

MRI, Retinotopic Maps, and the HCP

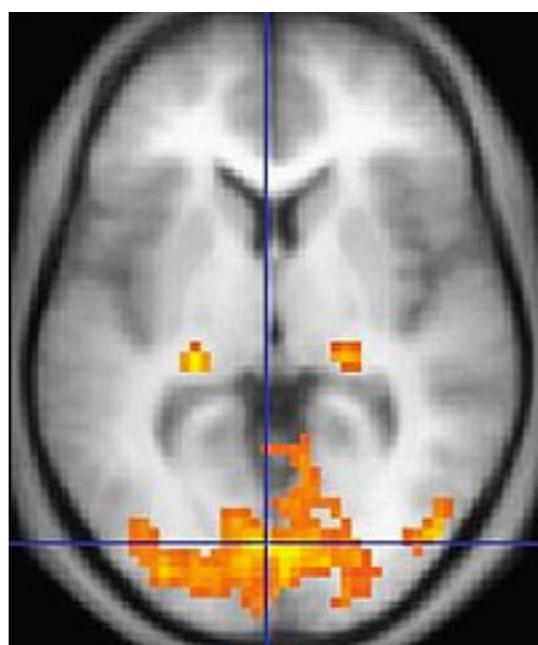
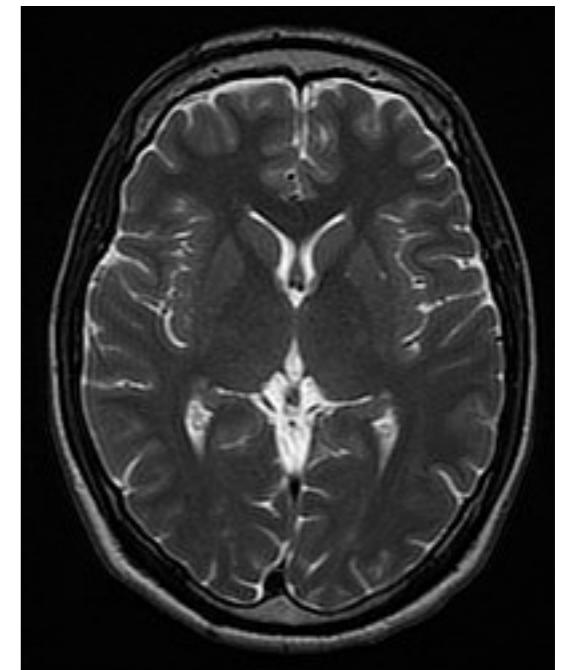
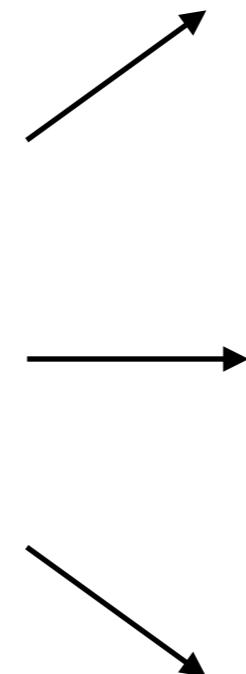
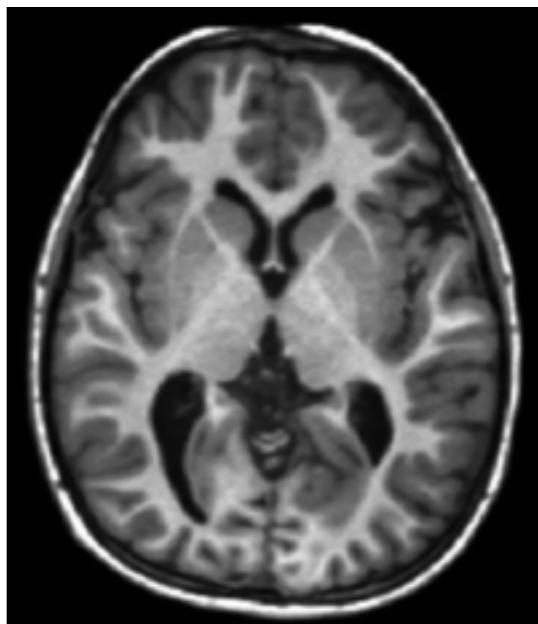
Noah C. Benson
Winawer Lab, Department of Psychology, NYU

Tutorial Outline: Goals

At the end of this tutorial, you will...

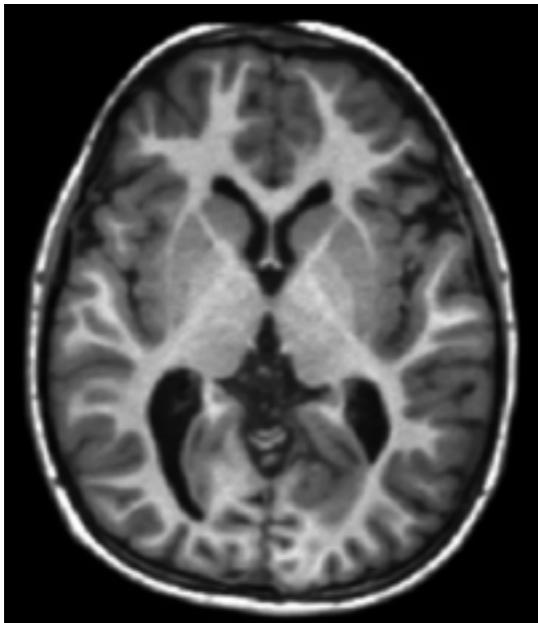
- [Slides] Understand the basics of structural MRI
- [Demo 1] Be able to load and plot structural MRI data from the Human Connectome Project in Jupyter
- [Slides] Understand the basics of functional MRI
- [Demo 2] Be able to fit a pRF model to functional MRI data
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- [Demo 3] Be able to plot retinotopic maps from the Human Connectome Project in Jupyter

What is MRI?



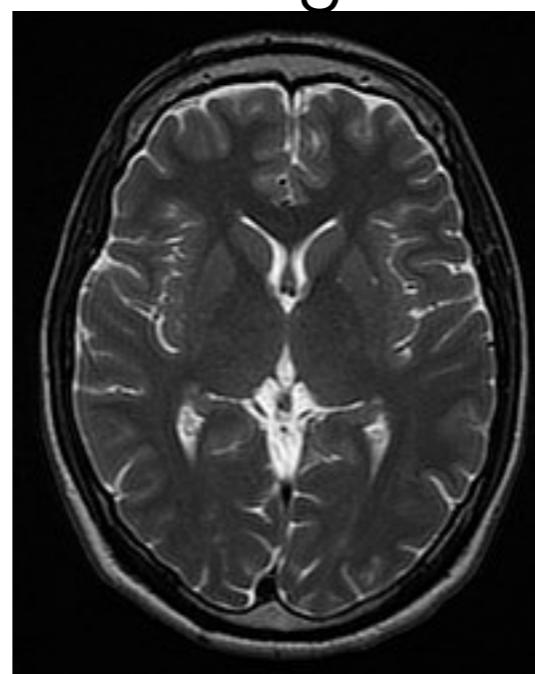
A Few Kinds of MR Images

T1-weighted



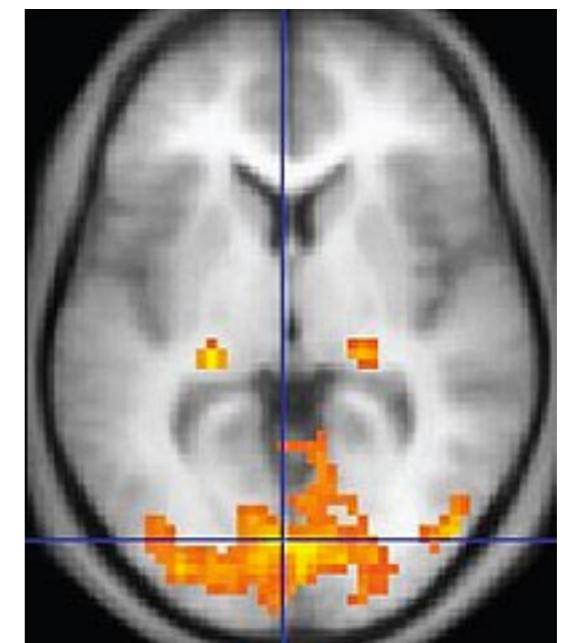
Fat is bright;
water is dark.

T2-weighted



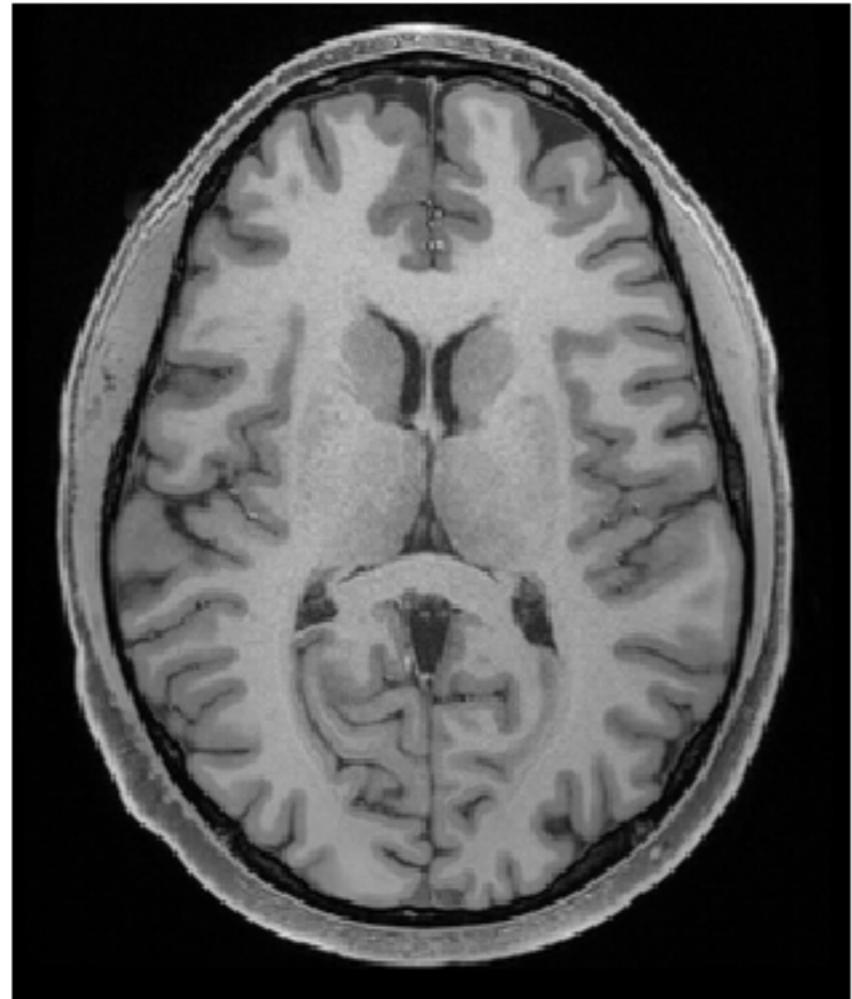
Water is bright;
fat is dark.

BOLD



Oxygenated
blood is light;
deoxygenated
blood is dark

Structural MRI: T1 -weighted Images



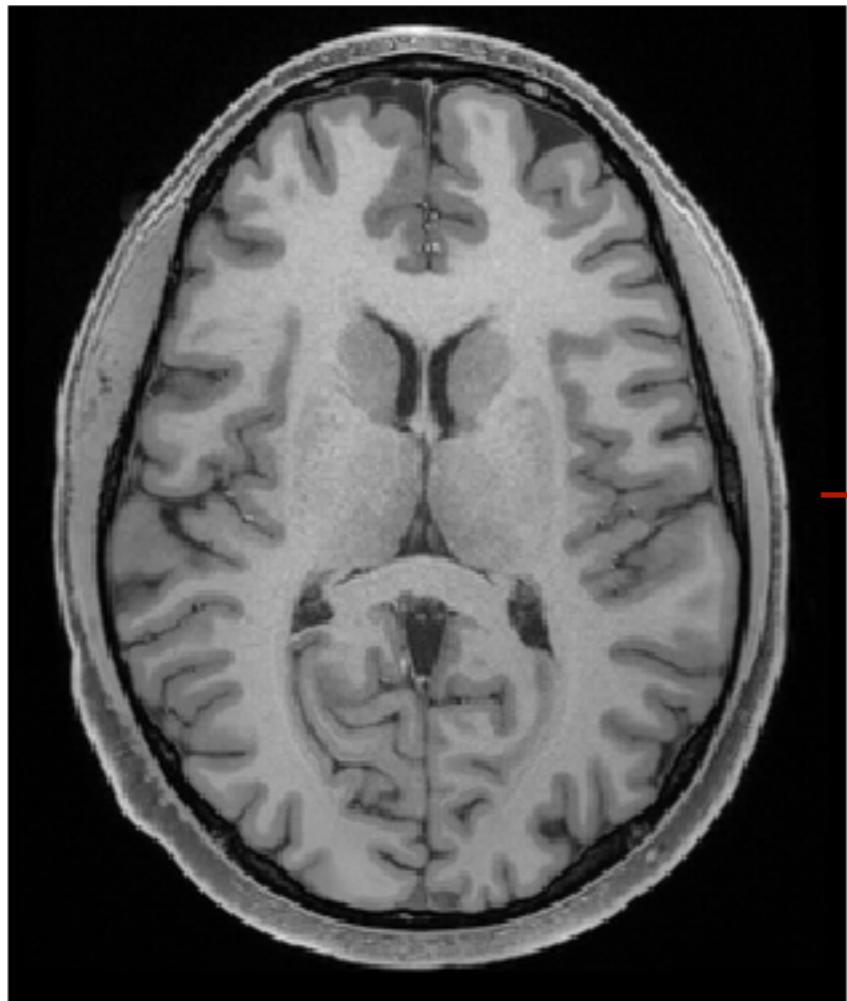
T1-weighted Image
(HCP Subject 100610)

- 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

- Main source of anatomical data about the human brain
- 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>

Segmentation



Segmentation

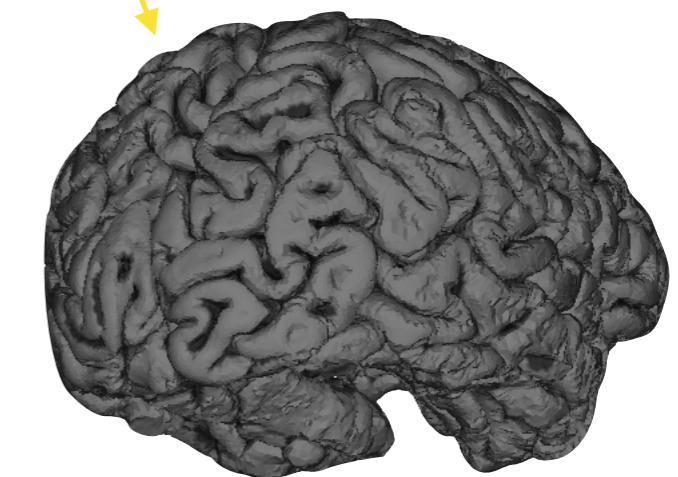
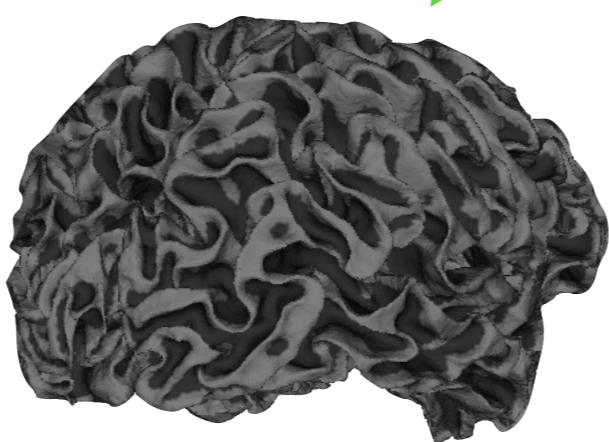
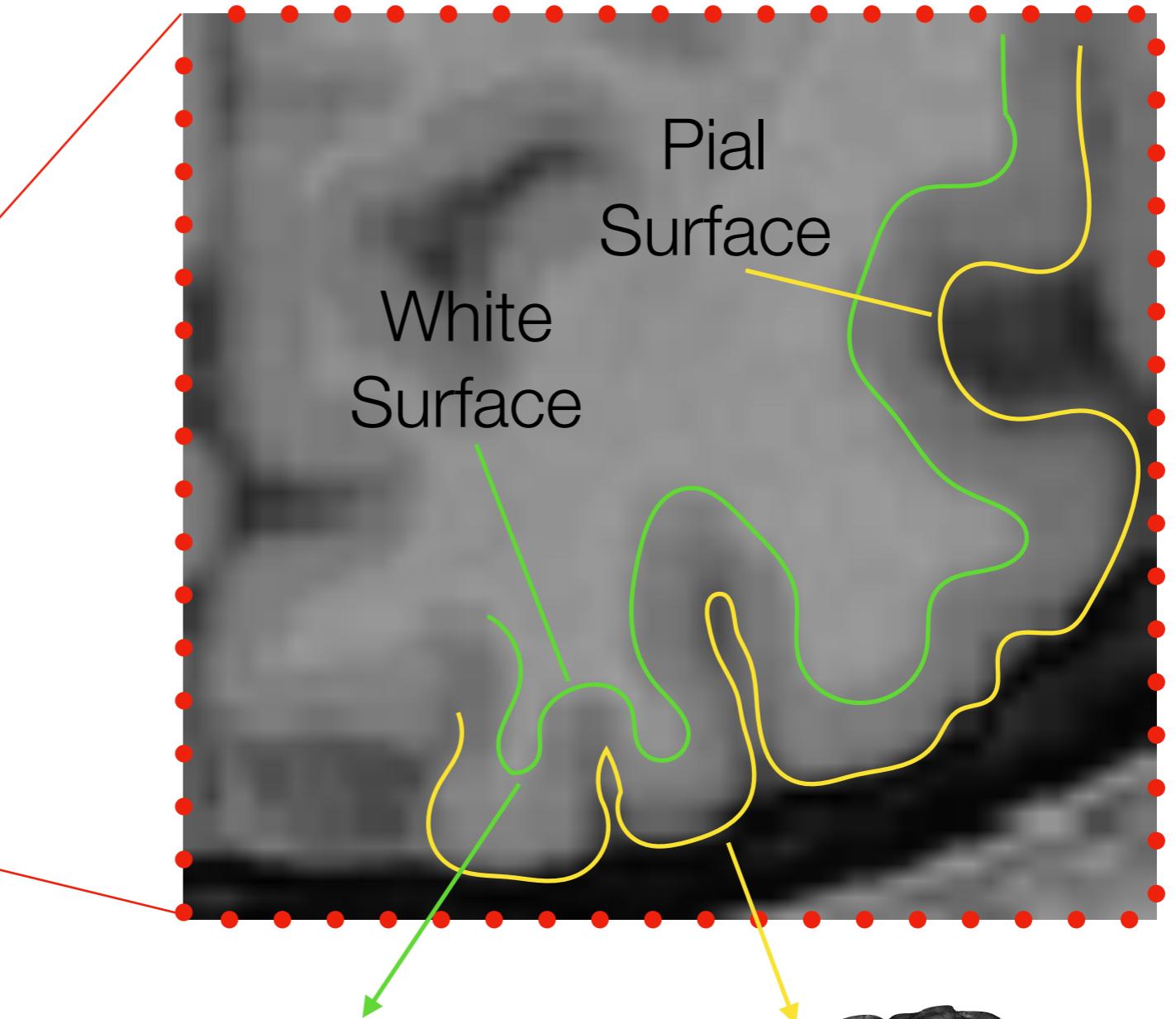
White-matter Mask



Gray-matter Mask



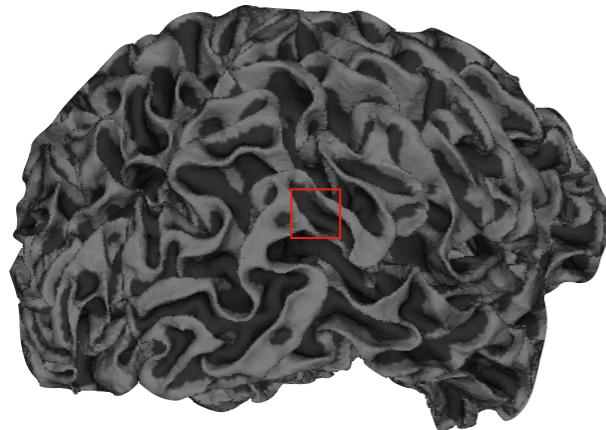
Tesselation



Tesselation

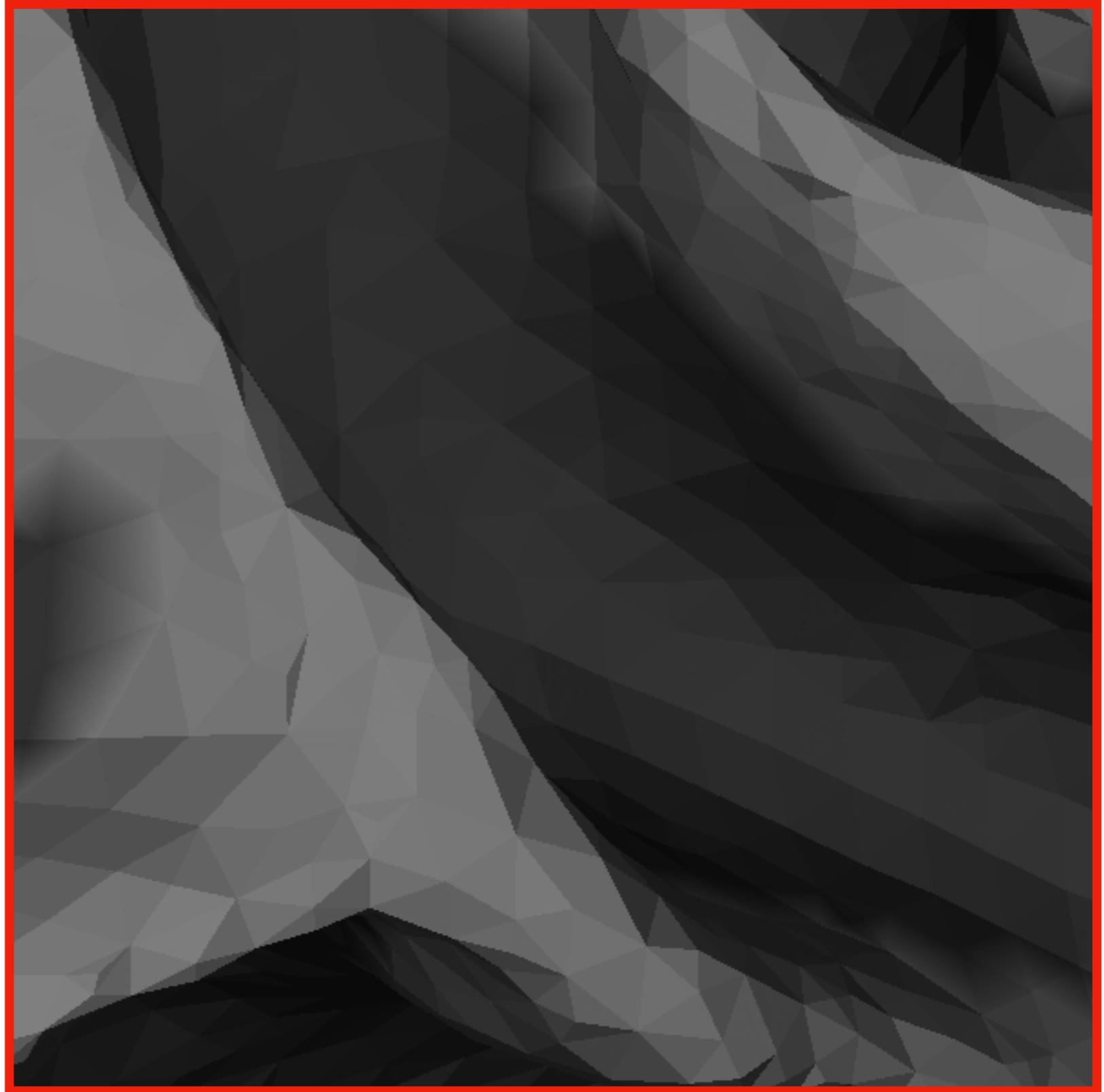
Describes the cortical surfaces as a set of vertices and triangles.

Surface files typically contain an $(n \times 3)$ matrix of coordinates and an $(m \times 3)$ matrix of triangles (integer indices into the coordinate matrix).



Data like cortical thickness and surface curvature are typically stored as vectors of values, one value per vertex.

Surfaces are represented as triangle meshes



The Human Connectome Project

- The Human Connectome Project (HCP) is an enormous effort to create a public database of human neuroimaging data
- <https://www.humanconnectome.org/>
- The HCP Young Adult dataset (headed by Kamil Ugurbil and David Van Essen) includes scans of almost 1,200 subjects
- Scans include structural data (processed with HCPPipelines) and a variety of functional data
- All data publicly available on Amazon S3 as well as from their database website: <https://db.humanconnectome.org/>

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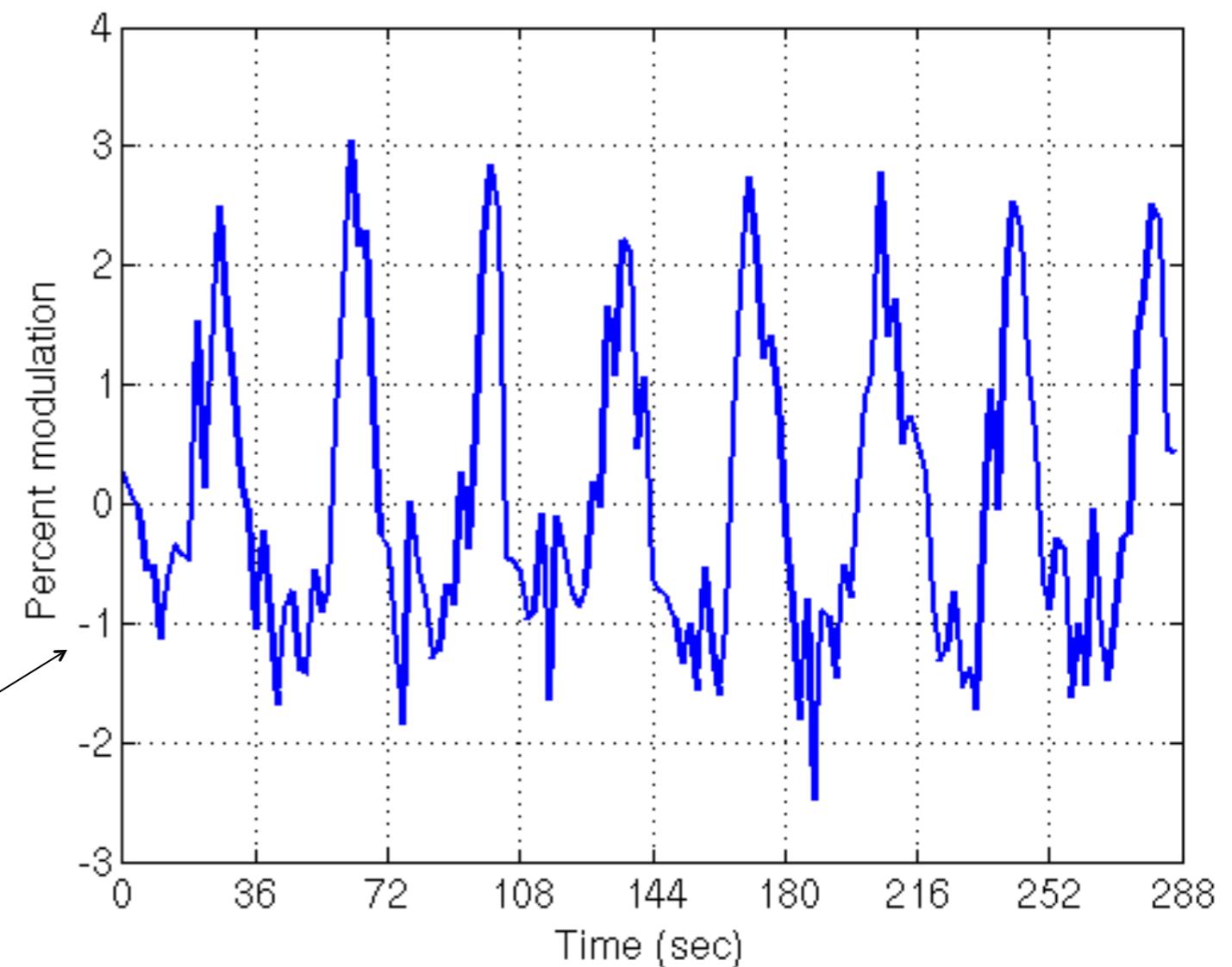
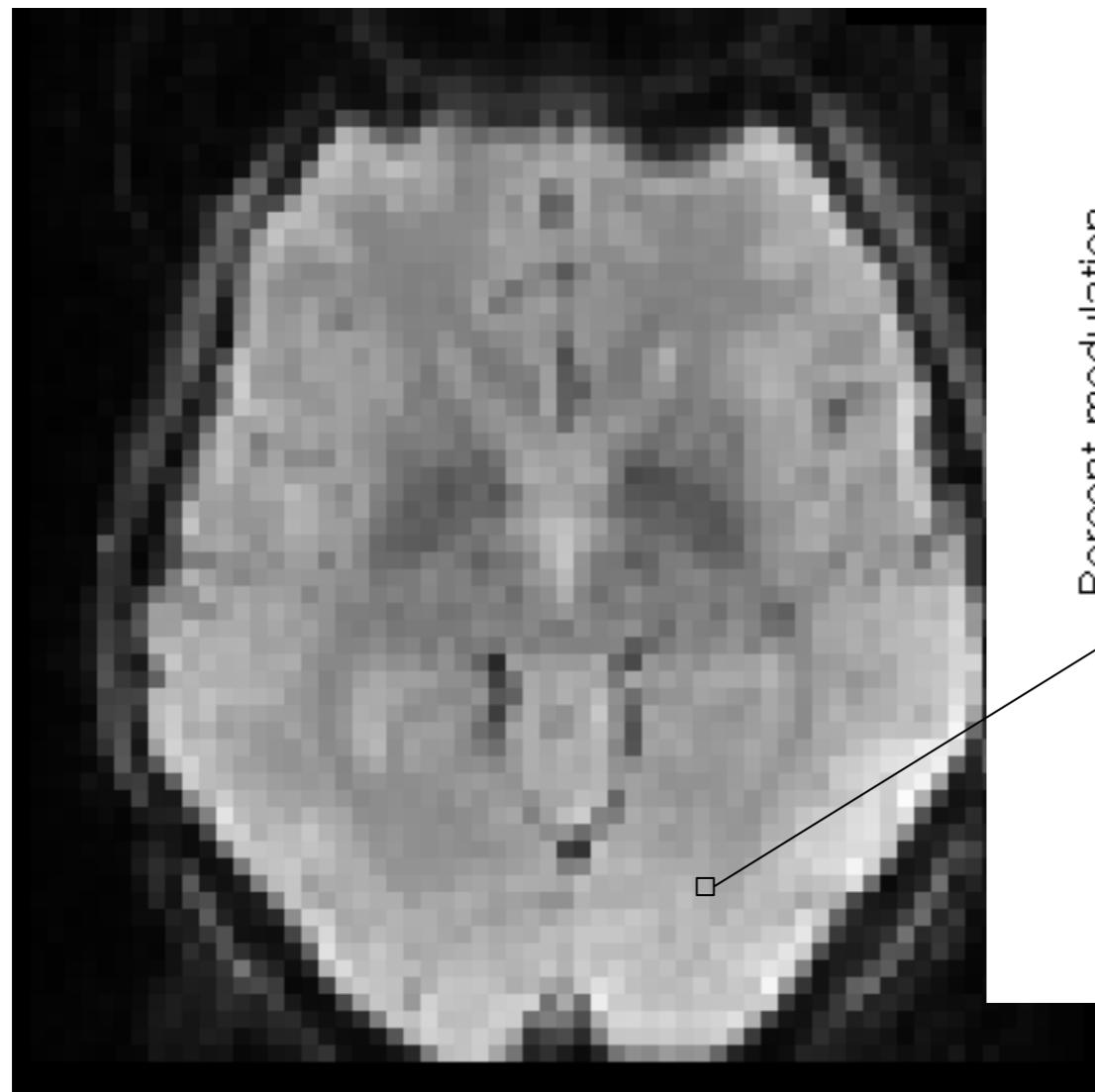
Functional MRI: BOLD Images



BOLD Image

- Lower spatial resolution
 - $2.5 \times 2.5 \times 2.5$ mm for 3T MRI
 - $1.6 \times 1.6 \times 1.6$ mm for 7T MRI
 - (varies a lot by scanner/parameters)
- Many 3D images taken in one scan:
~1s temporal resolution
(can also vary a lot)
- BOLD Signal:
Blood **O**xxygen-**L**evel **D**ependent
Signal
- Measures blood flow, **not** neural
activity, but can be used to infer neural
activity

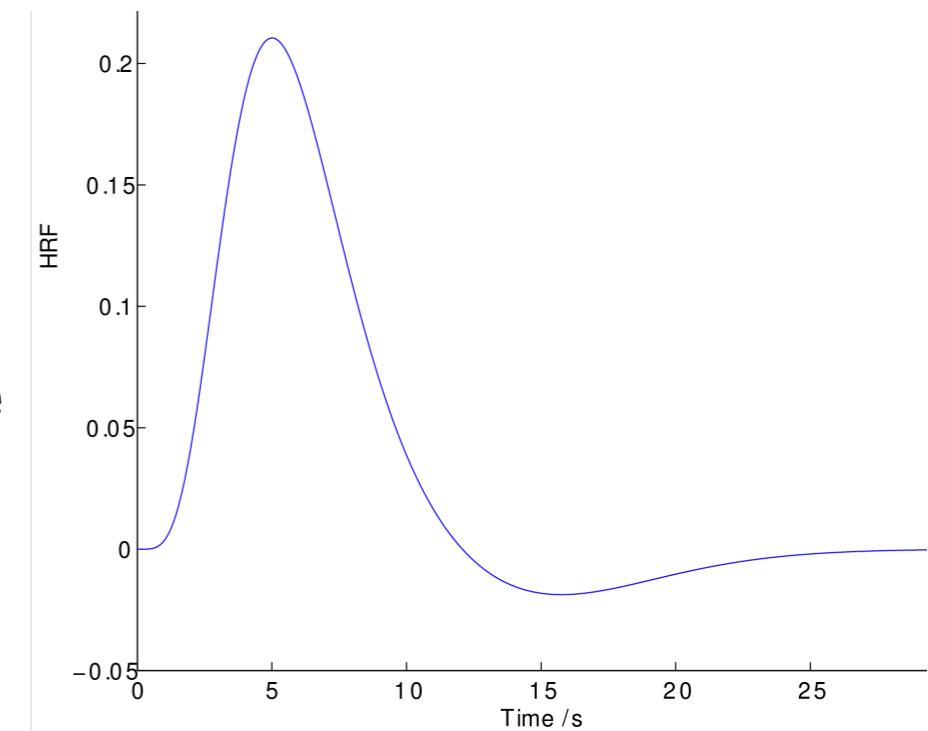
The BOLD response is small but reliable



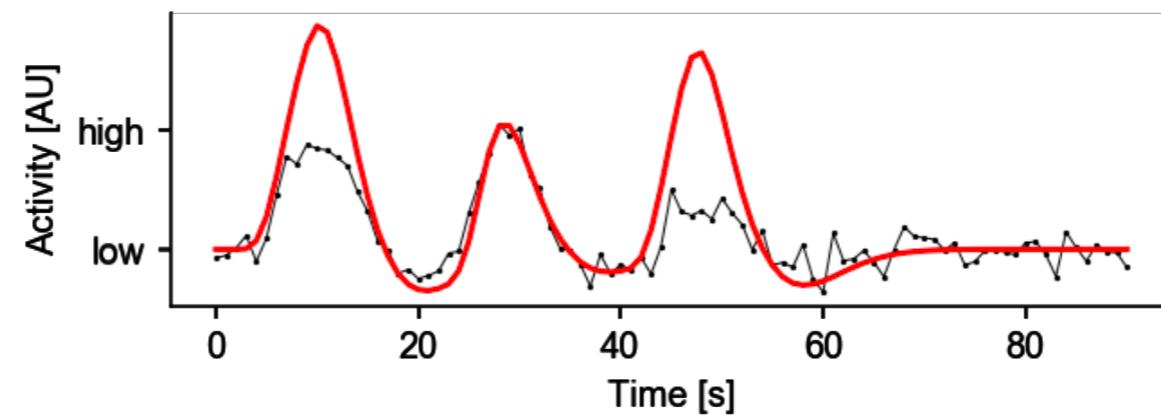
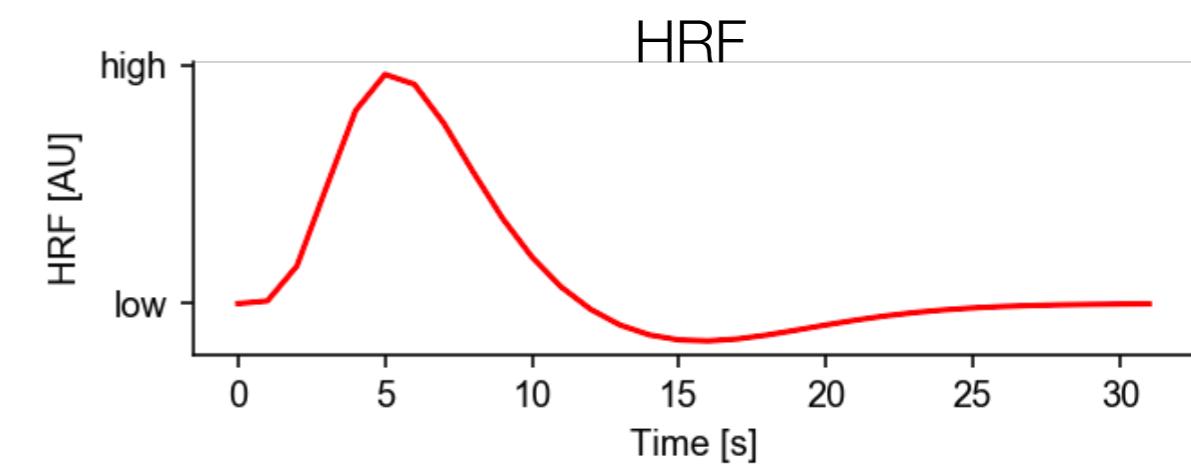
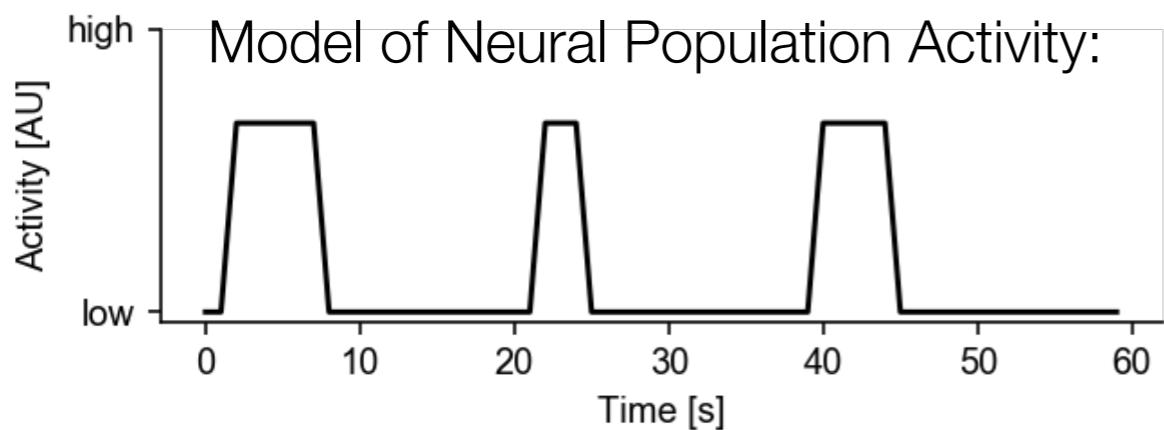
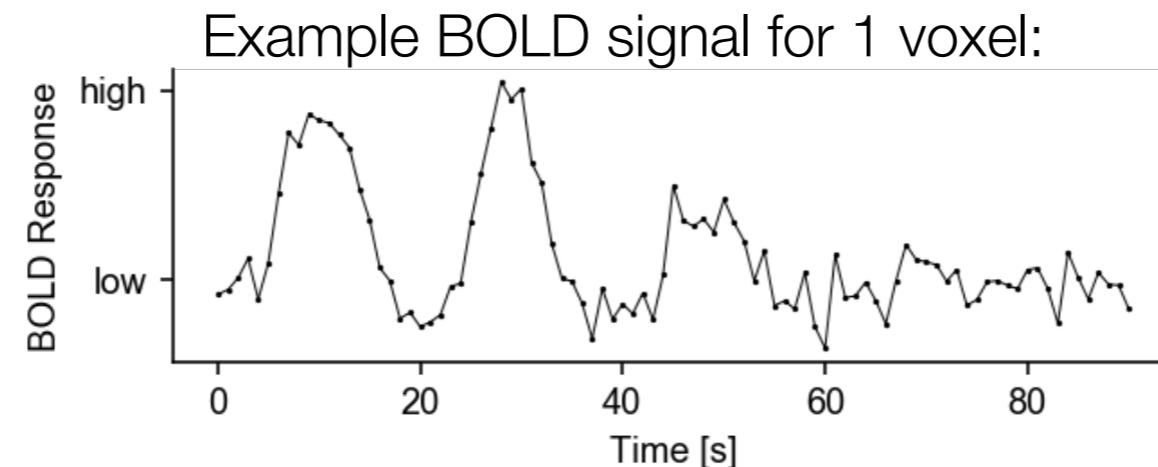
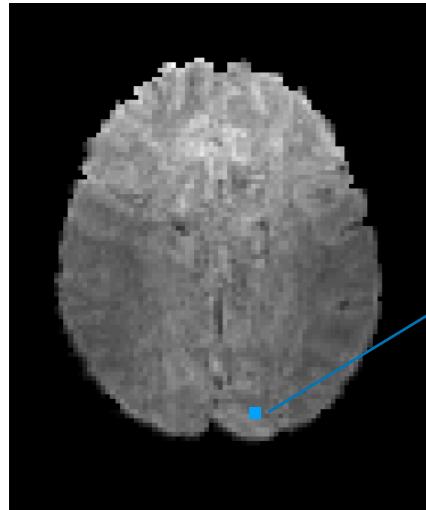
Why Measure Blood Oxygenation?

- Neurons have few energy reserves and need O_2 for metabolism
- So when they are active, they require fresh blood to arrive quickly
- The flow of blood in the brain is dynamic and routes blood preferentially to areas of higher neural activity, so:
- Higher blood flow correlates with higher neural activity; but:
- The rerouting of blood is not instantaneous; the change in blood flow over time is described by the Hemodynamic Response Function (HRF)
- If we have a measure of neural activity over time, $g(t)$, then we can estimate the BOLD response by convolving g with the HRF:

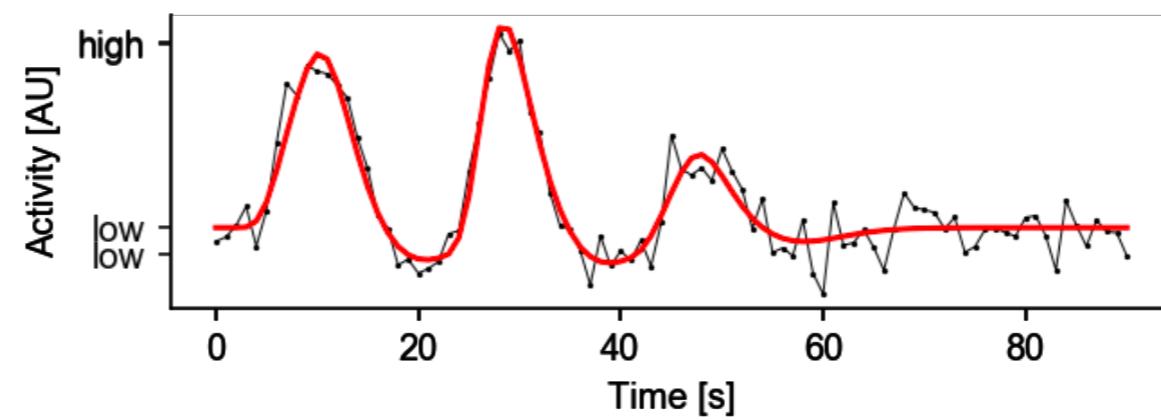
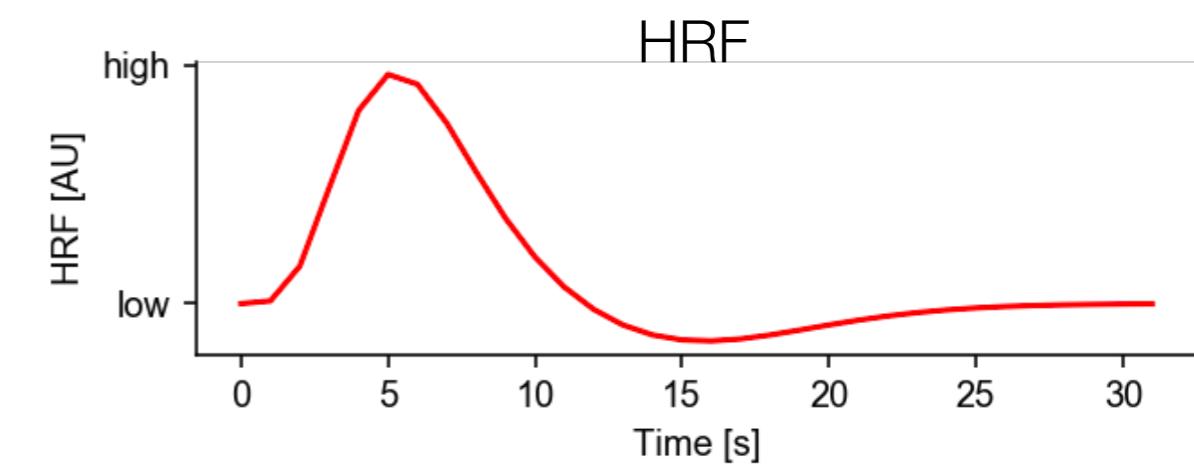
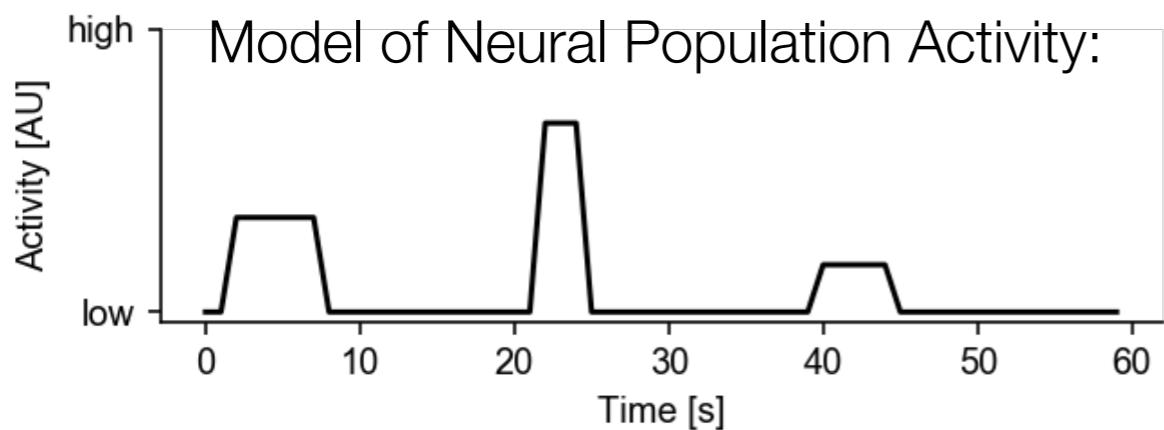
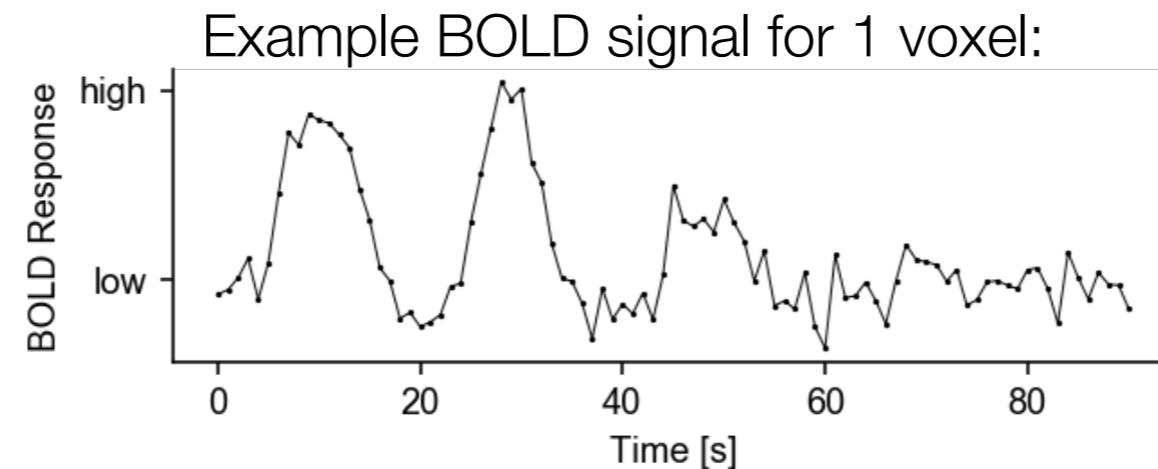
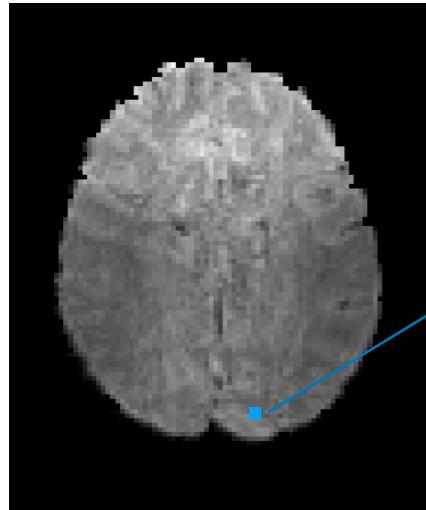
$$\text{BOLD}(t) \approx \text{HRF}(t) \otimes g(t)$$



Analyzing the BOLD Signal



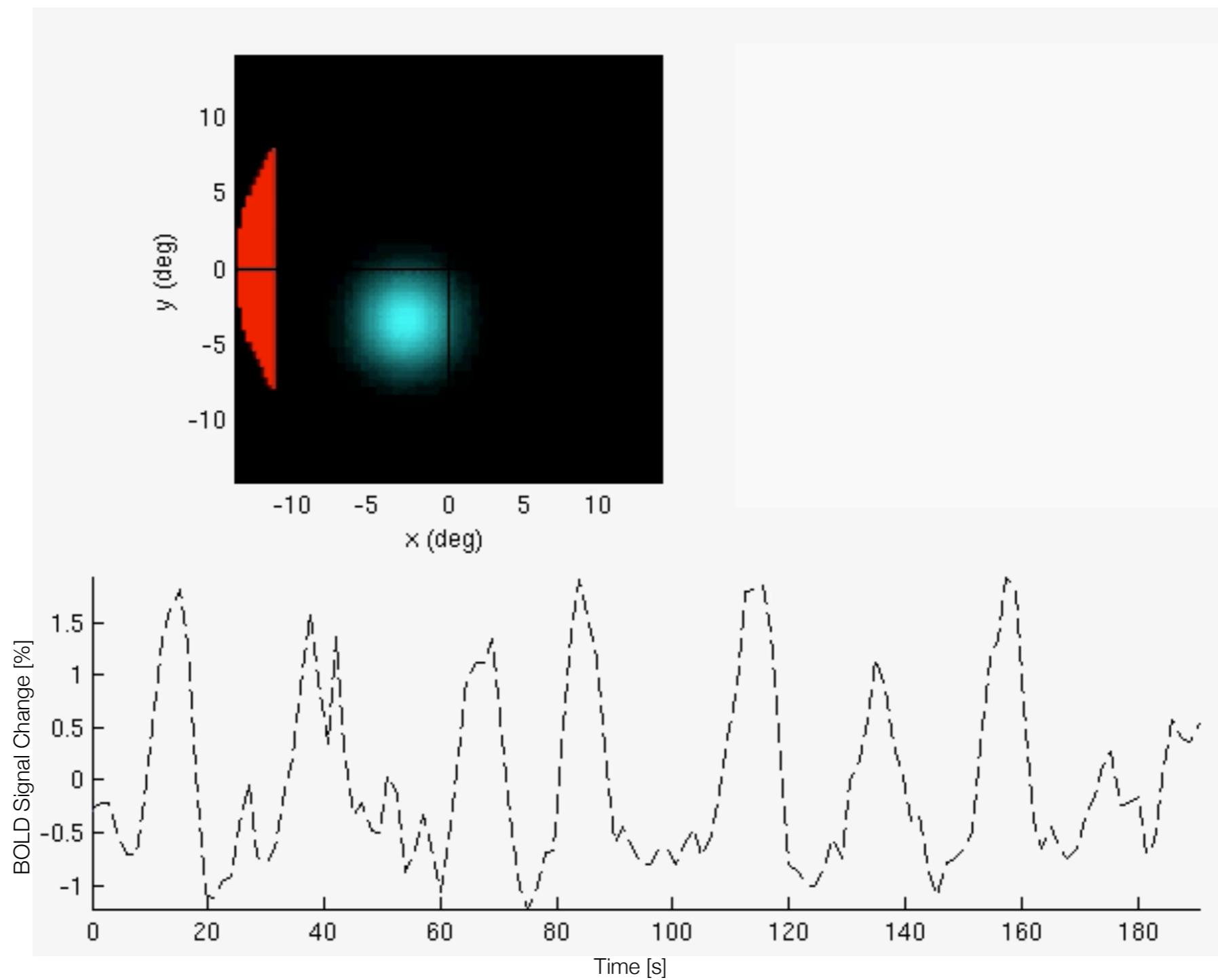
Analyzing the BOLD Signal



Visual Models: Receptive Fields

- Individual neurons in the visual system tend to respond to a set of image features that lie within a single “receptive field”, or region of the visual field
- Receptive fields for individual neurons can be quite large or small
- A population of neurons (a voxel or a cortical surface vertex) has a population receptive field (pRF)
- PRFs are usually modeled as a Gaussian blob over the visual field (in terms of x and y); high values of the Gaussian indicate high sensitivity to stimulus at that location

Model a Visual pRF



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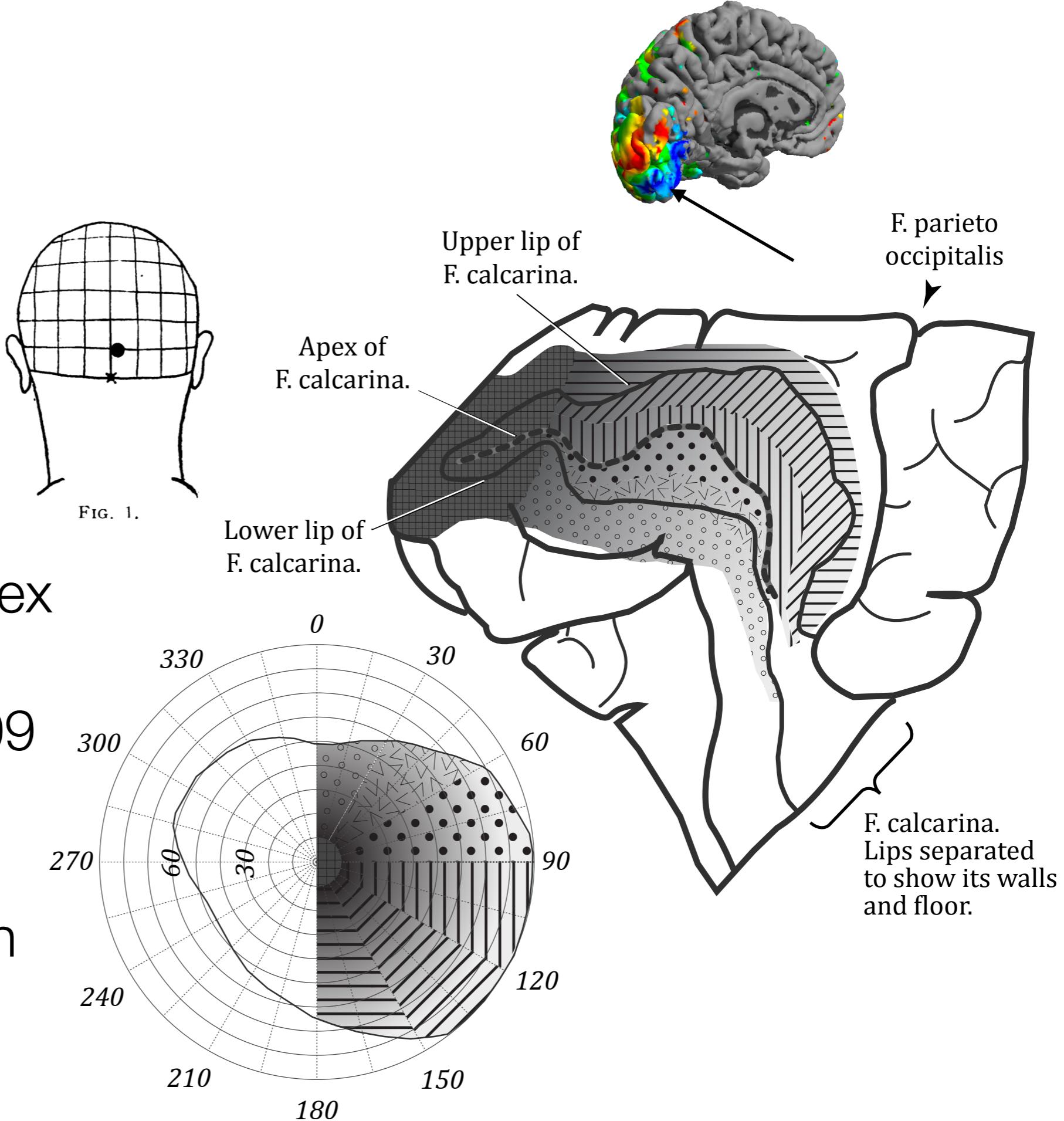
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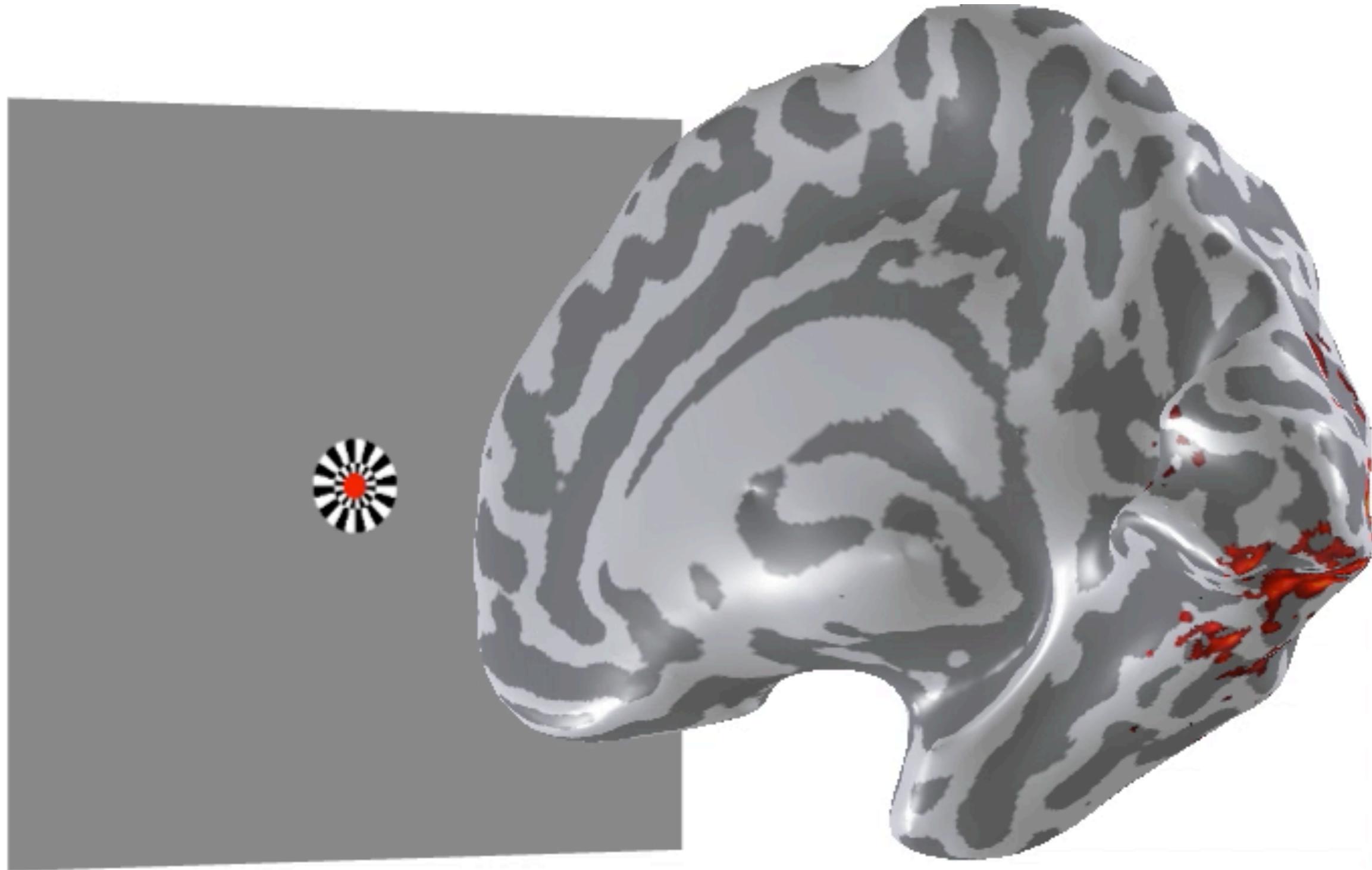
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Retinotopy

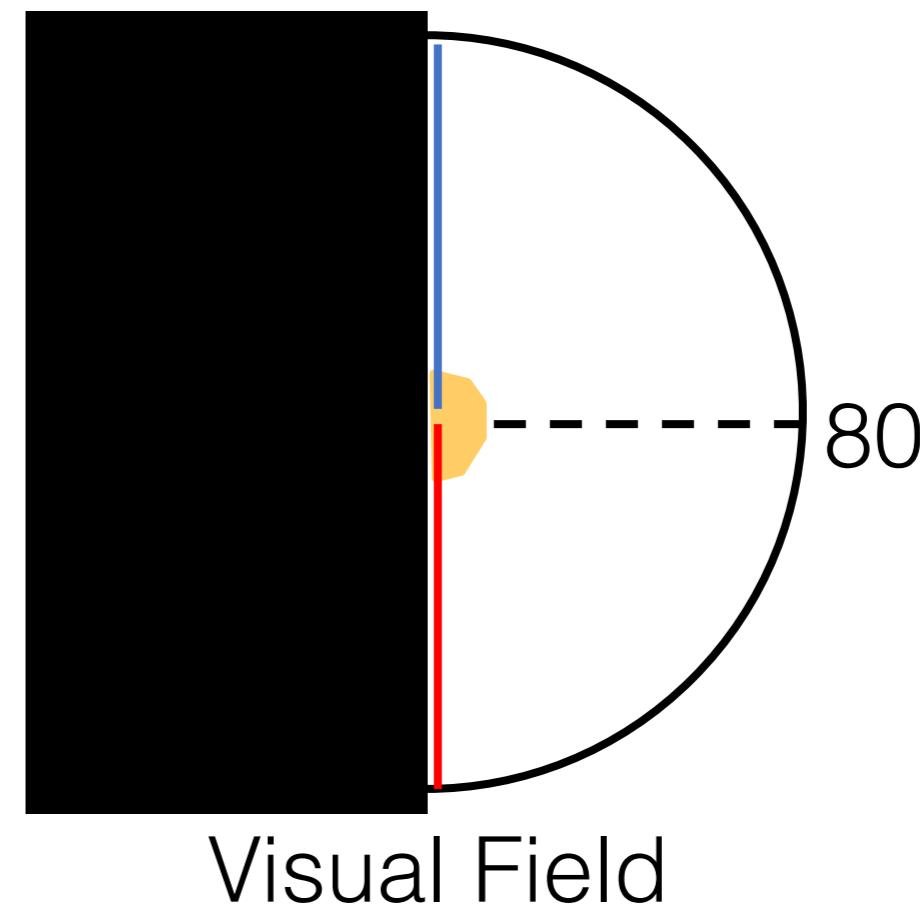
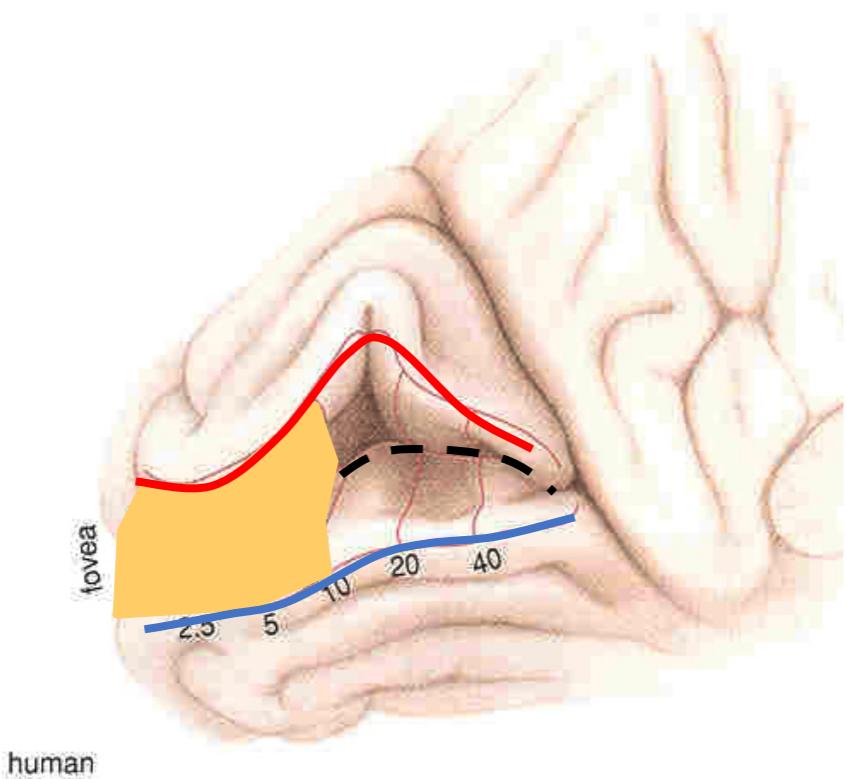
Retinotopic organization on cortex was discovered by Tatsuji Inouye in 1909 and later studied by Gordon Holmes in 1918, both via lesion studies.



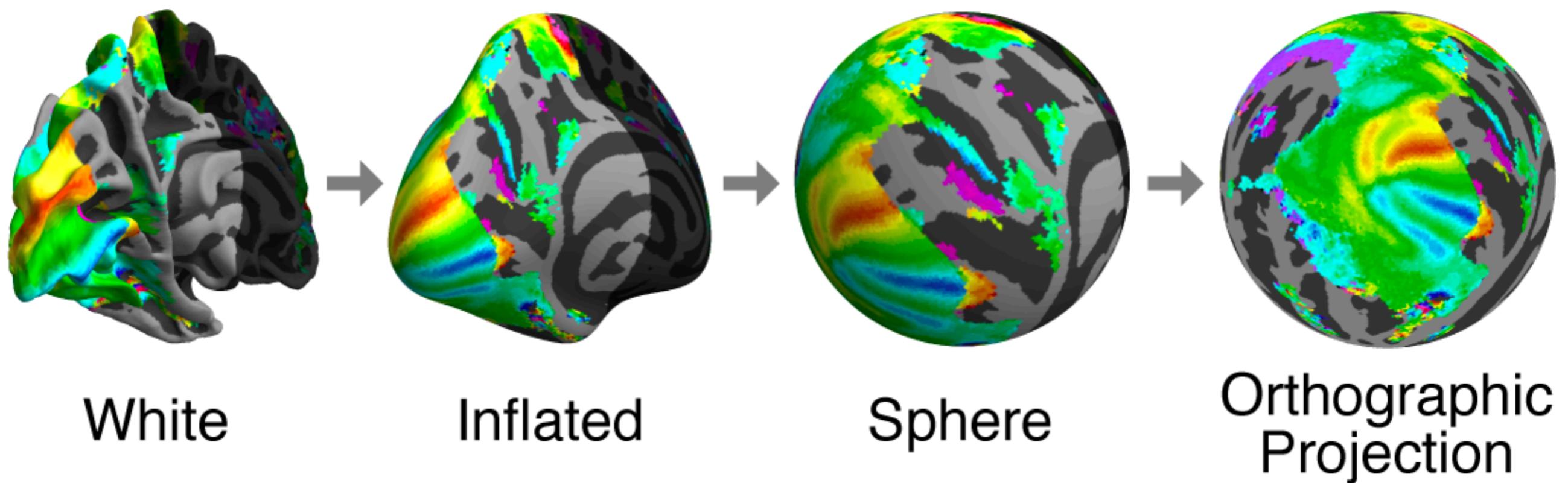
Retinotopic Mapping



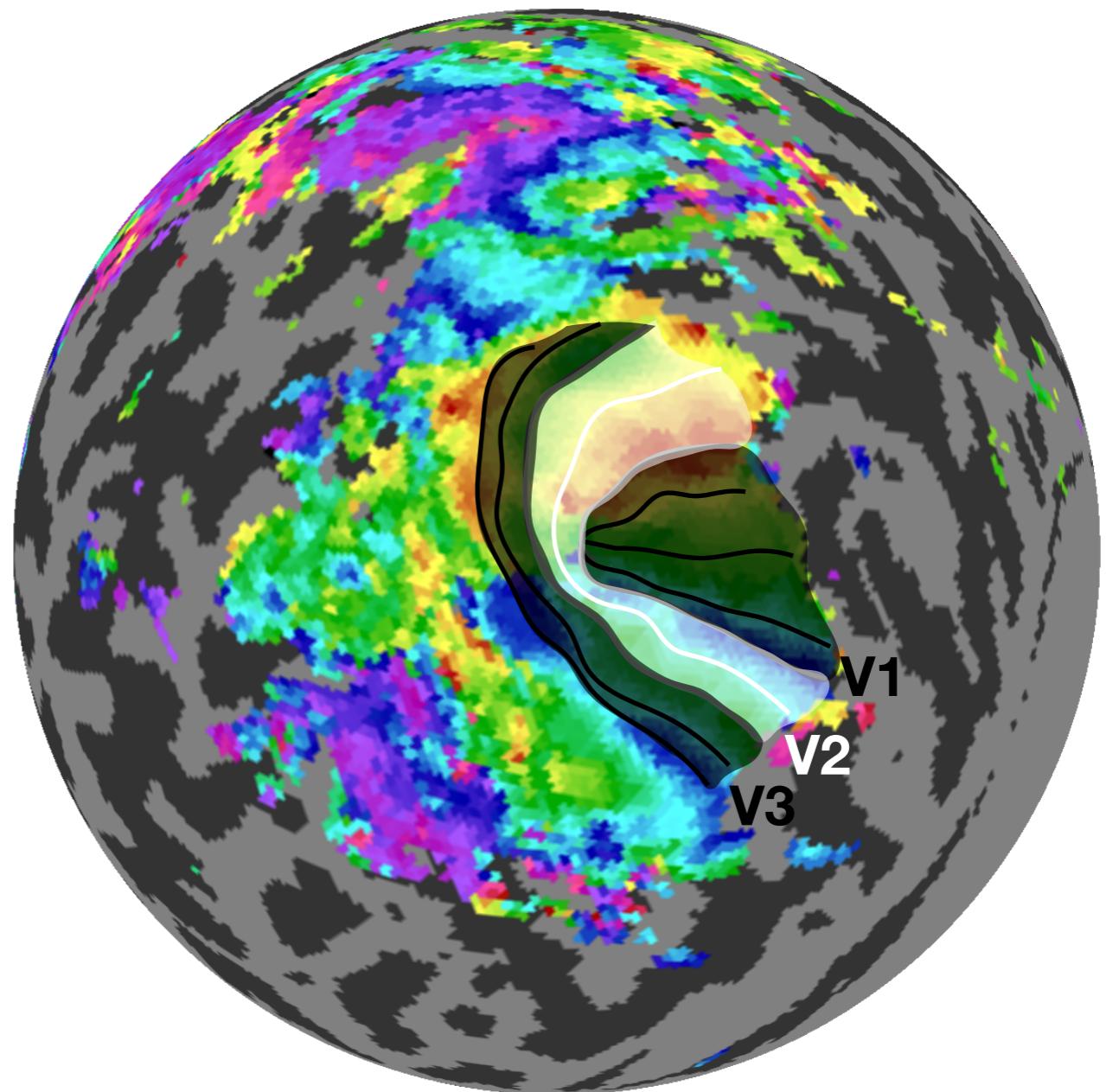
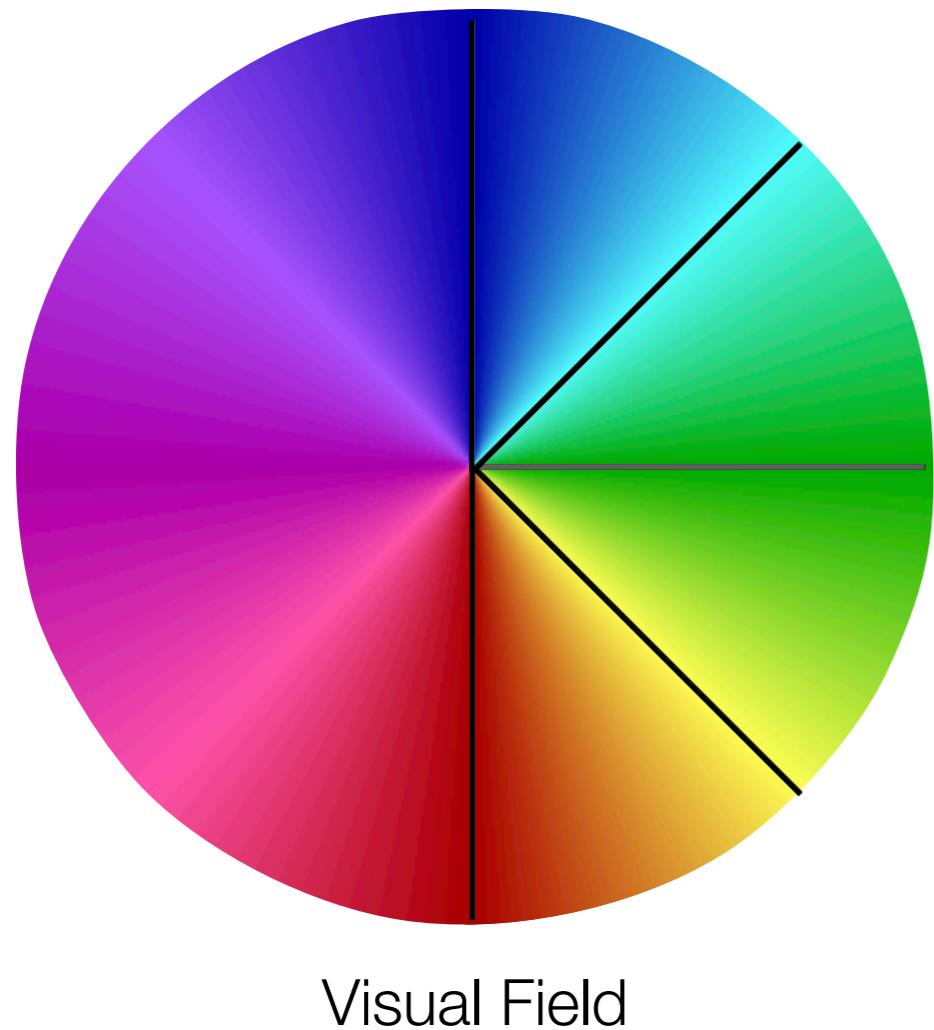
There is a conserved arrangement of the retina on cortex across subjects.



V1, V2, and V3 Organization



V1, V2, and V3 Organization



Retinotopy: Cortical Magnification



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Conclusions

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

<https://github.com/noahbenson/neurohackademy2019>

If you have additional interests related to:

- The Human Connectome Project
- fMRI Modeling
- Retinotopic Maps
- Structural/Surface Alignment and Atlases
- MRI tools in Python...

... I'll be around until next Tuesday evening and would be happy to chat about any of these!

Neuropythy: <https://github.com/noahbenson/neuropythy>

HCP: <https://db.humanconnectome.org/>

HCP Retinotopy: <https://osf.io/bw9ec/>

More Tutorials: <https://nben.net/>