

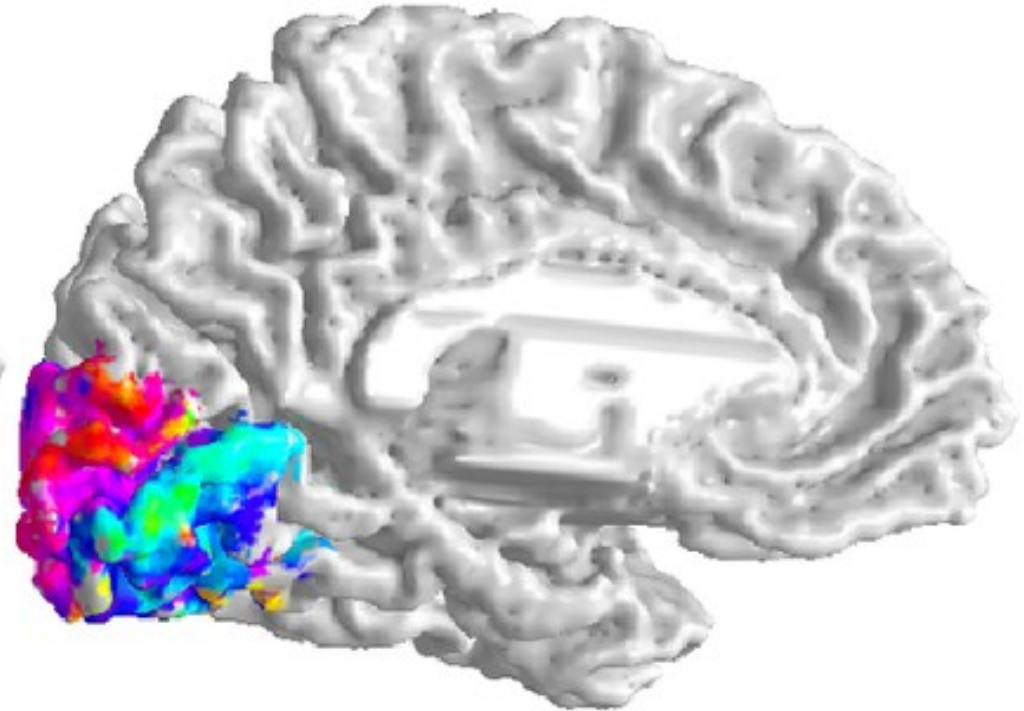
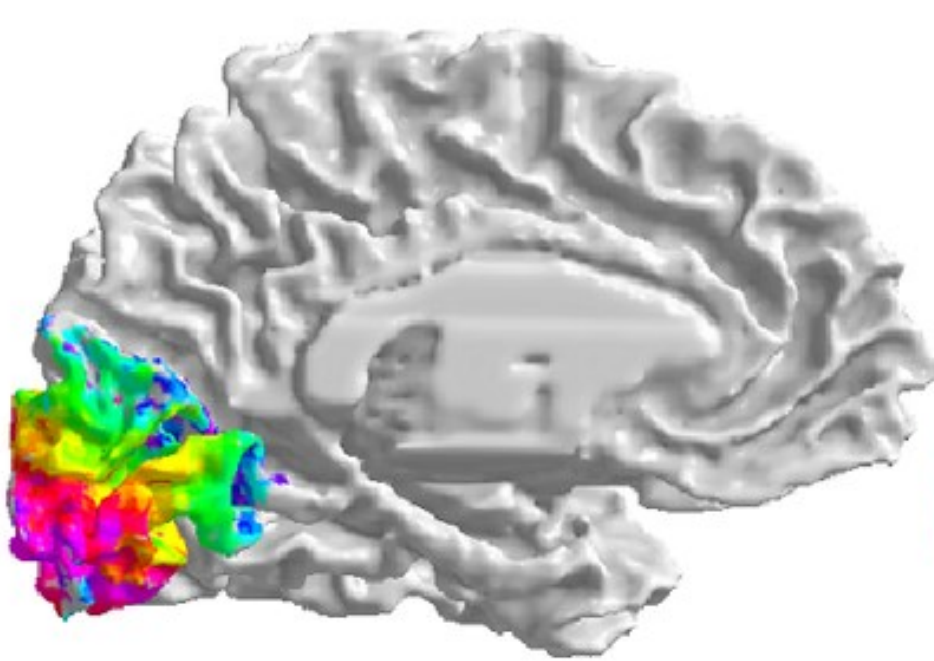
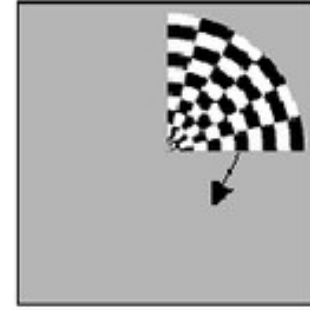
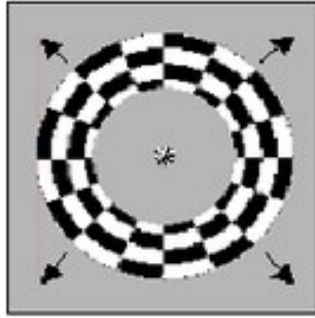
CS463/516

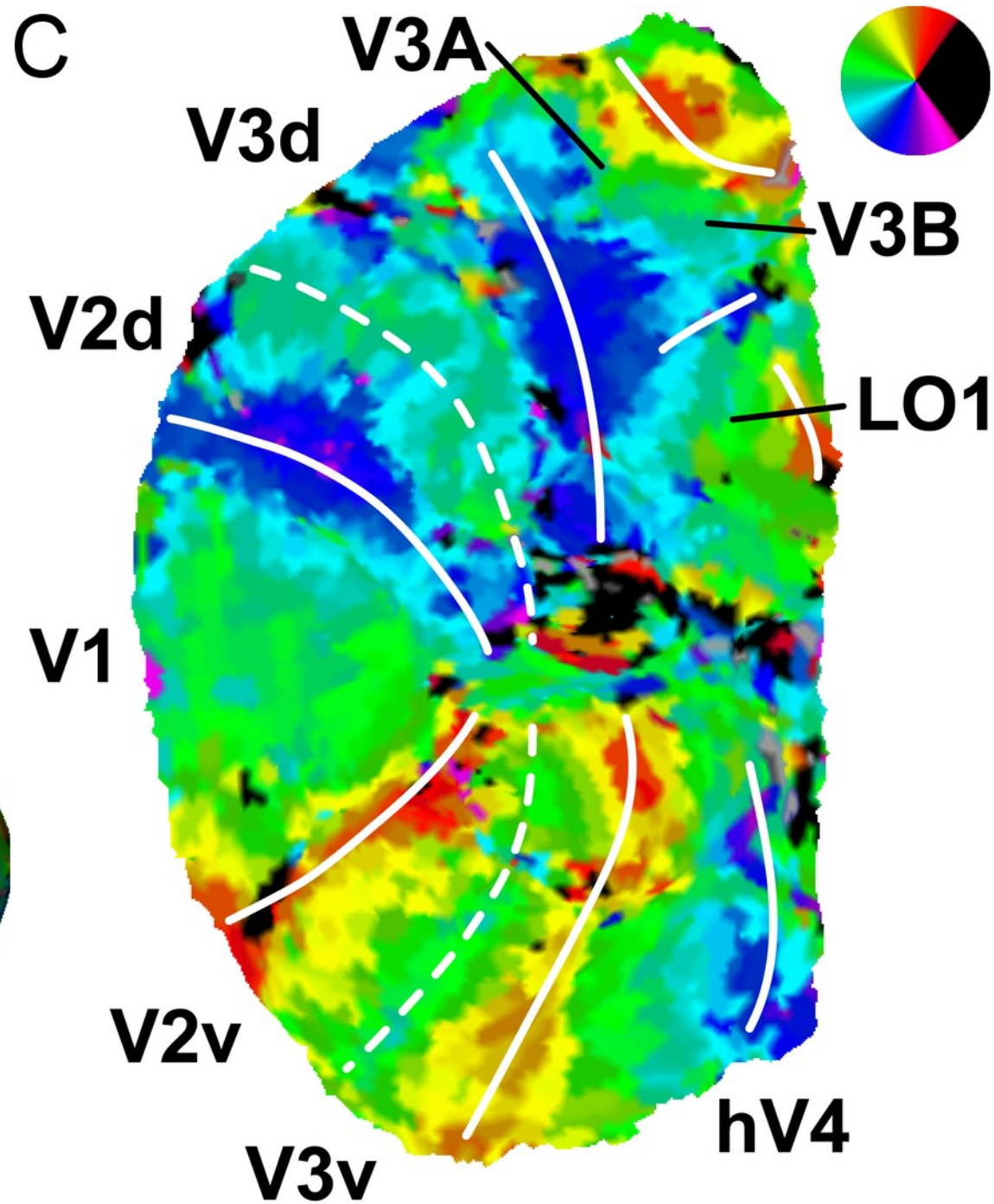
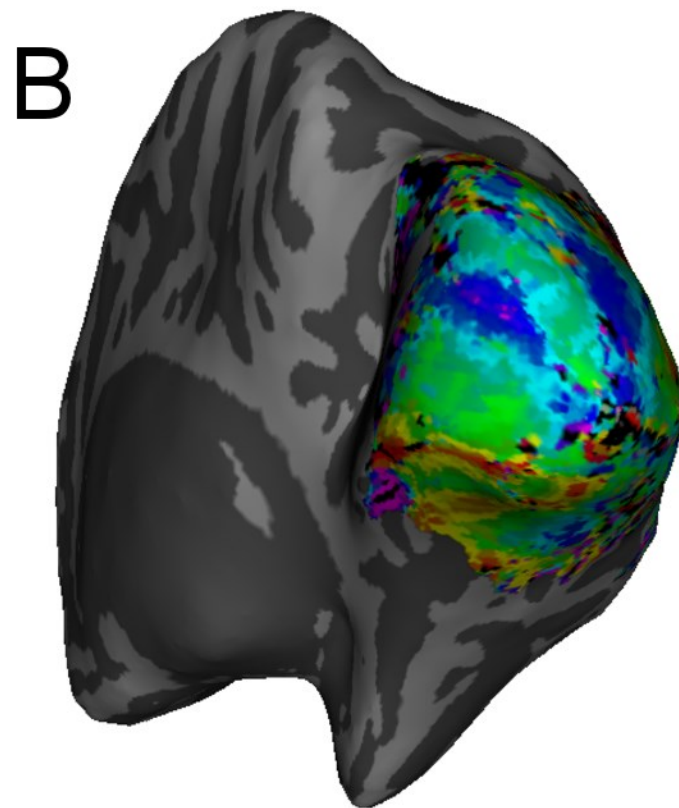
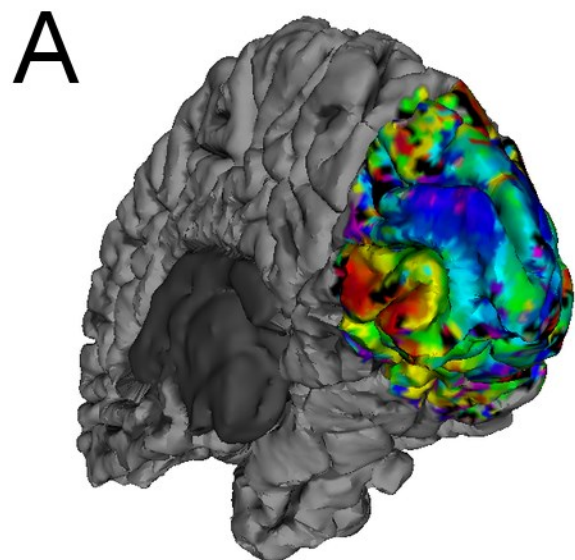
Lecture 18

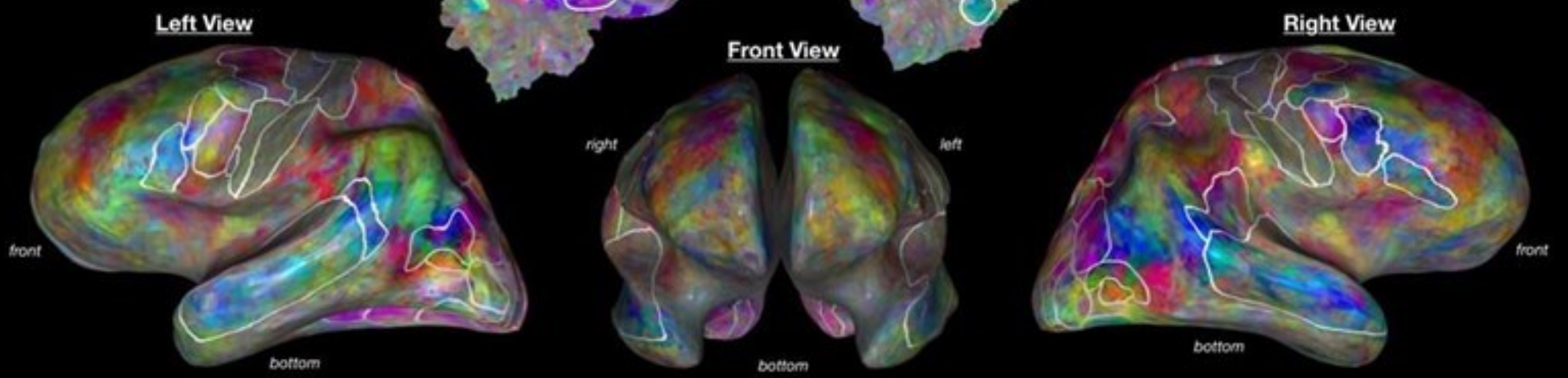
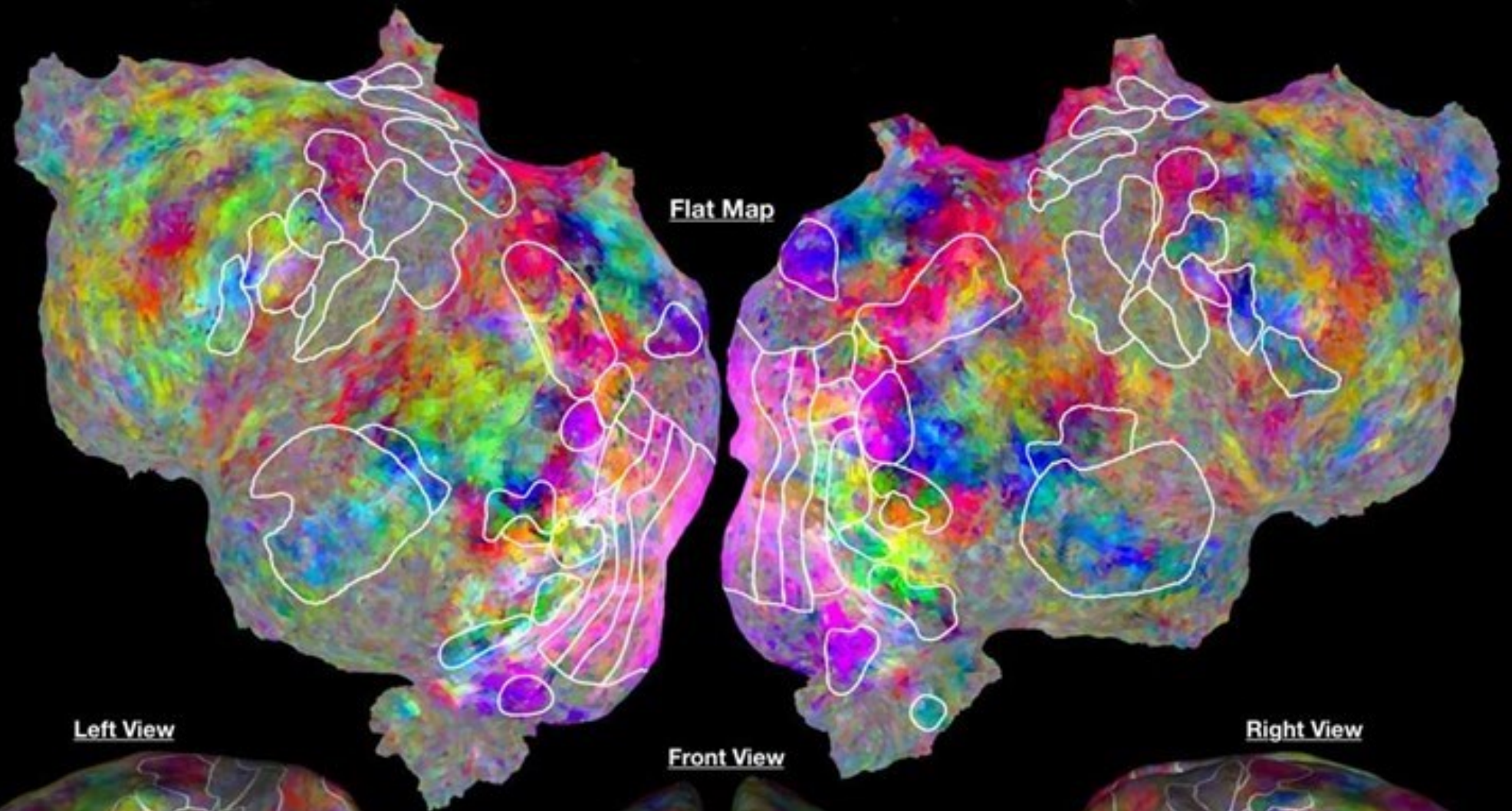
More remarks on final project

Final project due Friday august 15th !

Retinotopic mapping

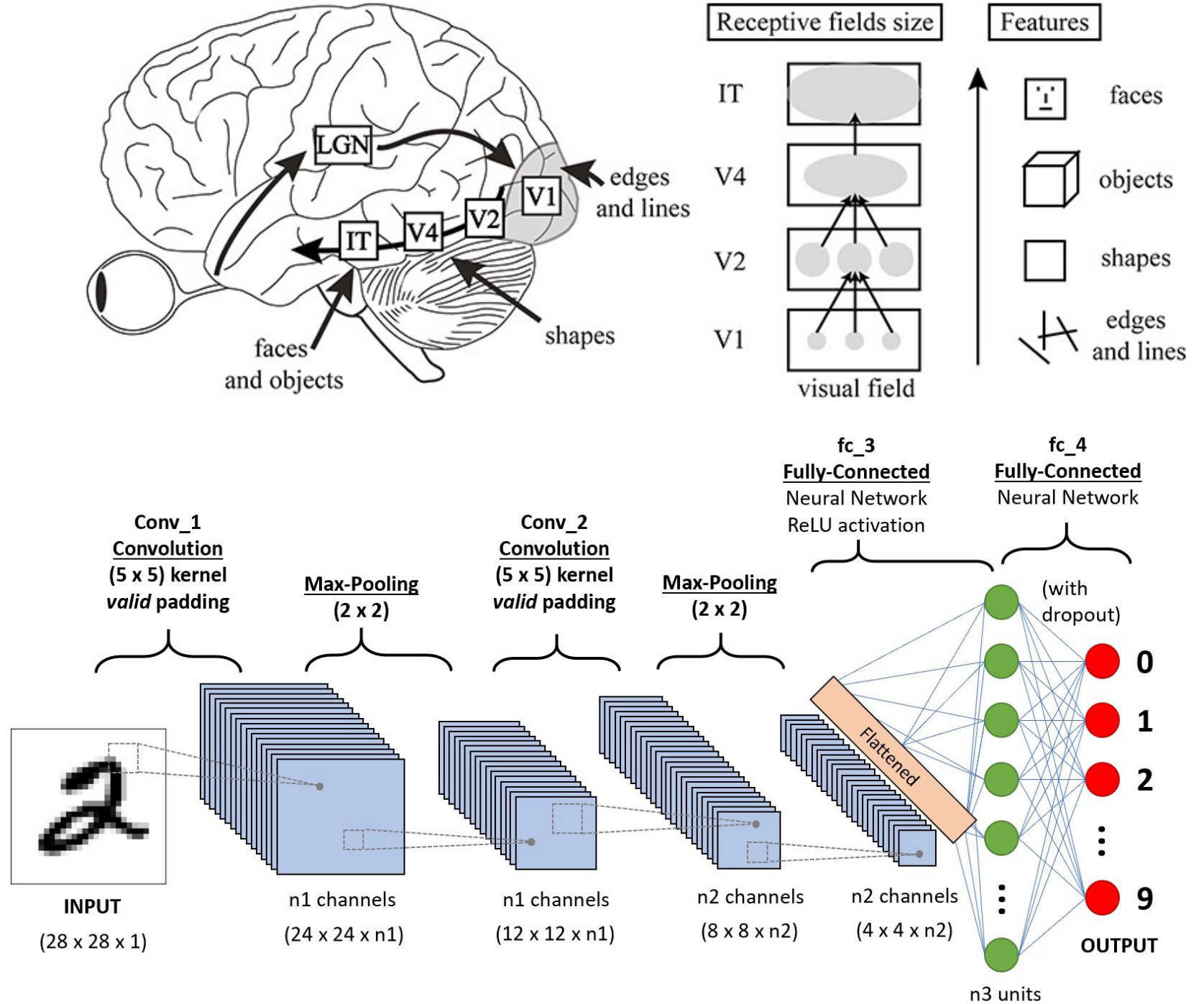






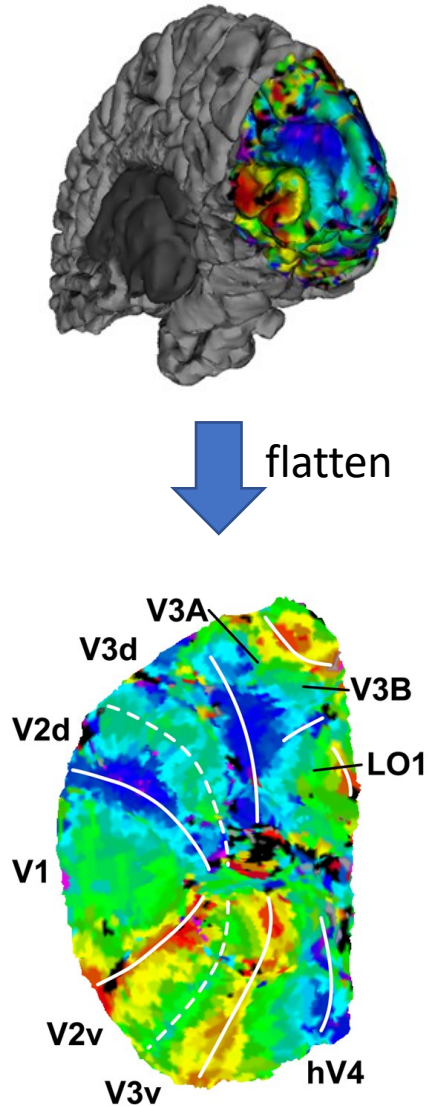
CNN vs mammalian visual system:

- Convolutional neural network (CNN)
- Some claim that the CNN 'recapitulates' the anatomy of the visual system:



Surface-based analysis

- <https://neurostars.org/t/converting-4d-3d-t-bold-image-to-3d-2d-t-flat-map/15765>



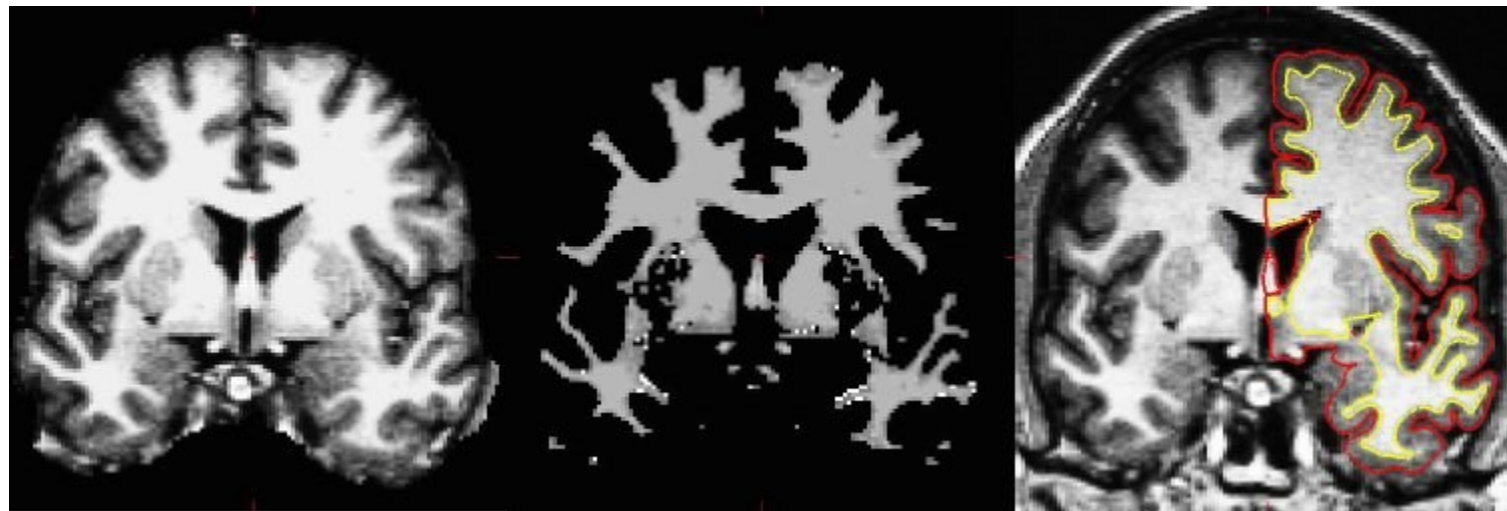
Can now
use 2d CNN

```
afni_proc.py
```

```
-subj_id FT.surf  
-blocks tshift align volreg surf blur scale regress  
-copy_anat FT/FT_anat+orig  
-dsets FT/FT_epi_r?+orig.HEAD  
-surf_anat FT/SUMA/FTmb_SurfVol+orig  
-surf_spec FT/SUMA/FTmb_?h.spec  
-tcats_remove_first_trs 2  
-align_opts_aea -cost lpc+ZZ -giant_move  
-volreg_align_to MIN_OUTLIER  
-volreg_align_e2a  
-blur_size 6  
-regress_stim_times FT/AV1_vis.txt FT/AV2_aud.txt  
-regress_stim_labels vis aud  
-regress_basis 'BLOCK(20,1)'  
-regress_motion_per_run  
-regress_censor_motion 0.3  
-regress_opts_3dT -jobs 2 -gltsym 'SYM: vis -aud'  
-glt_label 1 V-A
```

Freesurfer

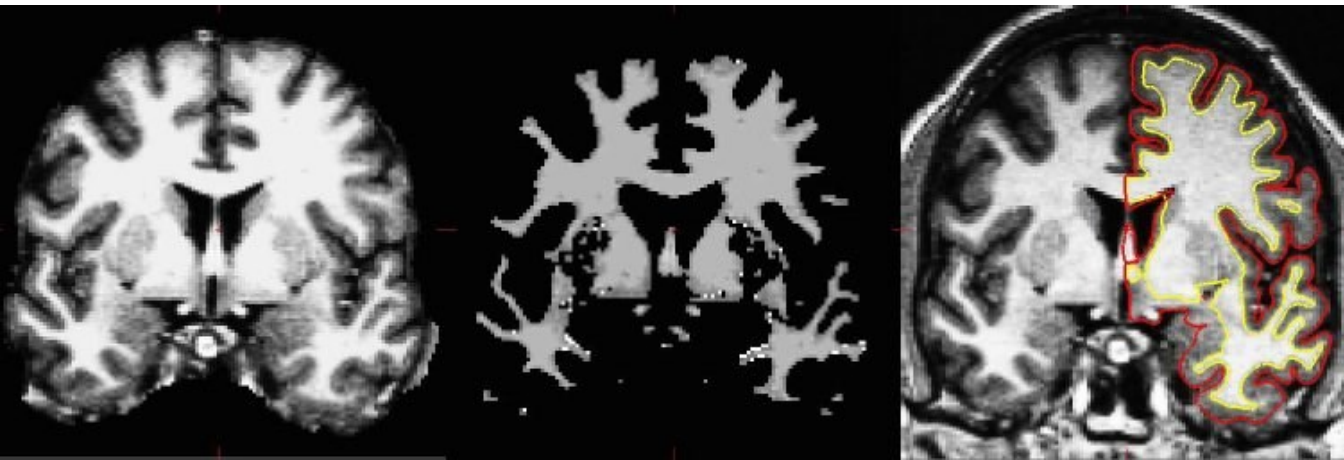
- Freesurfer is a set of tools for study of cortical and subcortical anatomy
- Constructs model of boundary between white matter and cortical gray matter as well as the pial surface
- Once these surfaces are known, can quantify many anatomical measures:
 - Cortical thickness, surface area, curvature, surface normal at each patch
- Surfaces can be inflated and/or flattened for improved visualization
- Most of the pipeline is automated



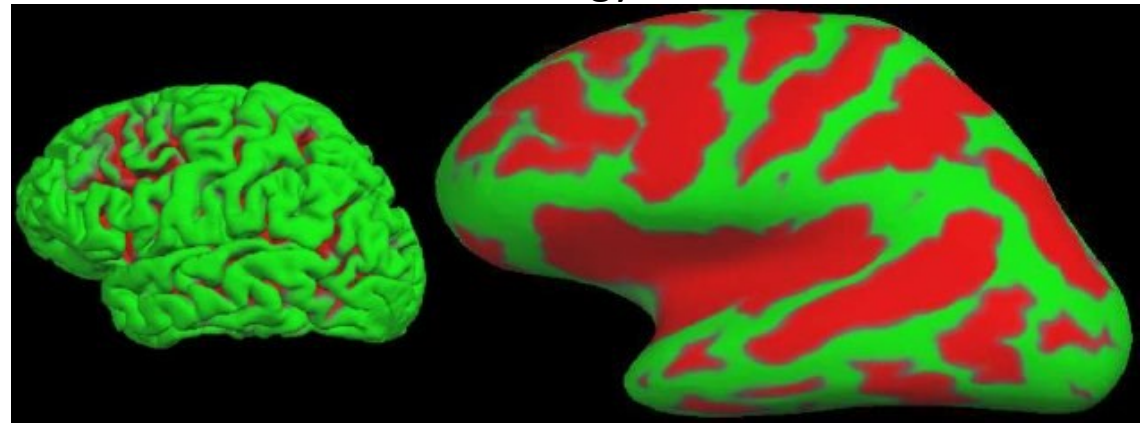
Surface-based stream

- Surface-based pipeline (applied to raw T1) consists of several stages:
 - 1) T1 is registered to an MNI atlas, which allows freesurfer to find seed points for later stages
 - 2) magnetic field bias is estimated using variation in white matter intensity and then subtracted out
 - 3) skull is stripped using deformable template model
 - 4) voxels classified as white matter/non-white matter based on intensity and neighbor constraints
 - 5) cutting planes chosen to separate hemispheres from each other, and remove cerebellum/brainstem (location of cutting plane based on seed points from MNI template)
 - 6) initial surface generated for each hemisphere by *tiling* the outside of the white matter mass for that hemisphere
 - 7) initial surface refined, to follow intensity gradients between white and gray matter (white surface)
 - 8) white surface nudged to follow intensity gradient between gray matter and CSF (pial surface)
 - Distance between white and pial surface gives cortical thickness
 - Can also compute local curvature, surface area, and surface normal

Three stages from freesurfer cortical analysis pipeline



3d view of pial surface. Can be inflated to show the areas in the sulci. Green indicates a gyrus, red indicates sulcus

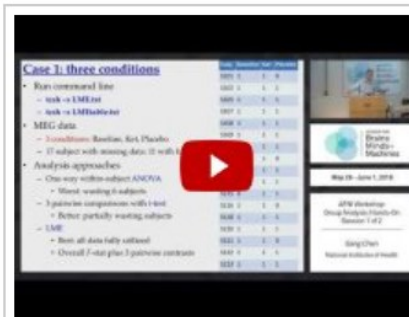


AFNI bootcamp on SUMA (and others)

- <https://cbmm.mit.edu/afni>
- Lectures 24-28



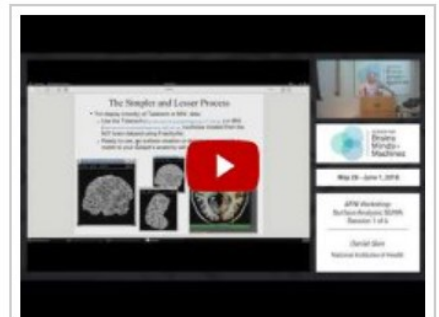
21 - Group Analysis: Part 2 of 2



22 - Group Analysis - Hands-On: Part 1 of 2



23 - Group Analysis - Hands-On: Part 2 of 2



24 - Surface Analysis: SUMA: Part 1 of 5



25 - Surface Analysis: SUMA: Part 2 of 5



26 - Surface Analysis: SUMA: Part 3 of 5



27 - Surface Analysis: SUMA: Part 4 of 5



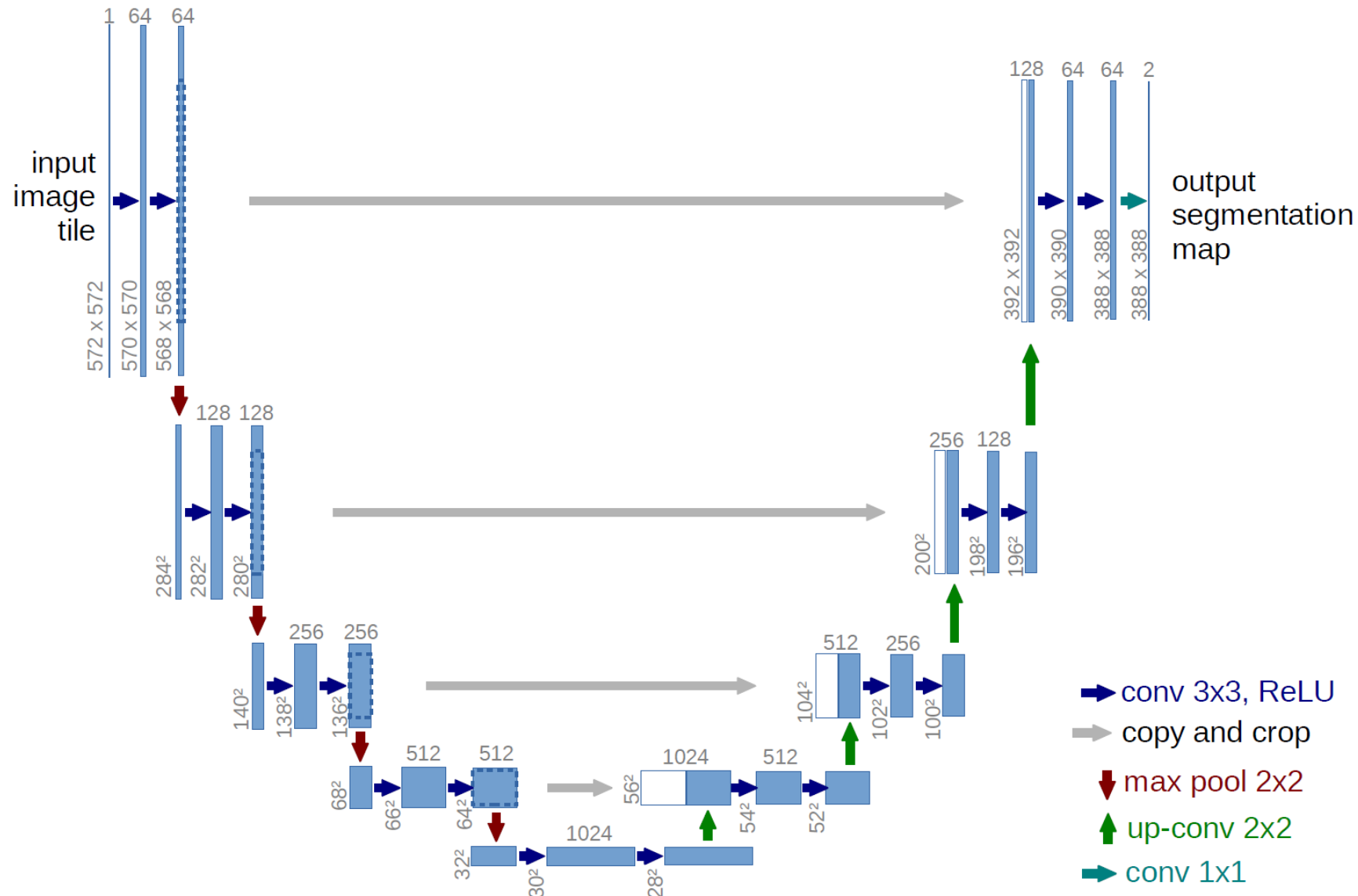
28 - Surface Analysis: SUMA: Part 5 of 5

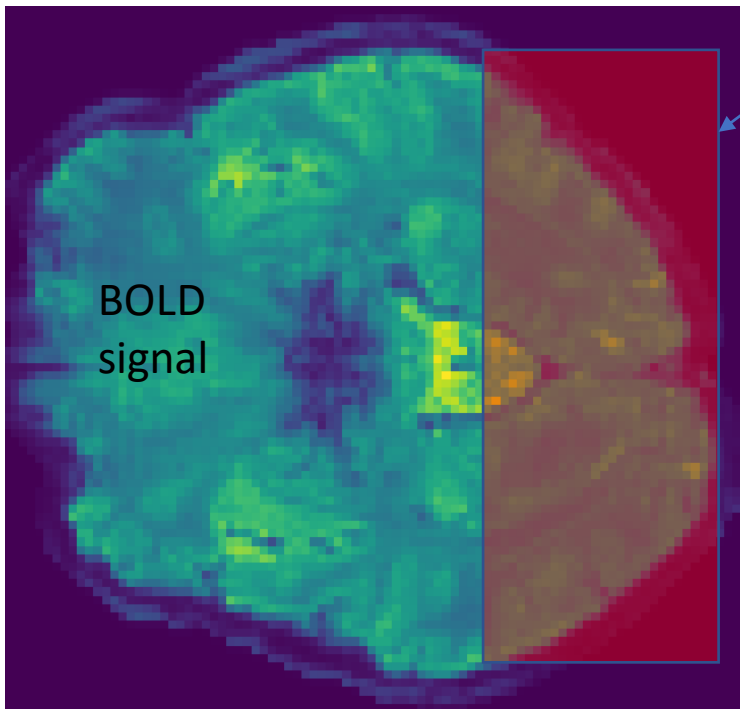
Demo – getting BOLD signal corresponding to images

- How to get the BOLD signal at the time when the image was presented?
- Use the .tsv, and knowledge of hemodynamic delay (4 seconds)
- Average the images in the specified time interval
- Load the corresponding image from disk
- At the end, you should have 2 matrices:
 - 1) $96 \times 96 \times 76 \times n_images$ matrix of BOLD data
 - 2) $500 \times 500 \times 3 \times n_images$ matrix of image data
 - Where n_images is the number of unique images used in the experiment (~1200)
 - Can also convert to grayscale (which gives $500 \times 500 \times n_images$) matrix
- You will then use these matrices to train your model

one possible approach: U-net

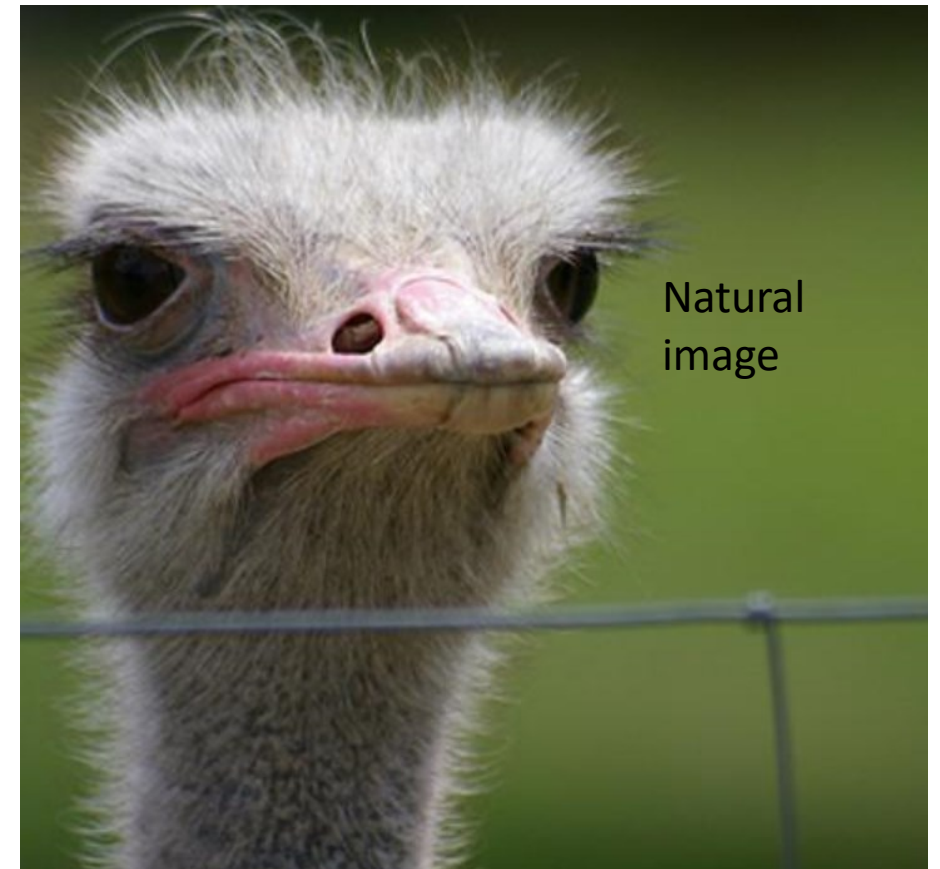
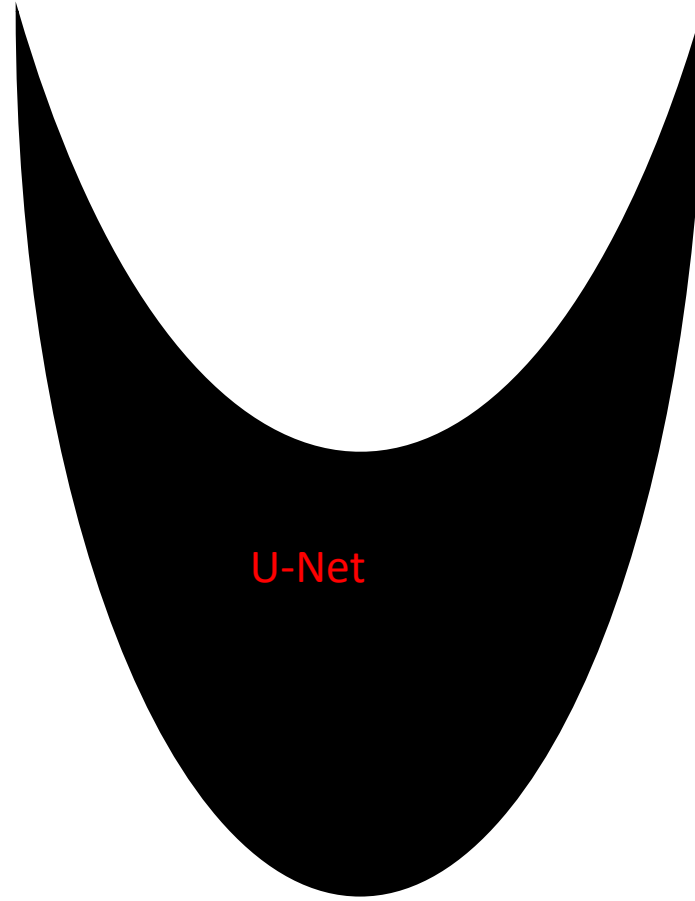
- U-net is a deep convolutional architecture that performs an image-to-image mapping, very popular in medical imaging for segmentation
 - Contracting and expanding path
 - Hence the name
- Can use U-net or similar architectures to map the BOLD signal directly to an image





(non-bandpass filtered image
shown here for simplicity)

Can use only back of
brain to reduce data size
(for colab)



U-net original article:
<https://arxiv.org/abs/1505.04597>

Can try this code: (or make your own)
<https://github.com/ellisdg/3DUnetCNN>