

# fMRI data analysis in mrVista

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PSYCH 204B

# Functional data processing stream

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- Organize session directory
- Initialize and preprocess functional data
- Between-scan motion correction
- Align functional data to T1 volume anatomy
- Install gray matter segmentation and transform an ROI from volume to inplane
- GLM and pRF analyses (Part 2)
- Visualization on inflated cortical surface (Part 2)

## **Part 6: GLM and pRF analyses**

# Analysis overview

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- Analyzing the Localizer and Adaptation datasets require running a GLM
  - Experimental parameter files (parfiles) for each run are located in the session directories in /Stimuli/parfiles/
  - Parfiles are text files containing 4 columns: (1) block onset time, (2) condition number, (3) condition name, and (4) condition plotting color (RGB values)
- Analyzing the Retinotopy dataset requires running a pRF (population receptive field) model
  - Experimental parameter files for Bar experiment are located in the session directory in /Stimuli/

# GLM analysis

```
script_fLocFilter_1Hz_run1.par
1 0 Fixation 1 1 1
2 8 0 Fixation 1 1 1
3 16 0 Fixation 1 1 1
4 24 5 lsf_car 1 1 0
5 32 8 lsf_house 0 8.000000e-001 0
6 40 0 Fixation 1 1 1
7 48 10 lsf_number 2.000000e-001 2.000000e-001 2.000000e-001
8 56 5 lsf_car 1 1 0
9 64 3 lsf_body 0 0 1
10 72 6 lsf_instrument 8.000000e-001 8.000000e-001 0
11 80 1 lsf_adult 1 0 0
12 88 8 lsf_house 0 8.000000e-001 0
13 96 2 lsf_child 8.000000e-001 0 0
14 104 0 Fixation 1 1 1
15 112 4 lsf_limb 0 0 8.000000e-001
16 120 4 lsf_limb 0 0 8.000000e-001
17 128 10 lsf_number 2.000000e-001 2.000000e-001 2.000000e-001
18 136 2 lsf_child 8.000000e-001 0 0
19 144 3 lsf_body 0 0 1
20 152 7 lsf_corridor 0 1 0
21 160 9 lsf_word 0 0 0
22 168 7 lsf_corridor 0 1 0
23 176 0 Fixation 1 1 1
24 184 1 lsf_adult 1 0 0
25 192 0 Fixation 1 1 1
26 200 7 lsf_corridor 0 1 0
27 208 6 lsf_instrument 8.000000e-001 8.000000e-001 0
28 216 5 lsf_car 1 1 0
29 224 9 lsf_word 0 0 0
30 232 0 Fixation 1 1 1
31 240 6 lsf_instrument 8.000000e-001 8.000000e-001 0
32 248 1 lsf_adult 1 0 0
33 256 10 lsf_number 2.000000e-001 2.000000e-001 2.000000e-001
34 264 2 lsf_child 8.000000e-001 0 0
35 272 6 lsf_instrument 8.000000e-001 8.000000e-001 0
36 280 0 Fixation 1 1 1
37 288 1 lsf_adult 1 0 0
38 296 2 lsf_child 8.000000e-001 0 0
39 304 0 Fixation 1 1 1
40 312 0 Fixation 1 1 1
```

*trial onset time*

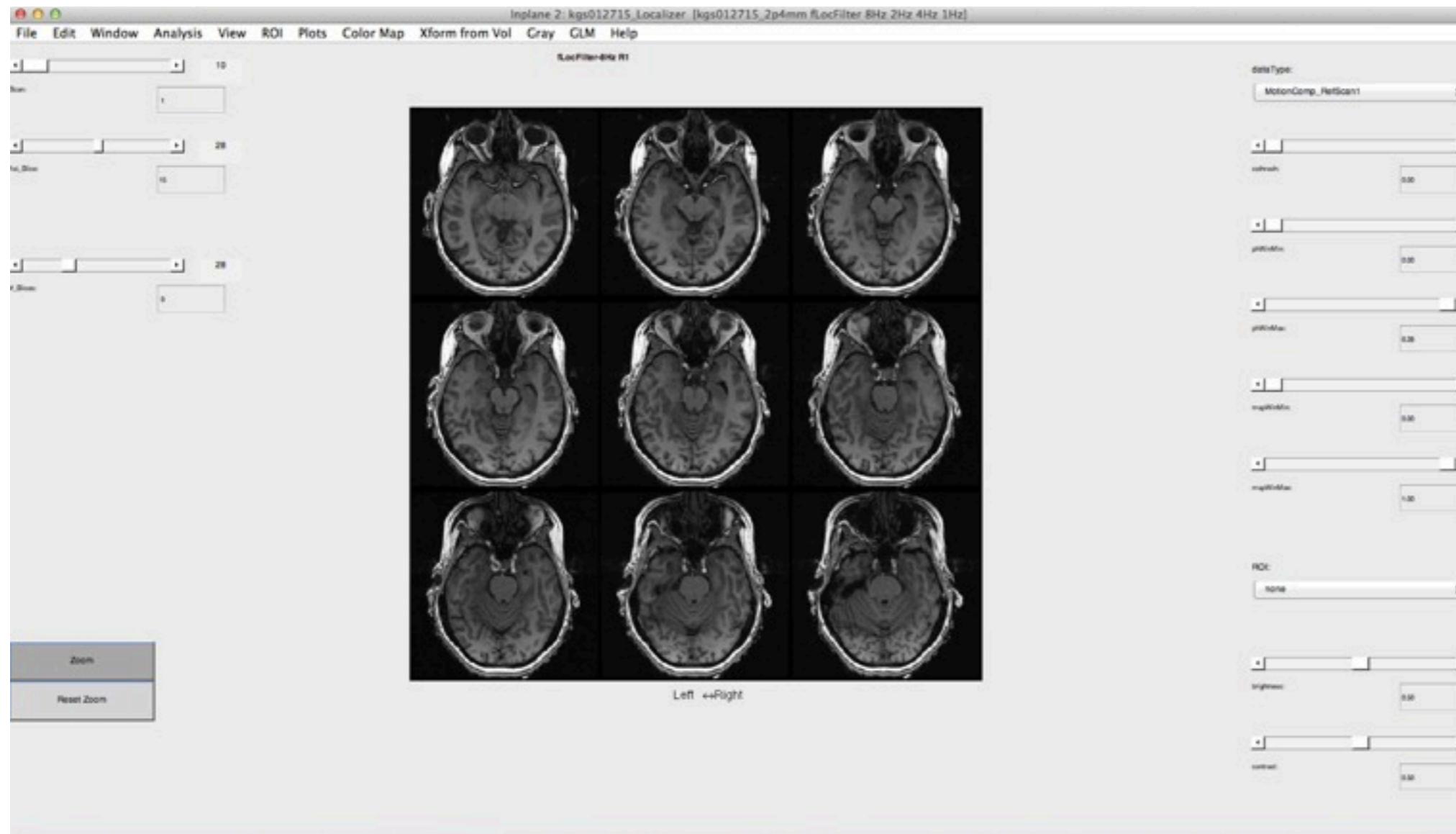
*condition number*

*condition name*

*RGB plotting colors*

*baseline condition number in parfile is 0*

# GLM analysis

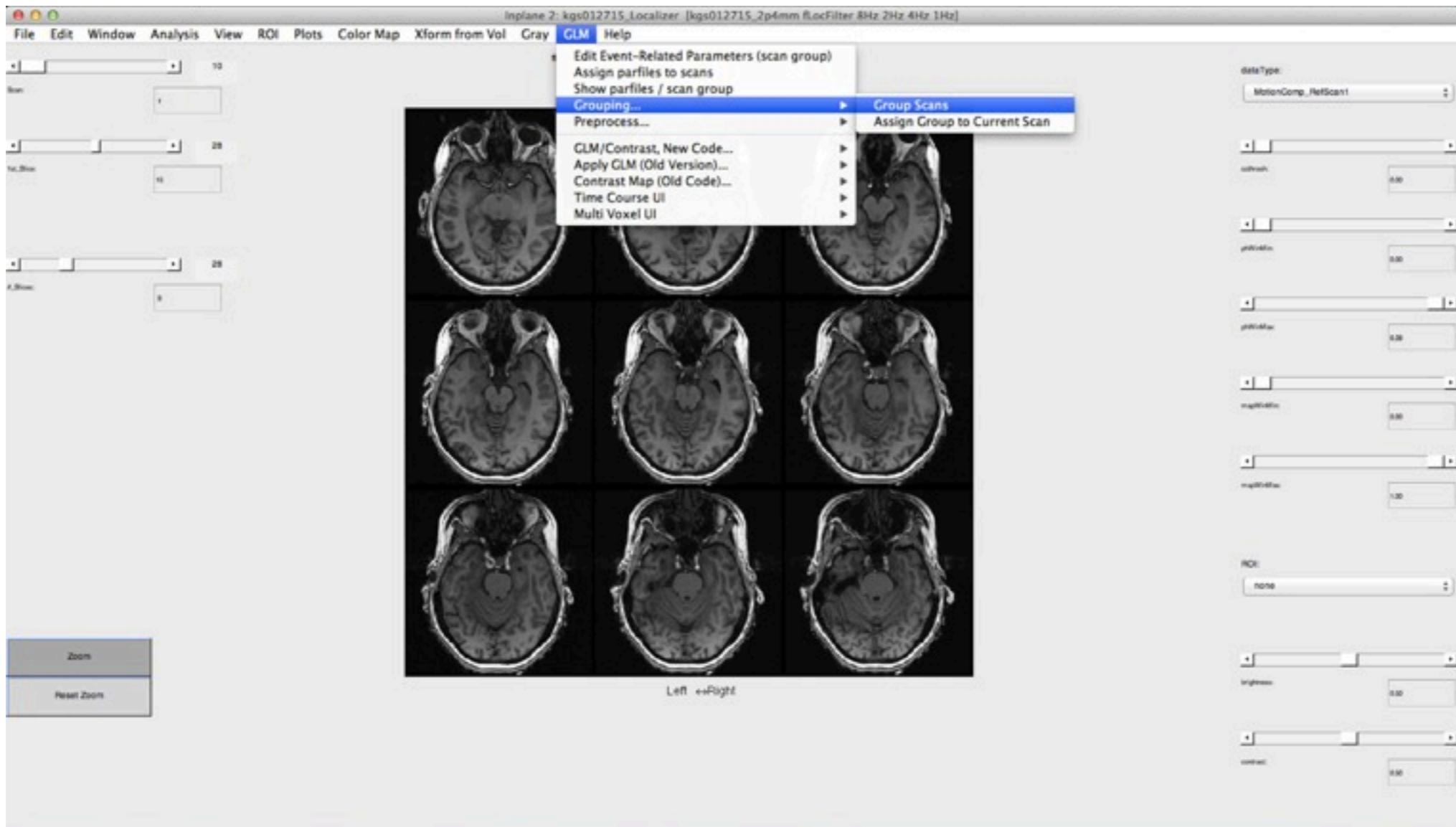


- Navigate to session directory and open inplane window by typing `mrVista` in the MATLAB command line (not `mrVista 3` which opens a gray window)

# GLM analysis

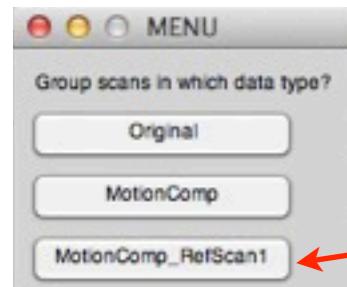
---

*set Data Type to MotionComp\_RefScan1*



*select group scans from GLM file menu*

# GLM analysis



*select MotionComp\_RefScan1*



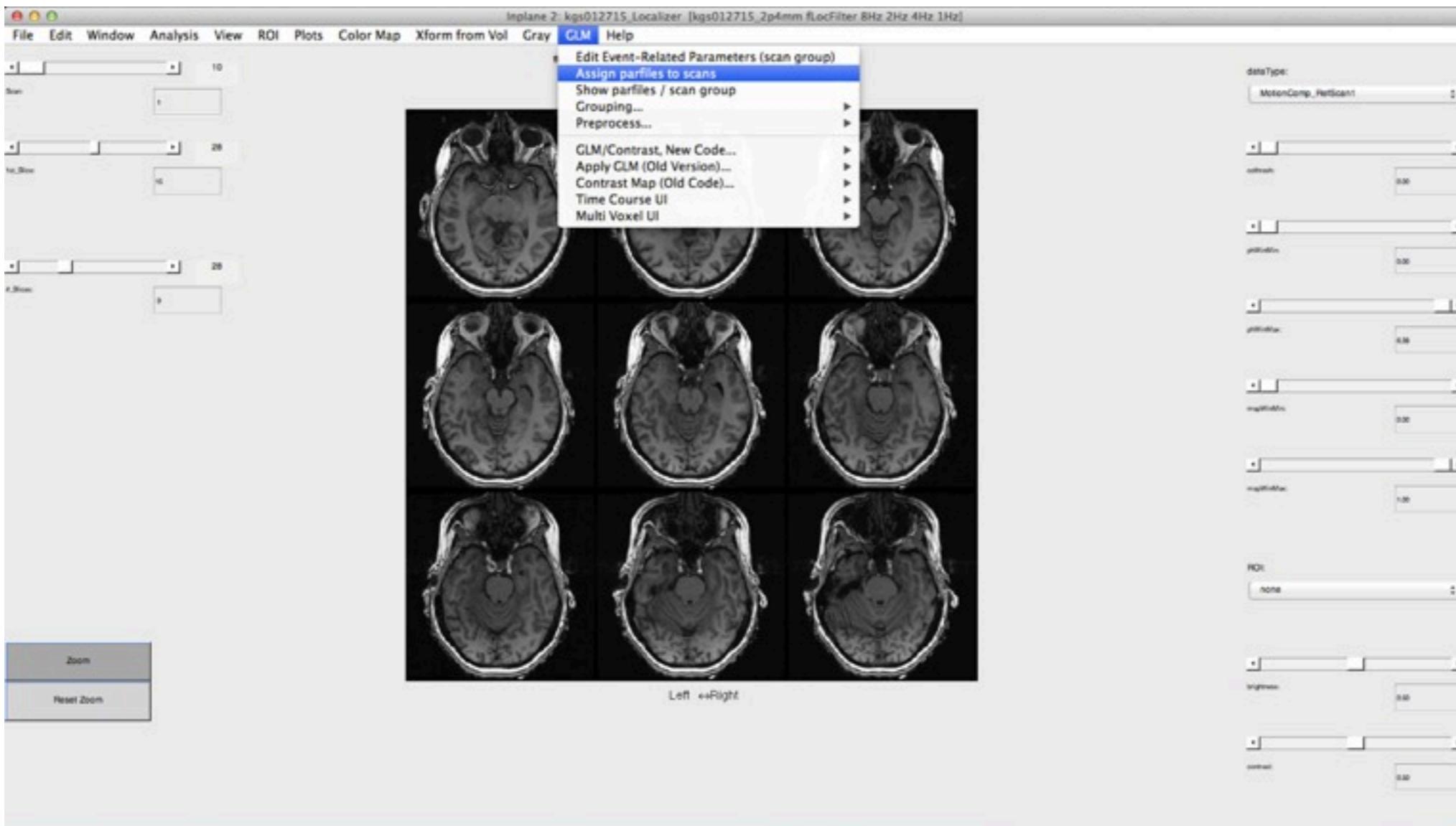
*highlight scans to group*

*click OK*

# GLM analysis

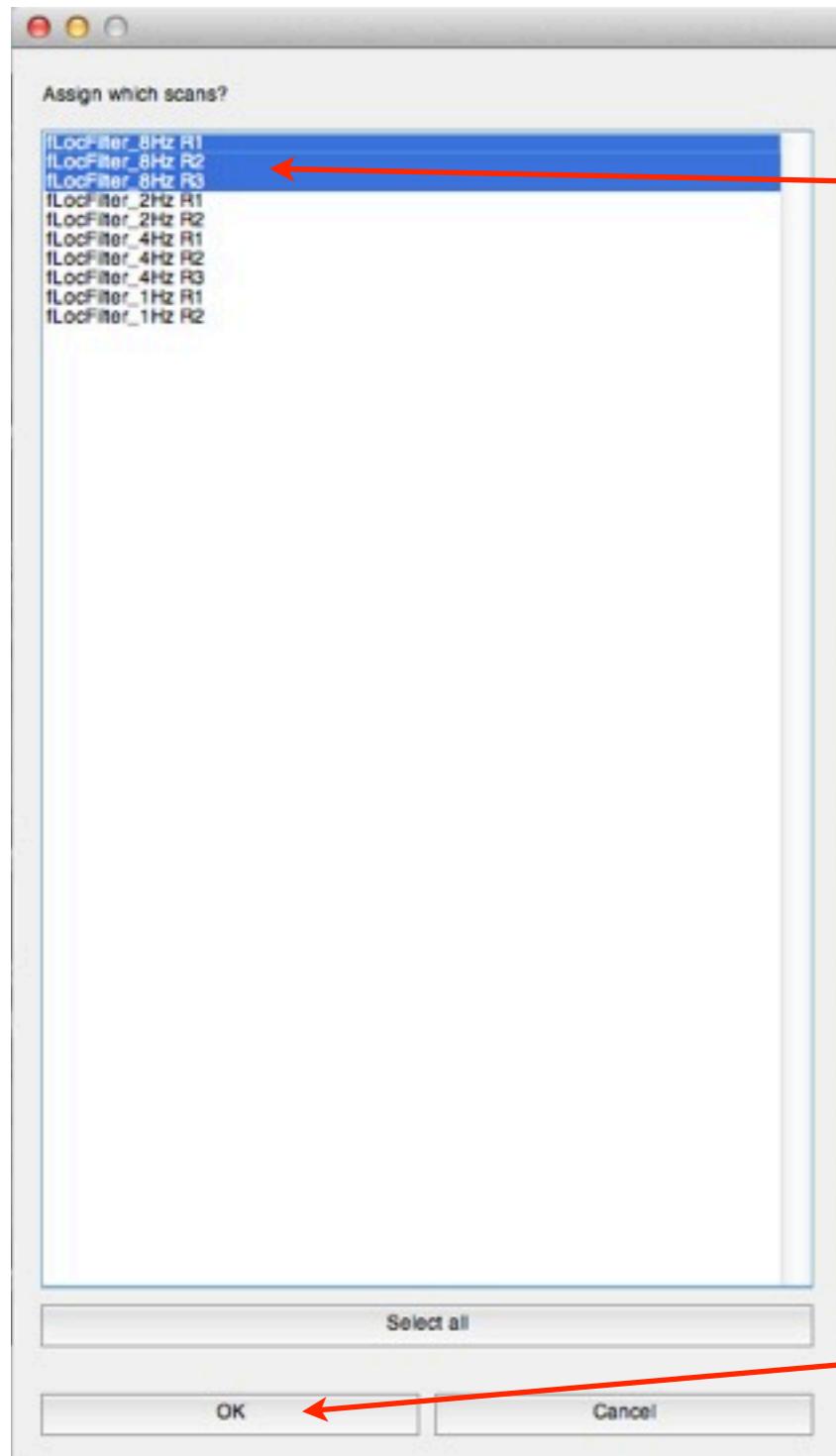
---

*select Assign parfiles to scans from GLM file menu*



# GLM analysis

---

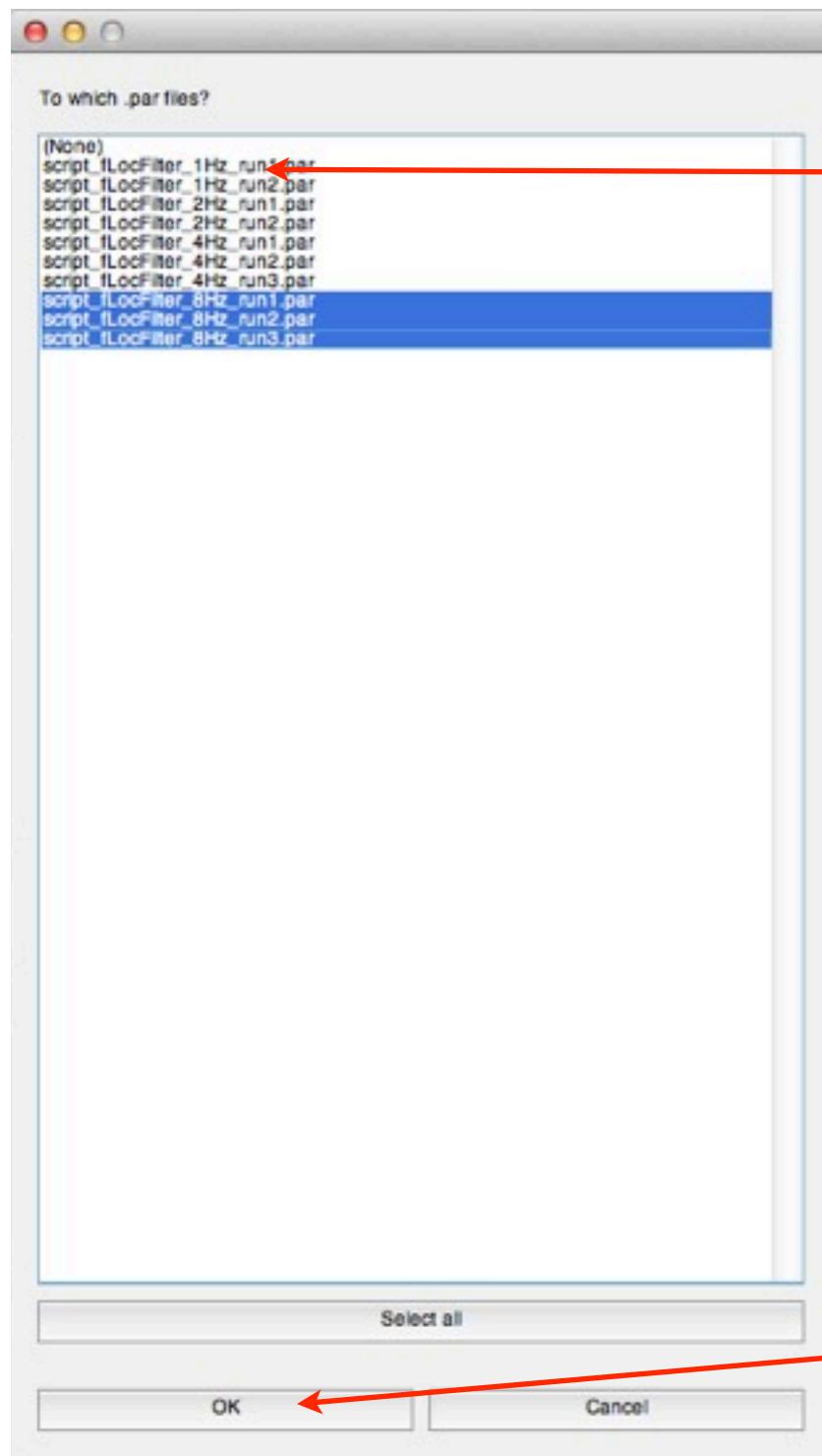


*highlight scans to attach parfiles*

*click OK*

# GLM analysis

---

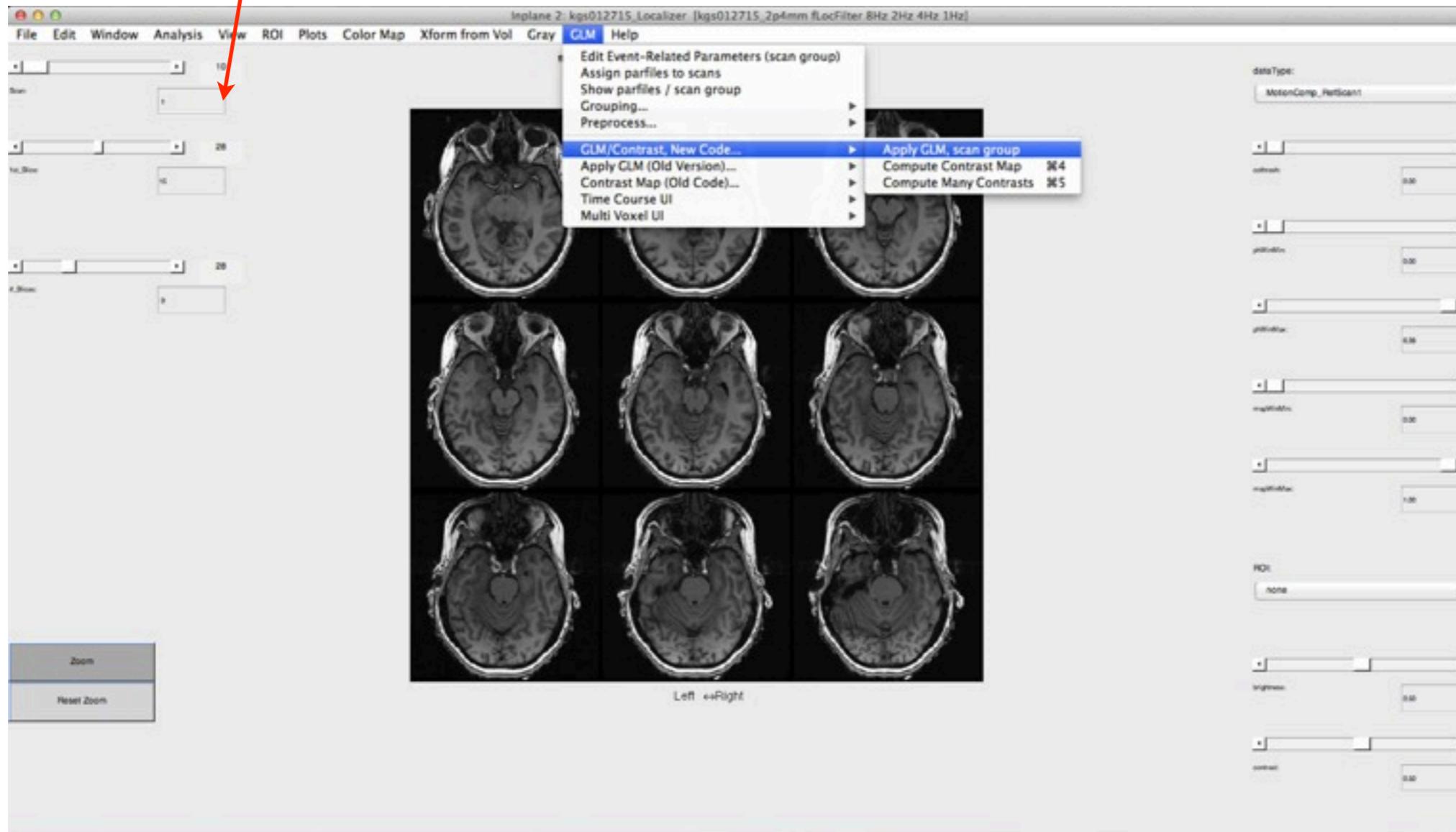


*select appropriate parfiles*

*click OK*

# GLM analysis

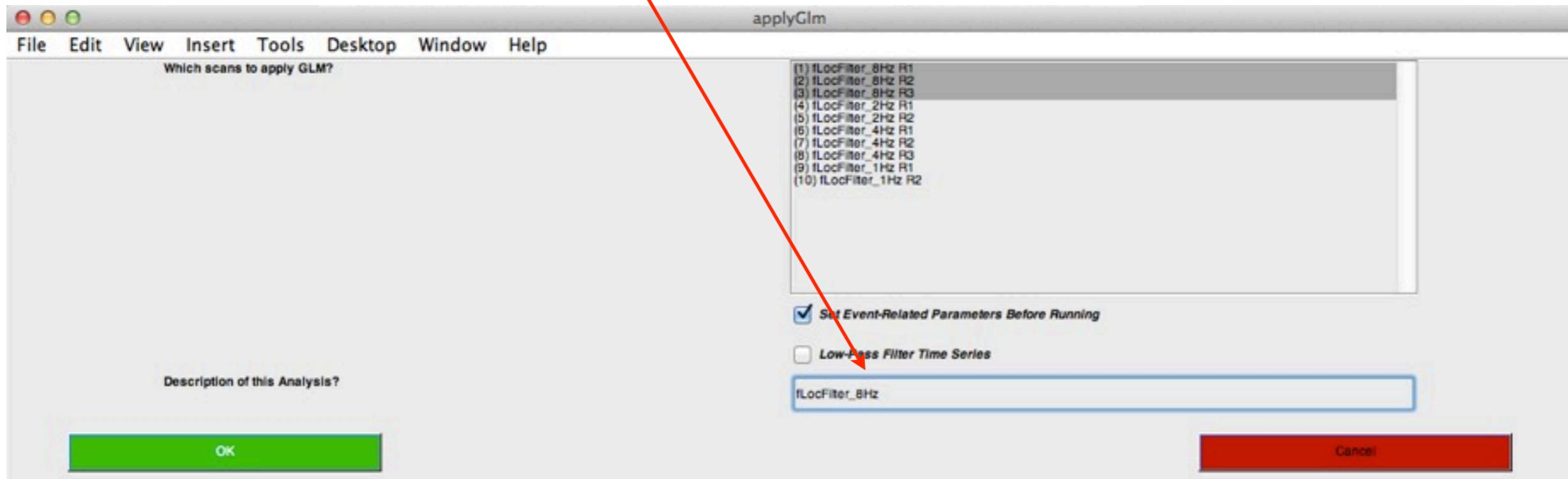
*set scan number to first run of grouped scans*



*select Apply GLM scan group from GLM file menu*

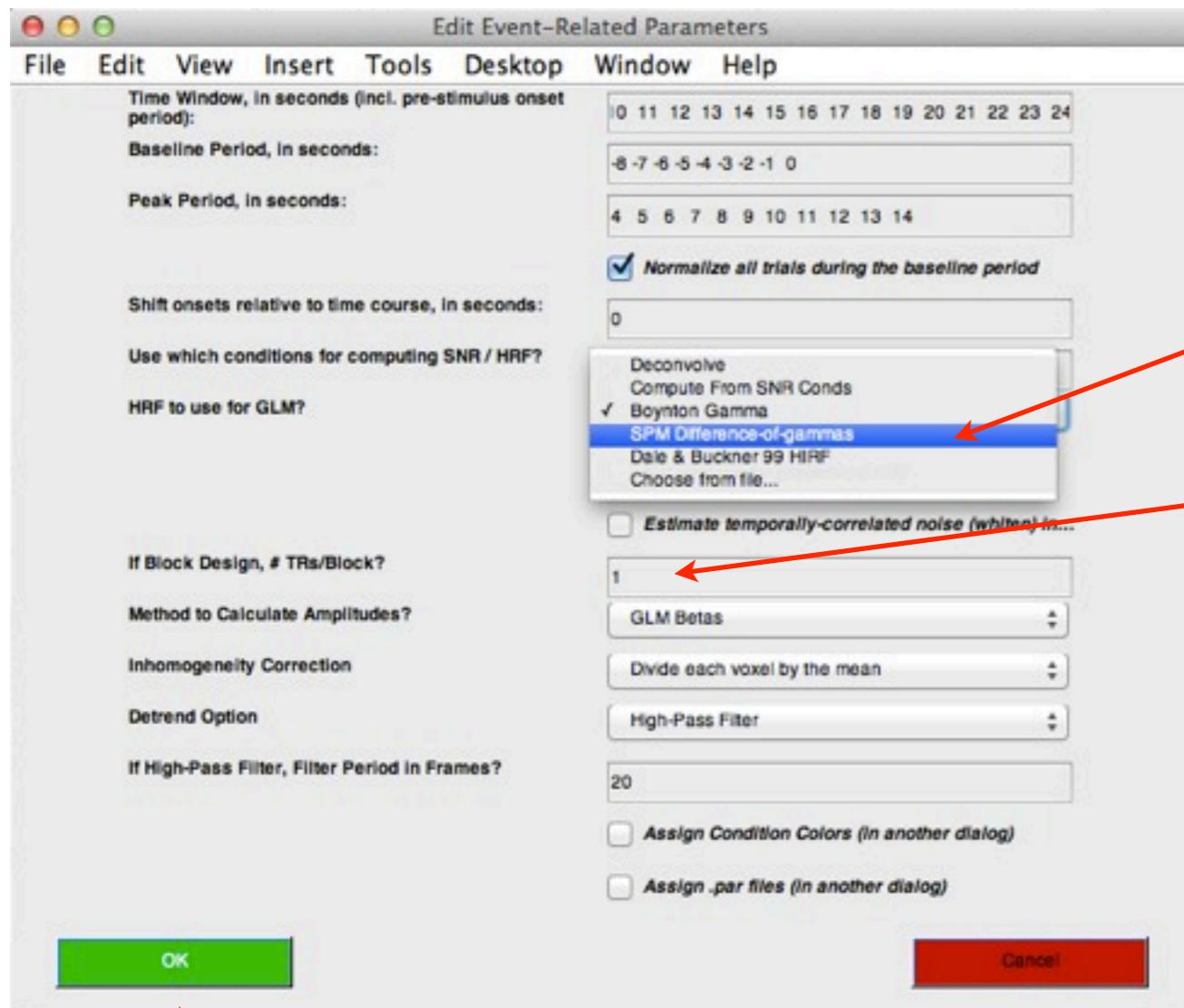
# GLM analysis

*enter a name for current GLM*



*press OK*

# GLM analysis



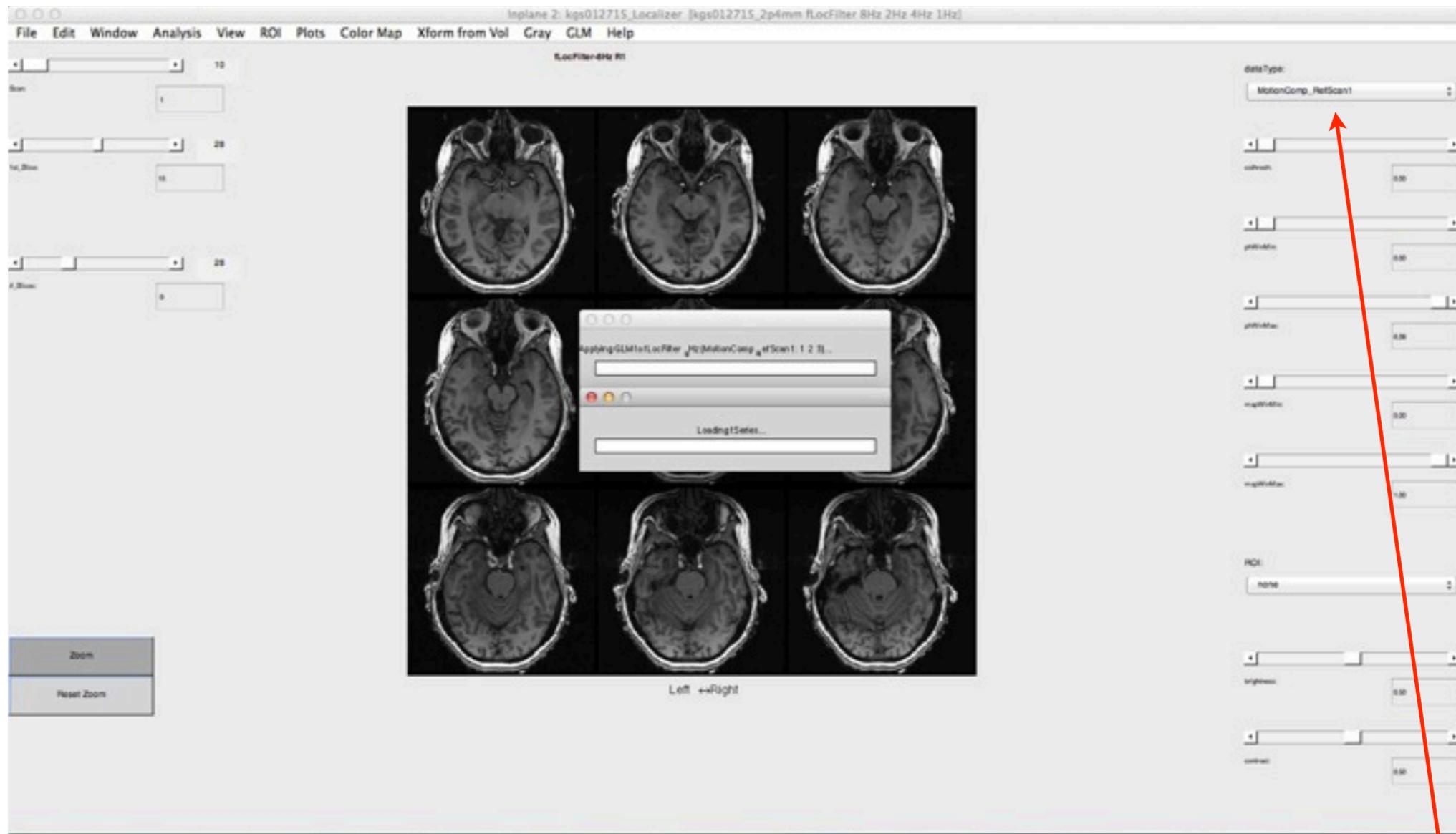
click OK

set *HRF*  
set number of *TRs* in  
each trial of parfile  
1Hz = 4 TR blocks  
2Hz = 2 TR blocks  
4Hz = 1 TR blocks  
8Hz = 1 TR blocks

# GLM analysis

---

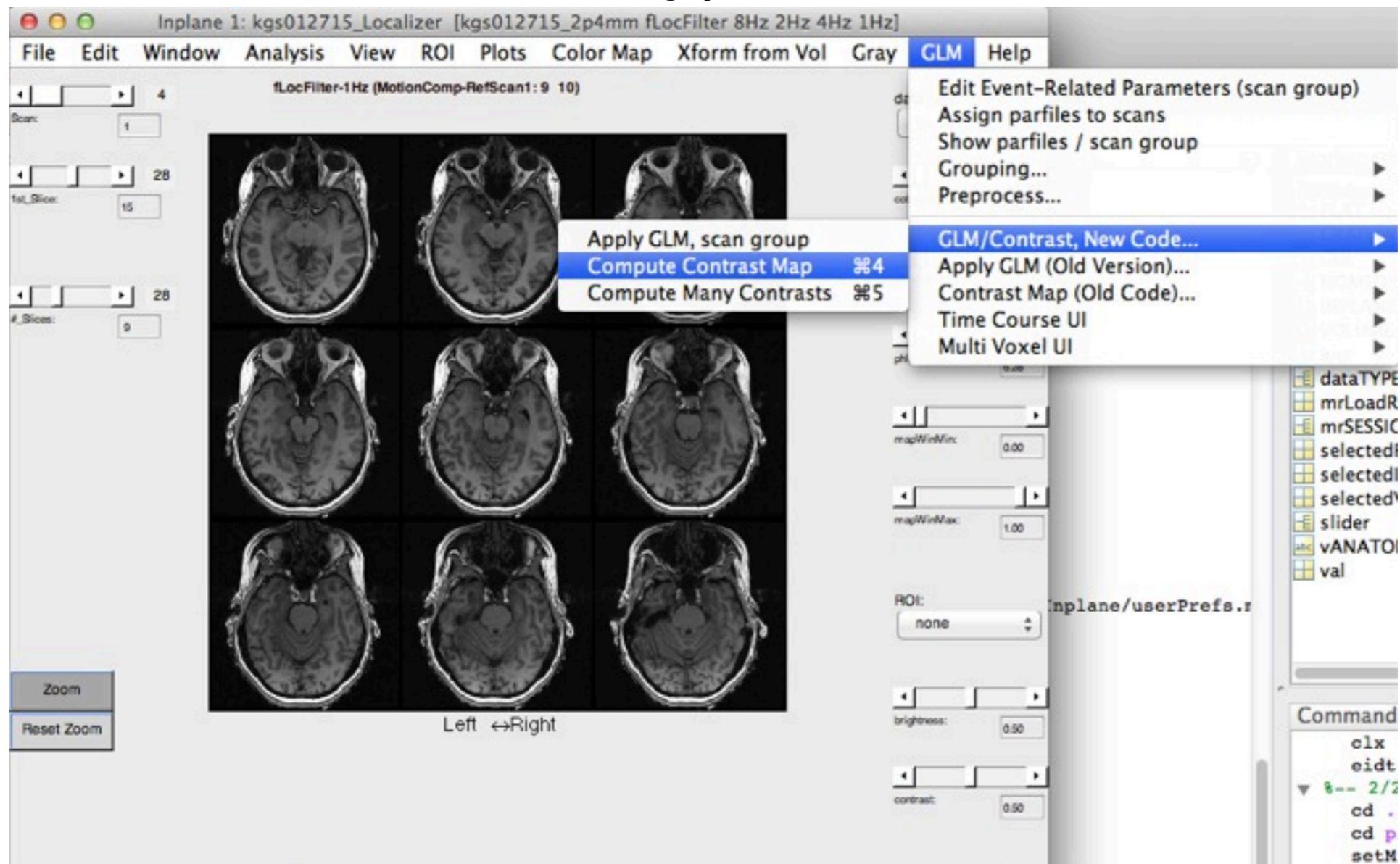
*wait...*



*you should now have a Data Type called GLMs*

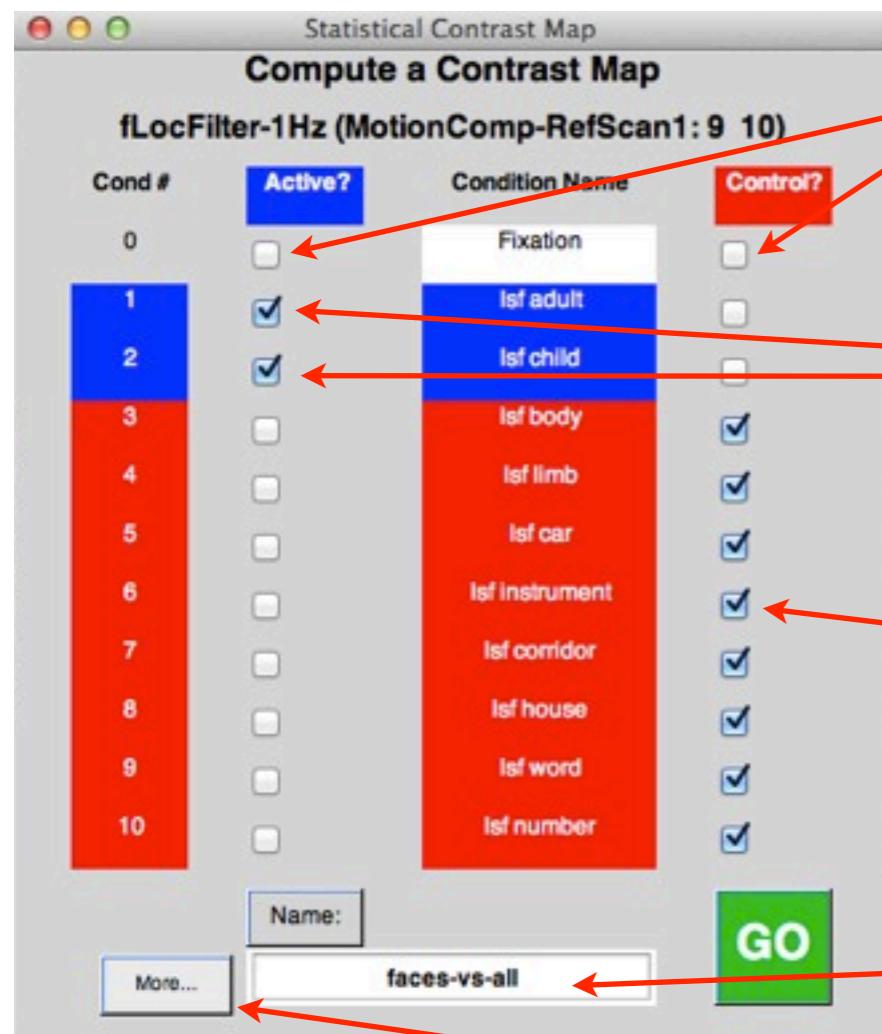
# GLM analysis

*set Data Type to GLM*



select Compute Contrast Map from GLM file menu

# GLM analysis



*never put baseline in contrast*

*select active conditions*

*select control conditions*

*name contrast*

*click More...*

# GLM analysis



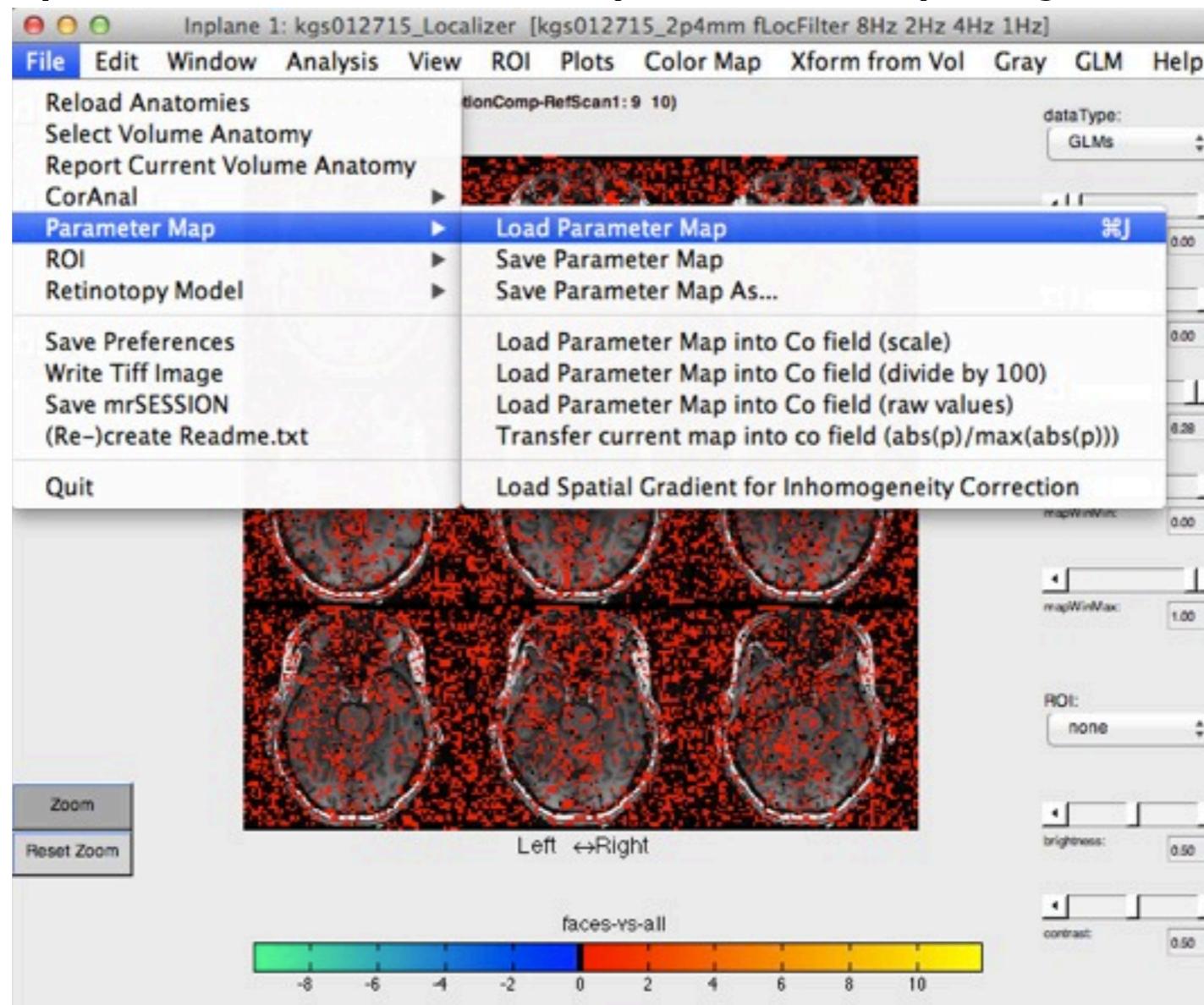
set units to  $T$ -values

click GO

# GLM analysis

---

*reload parameter map to display correctly*

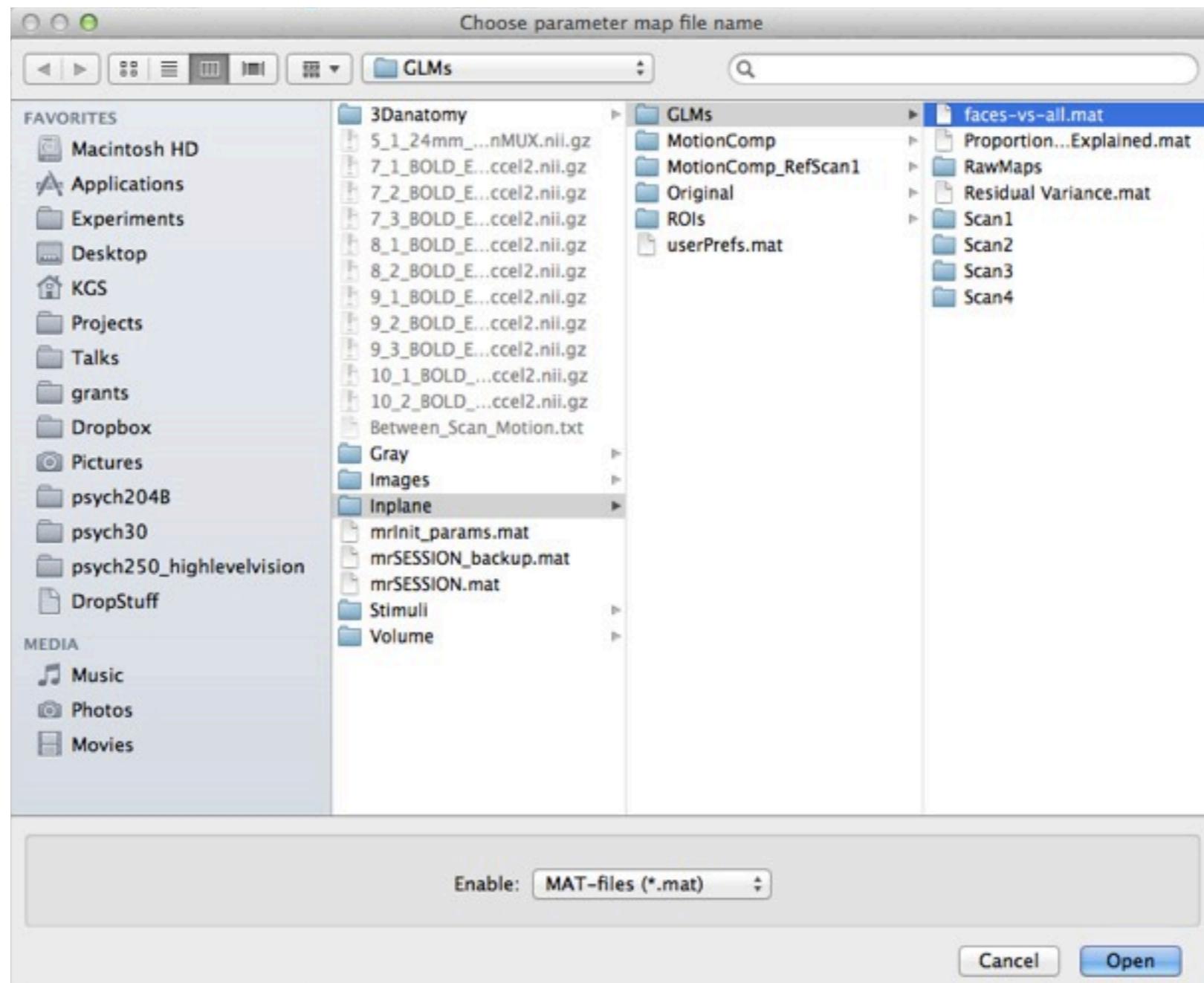


select Load Parameter Map from file menu

# GLM analysis

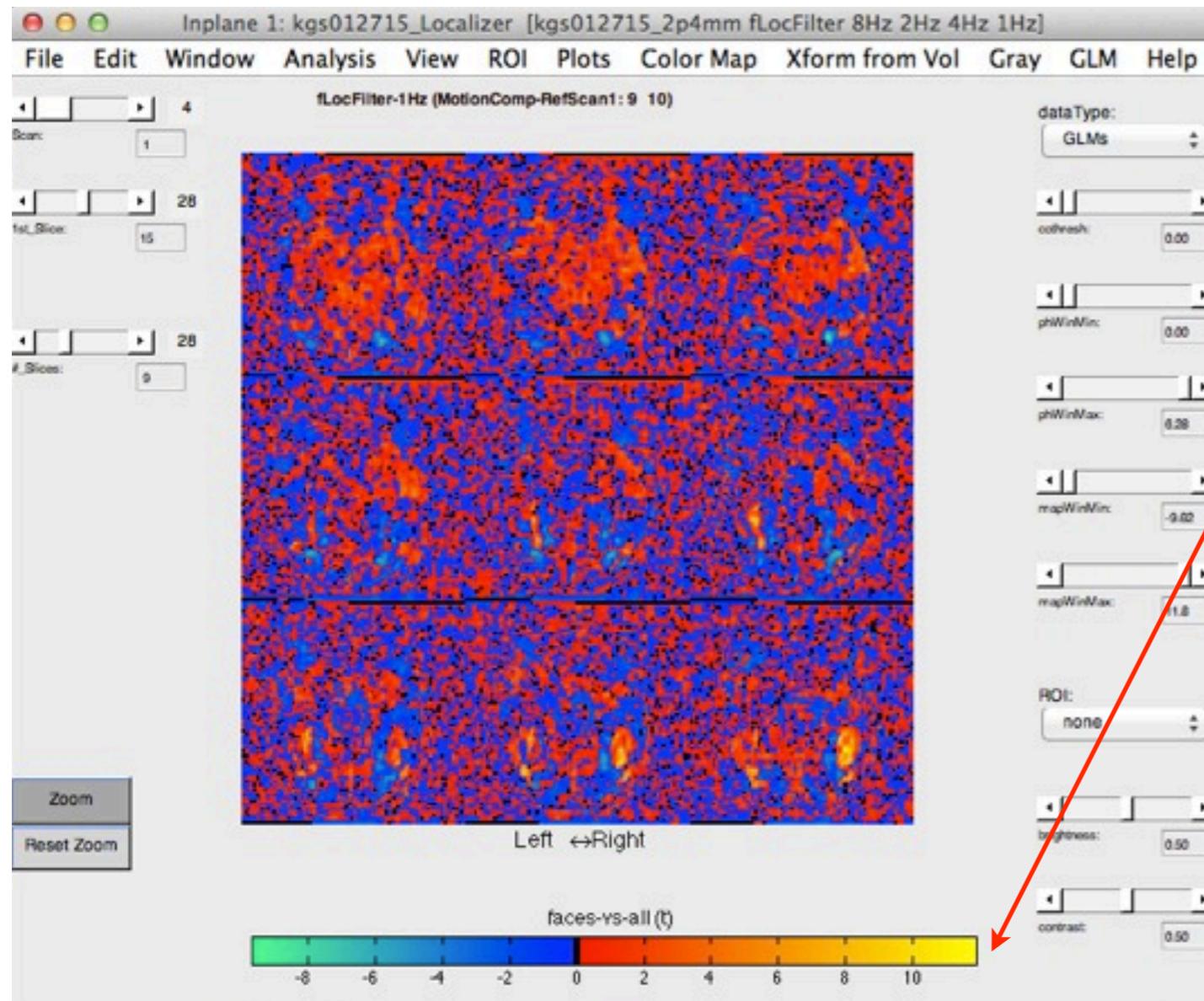
---

*open parameter map from GLMs directory*



# GLM analysis

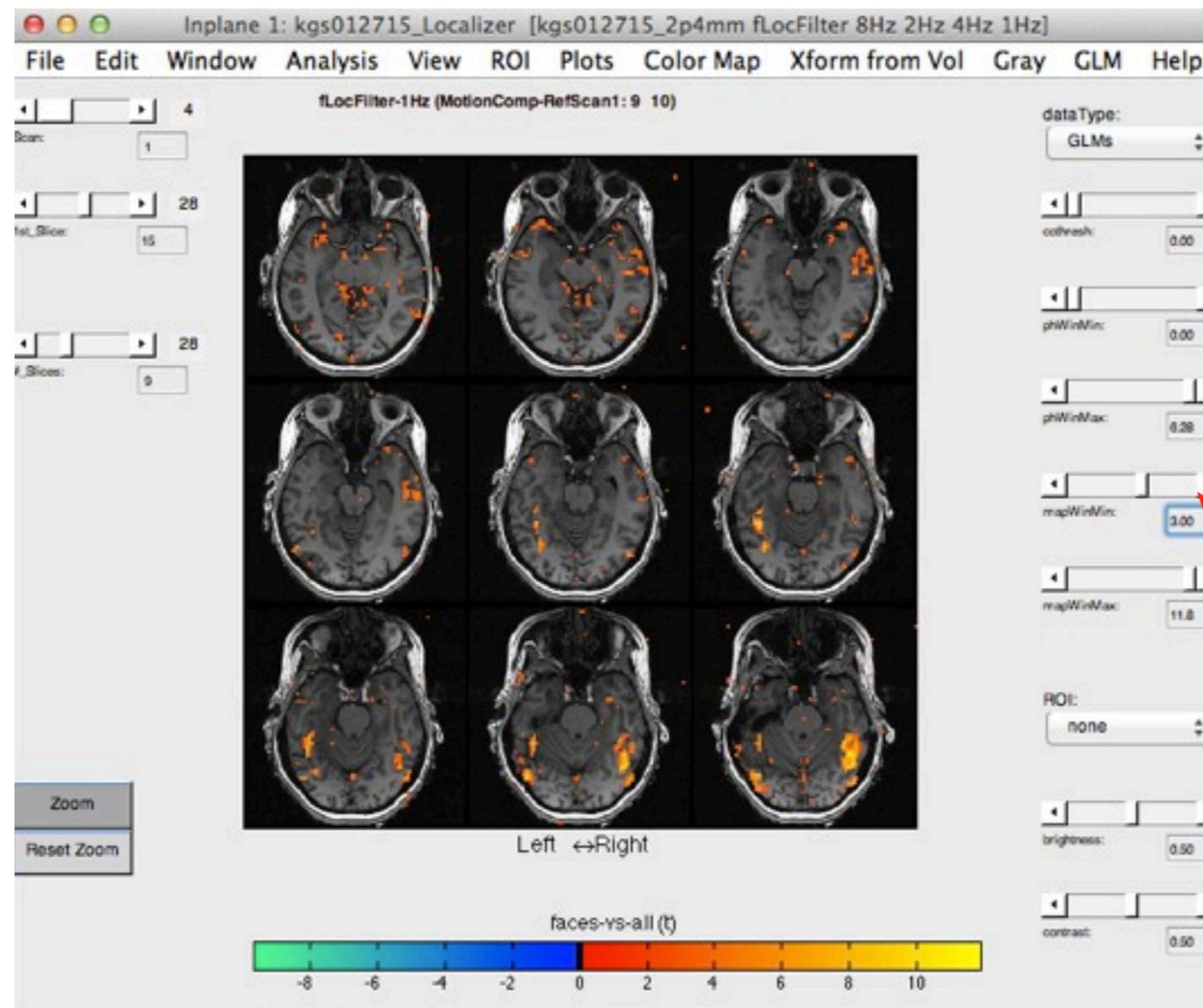
*unthresholded parameter map will display*



*right click color bar  
to change colormap  
(autumn is good)  
and scaling (set clip  
mode to 3 10 to  
scale colors between  
 $T = 3$  and  $T = 10$ )*

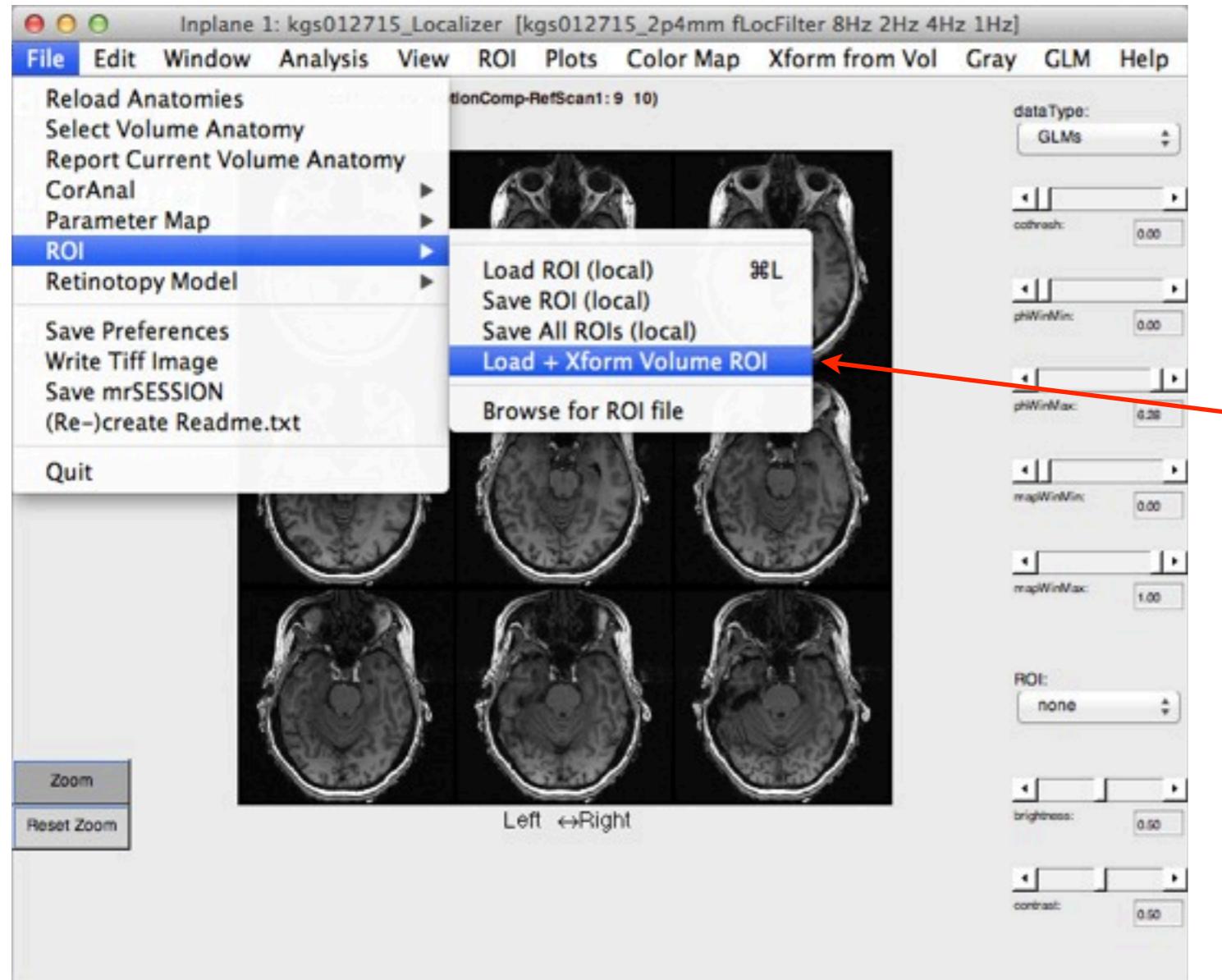
# GLM analysis

*threshold parameter map at  $T > 3$  or 4*



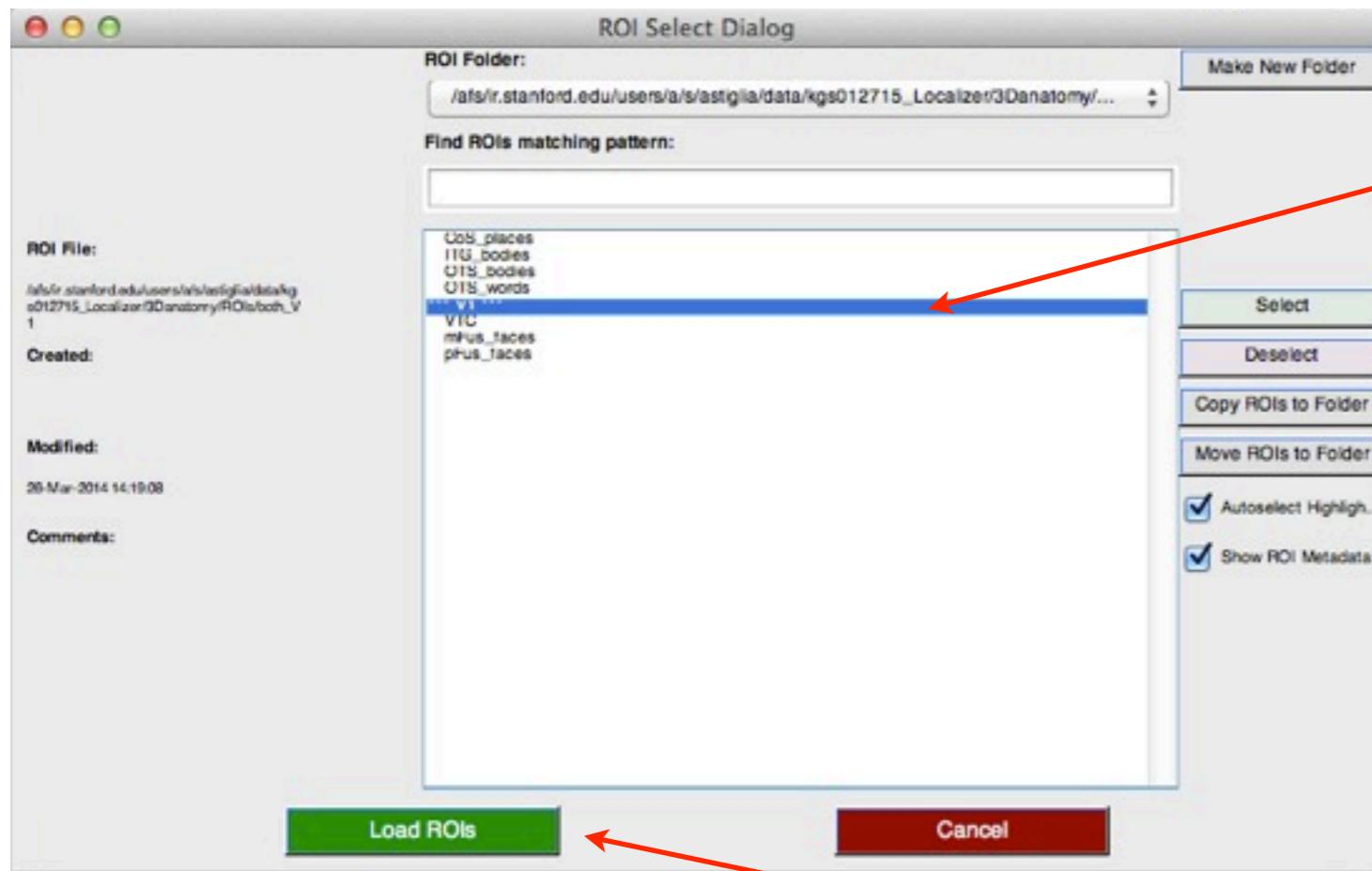
# GLM analysis

*a GLM can also be run across all voxels in a ROI*



*load a predefined volume ROI in the inplane view by transforming the from the gray view*

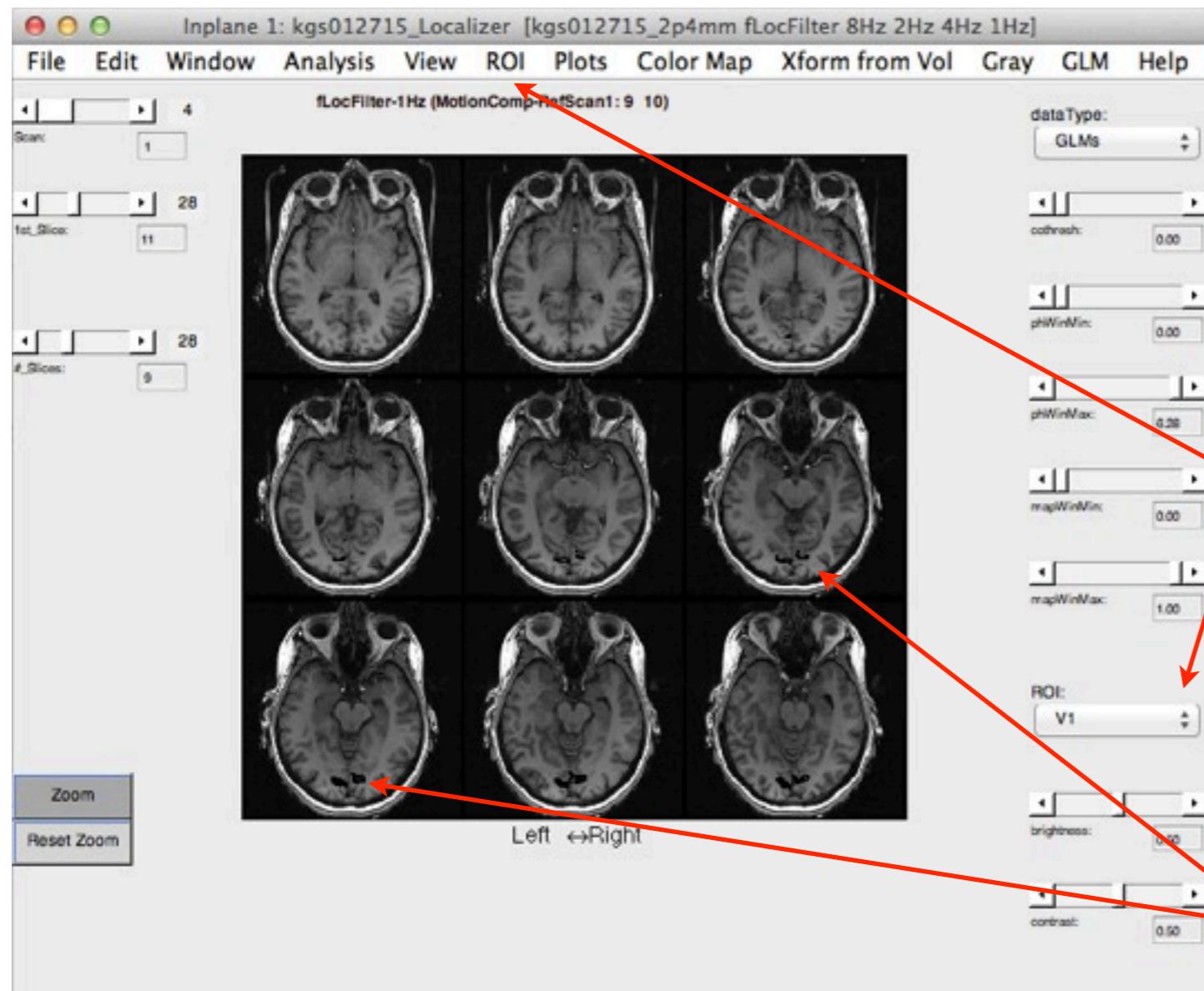
# GLM analysis



*select ROIs you would like to load*

*click load ROIs*

# GLM analysis



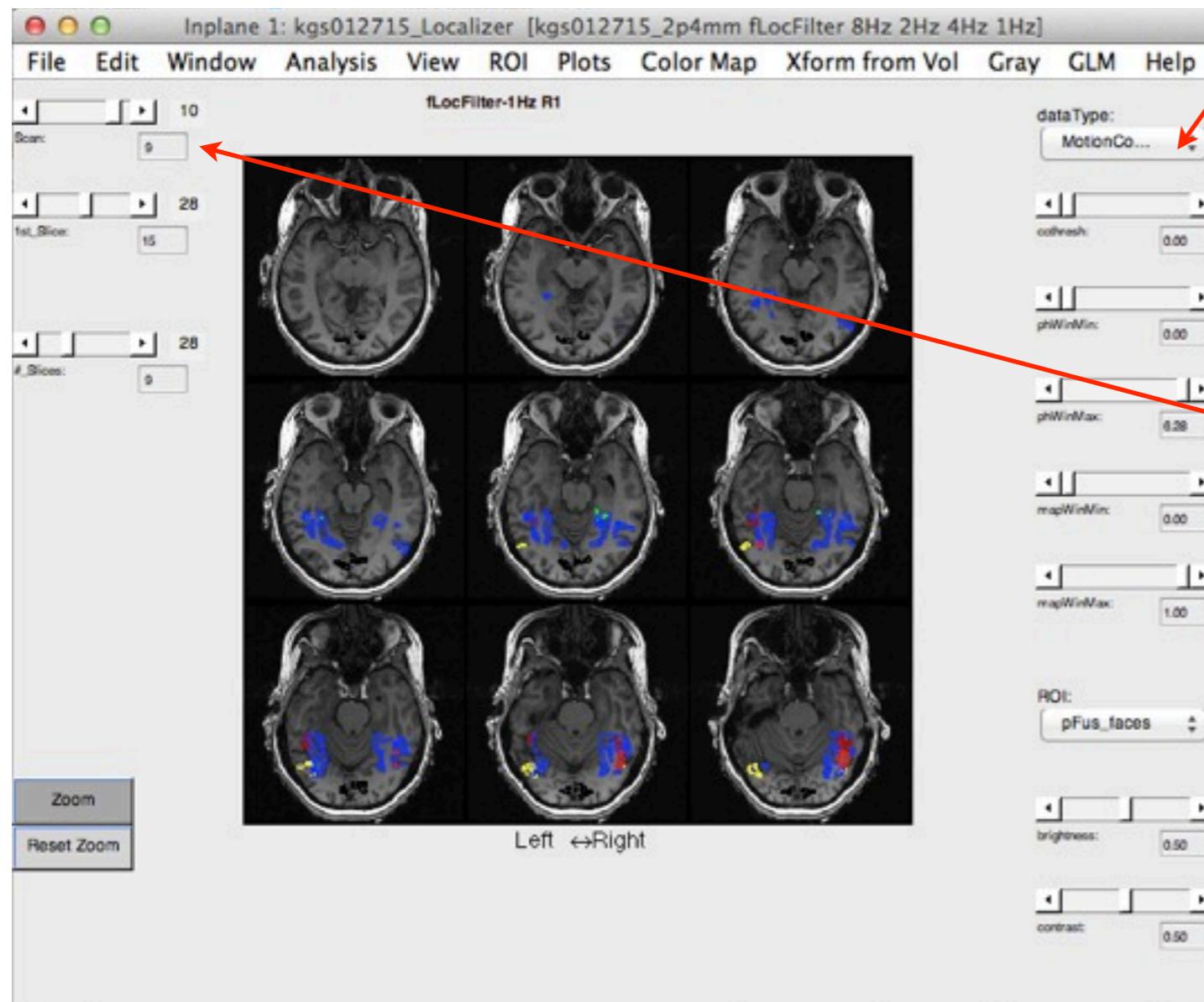
*loaded ROIs are listed in ROI field*

*you can change the color of the ROI here*

*V1 is colored black*

# GLM analysis

*set Data Type to MotionComp\_RefScan1*

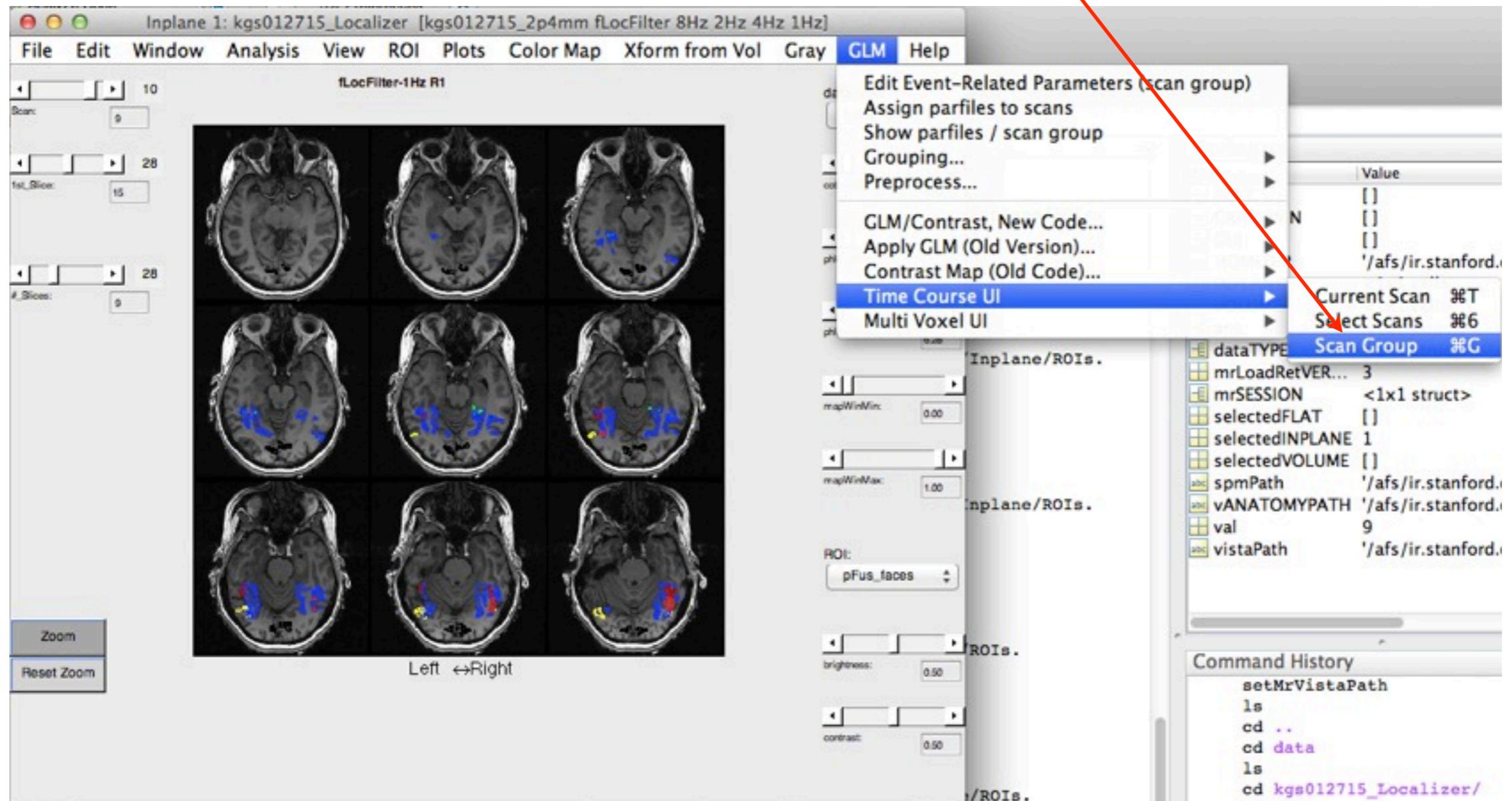


*set scan number  
to first run of scan  
group you want to  
analyze in ROI*

*make sure correct  
ROI is selected*

# GLM analysis

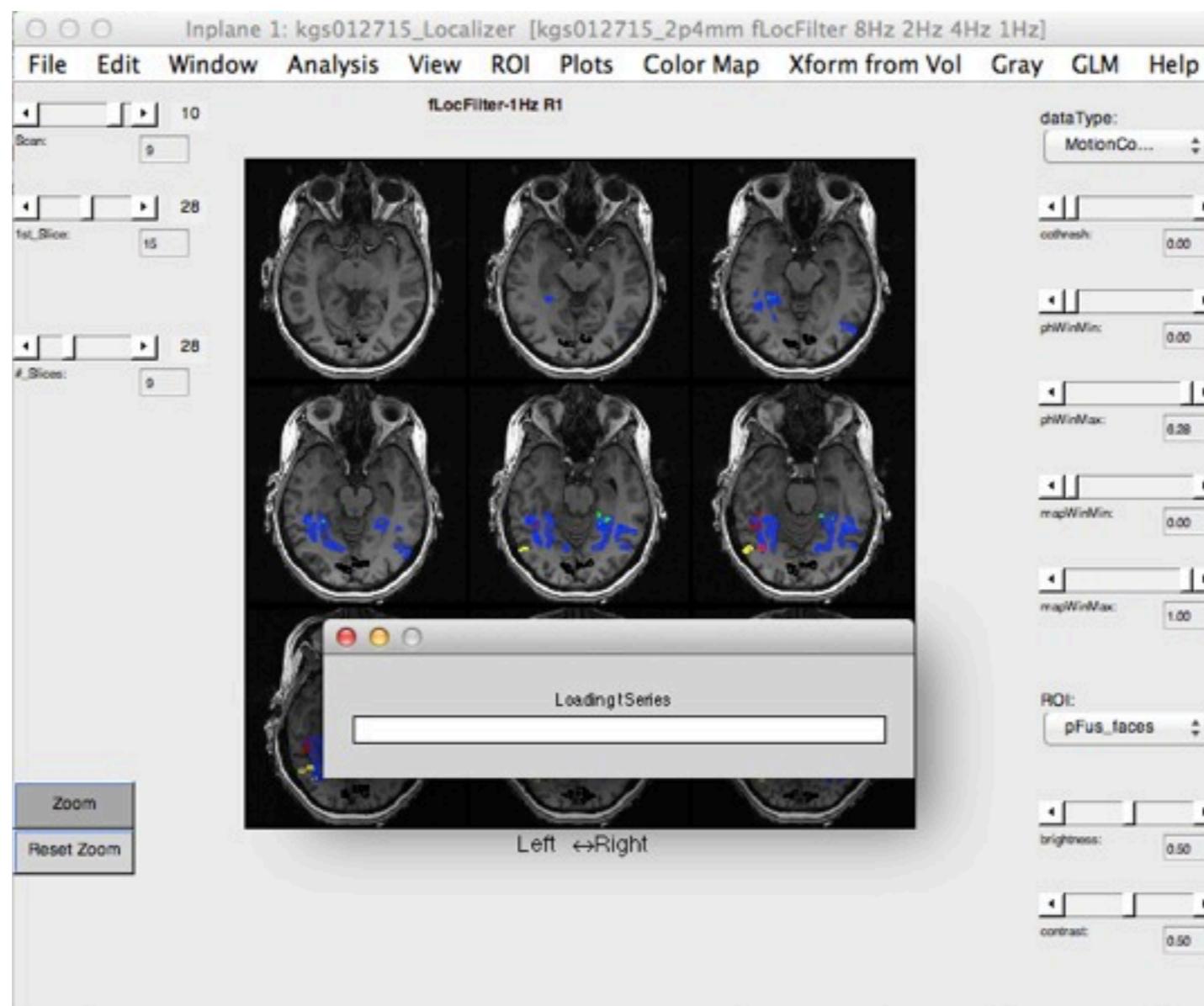
*ROI analysis on scan group from GLM file menu*



# GLM analysis

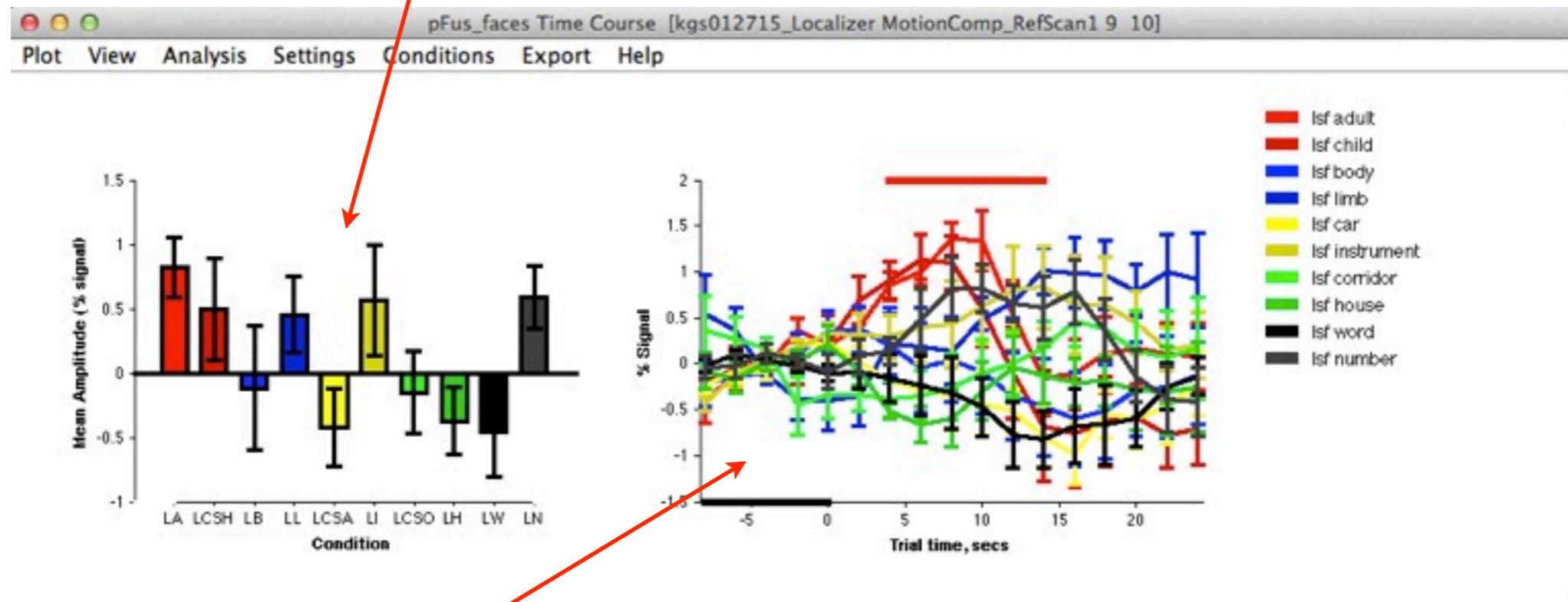
---

*wait...*



# GLM analysis

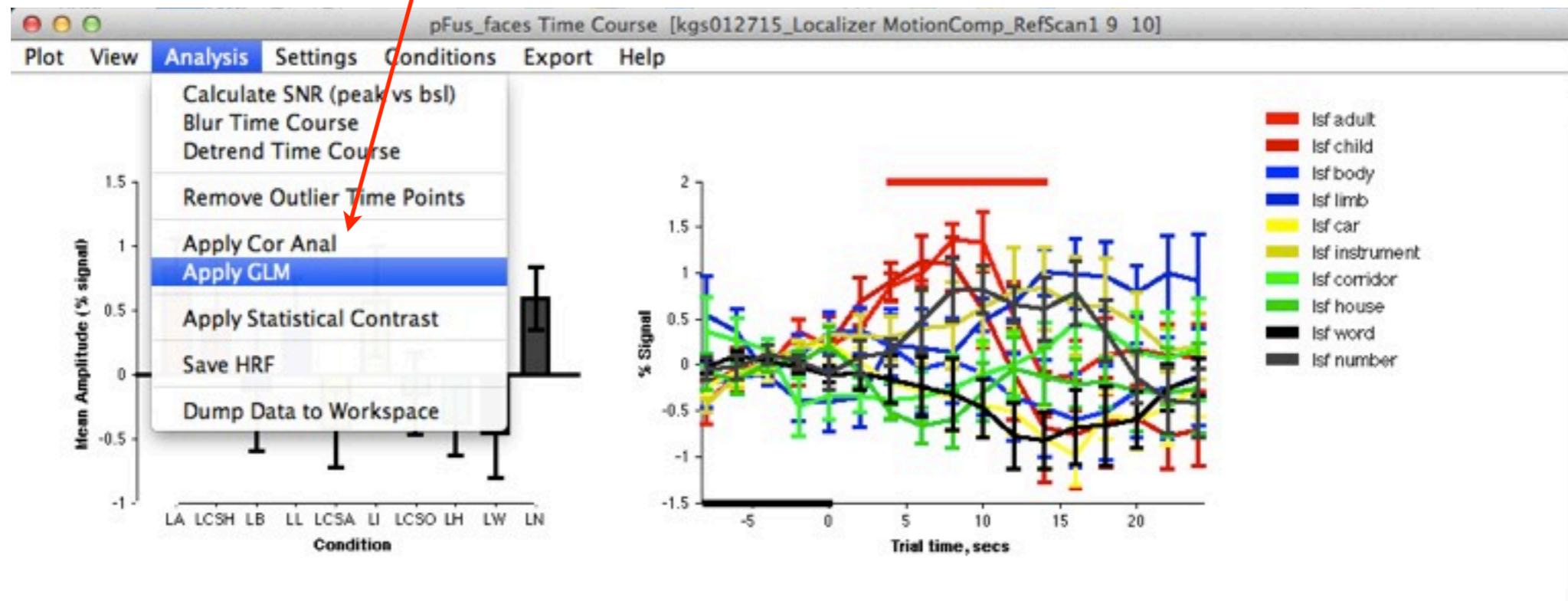
*mean percent signal change is plotted by default*



*ROI timecourse is plotted for each condition*

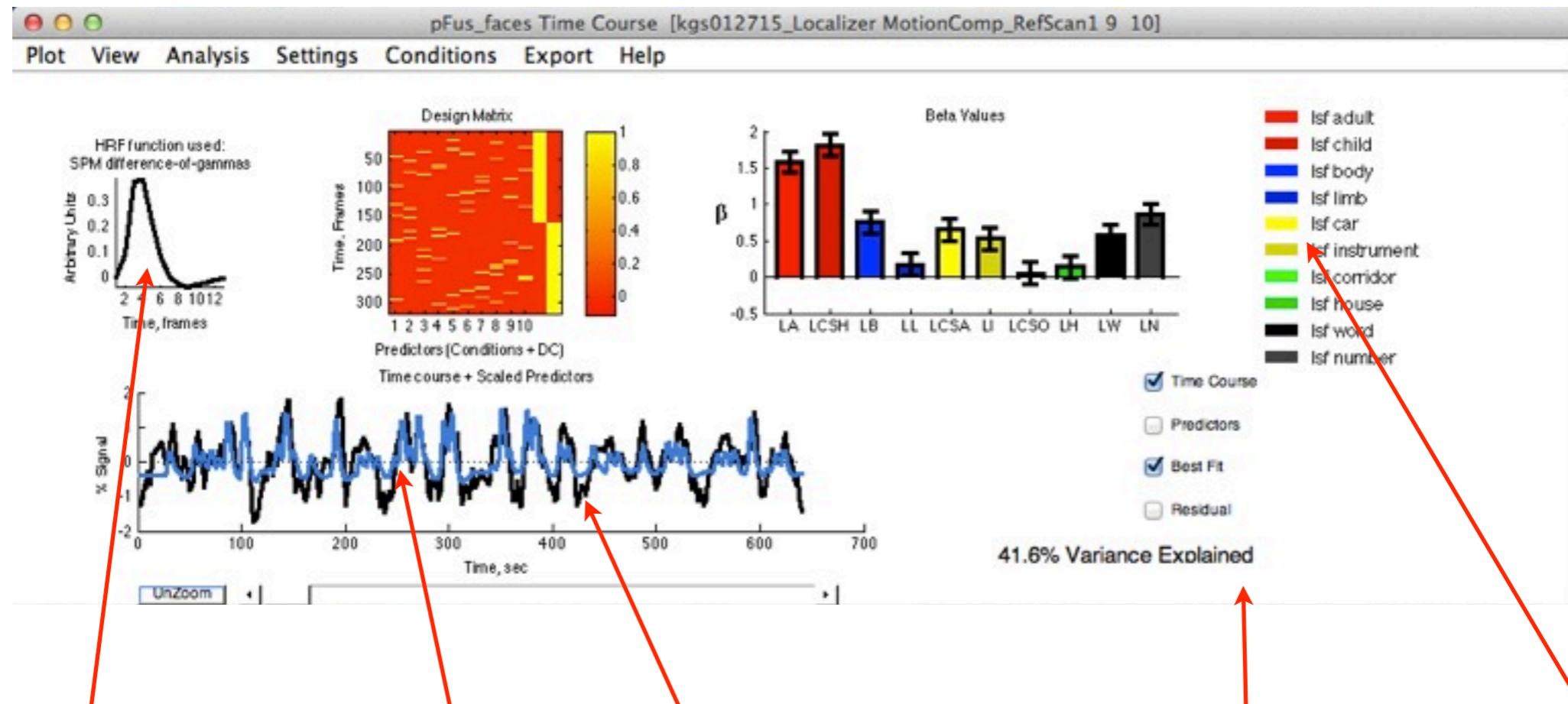
# GLM analysis

*select Apply GLM from Analysis file menu*



*this will plot betas instead of % signal change*

# GLM analysis



*make sure HRF  
is set correctly*

*blue is predicted  
timeseries*

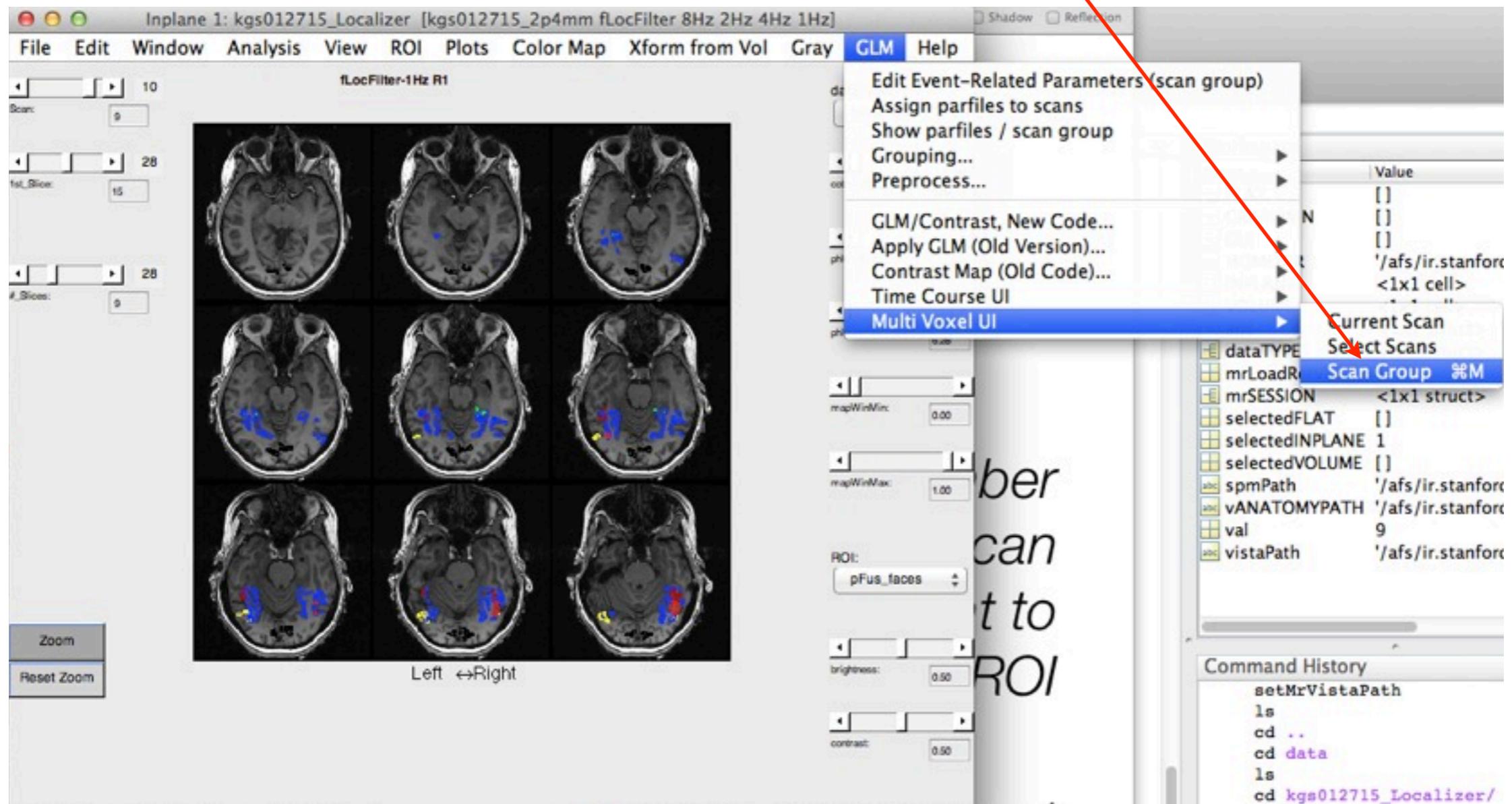
*black is measured  
timeseries*

*look at variance  
explained*

*plotting colors  
set in parfile*

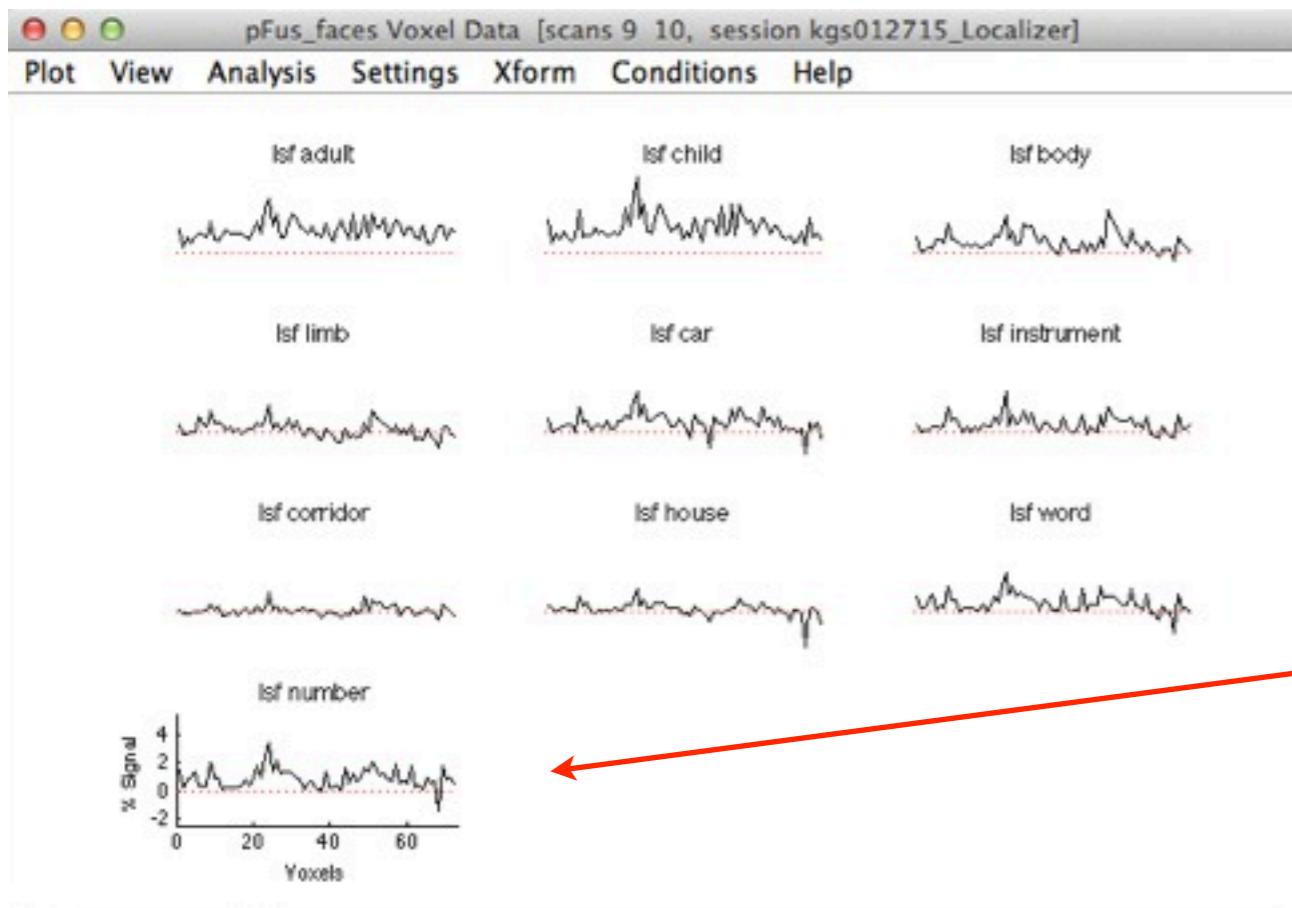
# MVP analysis

*MVP analysis in a ROI is run like a GLM*



# MVP analysis

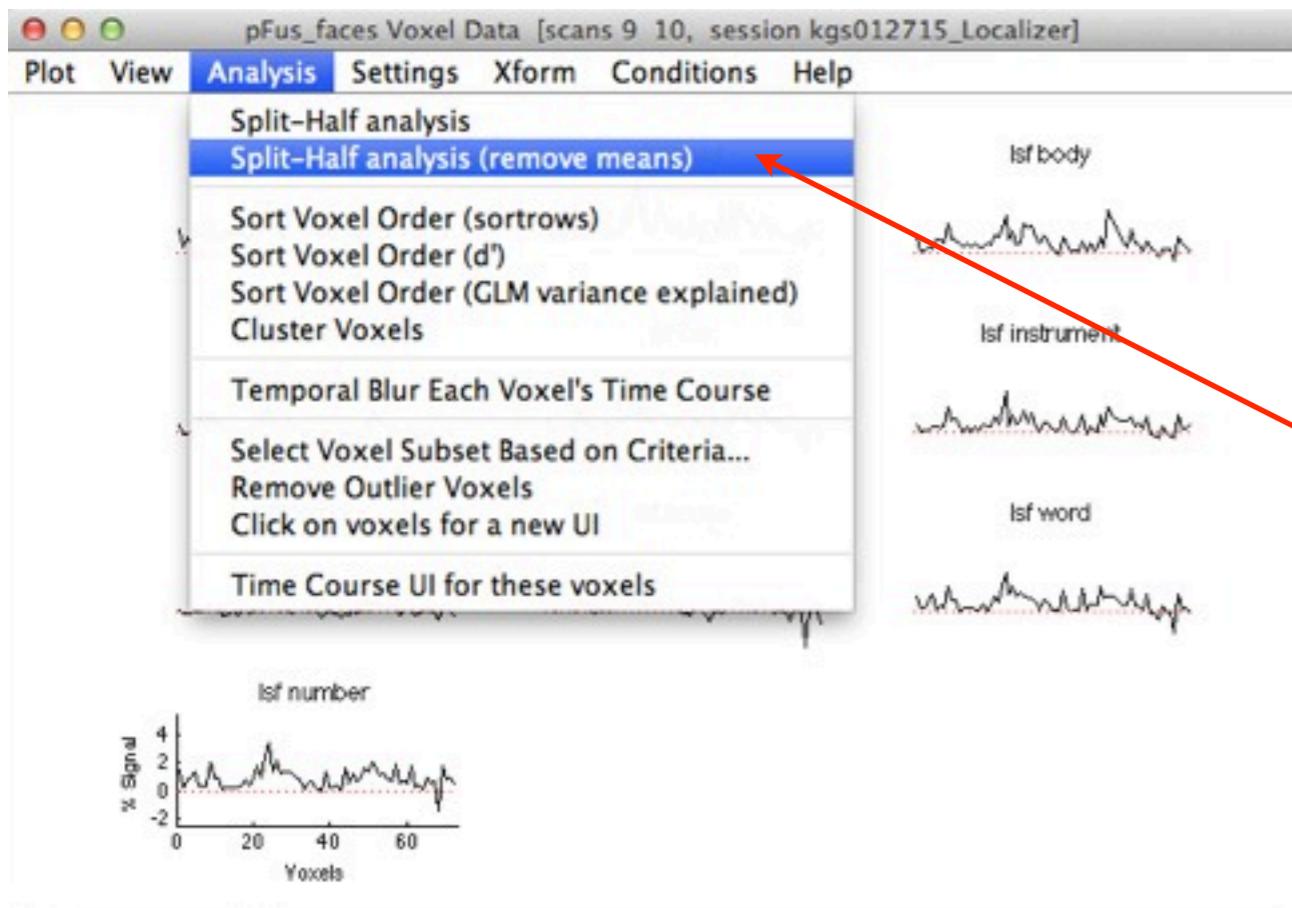
*% signal change plotted for each condition/voxel*



*voxels are sorted  
on x-axis arbitrarily  
from 1 to N*

# MVP analysis

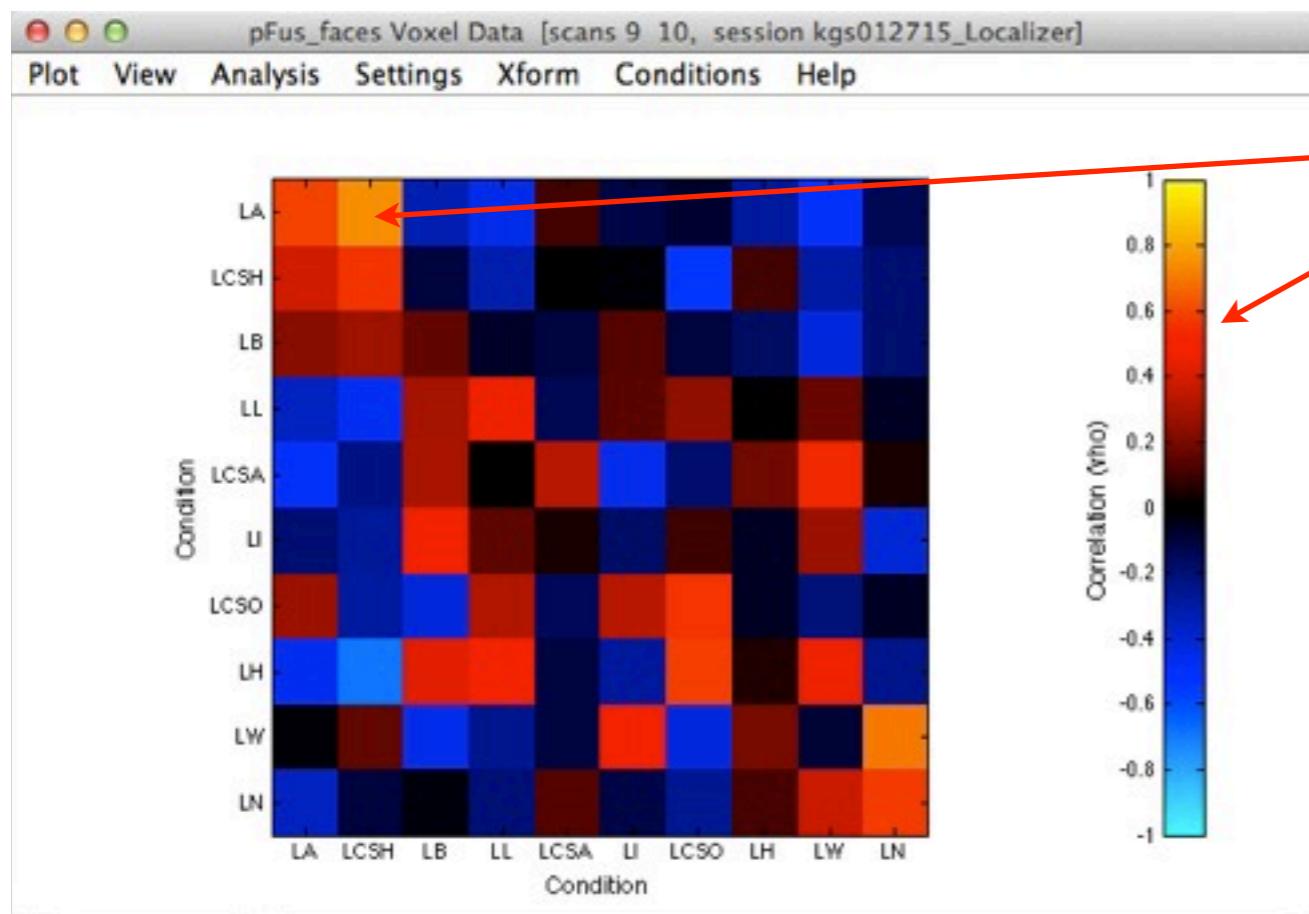
*run Split-Half analysis (remove means)*



*remove means  
option subtracts the  
average correlation  
from each voxel  
across all conditions*

# MVP analysis

## *MVP confusion matrix*

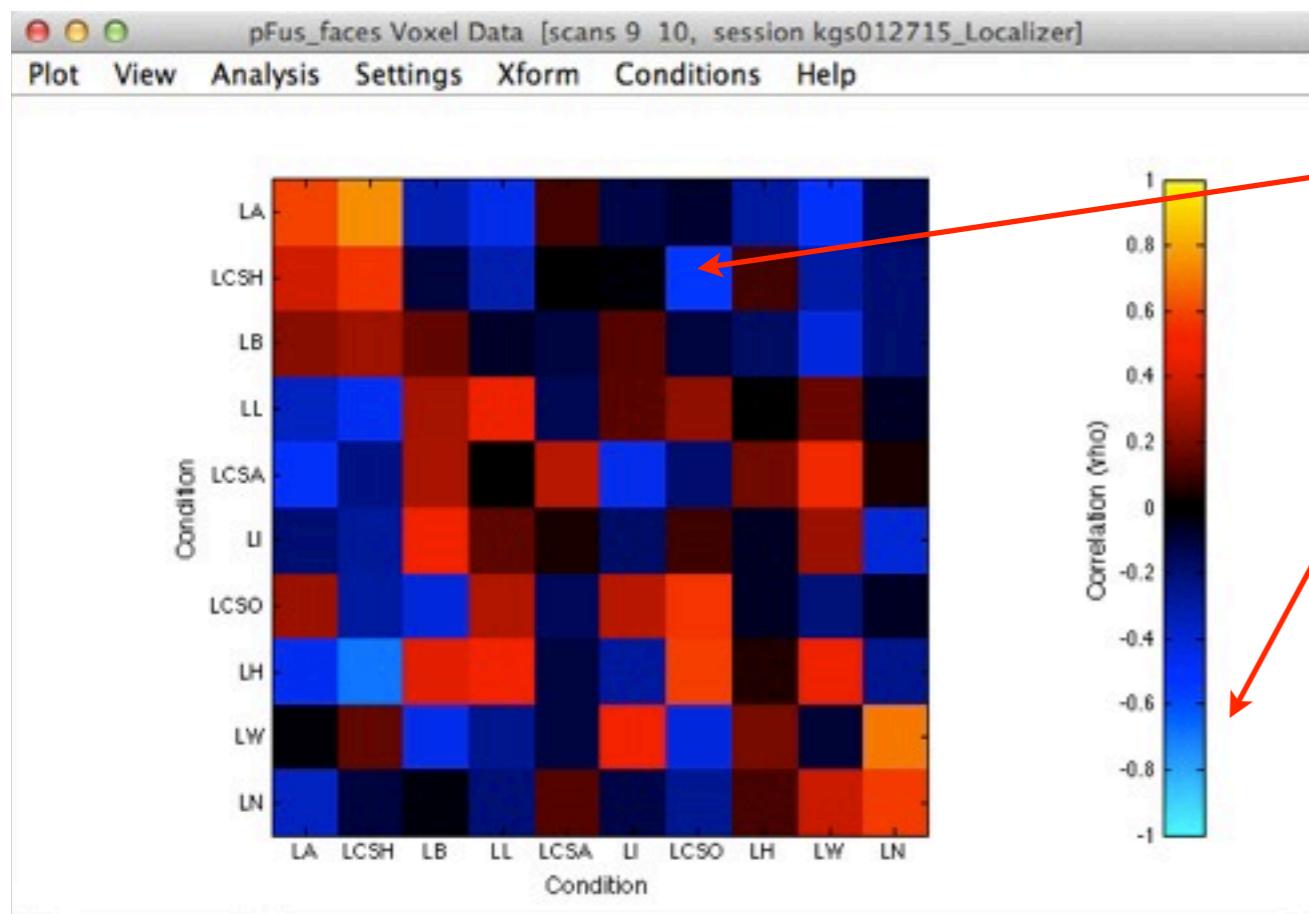


warm colors show conditions whose MVPs in this ROI are positively correlated across separate halves of the data

high correlations on diagonal suggests that MVPs in this ROI across different presentations of the same condition are reliably similar

# MVP analysis

## *MVP confusion matrix*

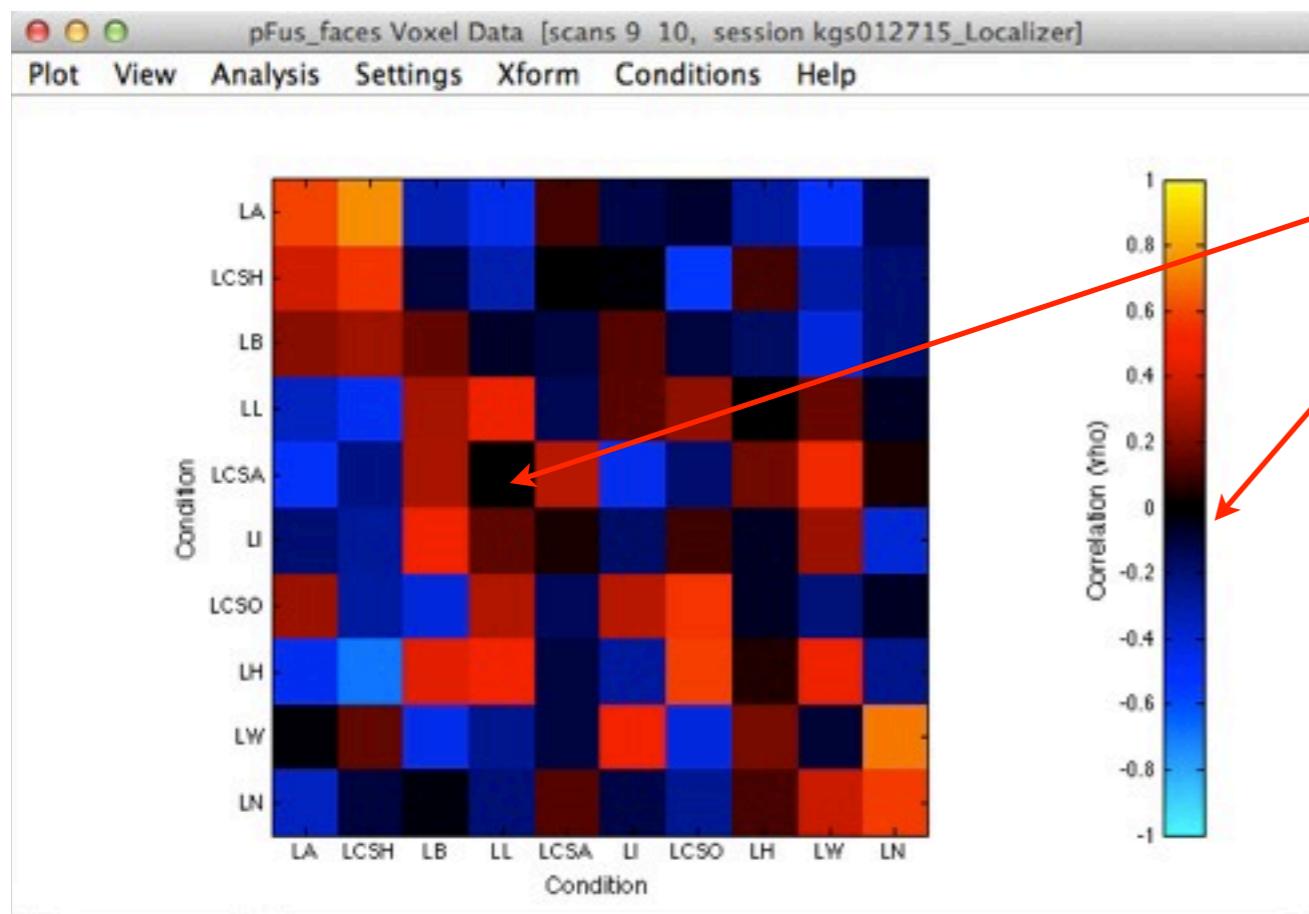


*cool colors show conditions whose MVPs in this ROI are negatively correlated across separate halves of the data*

*negative correlations suggest that response patterns in this ROI across different conditions are reliably anticorrelated*

# MVP analysis

## *MVP confusion matrix*



*dark colors show conditions whose MVPs in this ROI are uncorrelated across separate halves of the data*

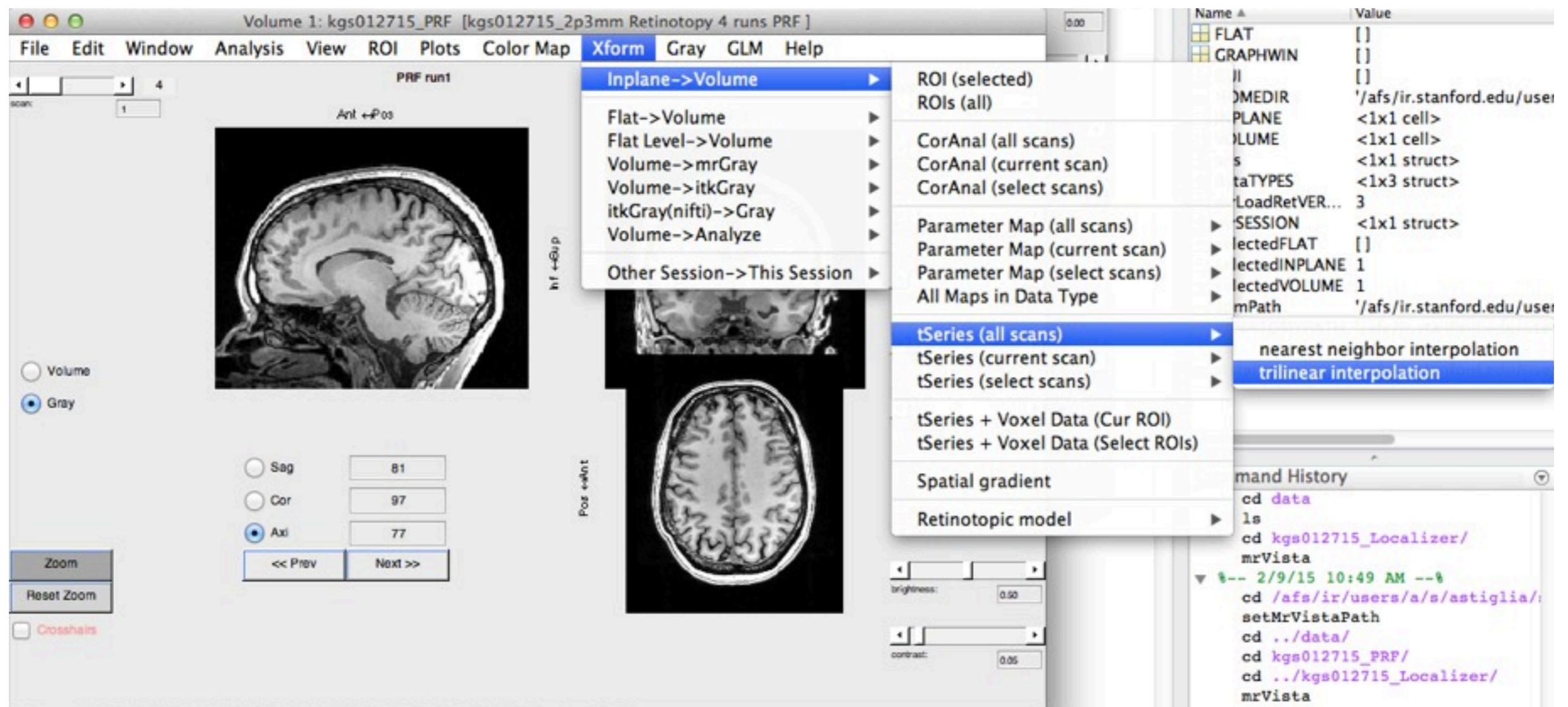
*small correlations suggest that response patterns in this ROI across the conditions are not reliable*

# pRF analysis

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- Running a population receptive field (pRF) model estimates each the preferred polar angle, eccentricity, and receptive field size of each voxel
- Maps are generated using the averaged timecourse of four runs of the same retinotopic mapping experiment in which bars sweep across the screen at eight different angles
- Unlike GLM analysis, which is typically run in the Inplane view (launched with `mrVista`), pRF analysis can only be run on the Gray view (launched with `mrVista 3`)
- You will need to transform the timeseries from the Inplane to the Gray views before averaging and running pRF

# pRF analysis

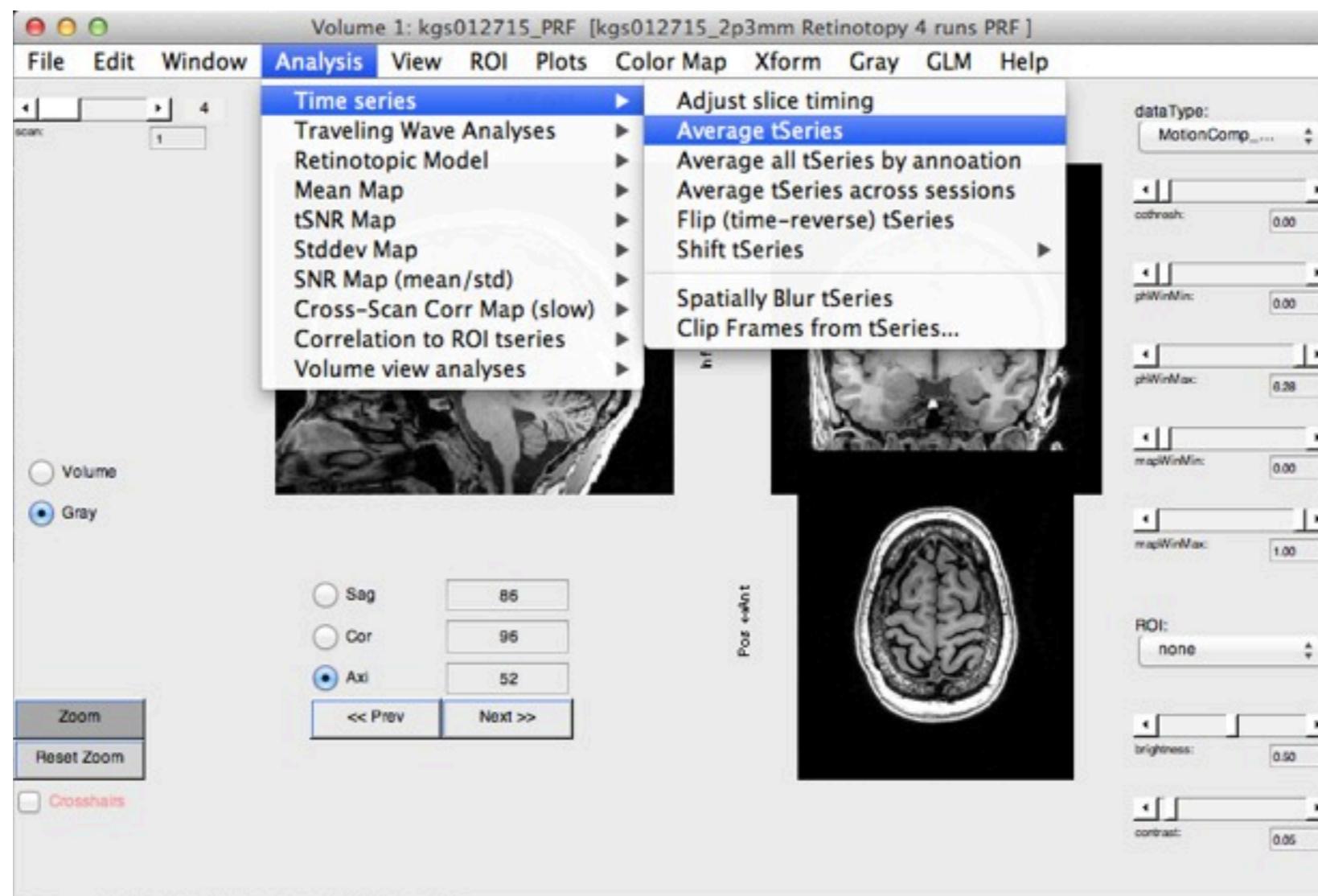


- Open Gray view by typing `mrVista 3` in Matlab command line and set the data type to MotionComp\_RefScan1 before transforming timeseries

# pRF analysis

---

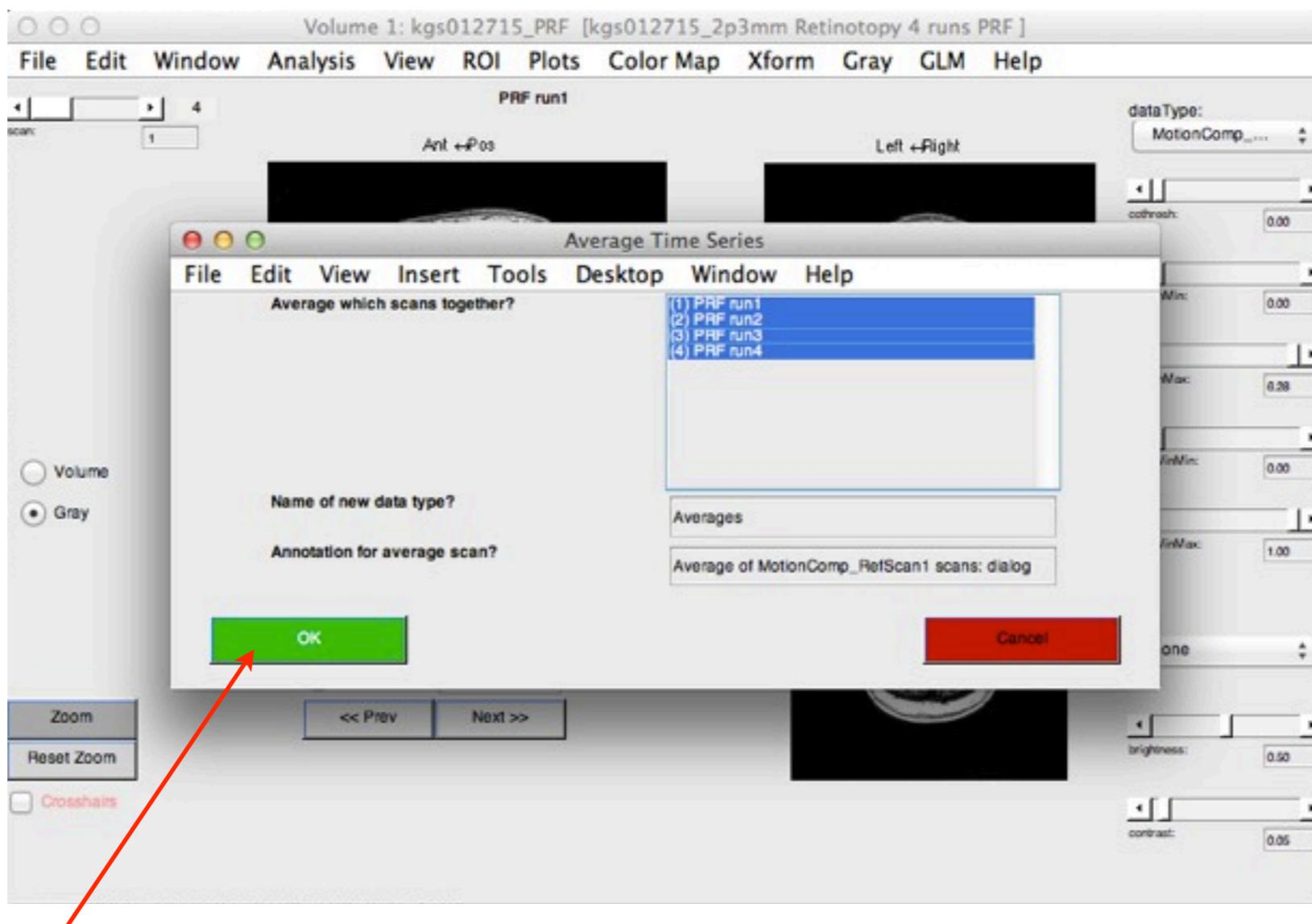
*select Average tSeries from Analysis menu*



# pRF analysis

---

*select all runs in MotionComp\_RefScan1*



*press OK*

# pRF analysis

---

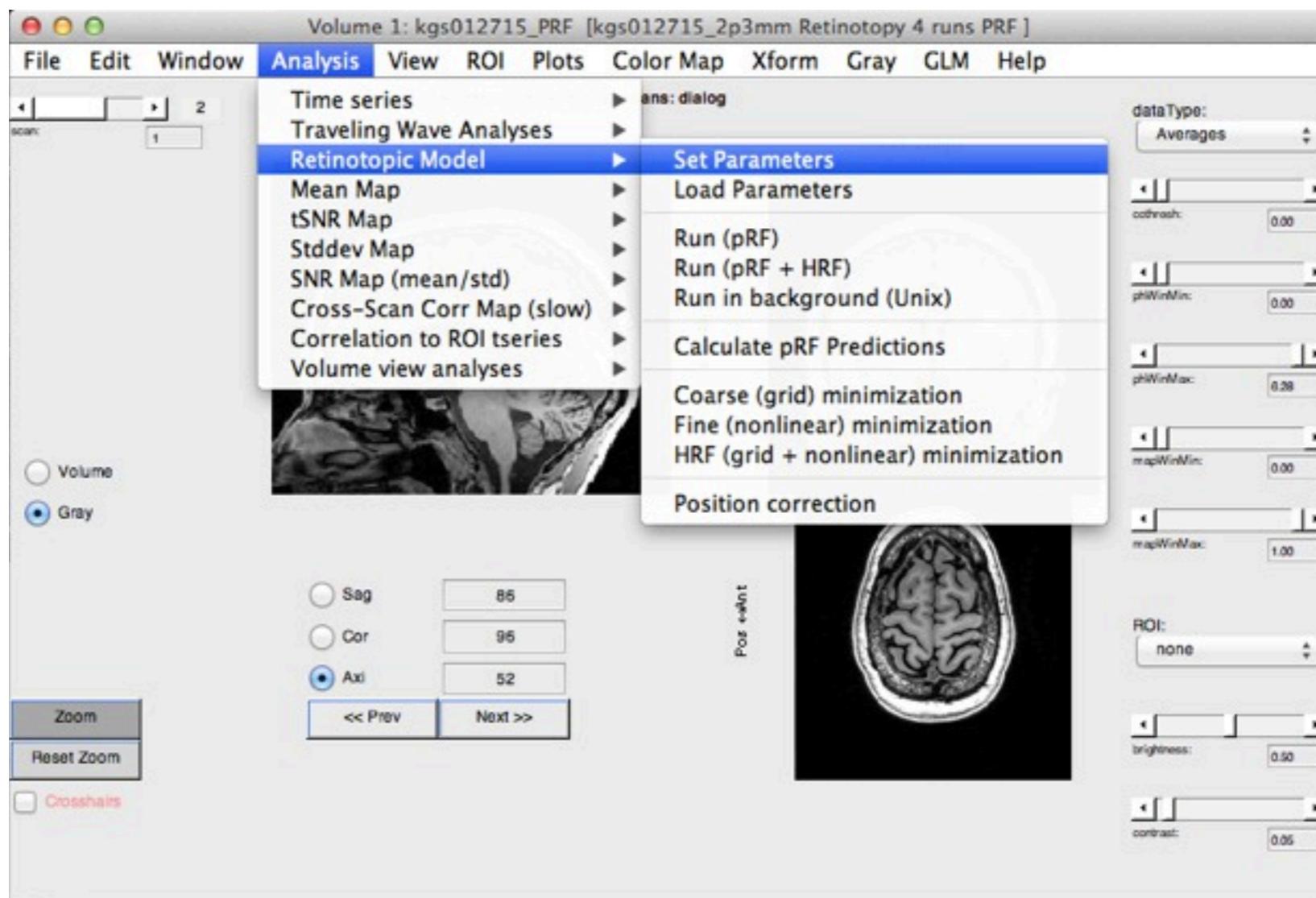


- There seems to be a small bug in the pRF code that will probably give you an error when you try to run the model, but the fix is simple
- Navigate to kgs012715\_PRF/Gray/Averages/TSeries/Scan1/ and if the file there is called tSeries.mat, you need to rename it to tSeries1.mat
- Then reopen the Gray view and set the data type to Averages

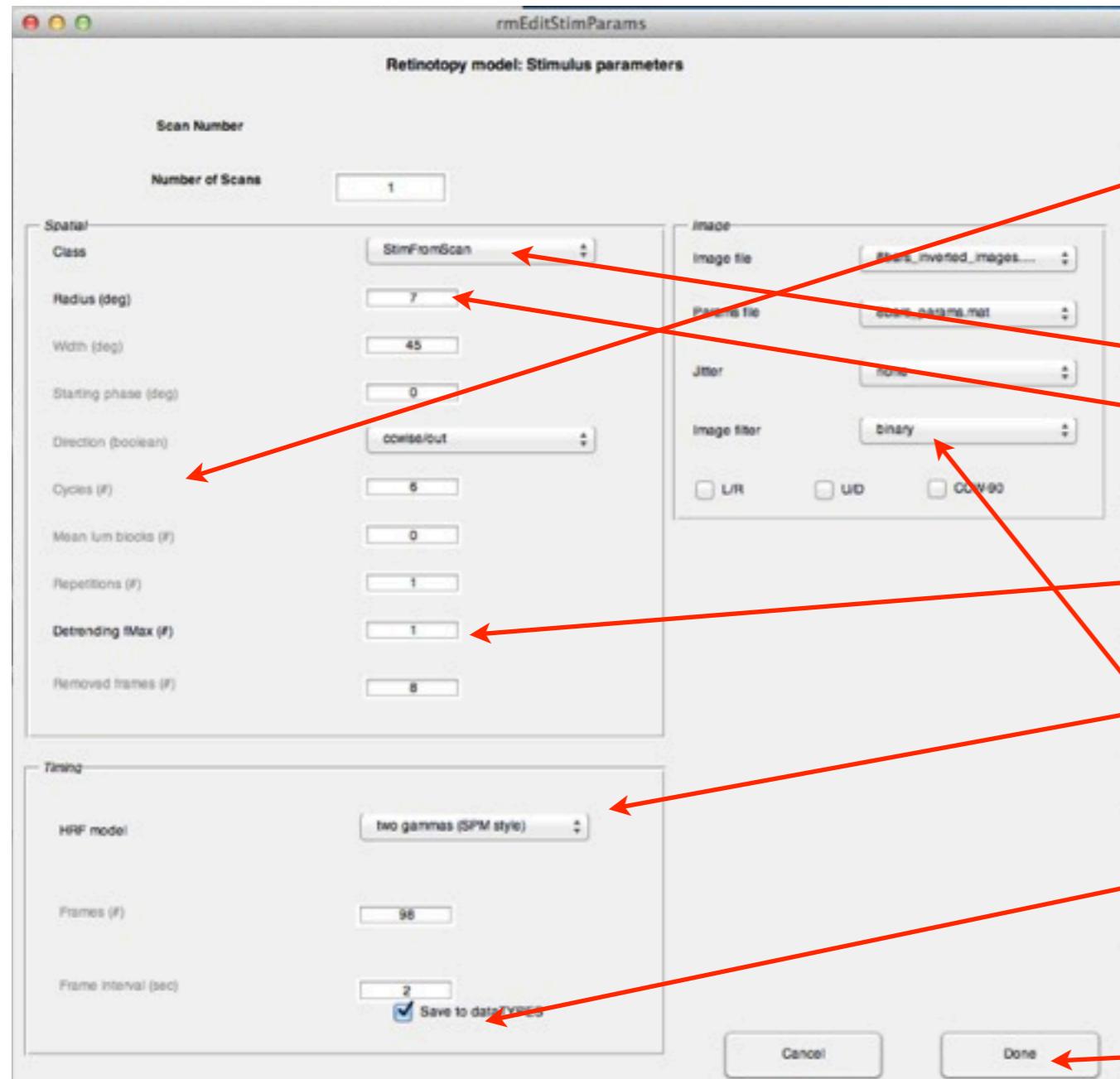
# pRF analysis

---

*select Set Parameters from Analysis menu*



# pRF analysis



*gray fields  
are irrelevant*

*class = StimFromScan  
radius = 7 deg*

*detrending fMax = 1*

*HRF = two gammas*

*select Save*

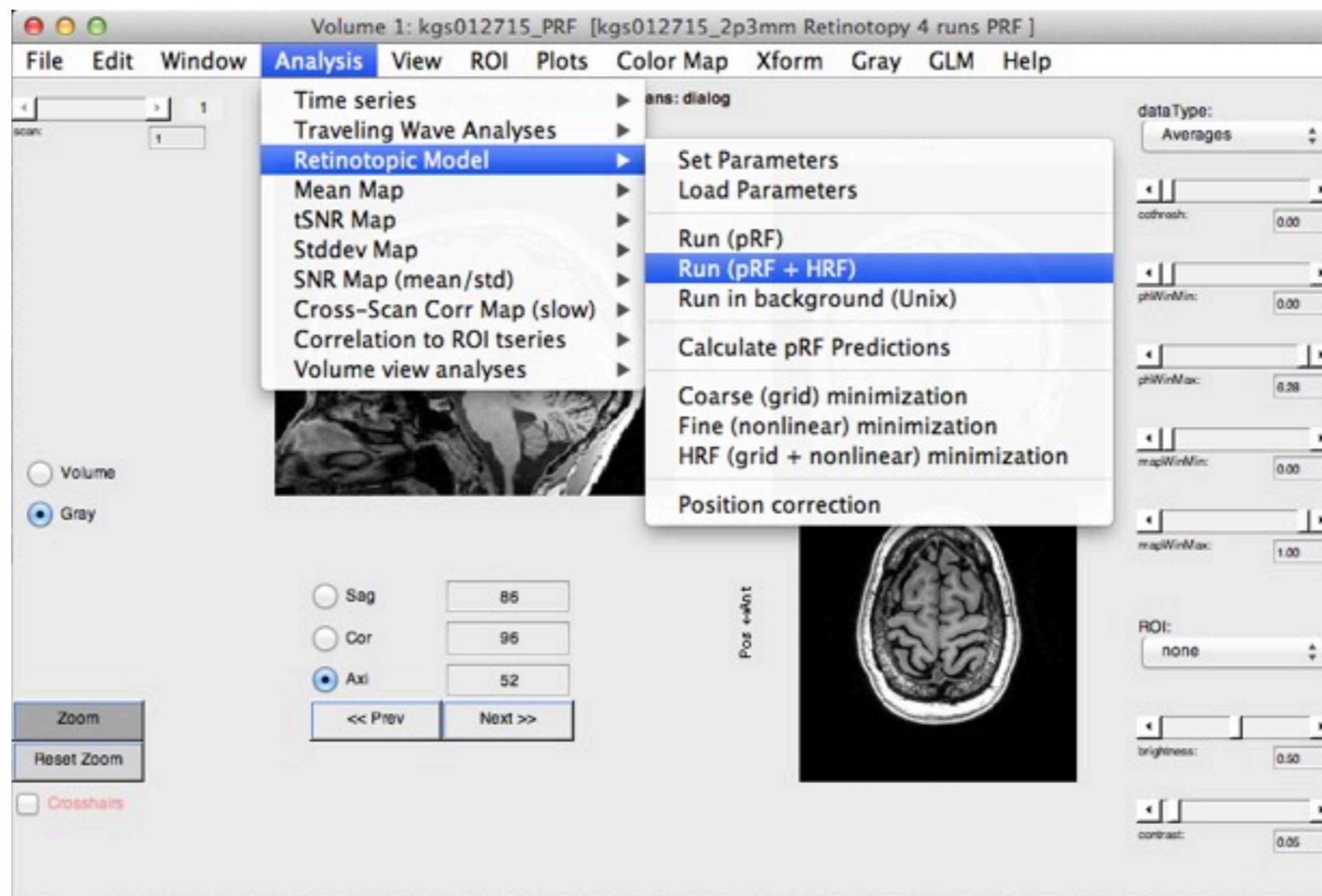
*image filter = binary*

*click Done*

# pRF analysis

---

*select Run (pRF + HRF) from Analysis menu*



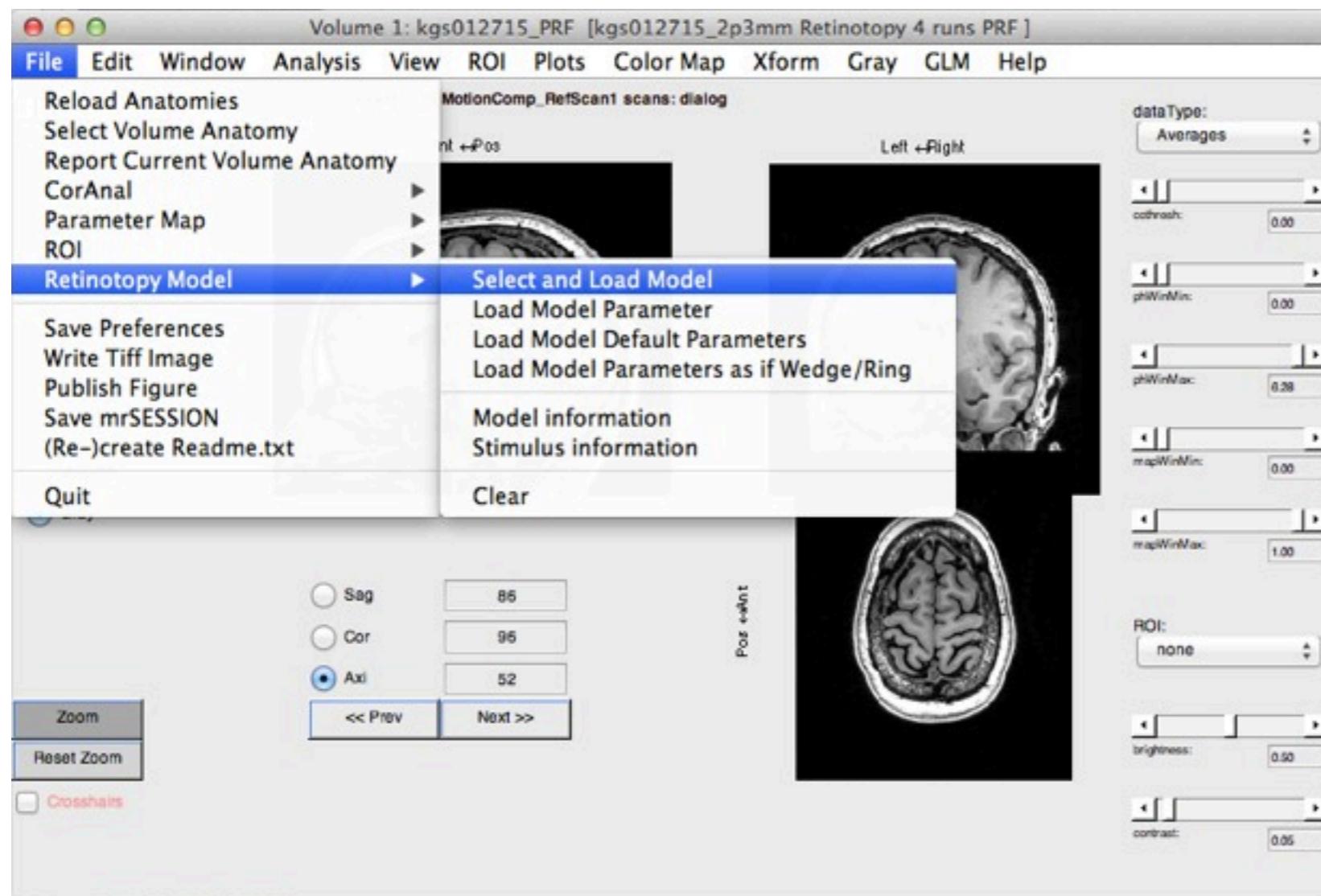
# pRF analysis

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- The pRF usually takes around an hour to finish running so be patient
- When complete there should a several mat files in kgs012715\_PRF/Gray/Averages/ one of which is called retModel-[some numbers]-fFit.mat
- This fFit model is the final version of the pRF model that you will load when visualizing maps on the cortical surface mesh

# pRF analysis

*Select and Load Model from file menu*

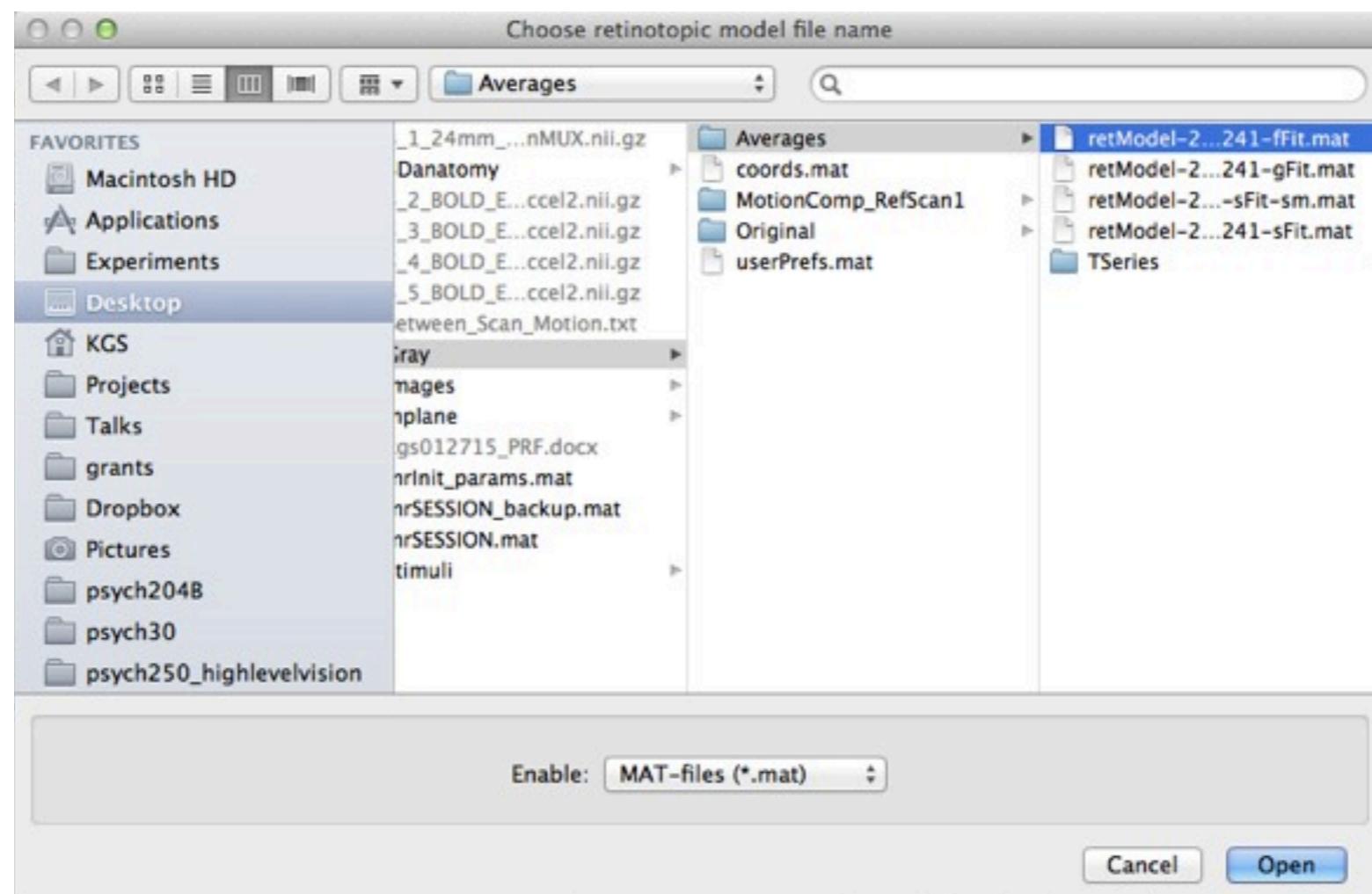


*make sure  
you are on  
the Averages  
data type*

# pRF analysis

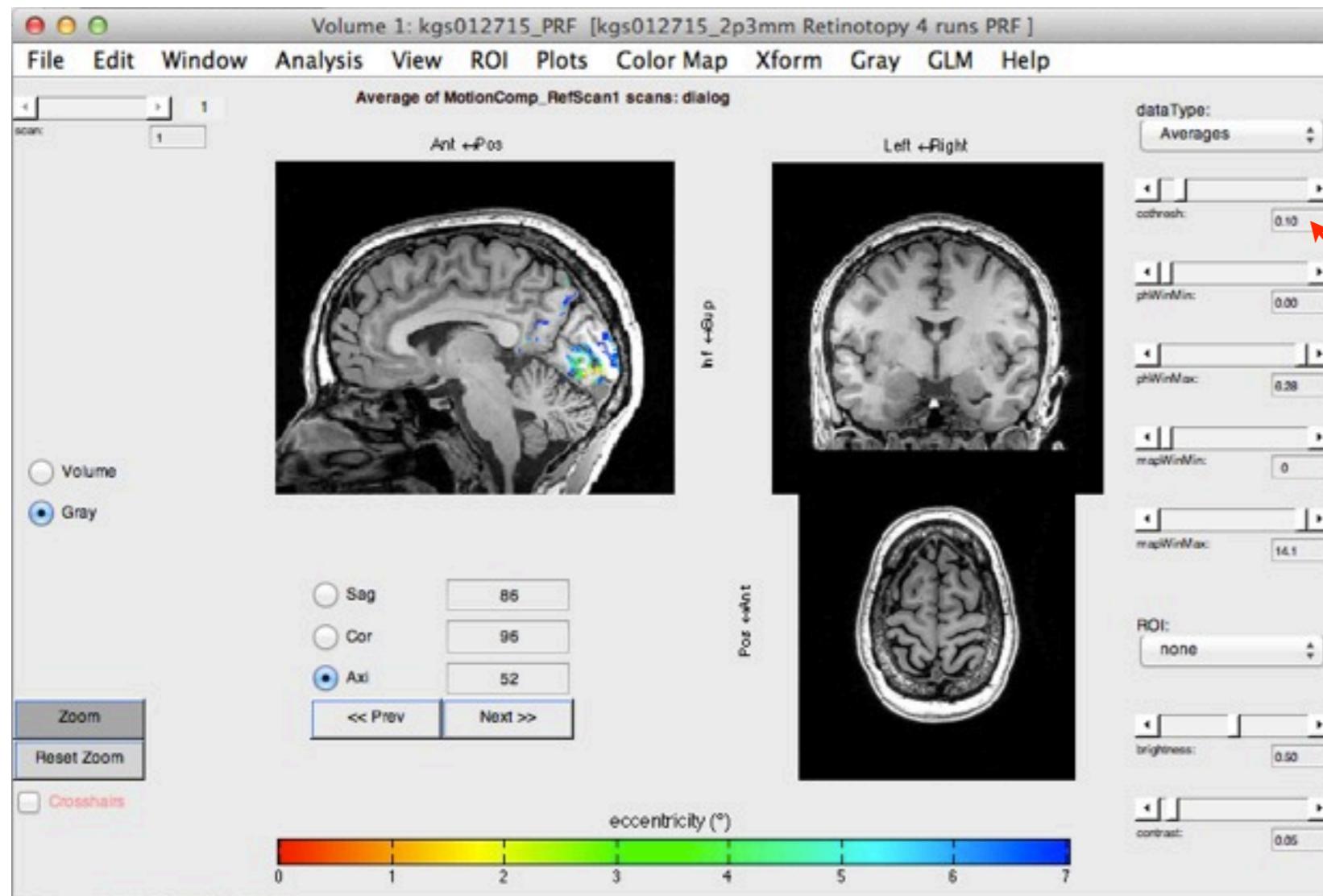
---

*select fFit model*



# pRF analysis

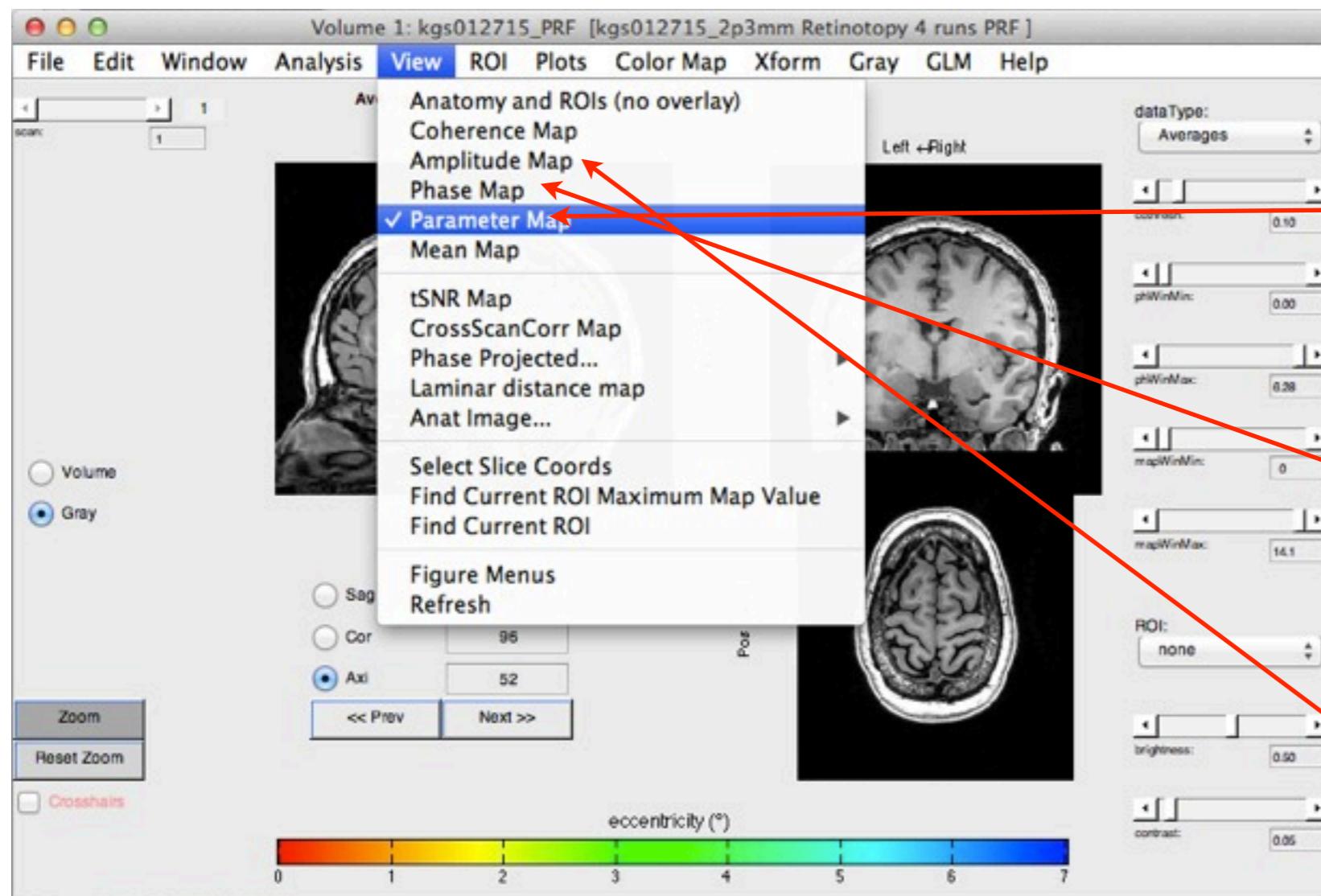
*eccentricity map displays first by default*



*threshold by proportion of variance explained (default is 0.1)*

# pRF analysis

*display different maps from View menu*



Parameter Map  
= eccentricity

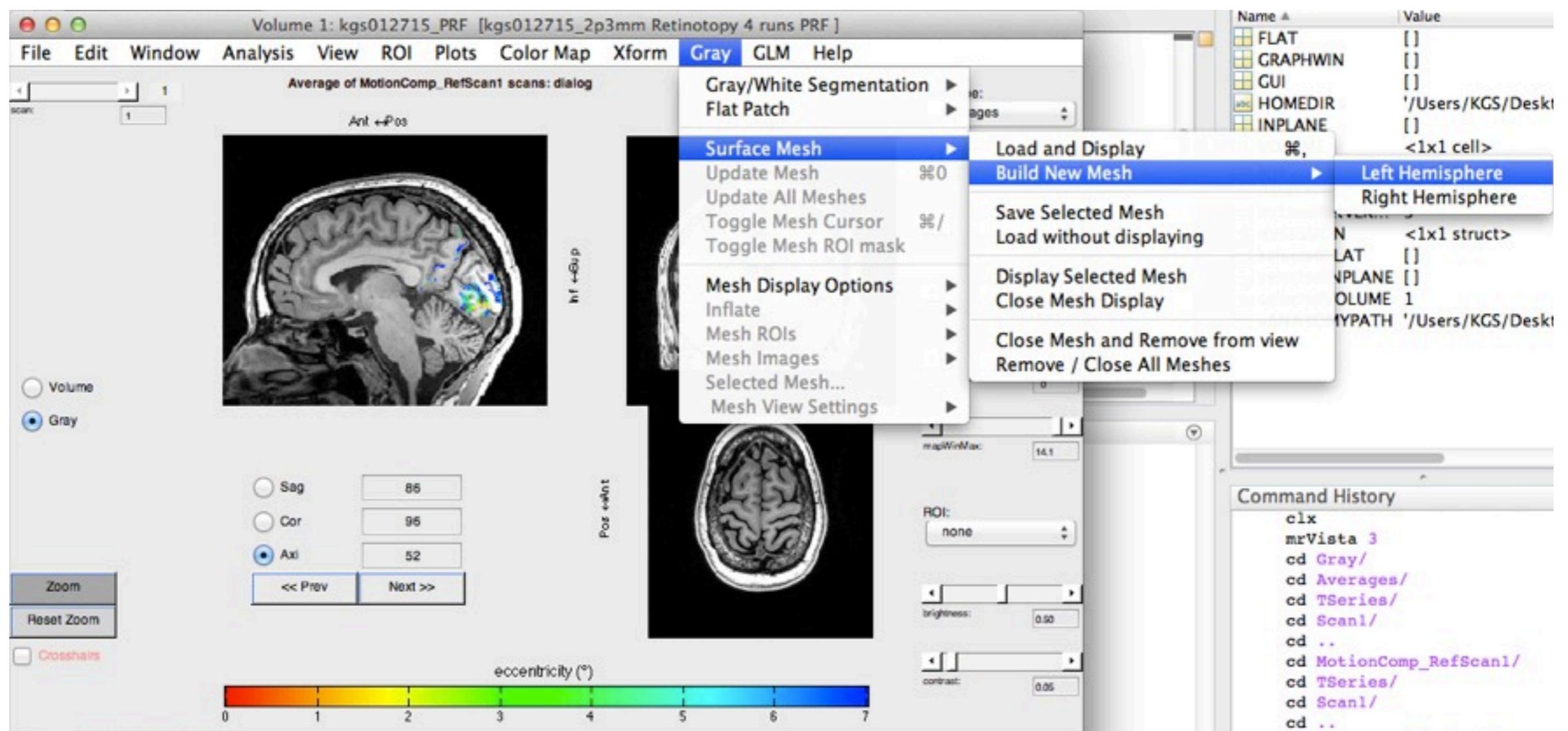
Phase Map =  
polar angle

Amplitude Map  
= pRF size

## **Part 7: Visualization on cortical surface**

# Visualization on inflated cortical surface

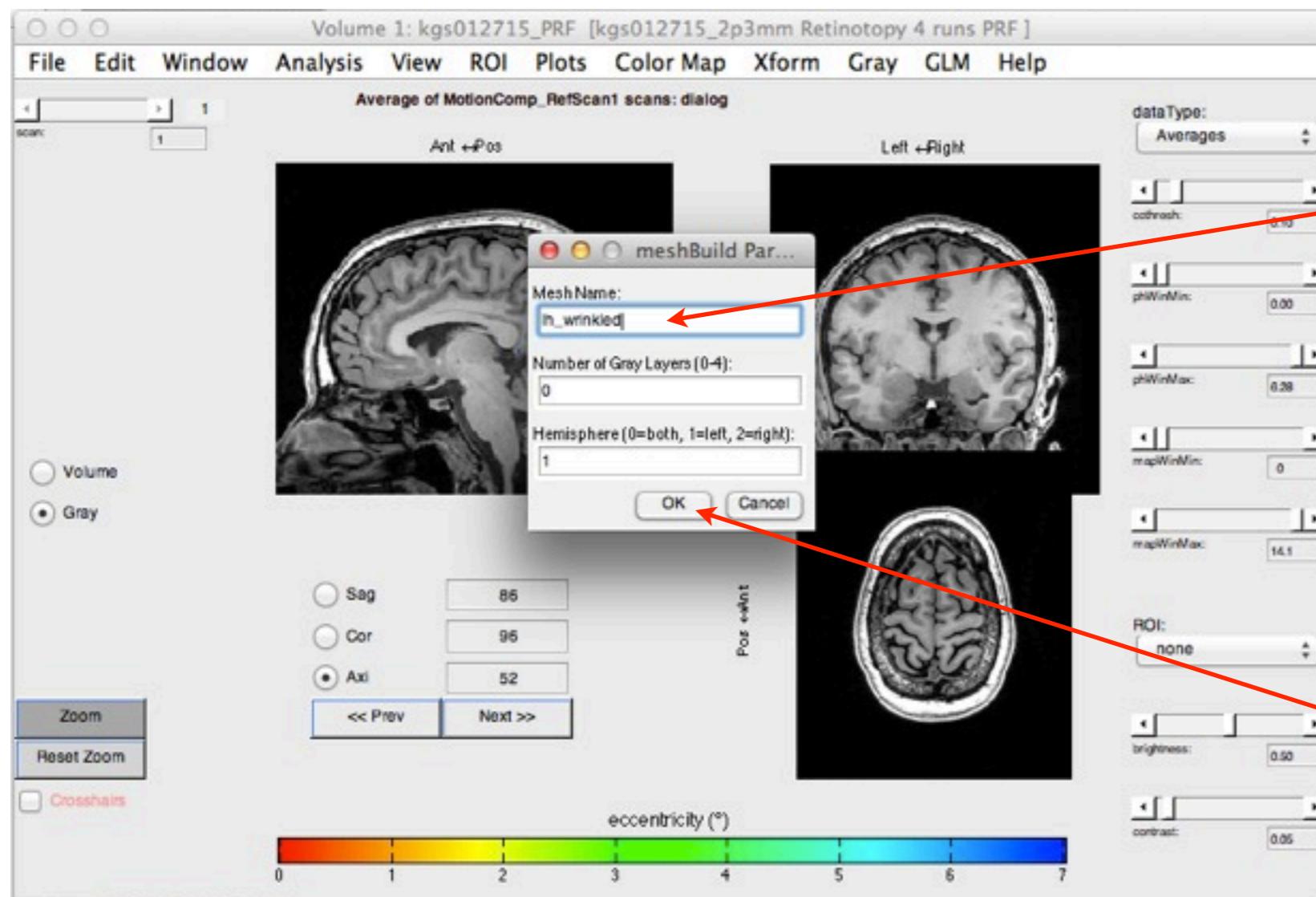
*choose hemisphere to build*



- Inflated cortical surface models are built in the Gray view (i.e., mrVista 3) using the t1\_class.nii file in the 3Danatomy directory

# Visualization on inflated cortical surface

*the first step is to created an uninflated mesh*

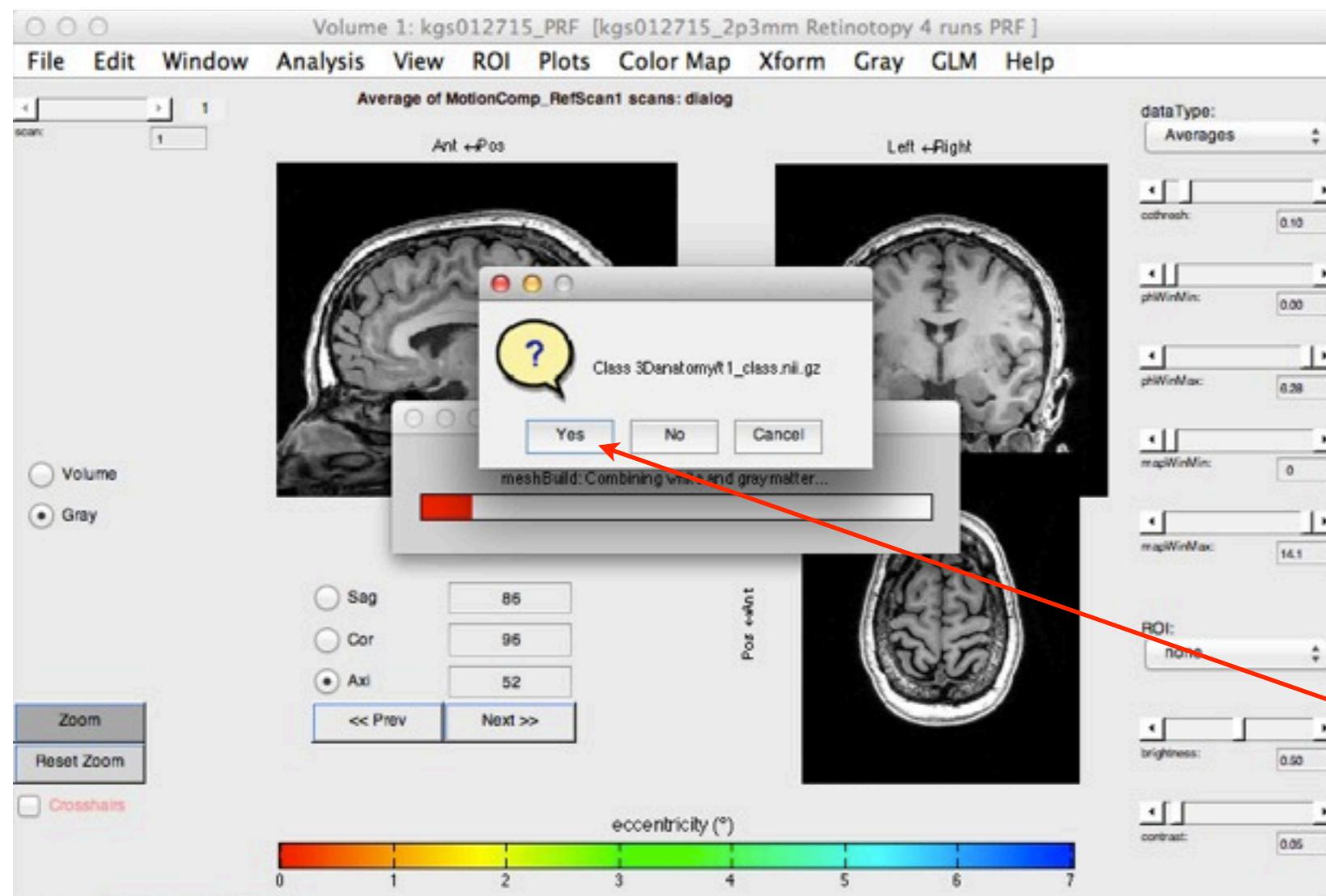


name the mesh  
lh\_wrinkled but  
don't change  
anything else

click OK

# Visualization on inflated cortical surface

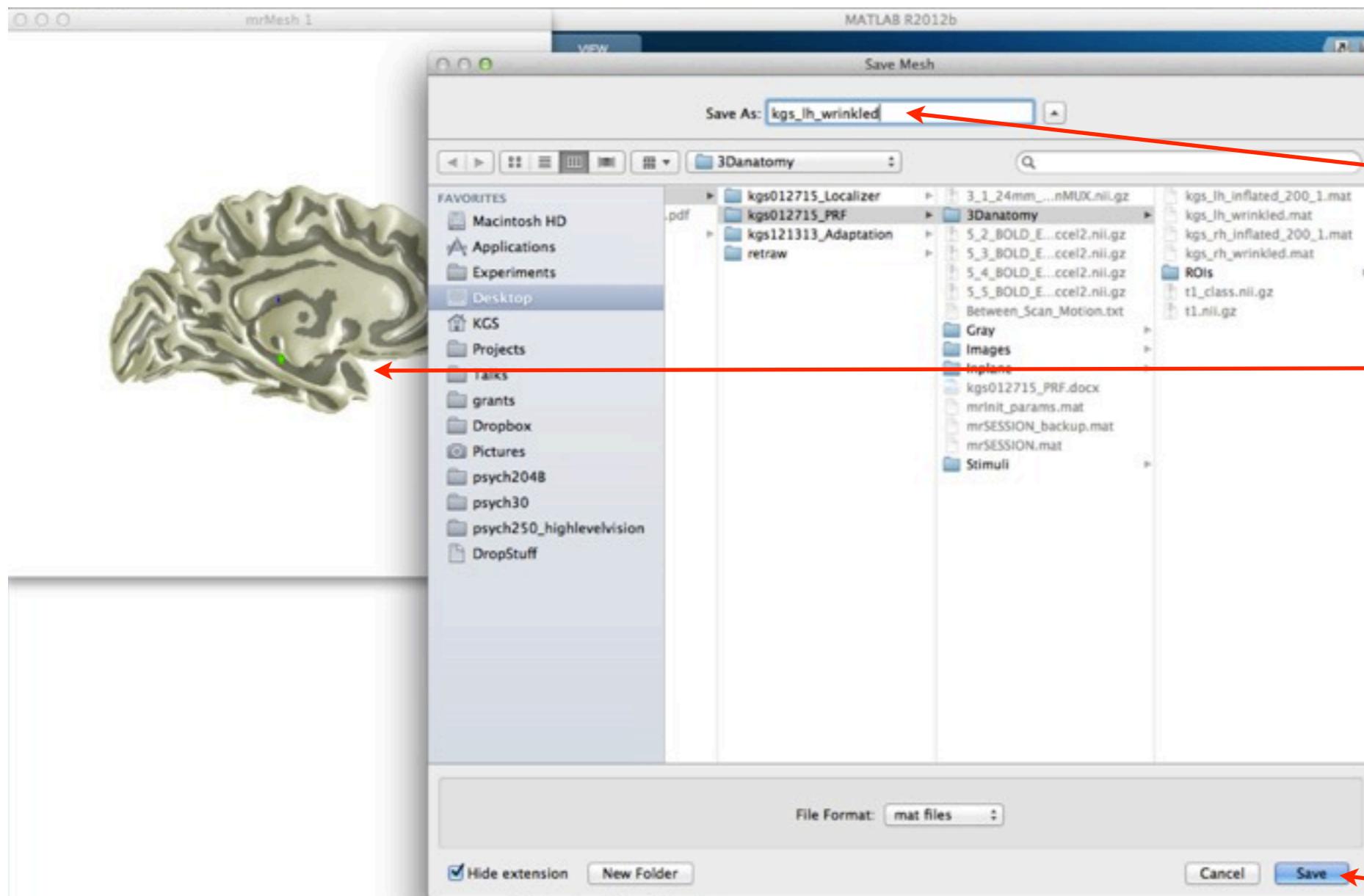
*feed mrVista the class file (t1\_class.nii.gz)*



*click Yes*

# Visualization on inflated cortical surface

*save the wrinkled mesh (overwriting old file)*



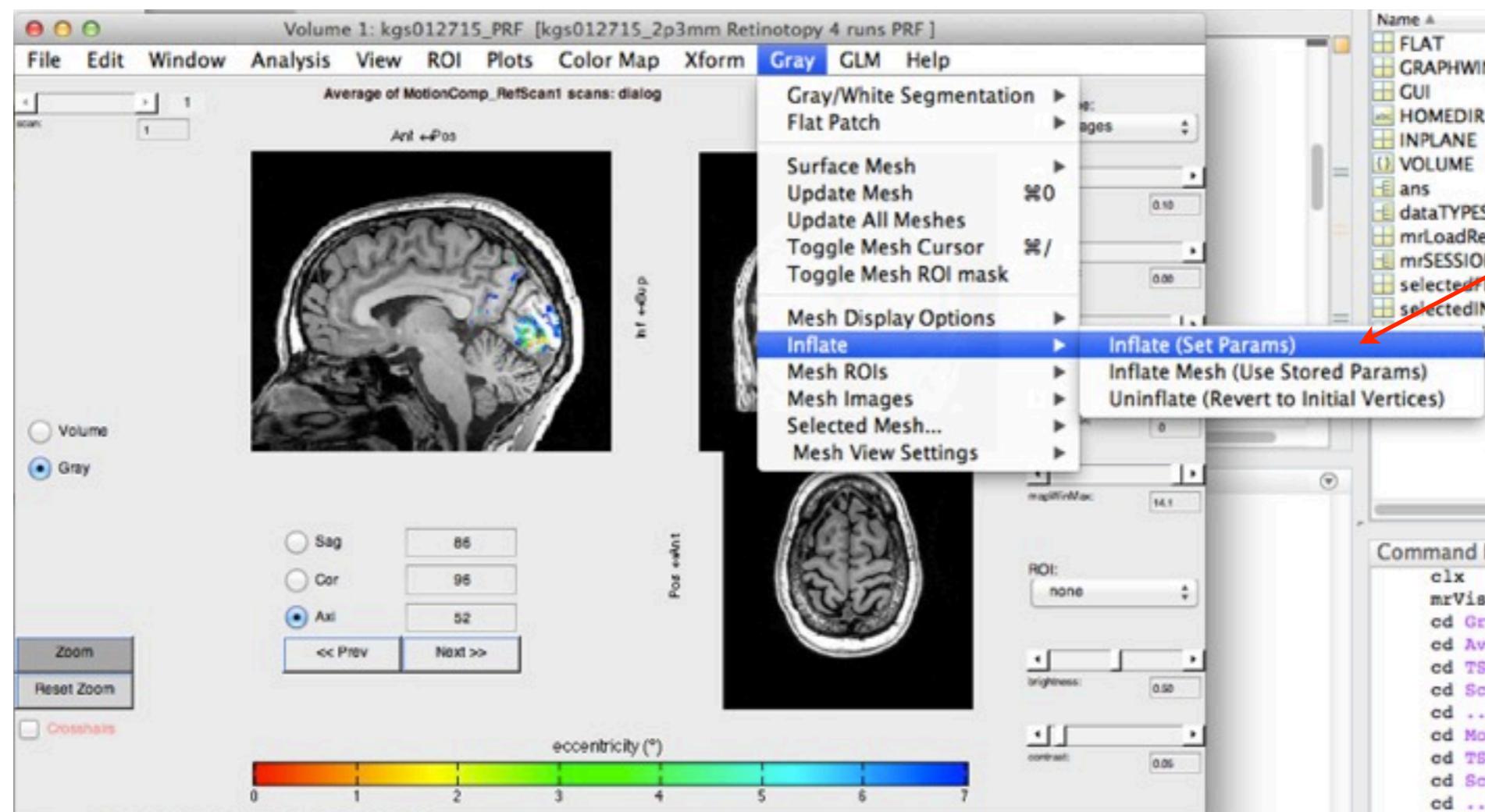
*name the  
mesh*

*this is the  
“wrinkled” or  
uninflated  
mesh saved*

*save the  
mesh*

# Visualization on inflated cortical surface

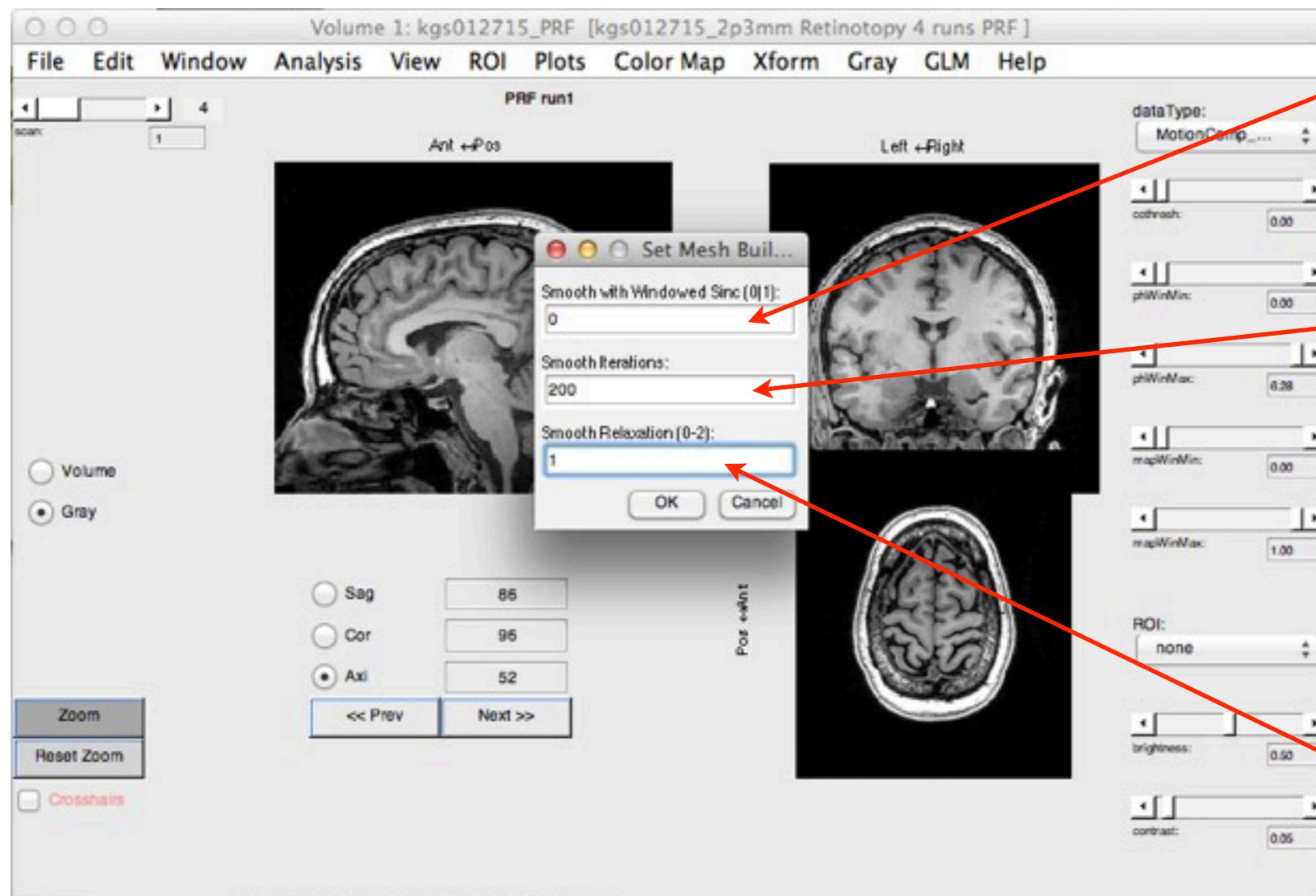
*with the wrinkled mesh still open...*



inflate  
wrinkled  
mesh from  
Gray menu

# Visualization on inflated cortical surface

*set some default parameters*



*Smoothing = 0*

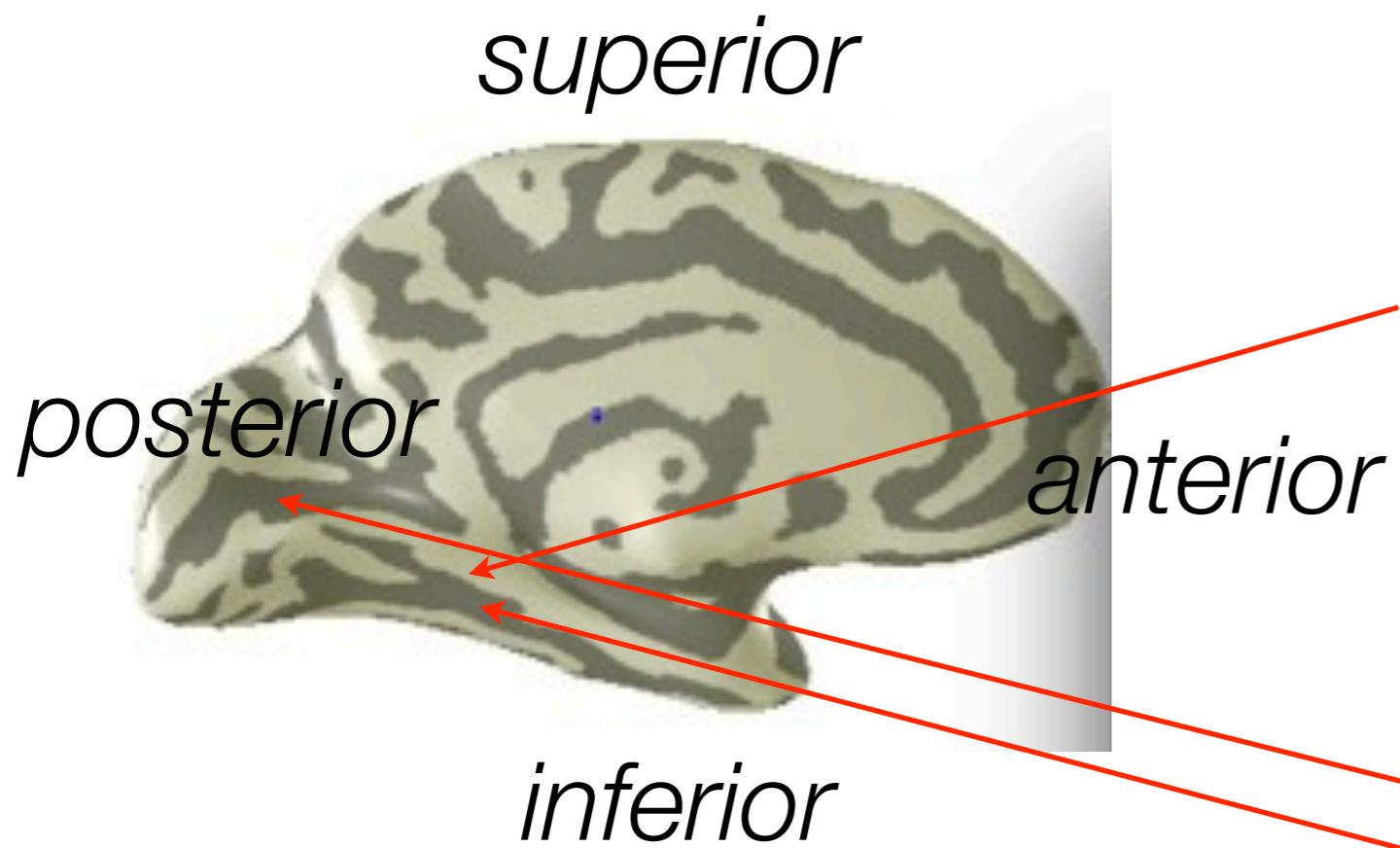
*Smooth Iterations:*  
32 = semi-inflated  
200=inflated

*Smooth Relaxation = 1*

# Visualization on inflated cortical surface

---

*inflated brain should look like this with 200 smoothing iterations*

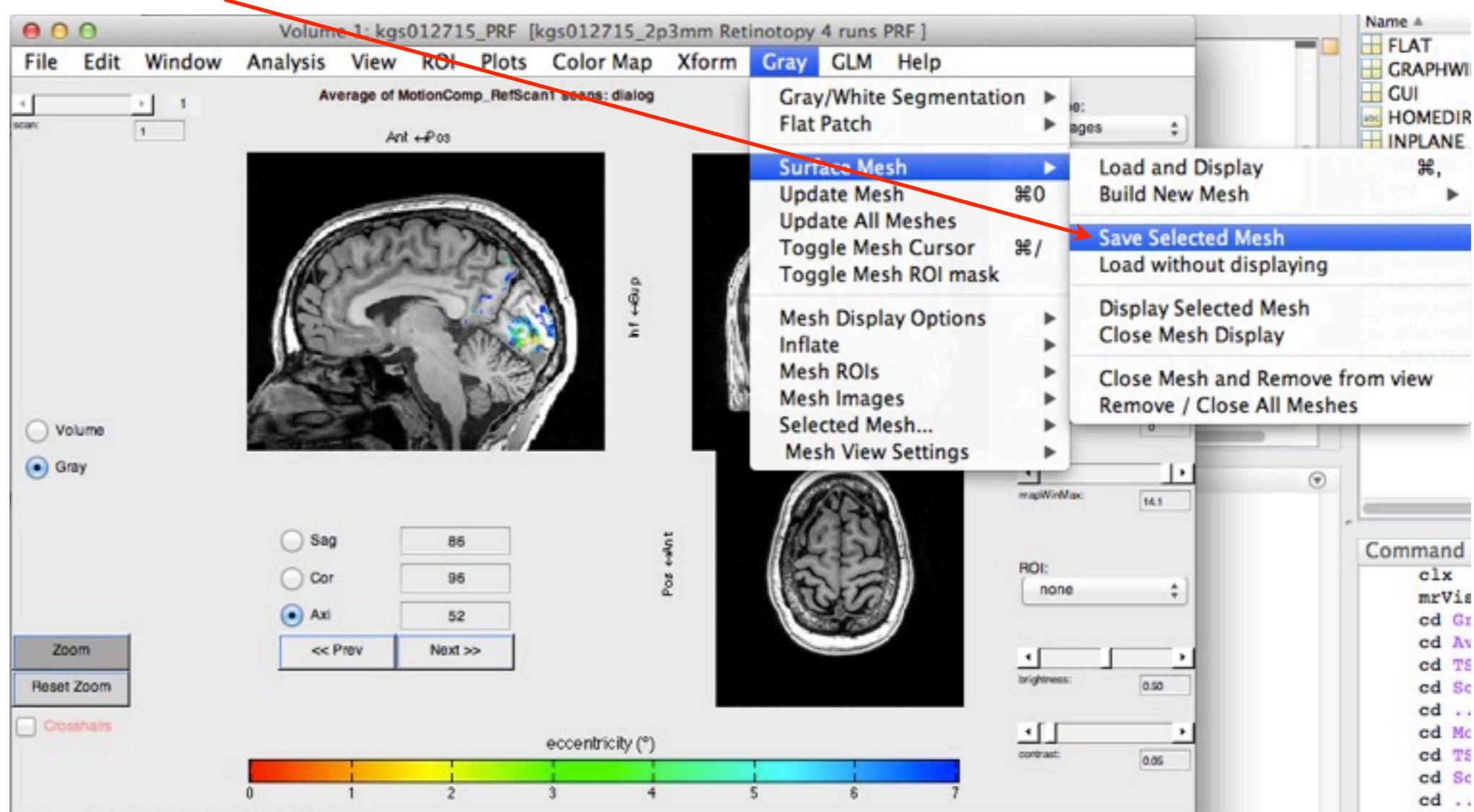


*light gray = gyrus*  
e.g., parahippocampal gyrus

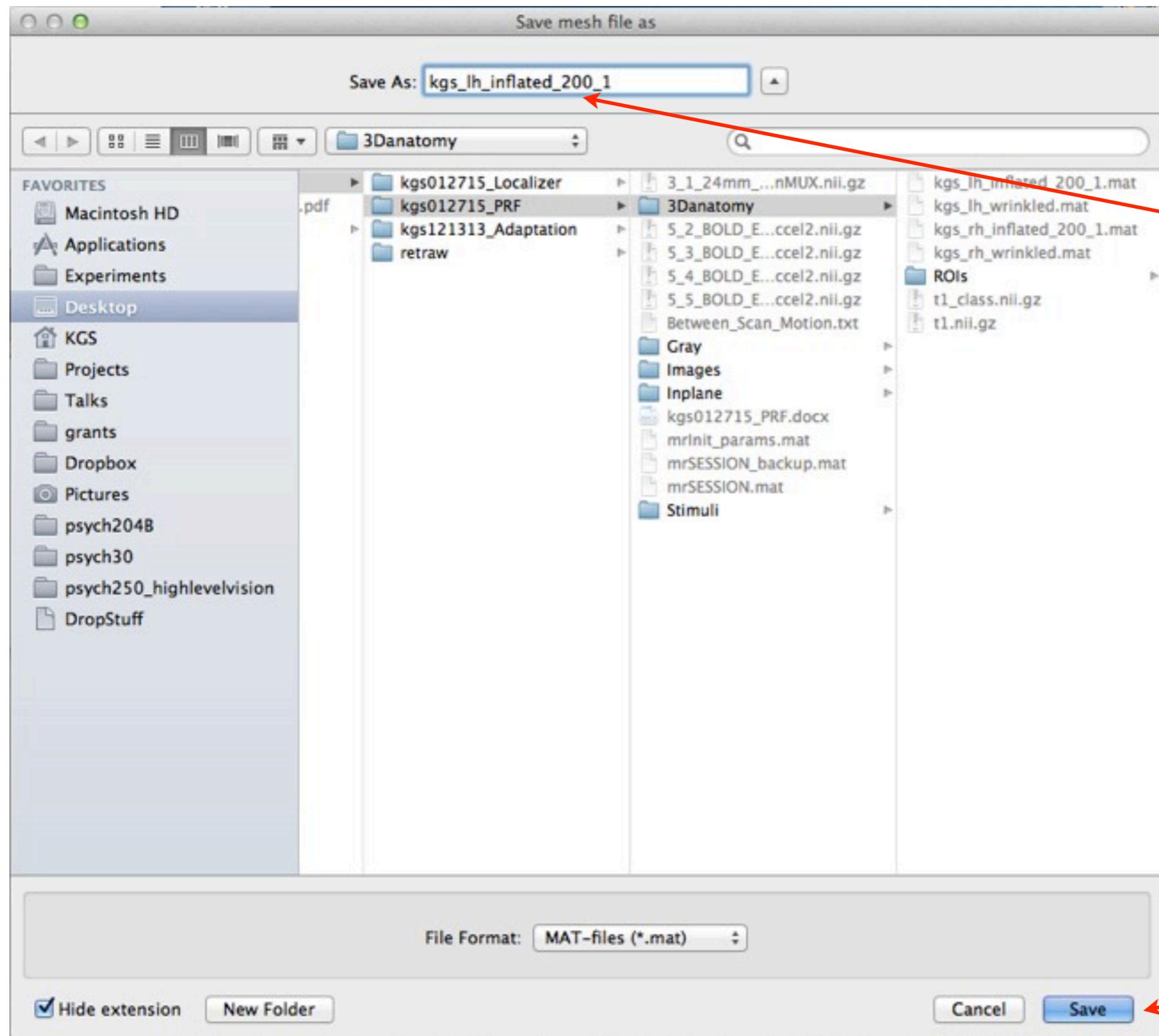
*dark gray = sulcus*  
e.g., calcarine sulcus  
collateral sulcus

# Visualization on inflated cortical surface

*save inflated version of the mesh from Gray menu*



# Visualization on inflated cortical surface

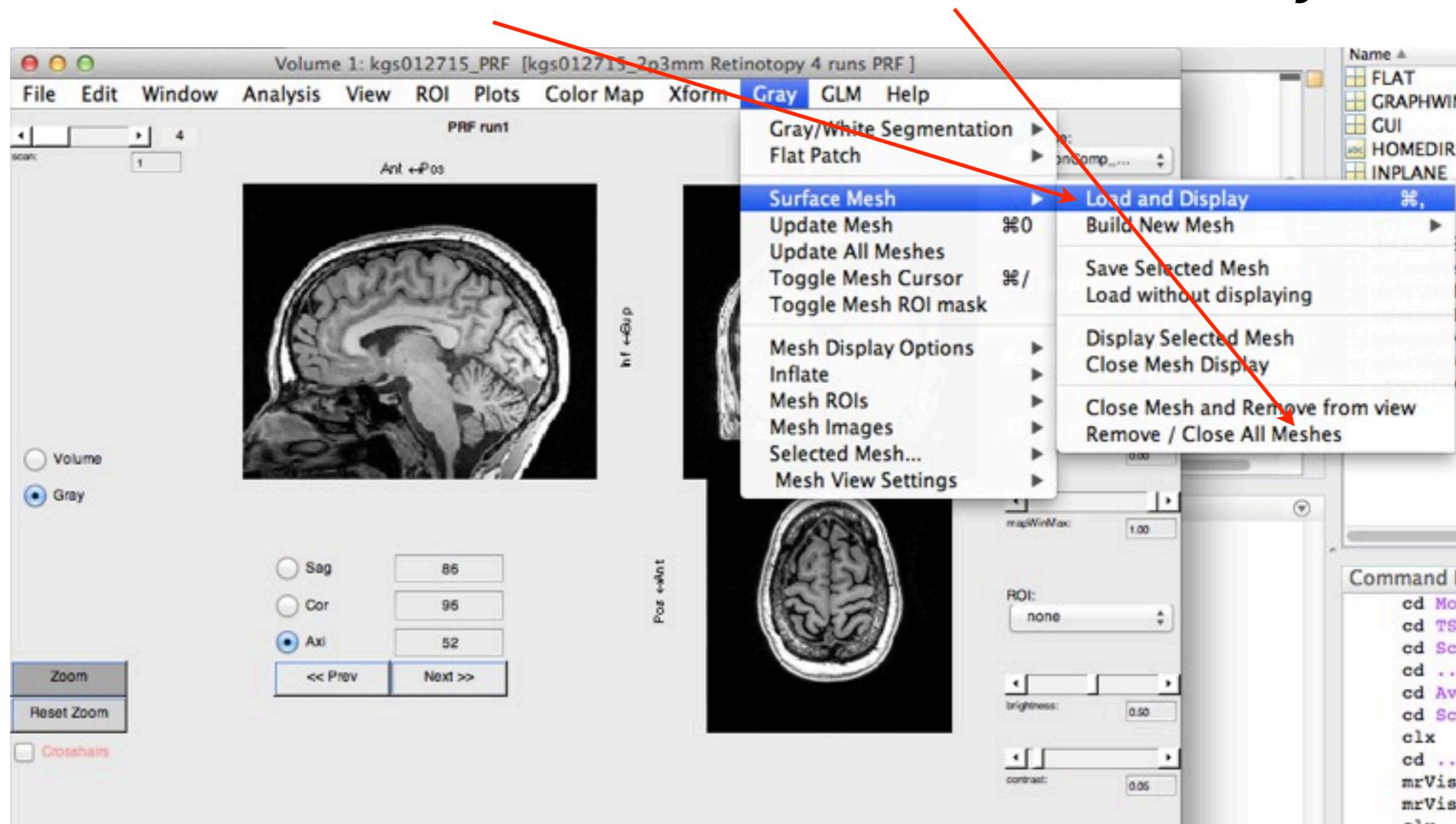


*name inflated  
mesh with  
smoothing  
iterations (200)  
and relaxation  
parameter  
(overwriting  
existing file)*

*click Save*

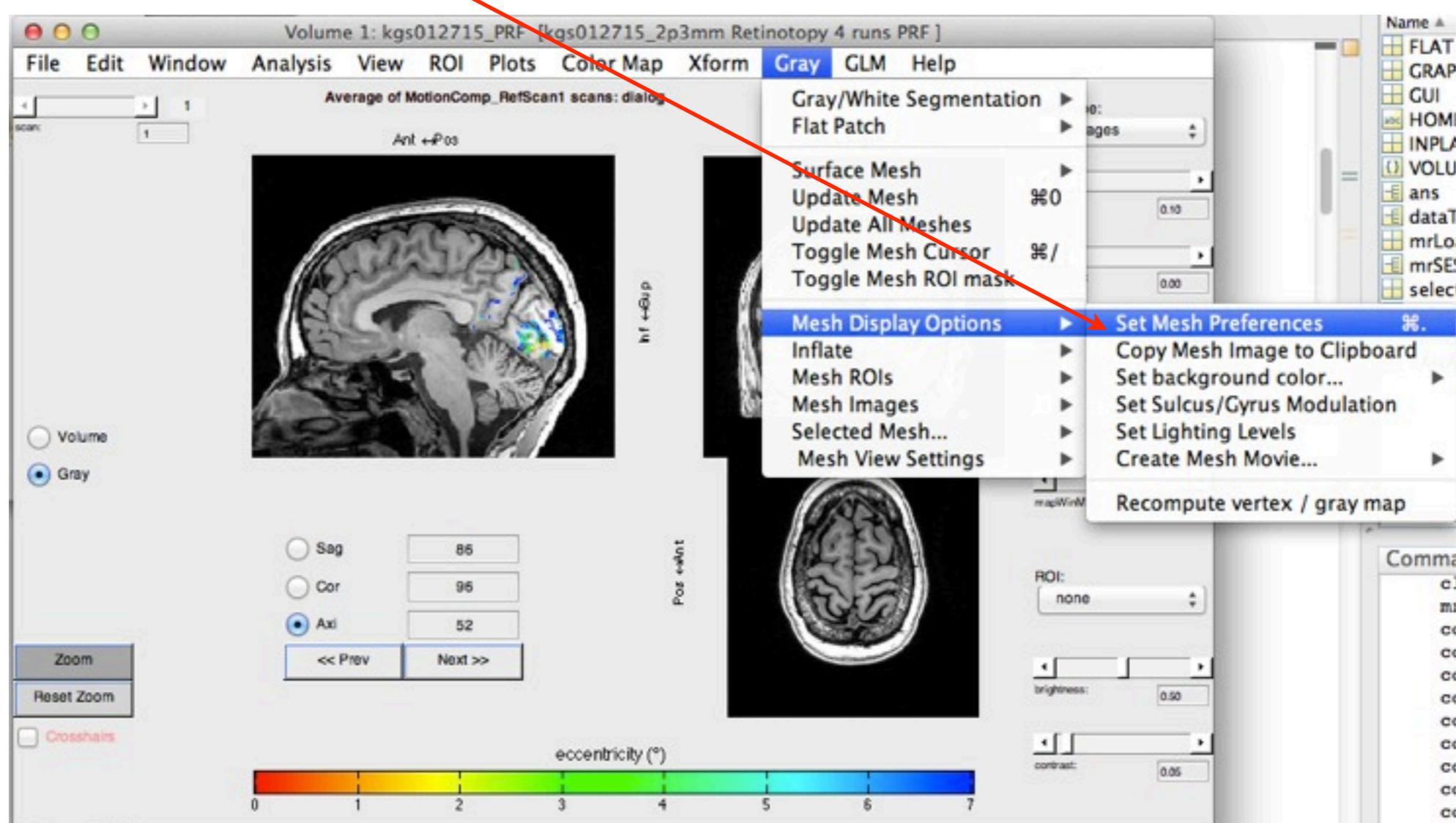
# Visualization on inflated cortical surface

*meshes are loaded and closed from Gray menu*

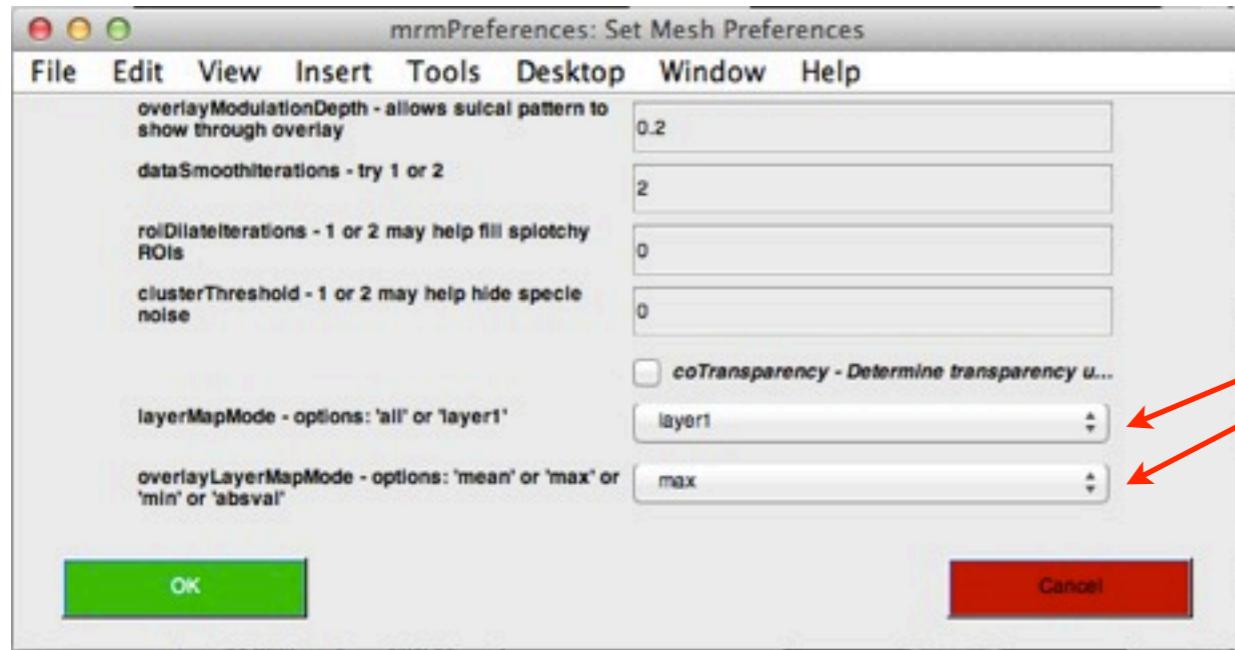


# Visualization on inflated cortical surface

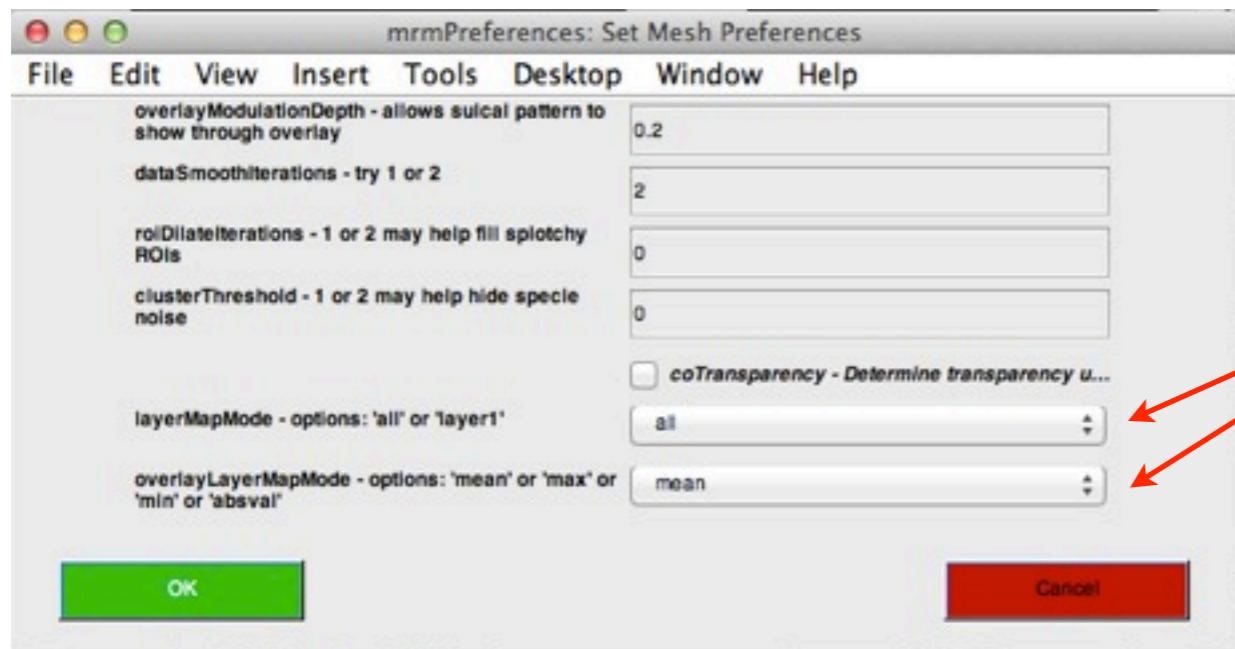
*set mesh preferences from Gray menu*



# Visualization on inflated cortical surface



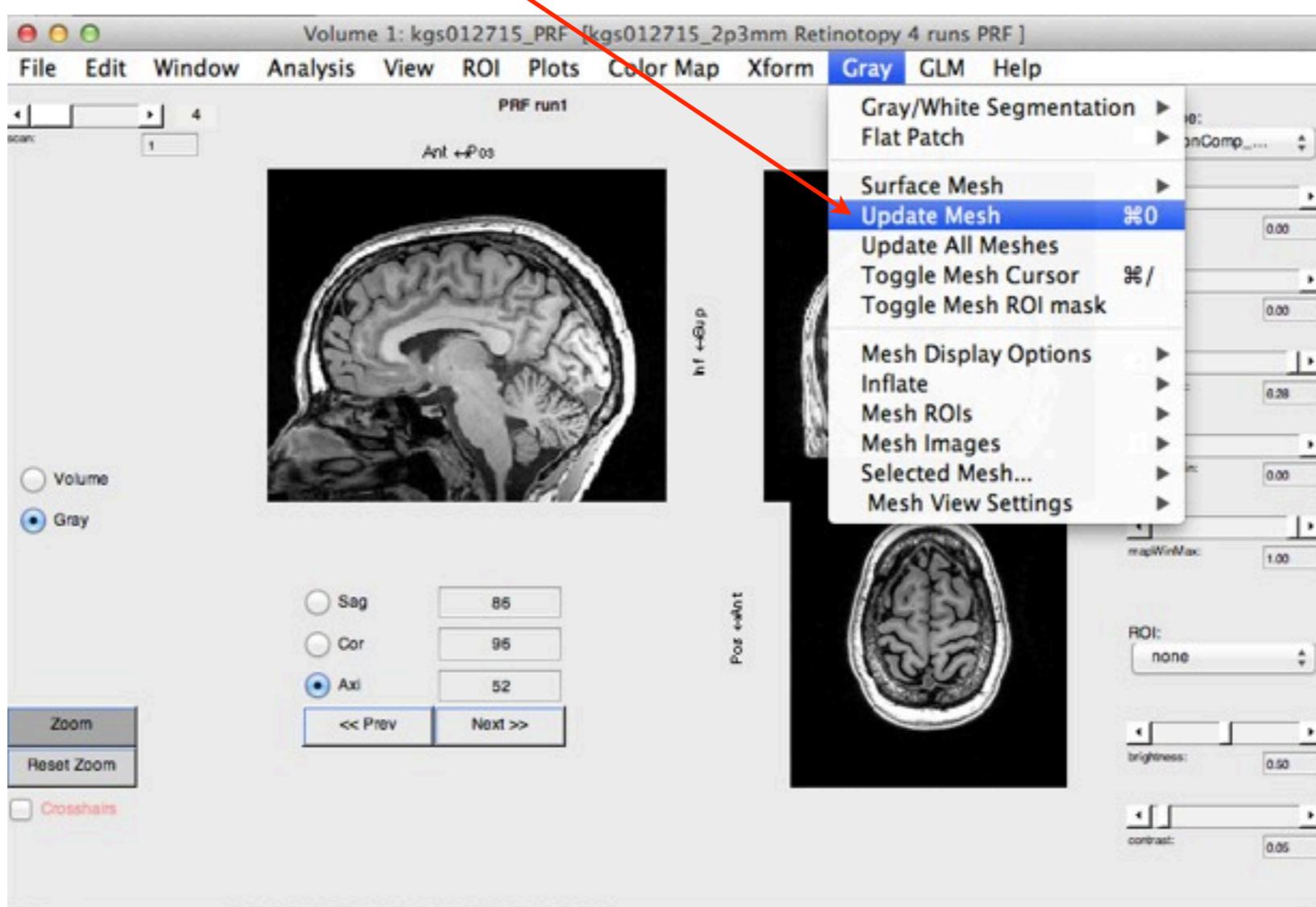
*retinotopy visualization  
preferences*



*otherwise use these  
visualization preferences*

# Visualization on inflated cortical surface

*select Update Mesh from Gray menu*

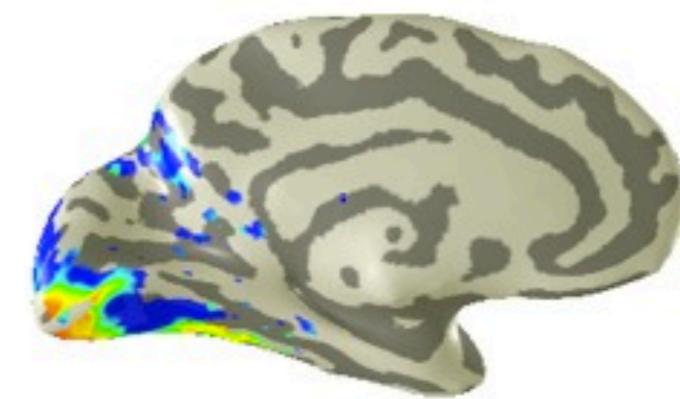


- Changes made in the Gray view window (e.g., loading a different map, changing the threshold, etc.) will not project to mesh until you update

# Visualization on inflated cortical surface

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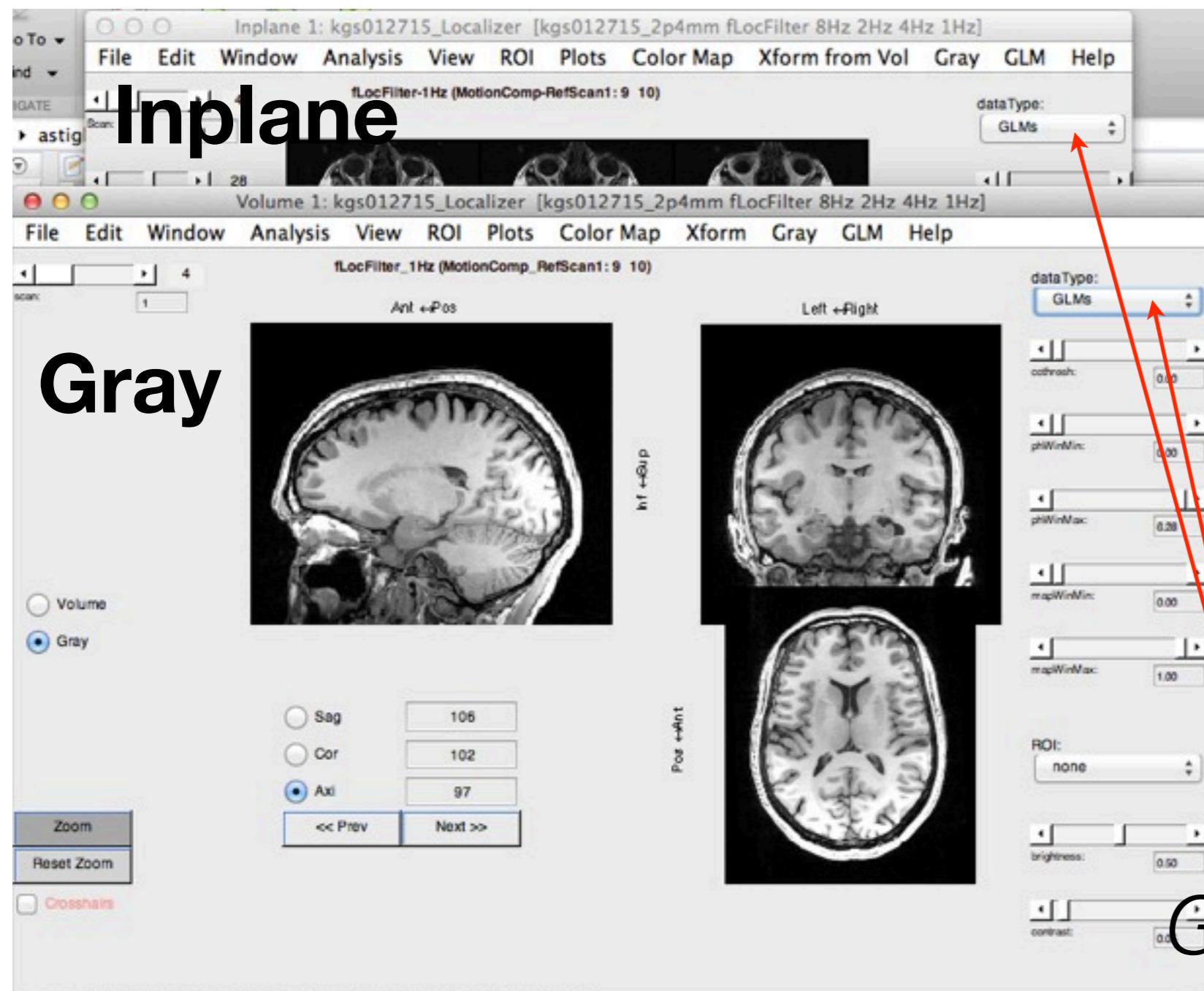
*updating the mesh should project parameter map loaded in Gray view window to inflated mesh*



e.g., eccentricity

# Visualization on inflated cortical surface

*to project GLM contrast map to surface*

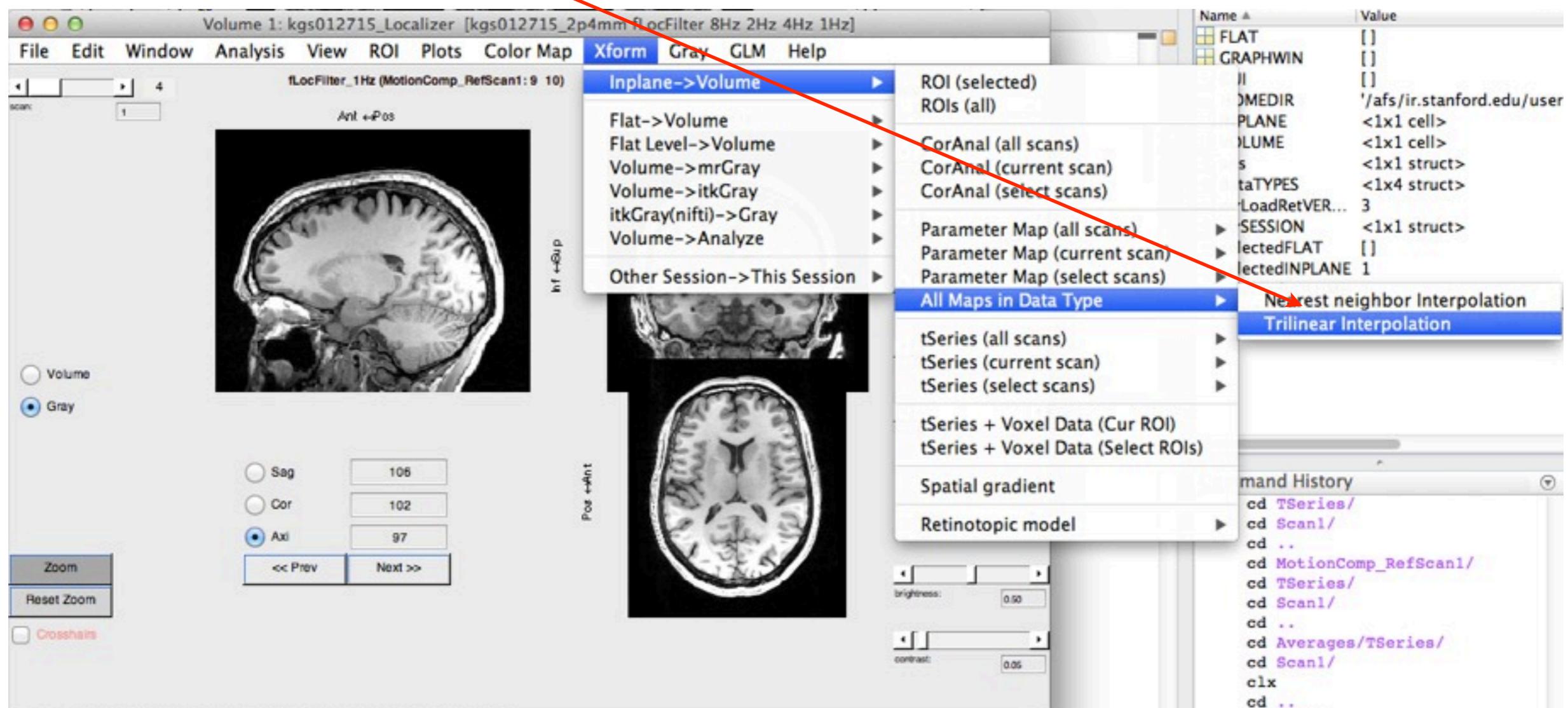


open *Inplane* and *Gray* view windows (type *mrVista*; *mrVista 3*; in Matlab command line)

set *data type* to *GLMs* in both views

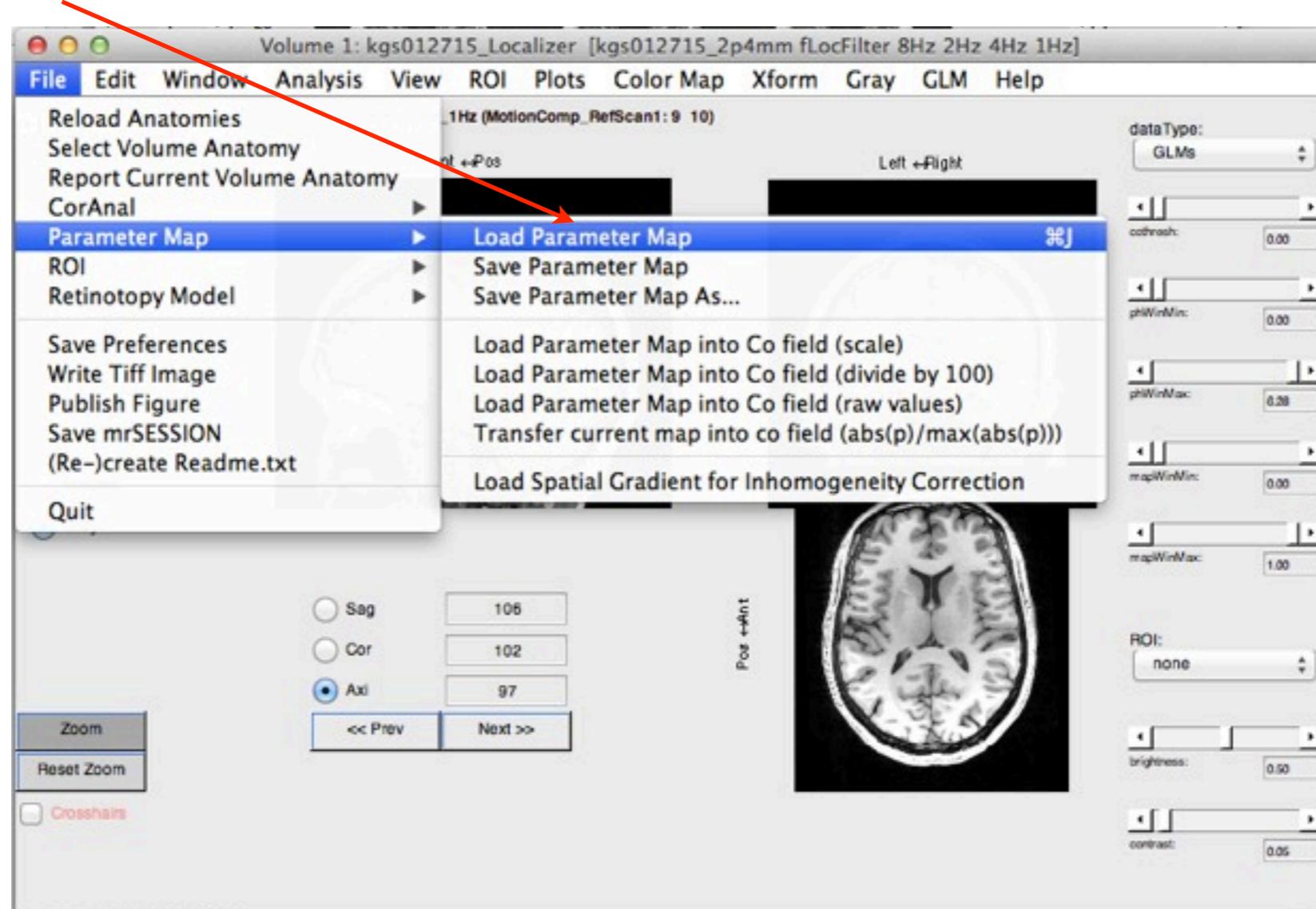
# Visualization on inflated cortical surface

*Transform all maps from Xform menu in Gray view*



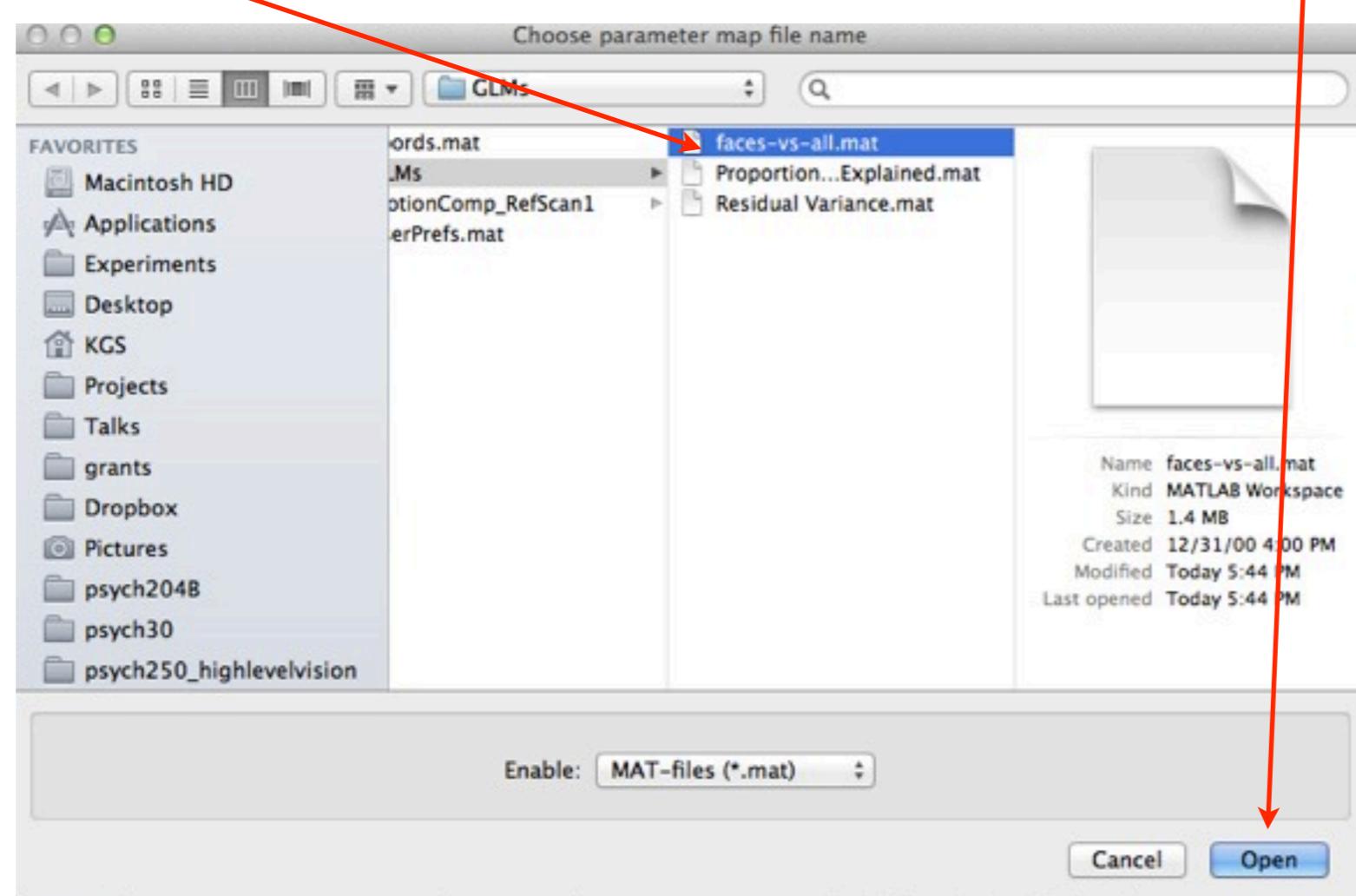
# Visualization on inflated cortical surface

*load contrast map just transformed from inplane*

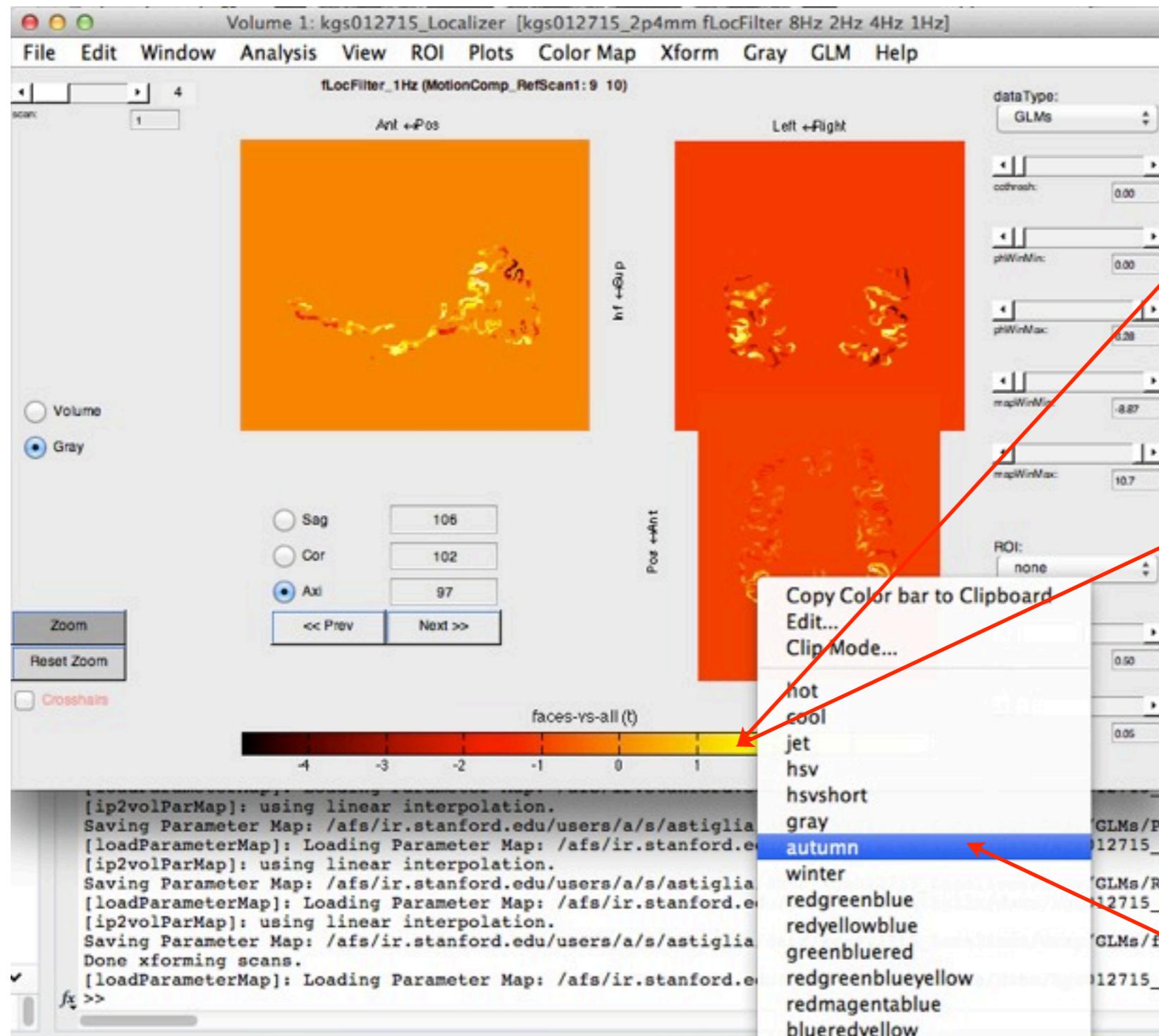


# Visualization on inflated cortical surface

*select map to load and click Open*



# Visualization on inflated cortical surface



if PC: right

click color bar

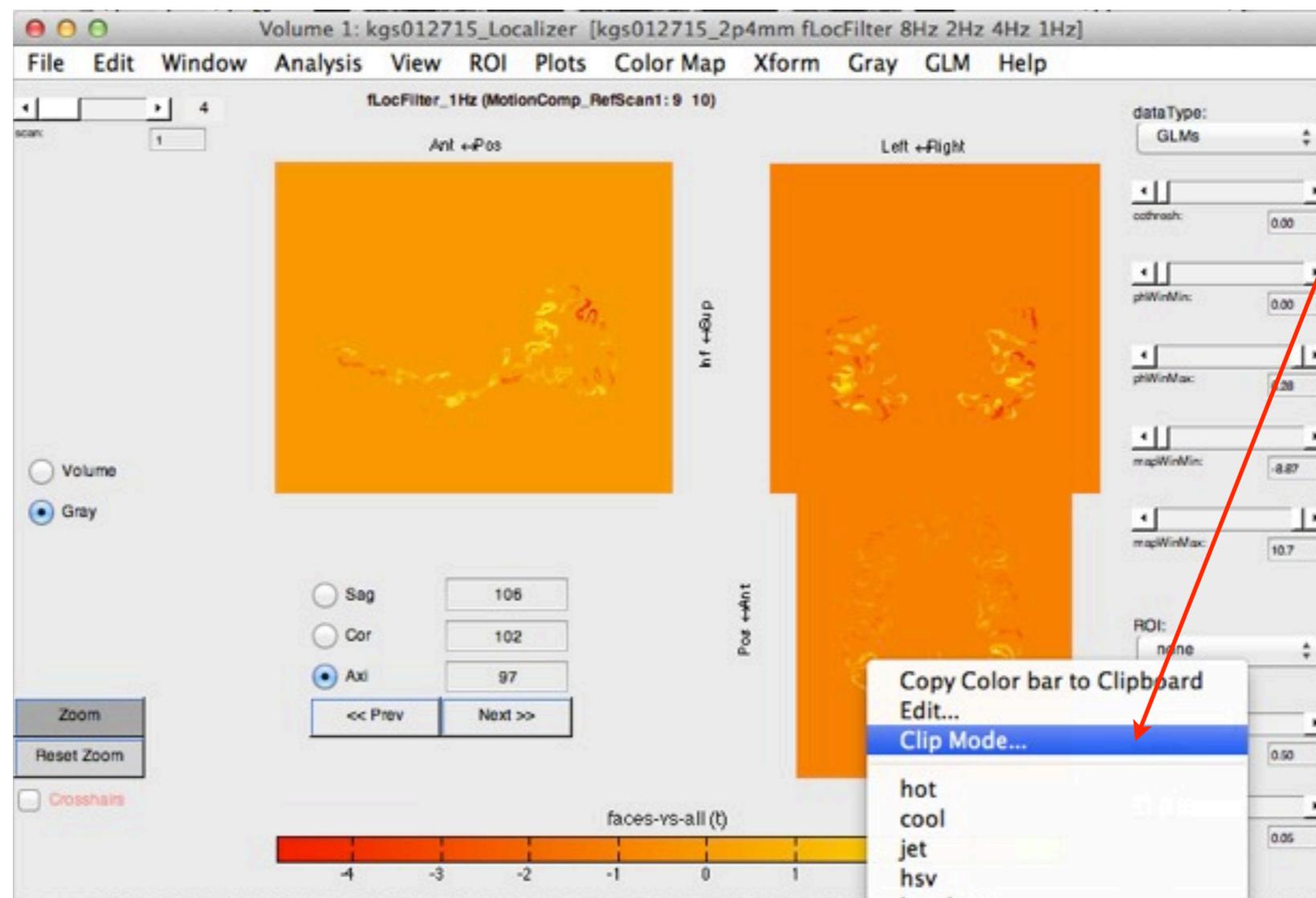
if Mac: click

color bar with  
two fingers

change colormap  
(autumn is good):

# Visualization on inflated cortical surface

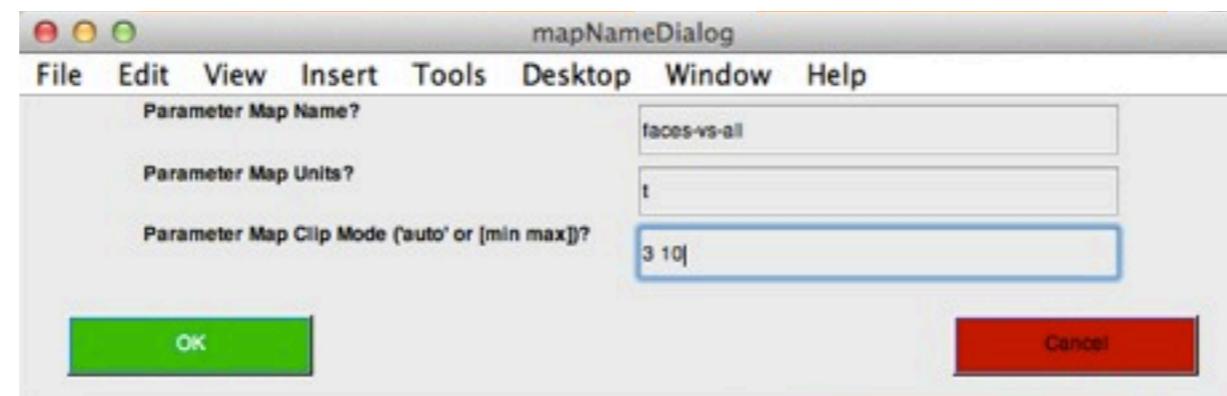
*scale colormap between specified values here*



# Visualization on inflated cortical surface

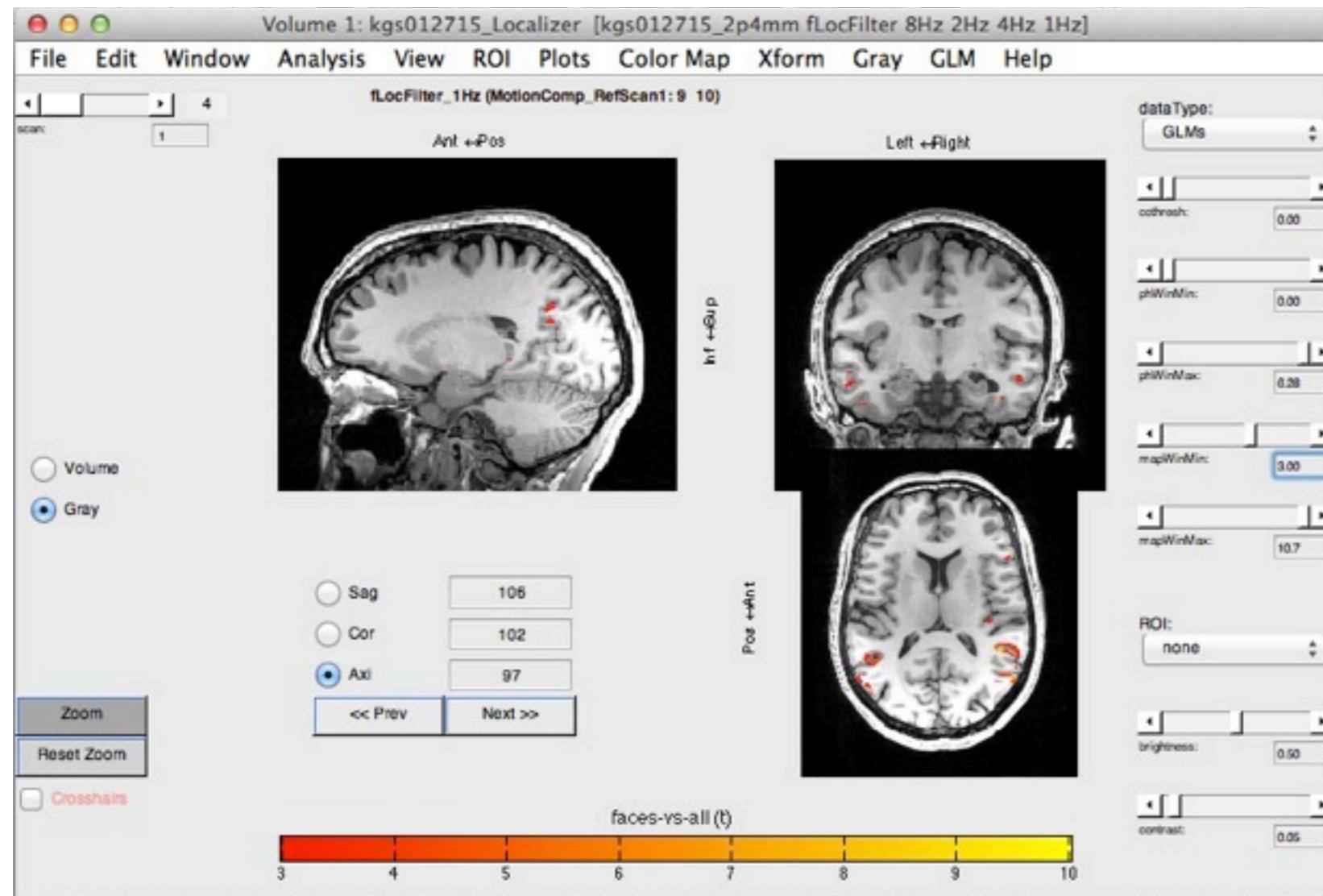
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*Specify min and max T-values for extremes of color scale in Parameter Map Clip Mode*



# Visualization on inflated cortical surface

*now you can open a mesh and look at the map*



*you will probably want threshold at  $T > 3$  or 4*

# Drawing ROIs on the mesh

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- Click on the mesh window
  - Press ‘d’ for draw
  - Press ‘delete’
  - Click around perimeter of blob
  - Click ‘c’ to close
  - Click ‘f’ to fill

# Drawing ROIs on the mesh

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- Click on the Gray view window
  - Press [CONROL + SPACE] to transform ROI from mesh to volume
  - Press [CONTROL + 'x'] to restrict ROI to
  - Press [CONTROL + 'n'] to save the ROI in 3Danatomy/ROIs/
- You can then transform this ROI to the Inplane view