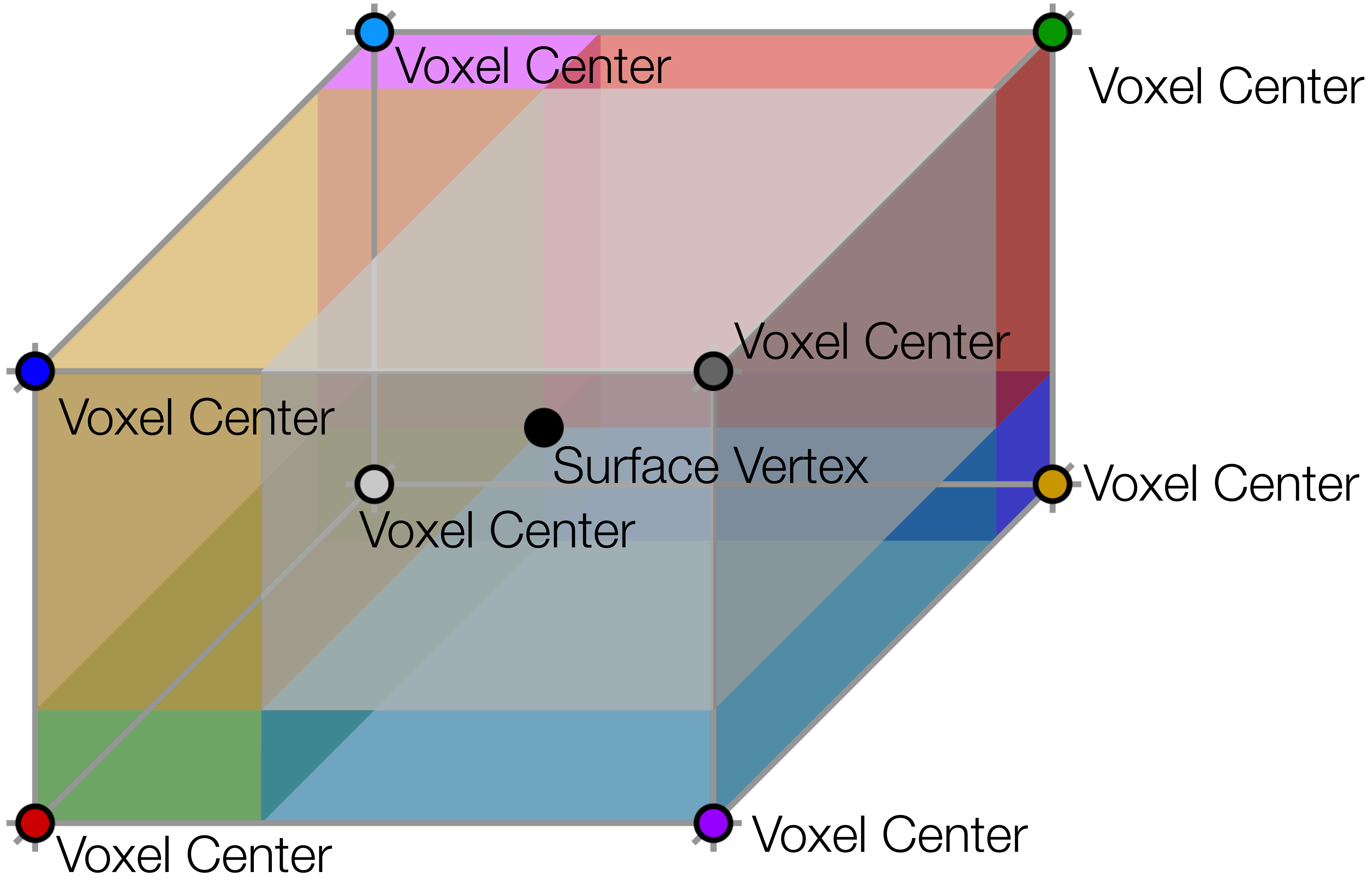
Cortical Surface Files

- Surface Files
  - Contain an $n \times 3$ floating-point matrix of vertex coordinates
  - Contains an $m \times 3$ integer matrix of triangles (indices into coordinate matrix)
  - Sometimes contain various other meta-data
  - FreeSurfer: no file extension (lh.white, rh.pial, lh.inflated, rh.sphere)
  - Human Connectome Project: GIFTI (XML-based; *.gii and *.gii.gz)
- Property Files
  - Can be just vectors or matrices of properties: one value per vertex
  - Often stored in MGH (*.mgh and *.mgz) volume files as $1 \times 1 \times n$ volumes
  - FreeSurfer: “curv” (also called “morph”) files (lh.curv, rh.thickness, lh.area)
  - Human Connectome Project: GIFTI, CIFTI (can store volume and vertex data together)

Transferring Data from Volume to Surface

- Step 1: Find the affine transformation that aligns the volume with the surface
- Step 2: Invert this transformation
- Step 3: Apply the inverse transformation to the surface vertices
  This gives each voxel an (*x*, *y*, *z*) equal to its (*row*, *column*, *slice*) position in the volume
- Nearest interpolation:
  Round (*x*, *y*, *z*) to get (*row*, *column*, *slice*)
- Linear Interpolation:
  - Each vertex is in a cube formed by the centers of the 8 nearest voxels…

Transferring Data from Volume to Surface



Transferring Data from Volume to Surface

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Volumetric Alignment

- Find the affine transformation that best-aligns an anatomical image to an “atlas" image

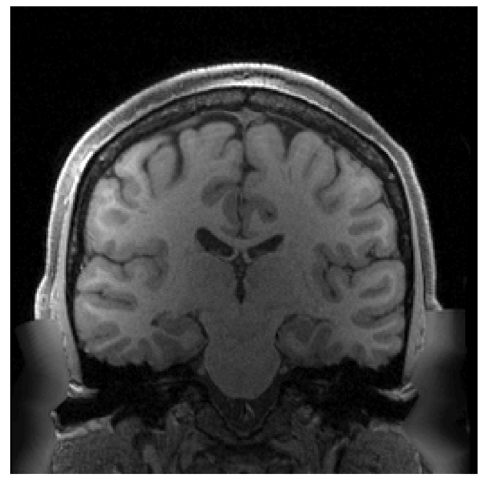
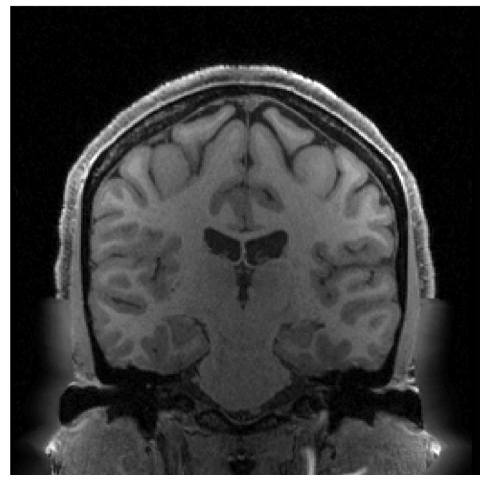
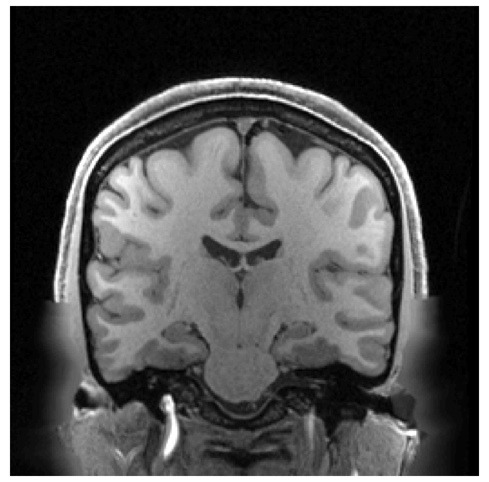
$$\begin{pmatrix} a & b & c & t_x \\ d & e & f & t_y \\ g & h & i & t_z \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

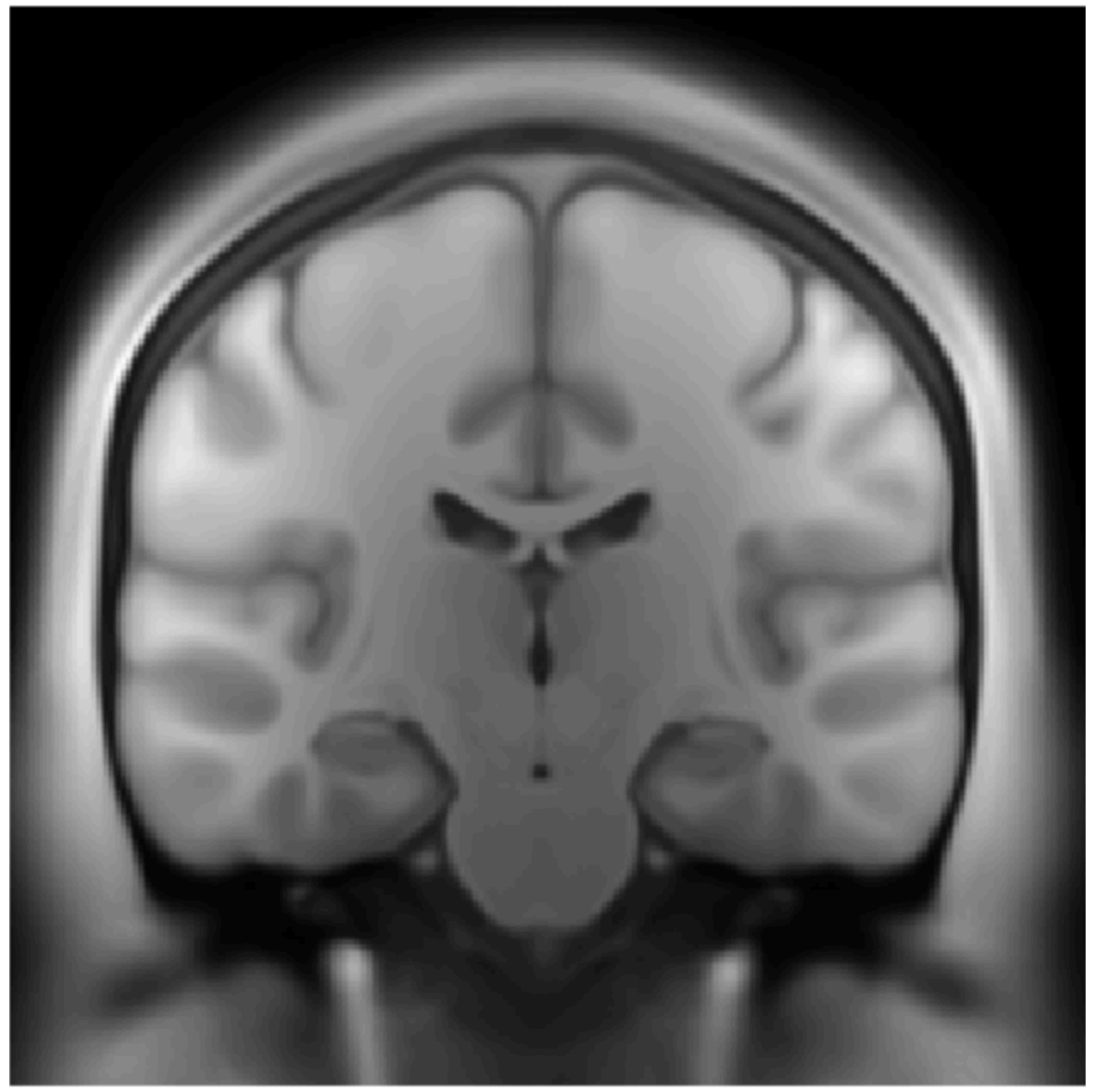
(relatively efficient because there are at most 12 parameters)

- MNI (McGill) publishes the *de facto* standard volumetric atlases: http://nist.mni.mcgill.ca/
- MNI Software: http://bic-mni.github.io/
- Many tools:
  - bbregister (FreeSurfer)
  - FSL
  - ITK-SNAP

Evans et al. (1992) *NeuroImage* 1:43–63
Collins et al. (1994) *J. Comput. Assist. Tomogr*. 18:192–205

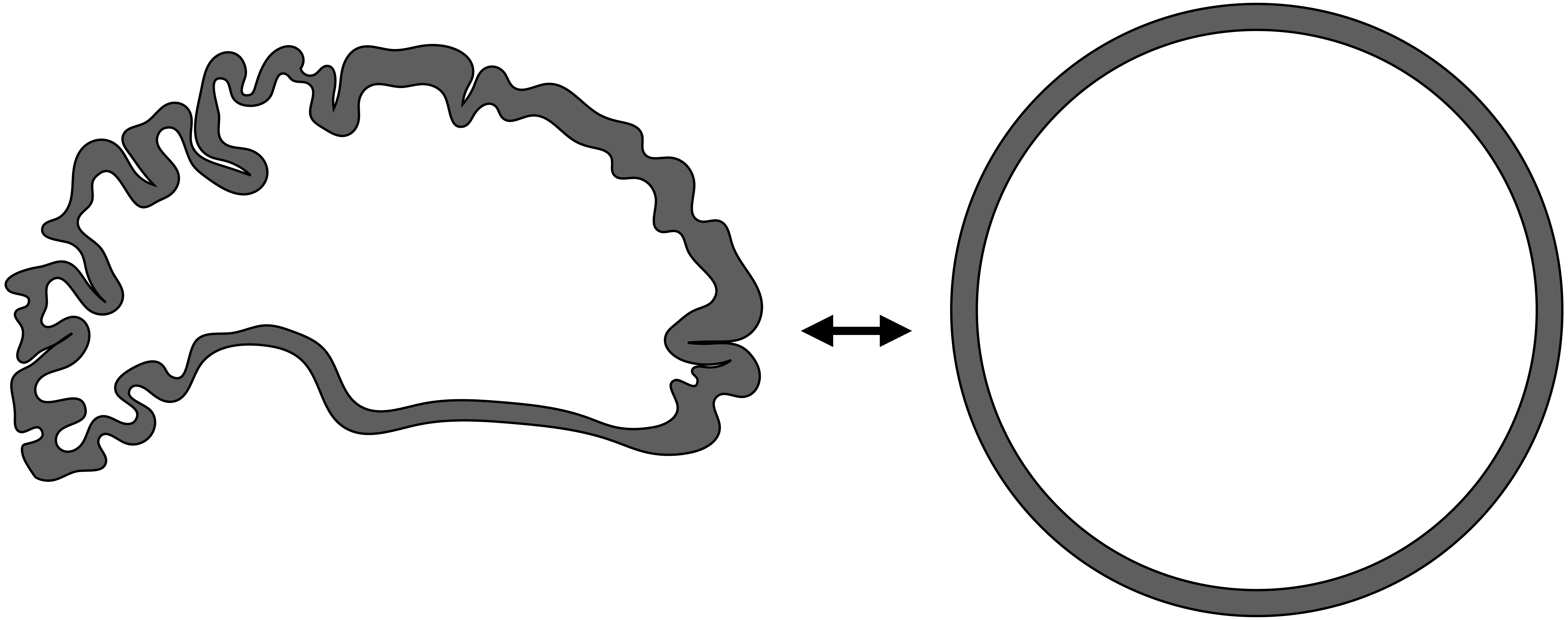
Surface-based Alignment

mean( ,  , … ) =



FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

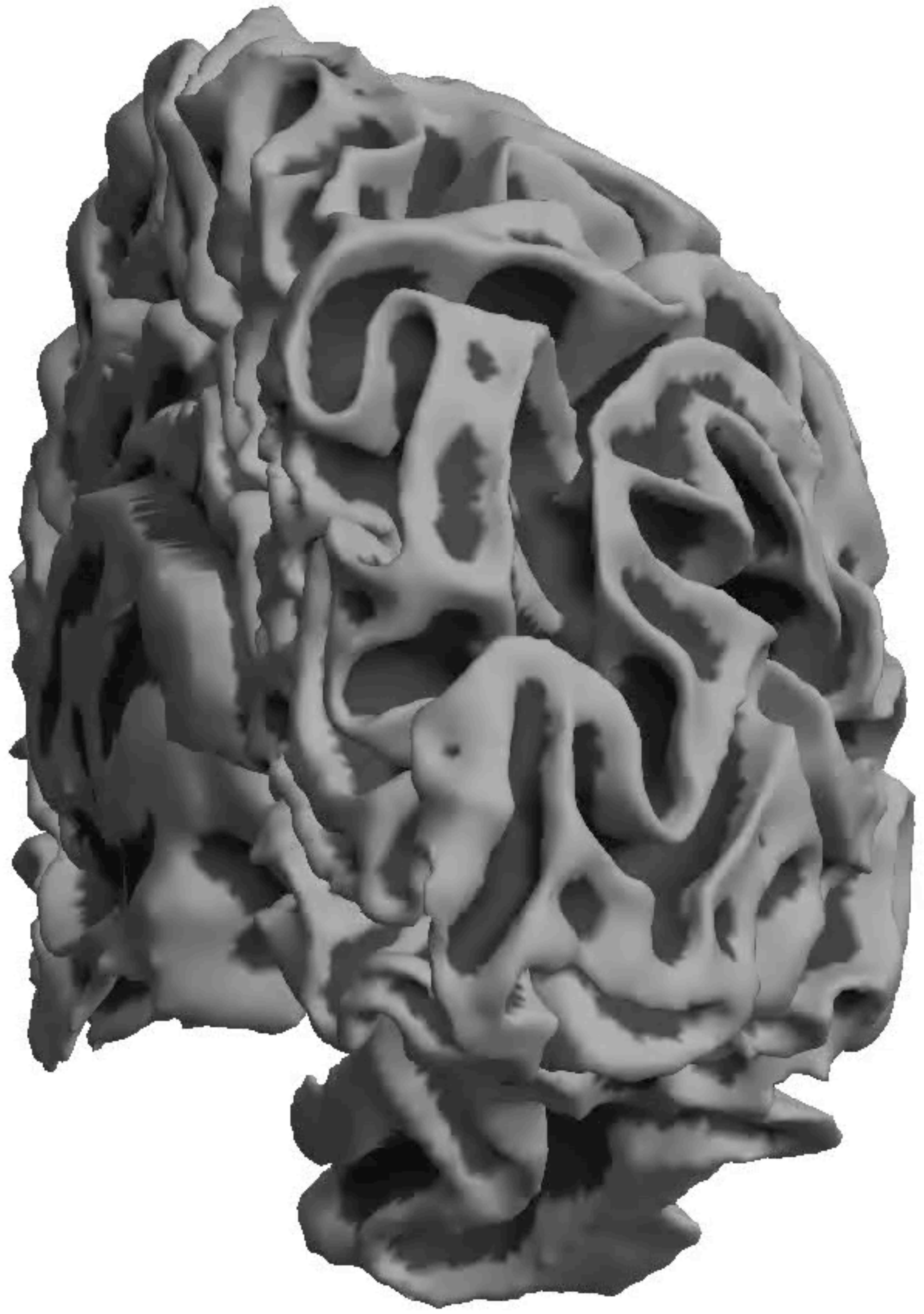
The gray matter surface is a topological sphere



Cortical “brain areas” exist on
the brain’s 2D surface

Surface-based Alignment

Atlas RH
("*fsaverage*")

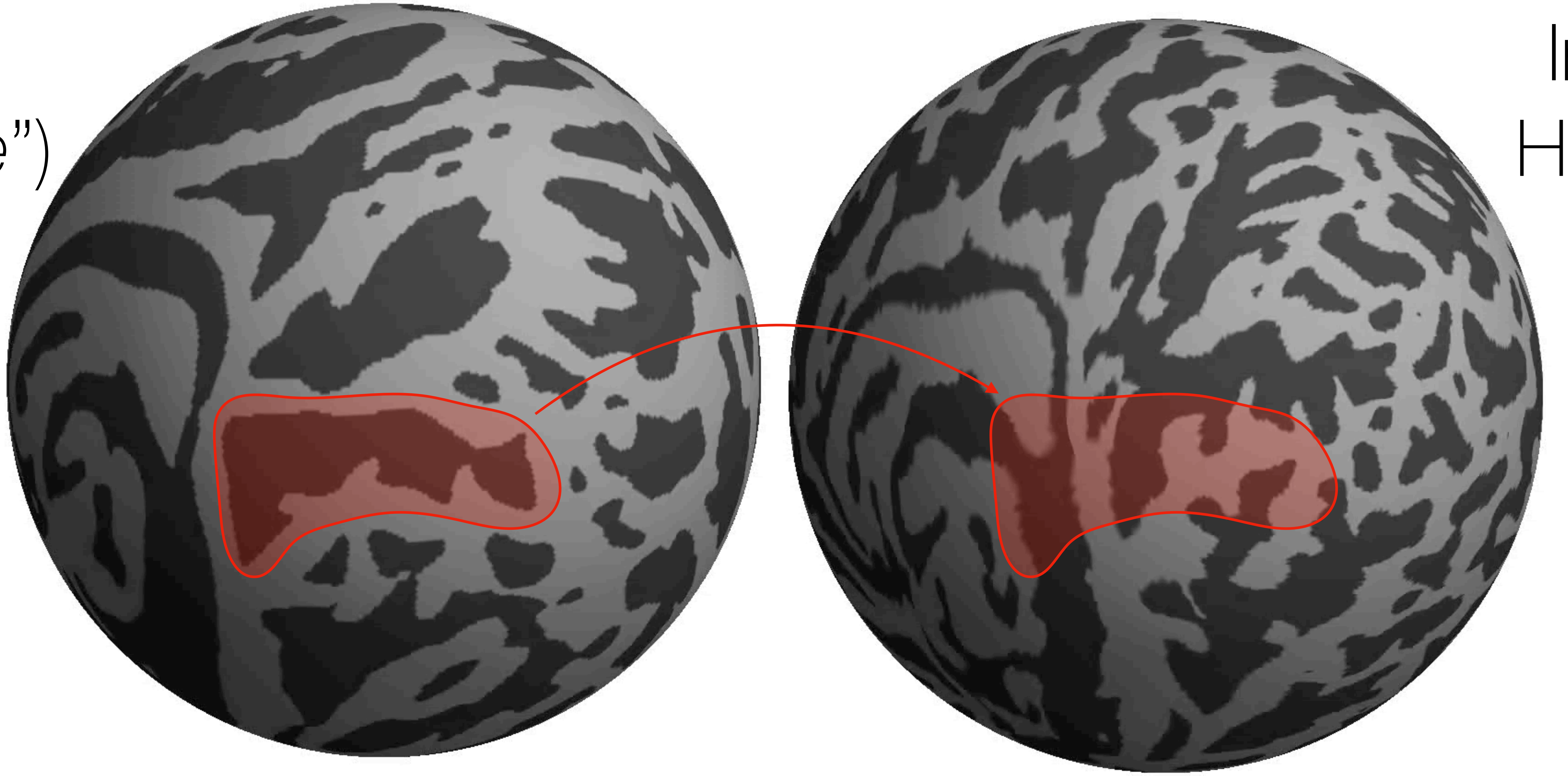


Individual
Human RH

FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

Surface-based Alignment

Atlas RH
("*fsaverage*")



Individual
Human RH

This creates a correspondence between points on the cortical surface.
We can use this to compare data across subjects.

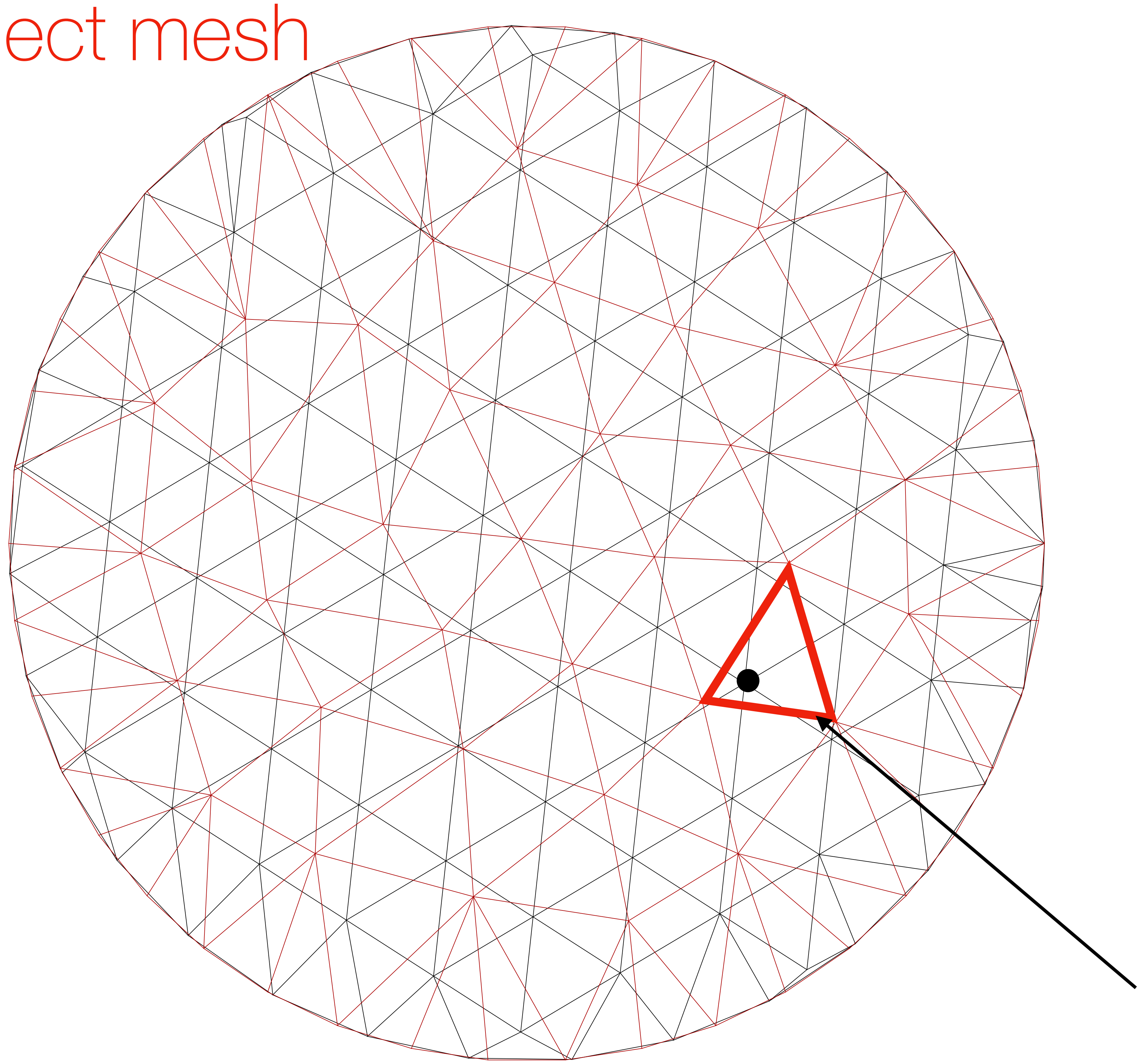
FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

Surface-based Interpolation

Using a correspondence between points on the cortical surface, we can interpolate data from the subject to the *fsaverage*.

fsaverage mesh

subject mesh



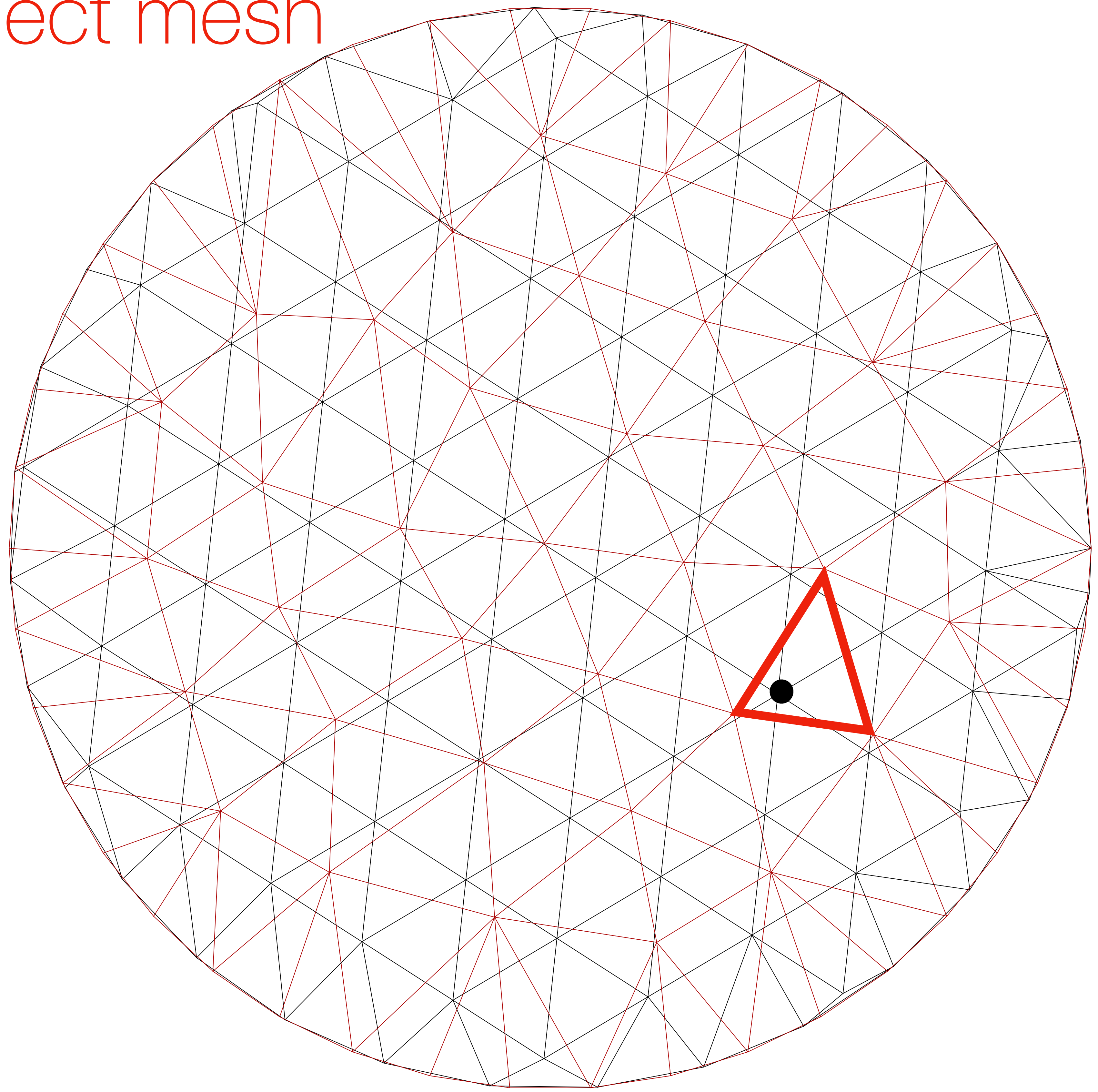
- Nearest interpolation:
  Each *fsaverage* vertex gets the value of the closest subject vertex
- Linear interpolation:
  Each *fsaverage* vertex gets a value depending on the values of the vertices of the subject triangle that contains the *fsaverage* vertex

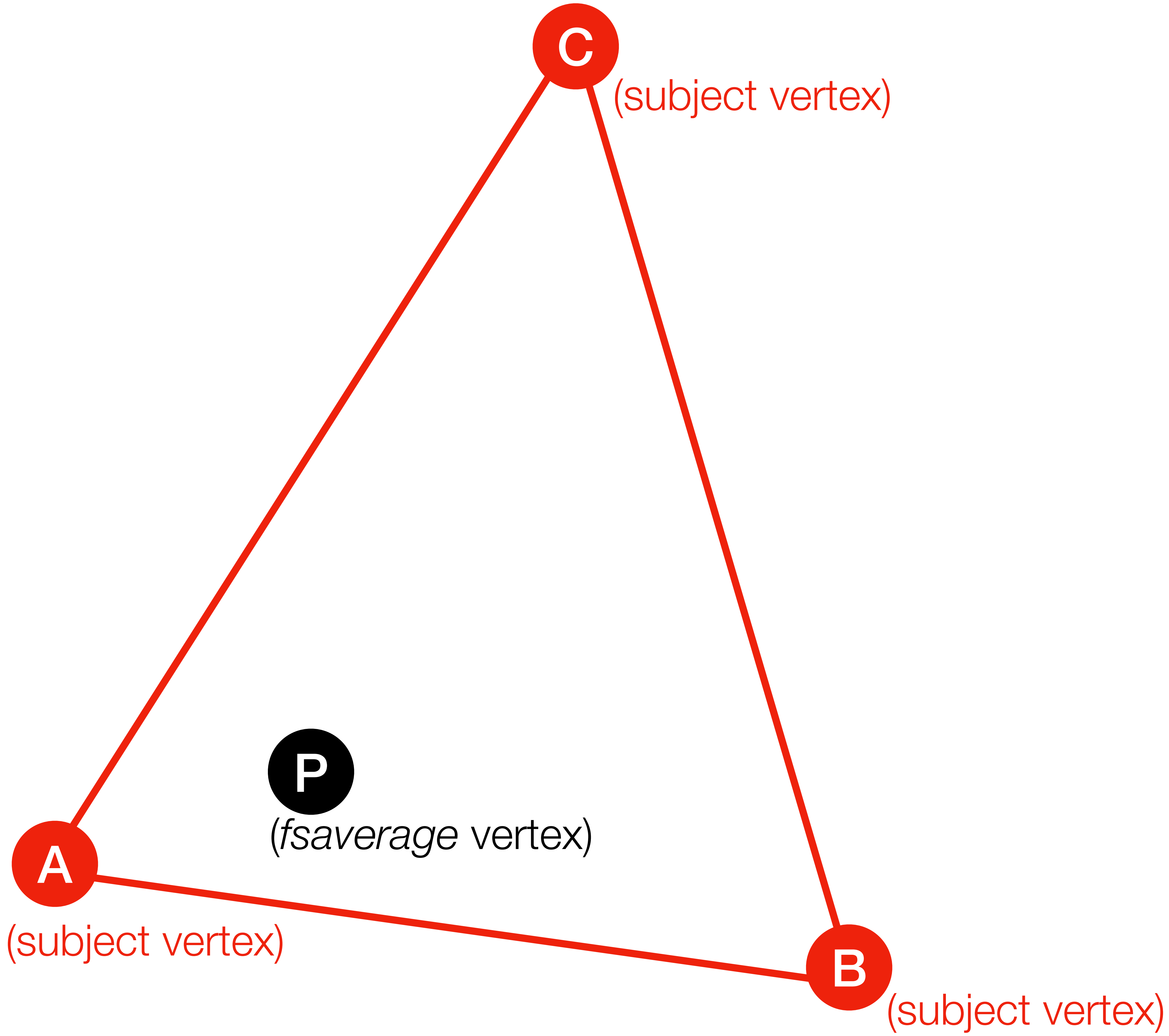
FreeSurfer: http://surfer.nmr.mgh.harvard.edu/

Surface-based Interpolation

Using a correspondence between points on the cortical surface, we can interpolate data from the subject to the *fsaverage*.

fsaverage mesh
subject mesh





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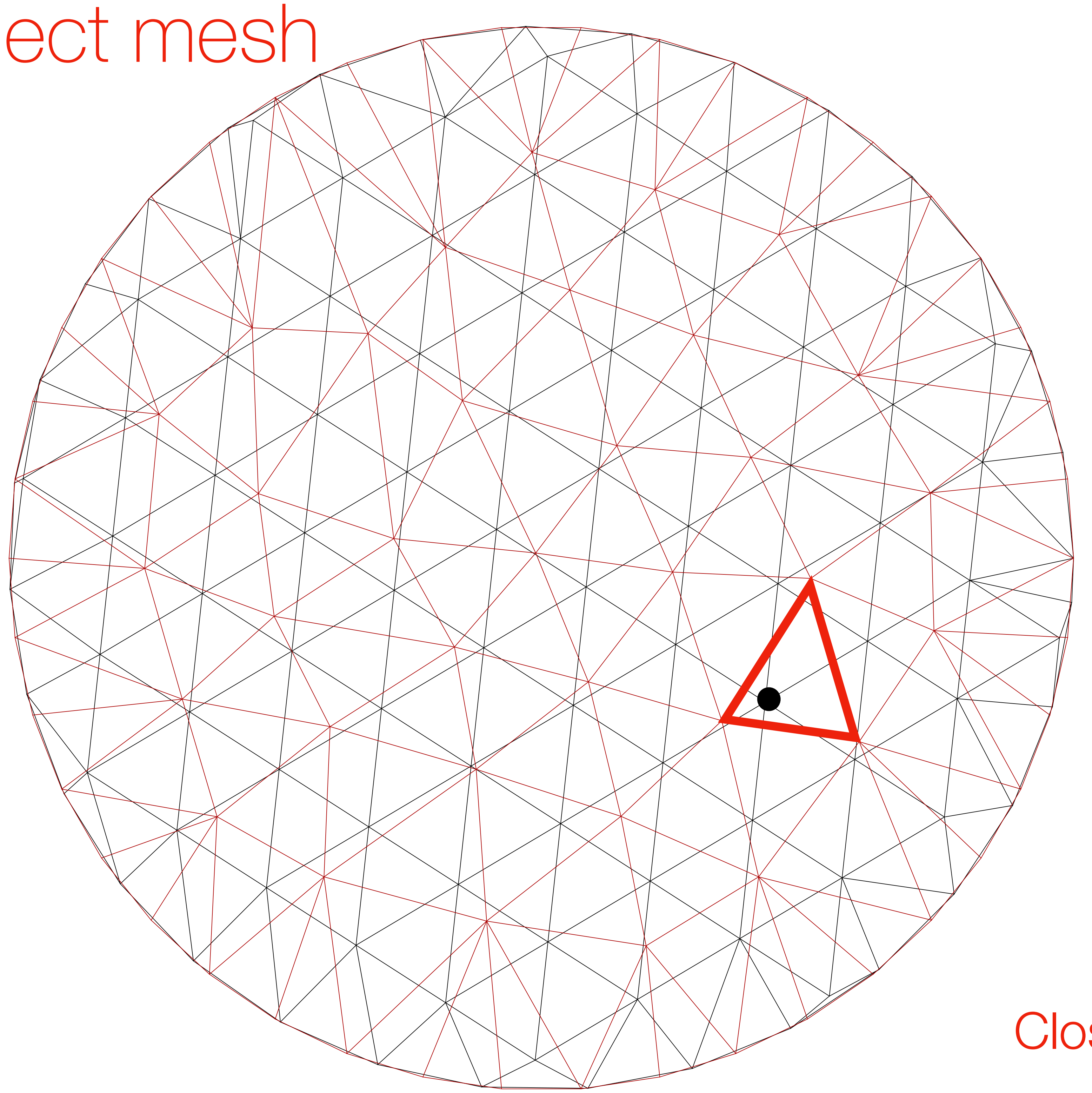

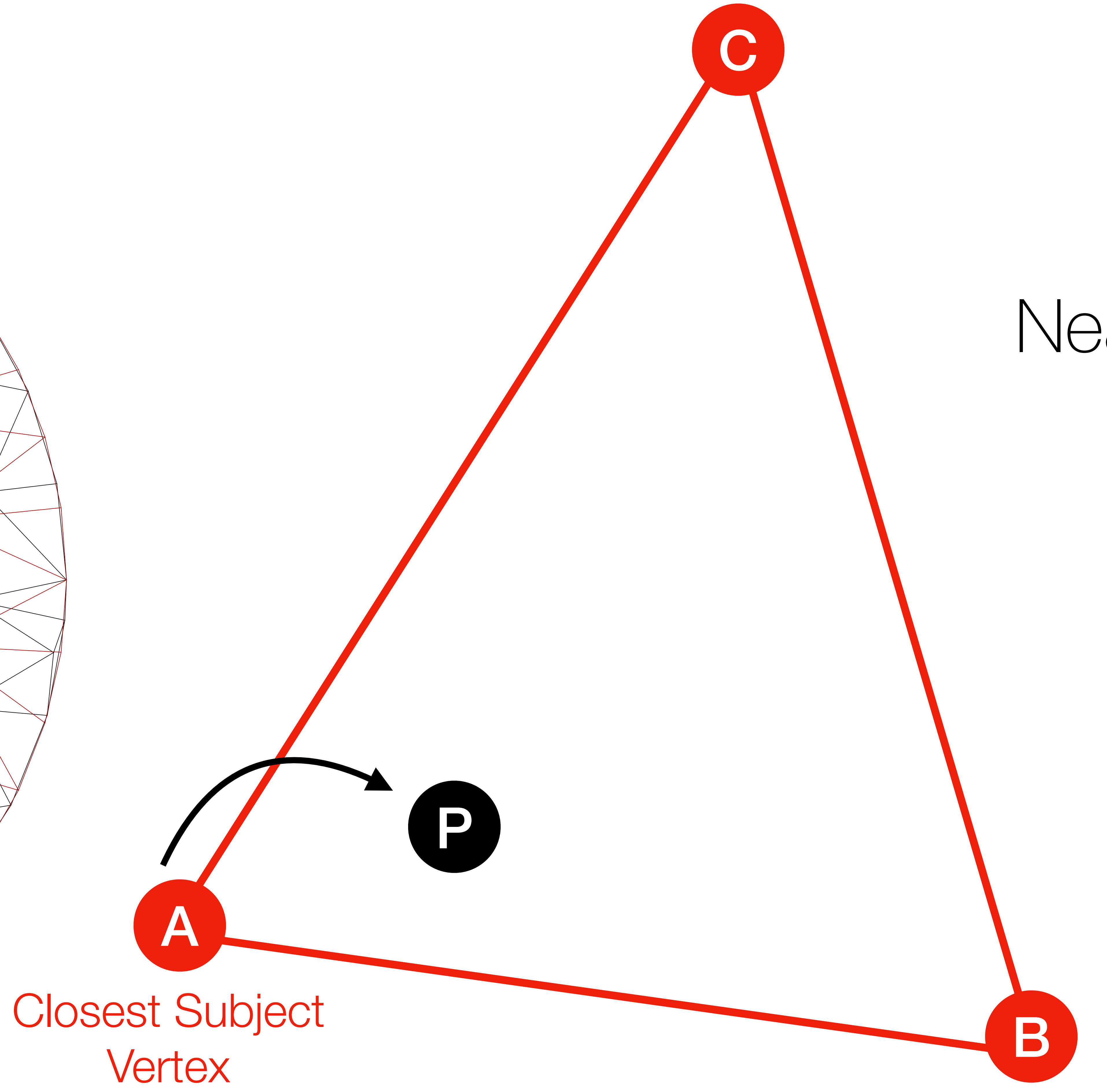

Nearest interpolation

Surface-based Interpolation

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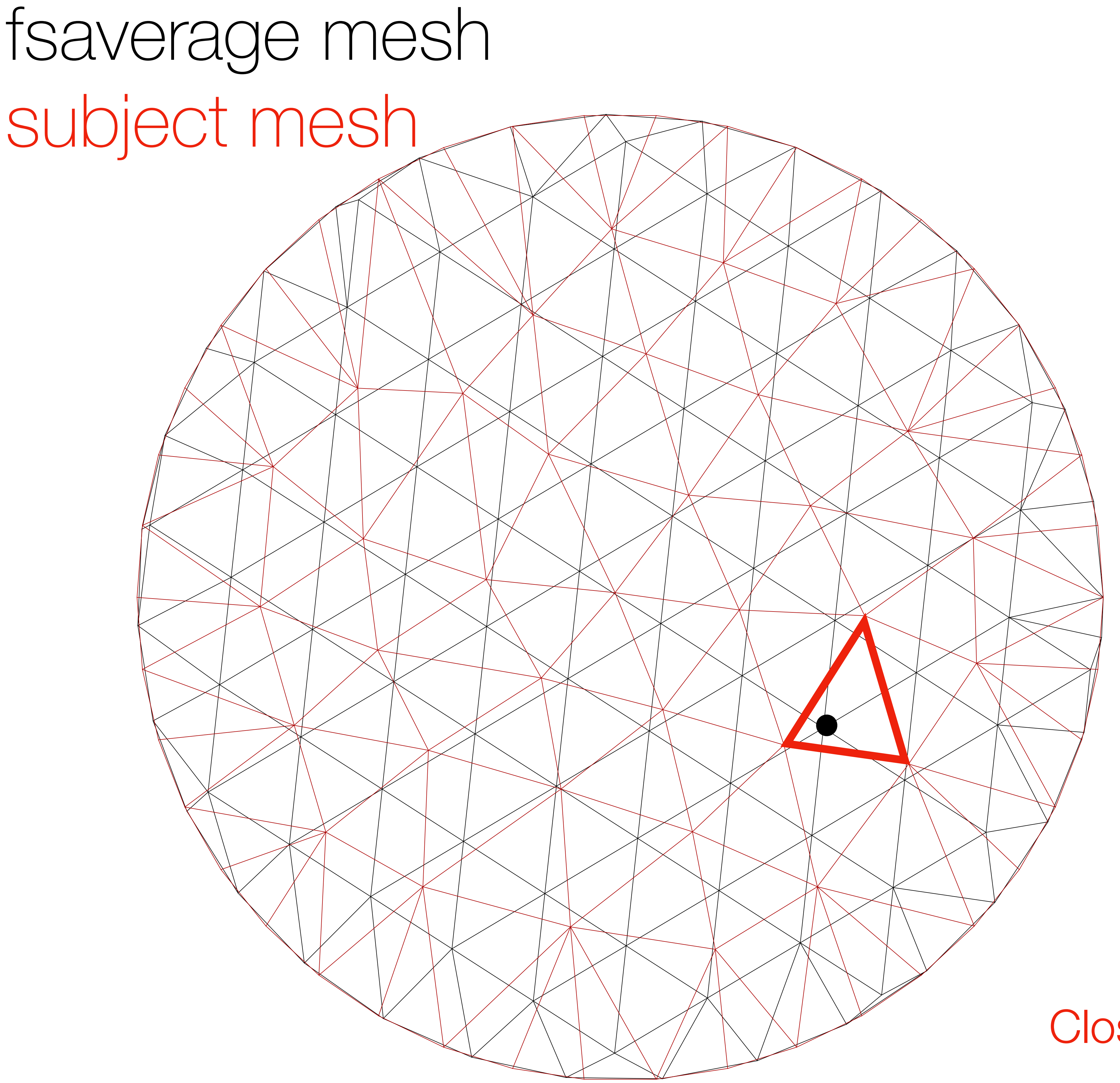
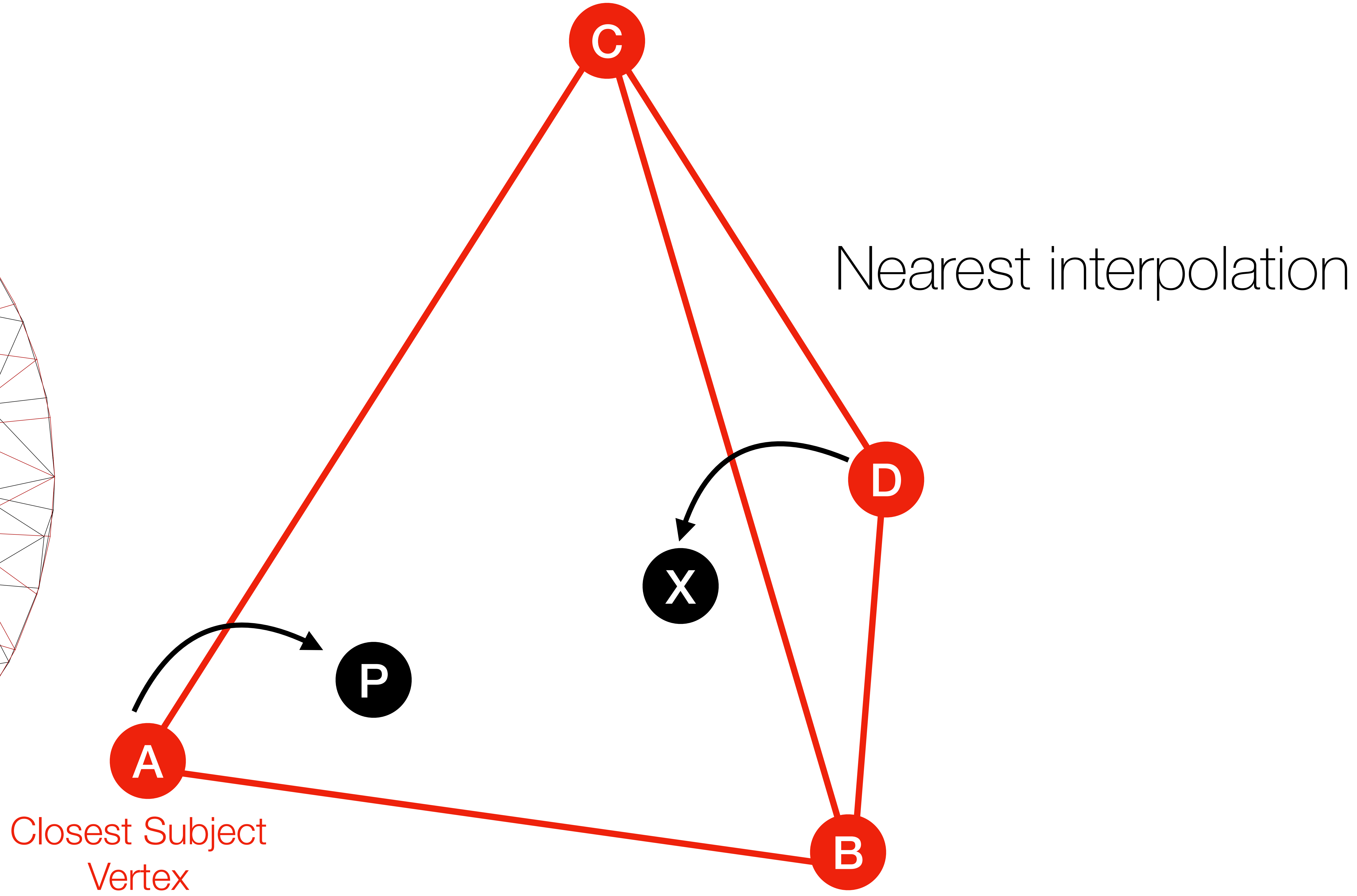
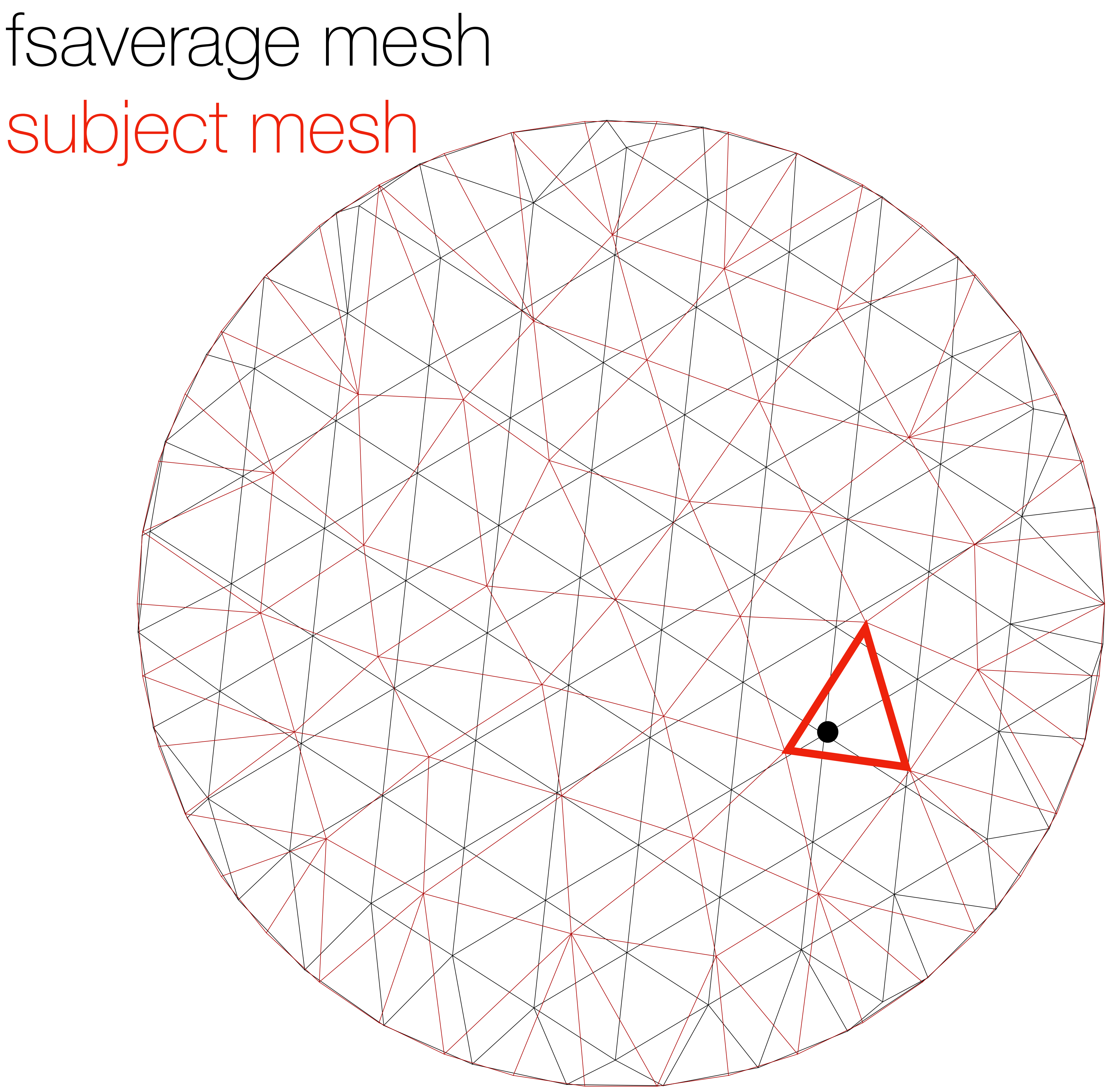
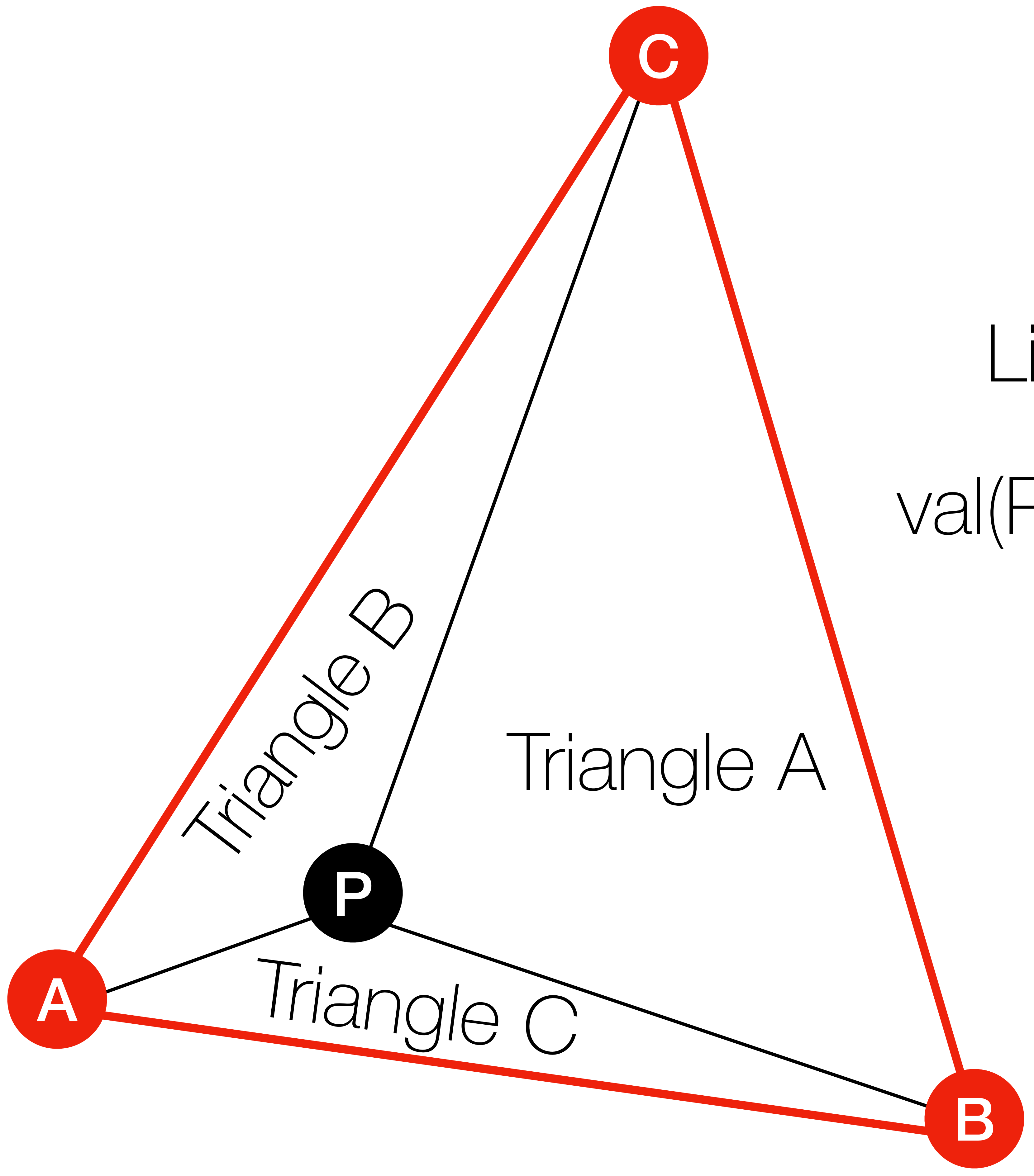




Surface-based Interpolation



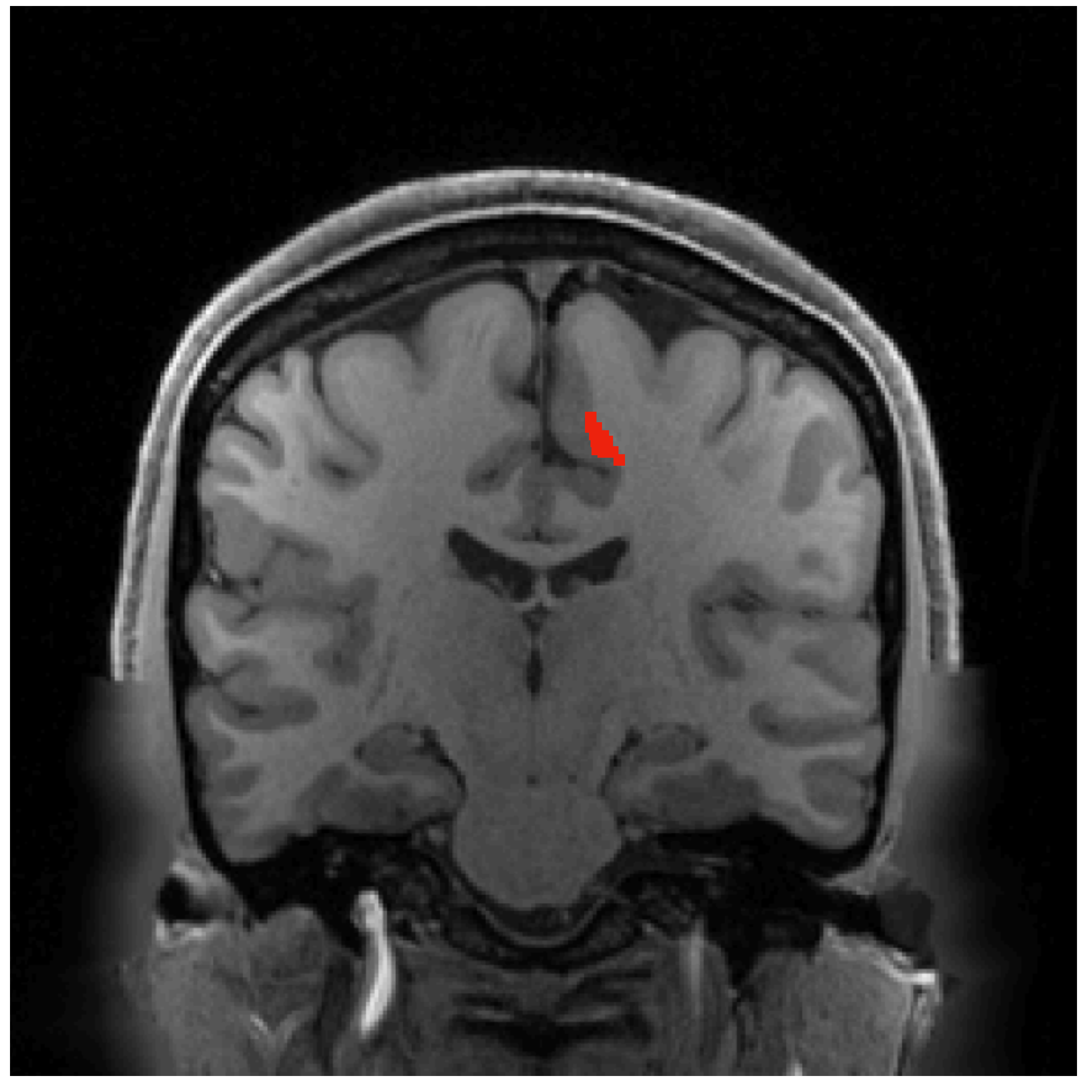


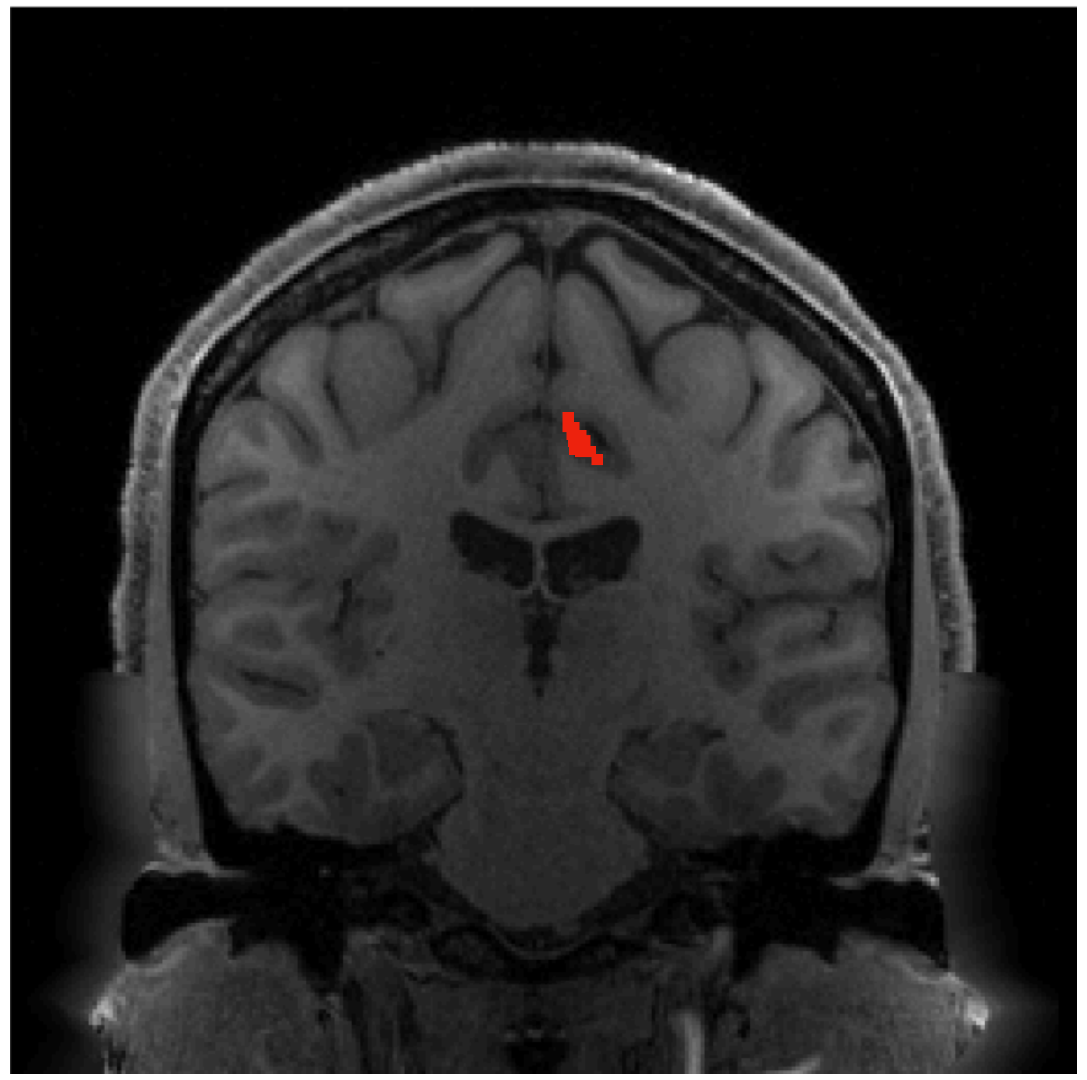
Linear interpolation

$$\mathrm{val}(P) = \frac{\mathrm{val}(A) \times \mathrm{area}(\mathrm{TriA}) + \mathrm{val}(B) \times \mathrm{area}(\mathrm{TriB}) + \mathrm{val}(C) \times \mathrm{area}(\mathrm{TriC})}{\mathrm{area}(\mathrm{TriABC})}$$

Surface versus Volumetric Comparison

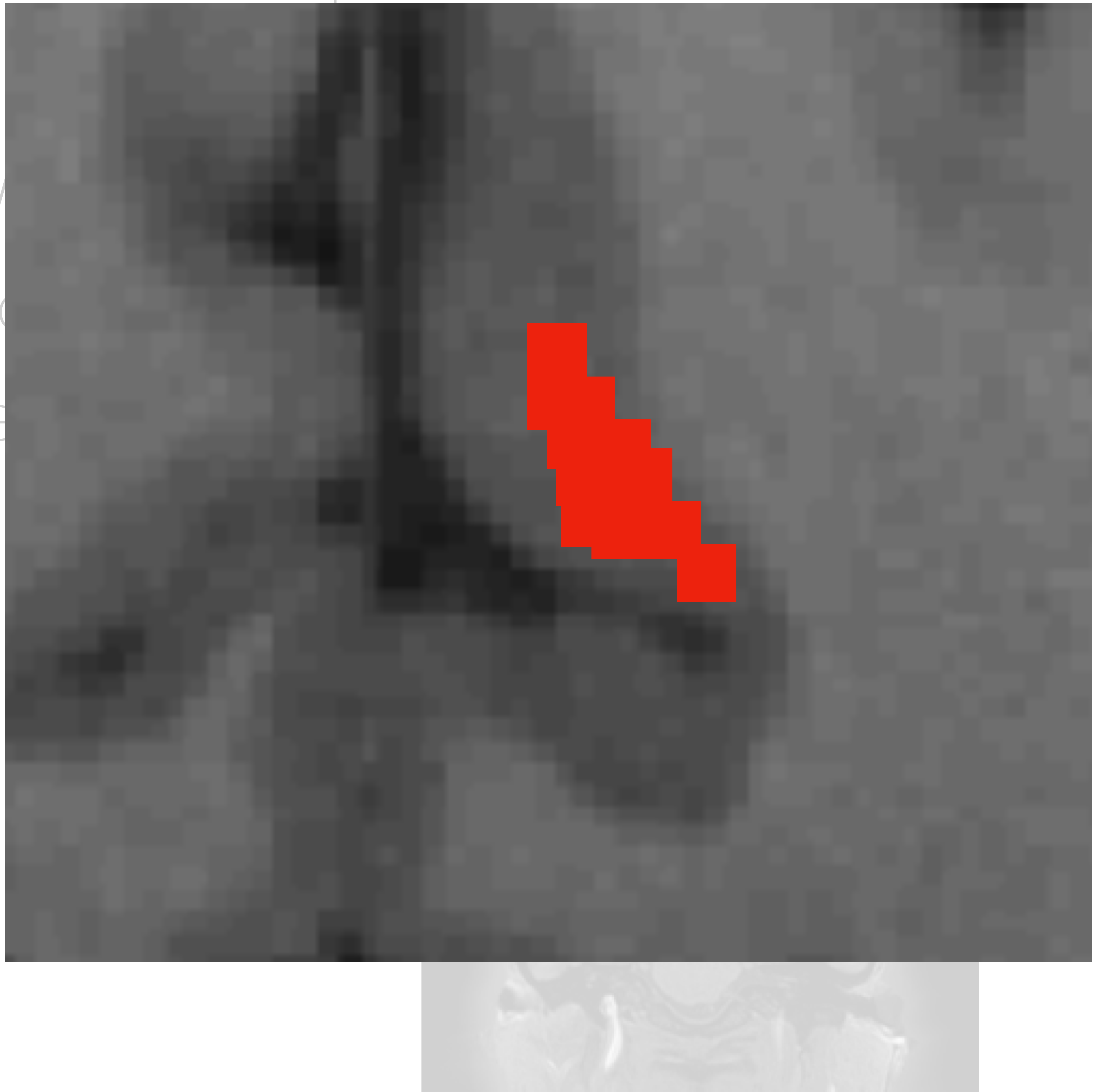
- Volumetric comparison
  - Rigid: few degrees of freedom
  - Whole-brain
  - Computationally cheap
  - Less complex
- Surface-based comparison
  - Diffeomorphic: many degrees of freedom
  - Cortex only
  - More computationally expensive
  - More complicated



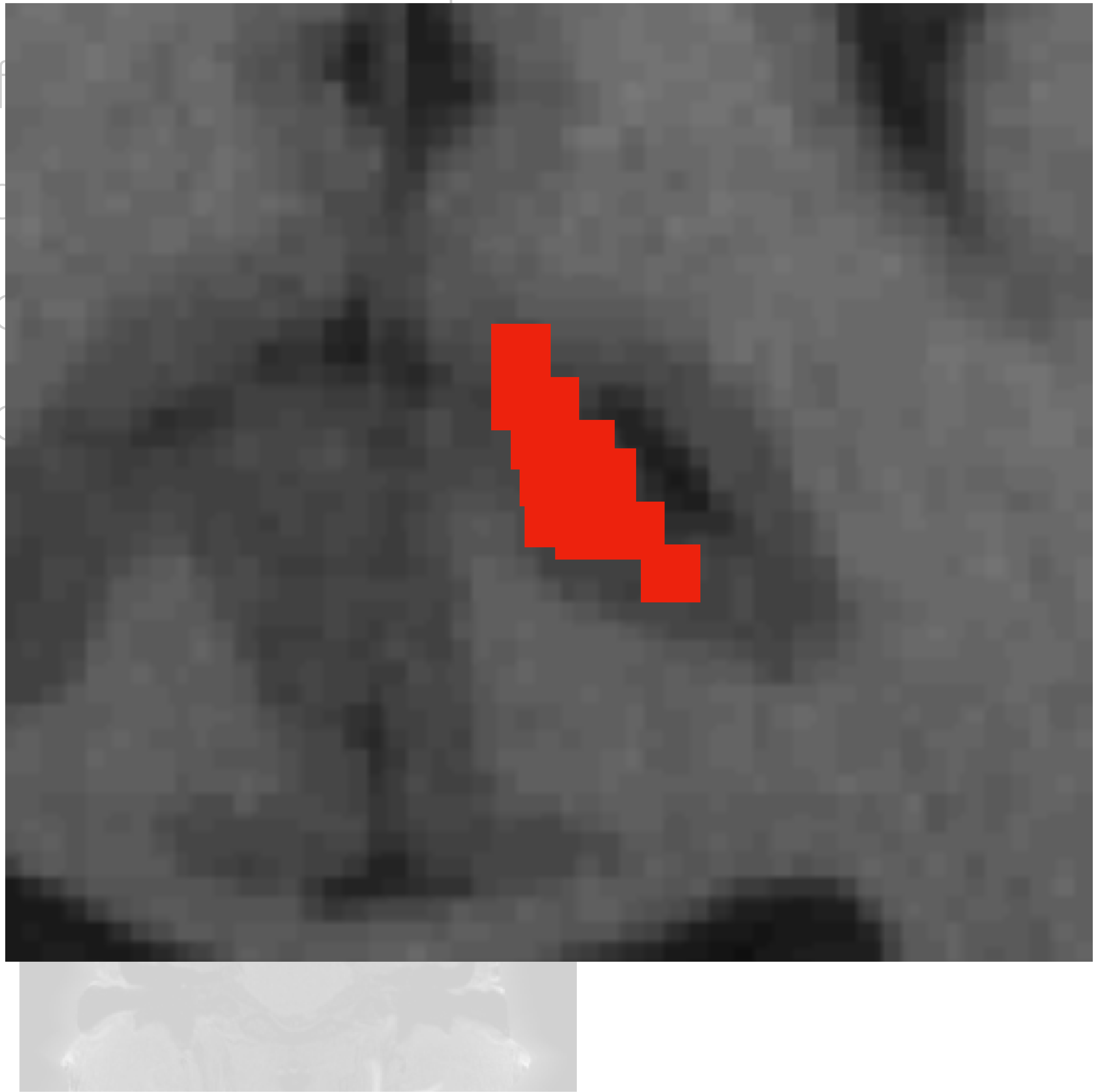


Surface versus Volumetric Comparison

- Volumetric comparison
  - Ri
  - W
  - Co
  - Le



- Surface-based comparison
  - Dif
  - Co
  - Mo
  - Mo



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- Many studies have concluded that surface-based anatomical alignment is superior for inter-subject comparison than volumetric alignment:
  - Rosenke *et al.* (2018) *Neuroimage* 170:257-270
  - Ghosh *et al.* (2010) *Neuroimage* 53:85-93
  - Coalson, Van Essen, Glasser (2018) *PNAS* 115:E6356-E6365
  - Many others

Conclusions

Hopefully this tutorial was helpful! You can try it out on your own later:

https://github.com/noahbenson/neurohackademy2020

Resources:

FreeSurfer: http://surfer.nmr.mgh.harvard.edu/
HCPpipelines: https://www.humanconnectome.org/software/hcp-mr-pipelines
MNI: http://nist.mni.mcgill.ca/
Neuropythy: https://github.com/noahbenson/neuropythy
More Tutorials: https://nben.net/

Email: nben@uw.edu

Github: noahbenson

Website: https://nben.net/