

# 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)

# Installation of vistisoft repository

Name	Date Modified	Size	Kind
mrMesh	Yesterday 11:57 AM	--	Folder
setMrVistaPath.m	Today 4:08 PM	227 bytes	Objec...Source
spm8	Jan 23, 2015 6:32 AM	--	Folder
vistasoft	Jan 29, 2015 12:27 PM	--	Folder

- Download datasets and analysis software at:  
<http://vpnl.stanford.edu/psych204b/ClassProject.zip>
  - Navigate to software directory in MATLAB and execute setMrVistaPath script by typing `setMrVistaPath` into the command line
  - For more information about *vistasoft* see:  
<http://white.stanford.edu/newlm/index.php/Software>

# Session directory structure

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Name	Date Modified	Size	Kind
▶ 3Danatomy	Jan 30, 2015 11:39 AM	--	Folder
5_1_24mm_Inplane_nonMUX.nii.gz	Jan 30, 2015 9:28 AM	2.2 MB	gzip compressed archive
7_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:28 AM	23.8 MB	gzip compressed archive
7_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:29 AM	23.8 MB	gzip compressed archive
7_3_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:29 AM	23.8 MB	gzip compressed archive
8_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:30 AM	38.1 MB	gzip compressed archive
8_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:31 AM	38.1 MB	gzip compressed archive
9_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:31 AM	23.8 MB	gzip compressed archive
9_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:32 AM	23.8 MB	gzip compressed archive
9_3_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:32 AM	23.9 MB	gzip compressed archive
10_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:33 AM	39.1 MB	gzip compressed archive
10_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 10:50 AM	39.1 MB	gzip compressed archive
▶ Stimuli	Jan 30, 2015 10:57 AM	--	Folder

- **3Danatomy:** directory containing T1 volume anatomy (t1.nii.gz), white matter segmentation (t1\_class.nii.gz), cortical surface meshes, and predefined ROIs
- **5\_1\_24mm\_Inplane\_nonMux.nii.gz:** T1-weighted inplane images
- **#\_#\_BOLD\_EPI\_24mm\_2sec\_Accel2.nii.gz:** T2\*-weighted functional images
- **Stimuli:** directory containing experimental parameter files

# **Part 1: Initialization and preprocessing**

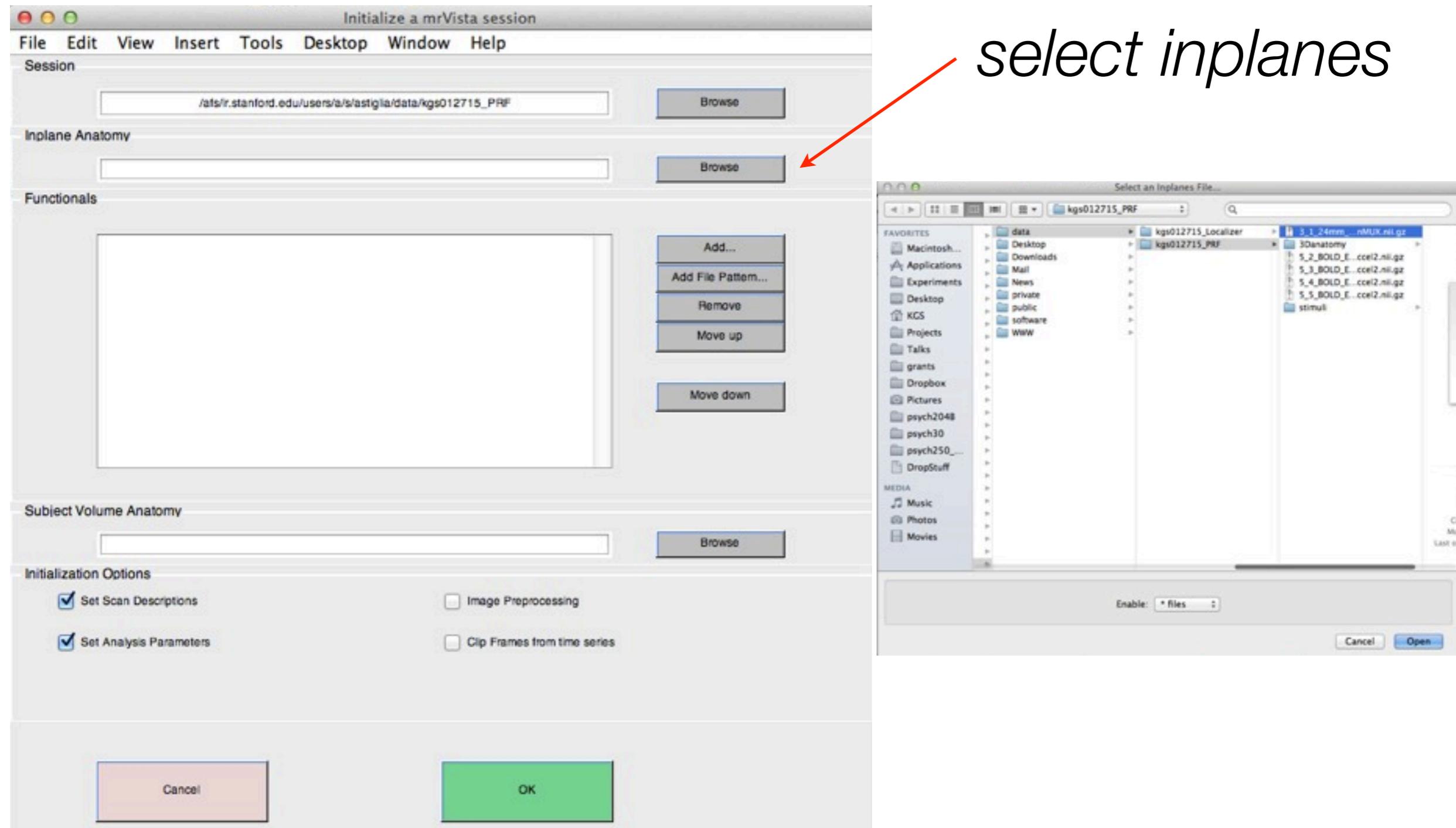
# Initialize and preprocess functional data

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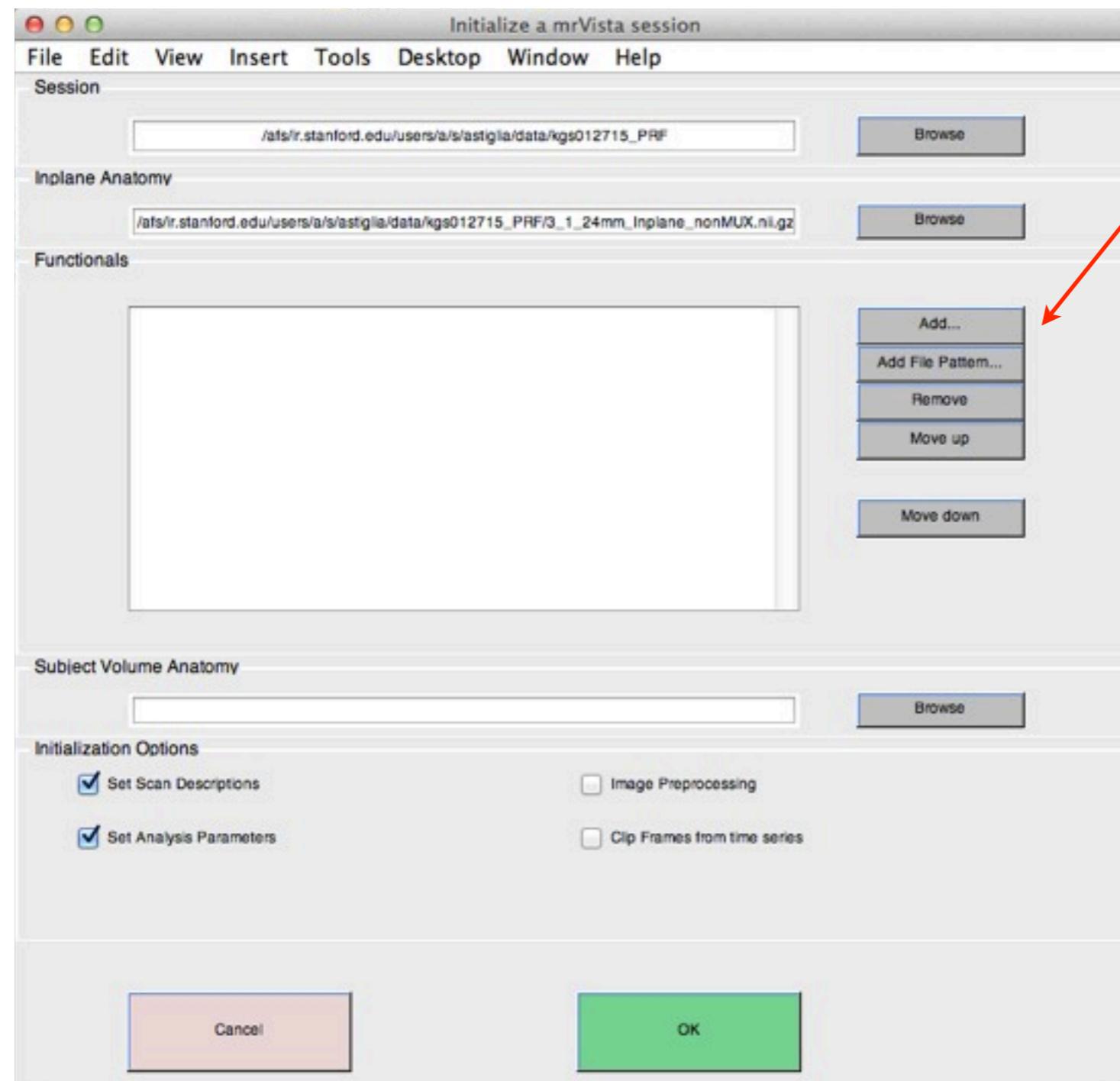
Name	Date Modified	Size	Kind
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7_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:28 AM	23.8 MB	gzip compressed archive
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7_3_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:29 AM	23.8 MB	gzip compressed archive
8_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:30 AM	38.1 MB	gzip compressed archive
8_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:31 AM	38.1 MB	gzip compressed archive
9_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:31 AM	23.8 MB	gzip compressed archive
9_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:32 AM	23.8 MB	gzip compressed archive
9_3_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:32 AM	23.9 MB	gzip compressed archive
10_1_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 9:33 AM	39.1 MB	gzip compressed archive
10_2_BOLD_EPI_24mm_2sec_Accel2.nii.gz	Jan 30, 2015 10:50 AM	39.1 MB	gzip compressed archive
▶ Stimuli	Jan 30, 2015 10:57 AM	--	Folder

- Navigate to a session in the data directory and prompt initialization of functional data by typing `mrInit` in the MATLAB command line
- **kgs012715\_Localizer:** functional localizer data
- **kgs012715\_PRF:** retinotopic mapping data
- **kgs#####\_Adaptation:** adaptation data

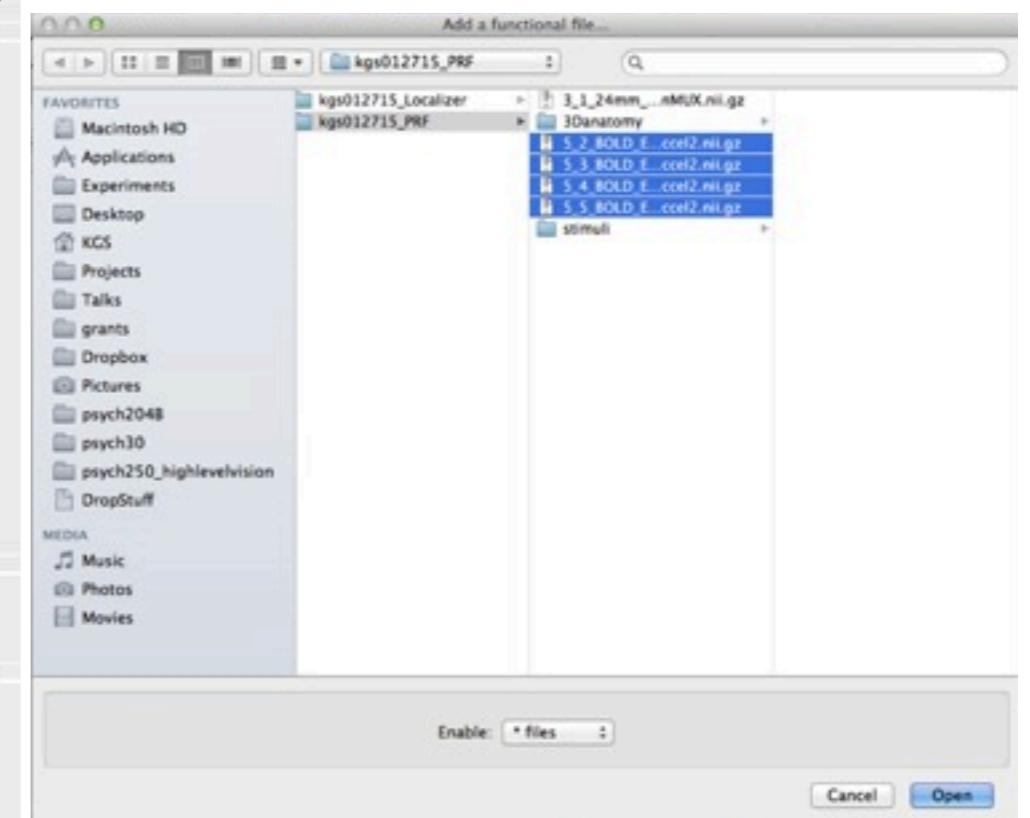
# Initialize and preprocess functional data



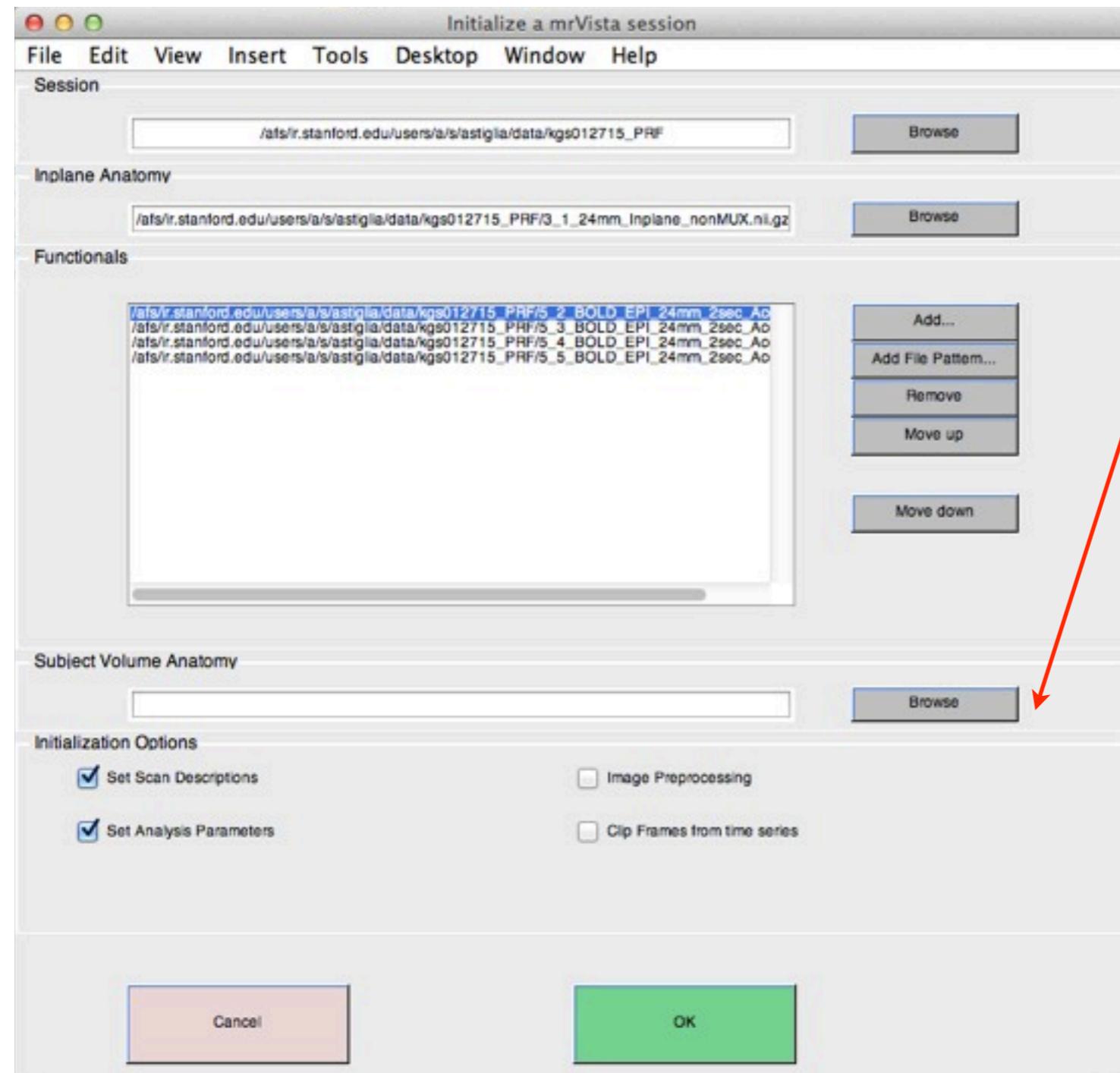
# Initialize and preprocess functional data



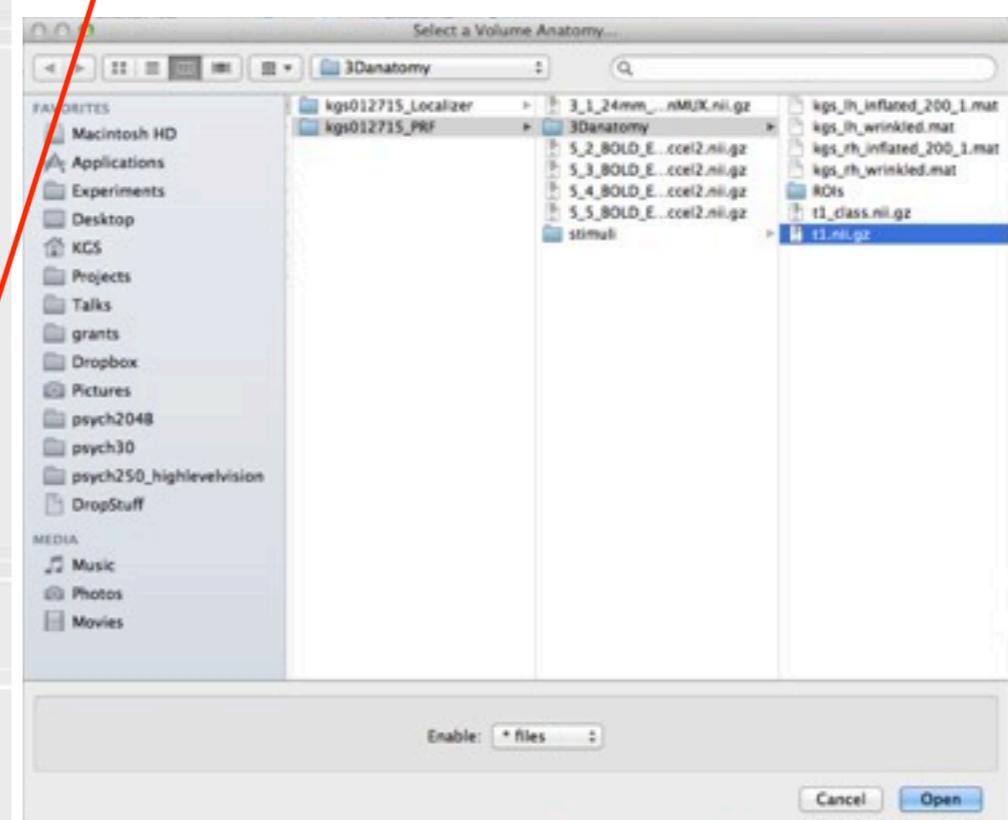
*select functionals*



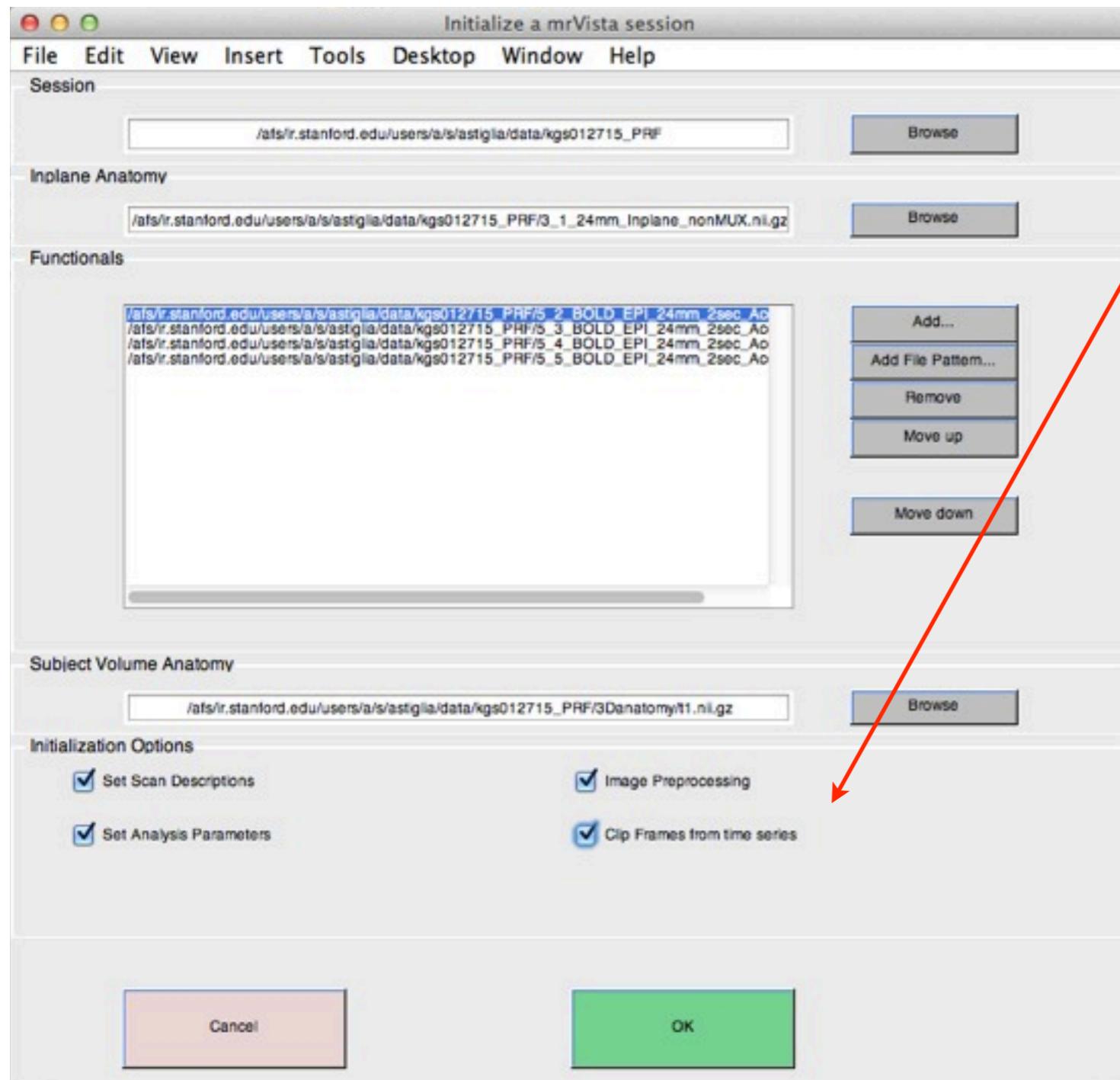
# Initialize and preprocess functional data



*select anatomy*

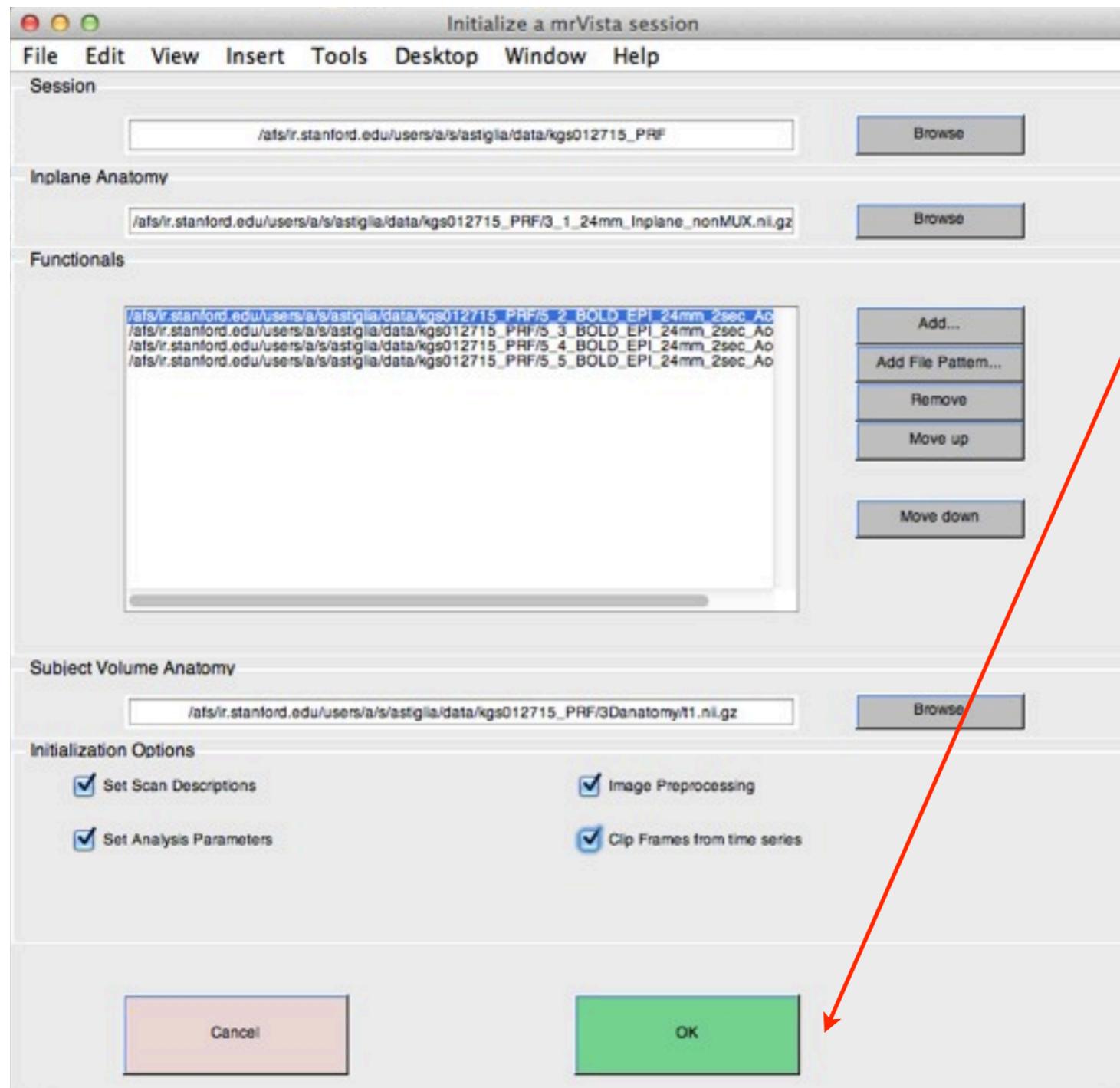


# Initialize and preprocess functional data



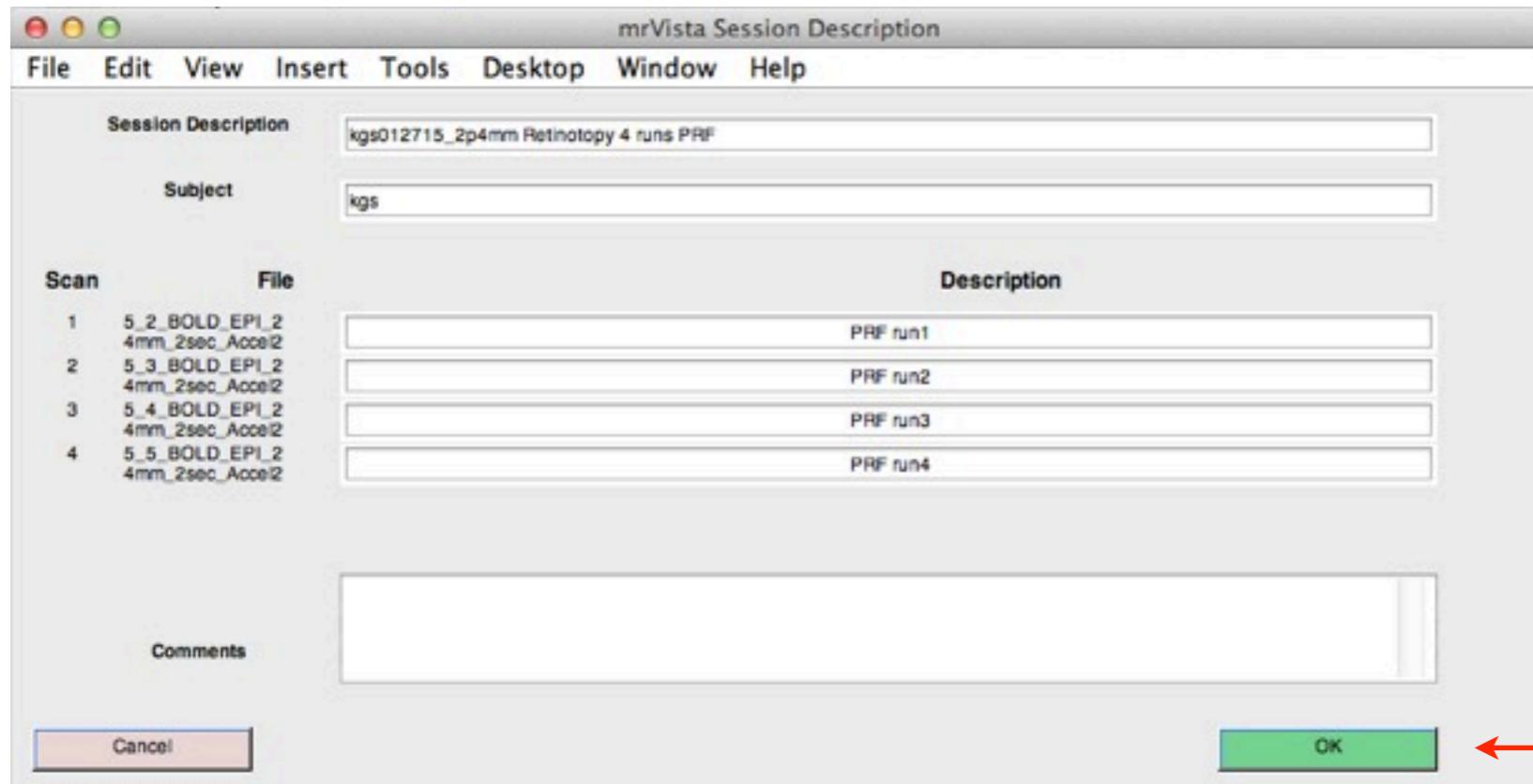
*select all options*

# Initialize and preprocess functional data



click OK

# Initialize and preprocess functional data

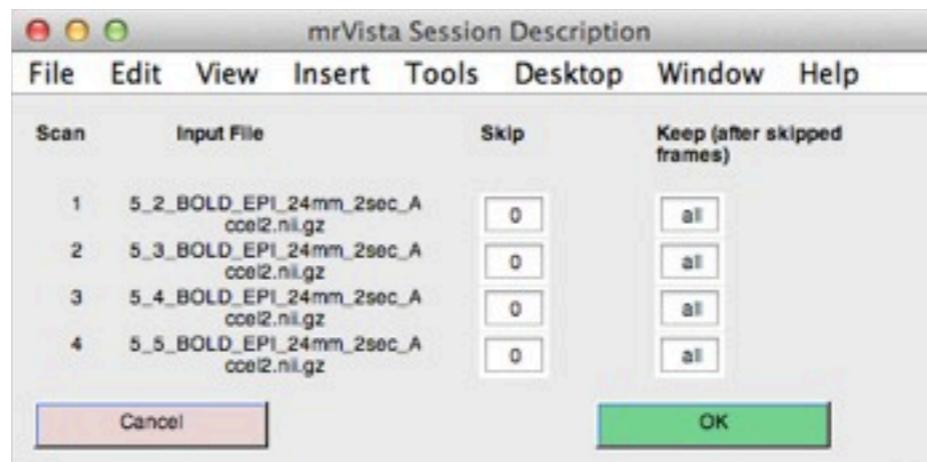


describe session

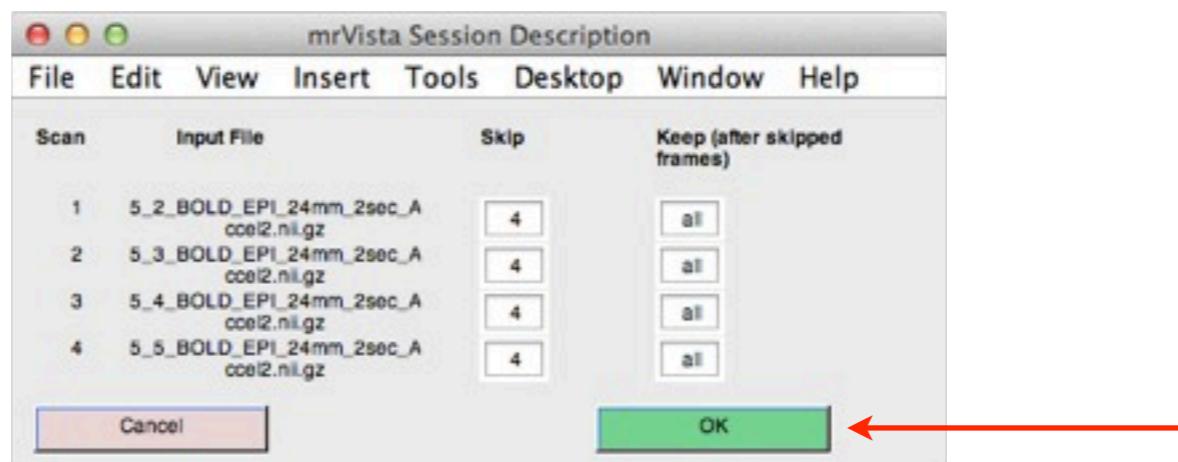
click OK

# Initialize and preprocess functional data

*clip first 4 frames of each run*



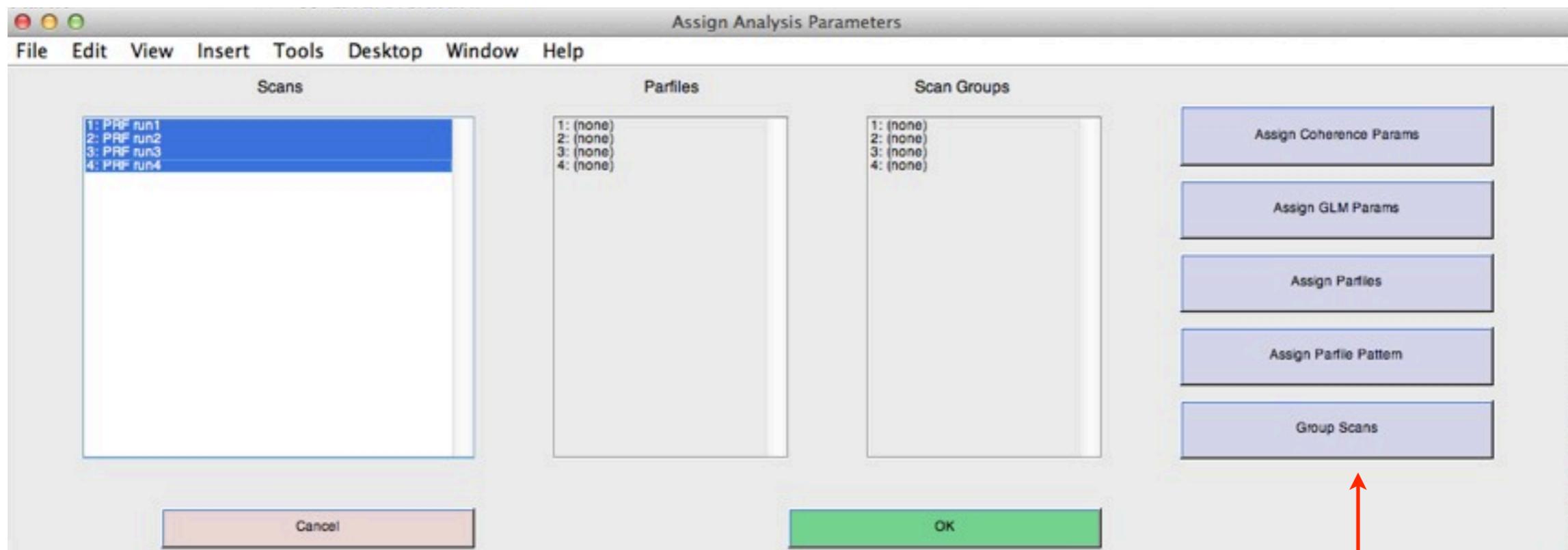
*keep all remaining frames*



click OK

# Initialize and preprocess functional data

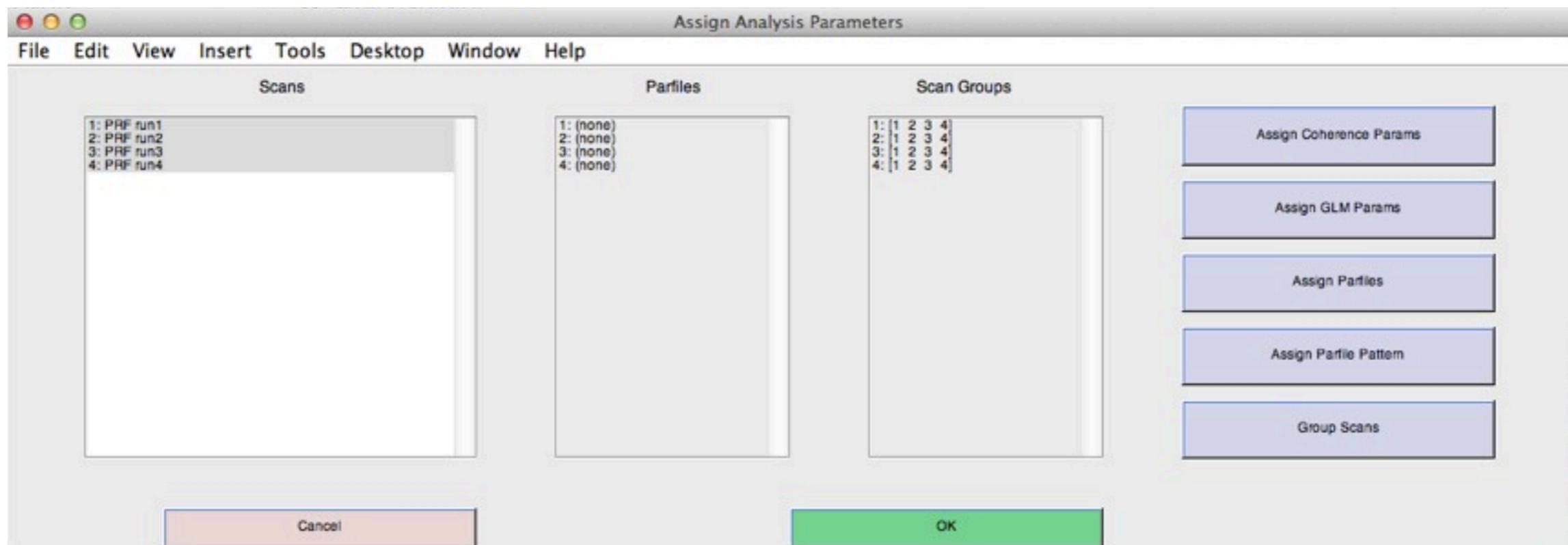
*select scans to group*



*click Group Scans*

# Initialize and preprocess functional data

see [1 2 3 4] in Scan Groups

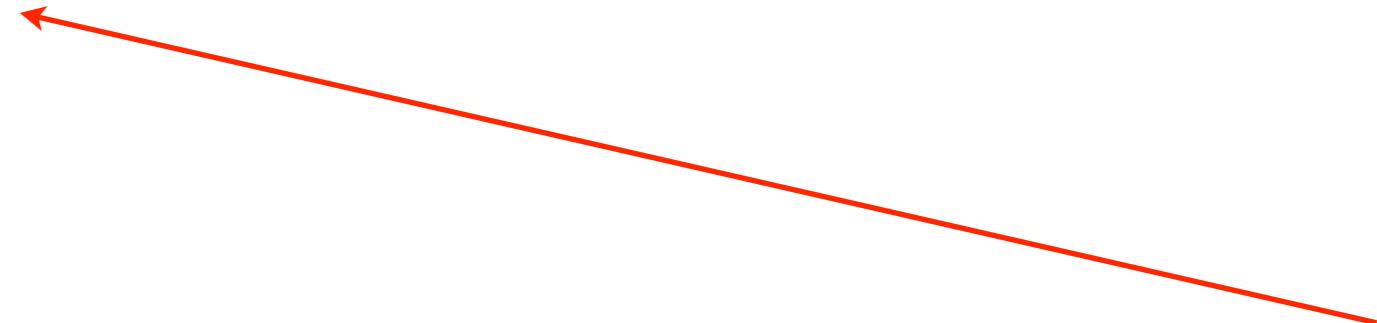
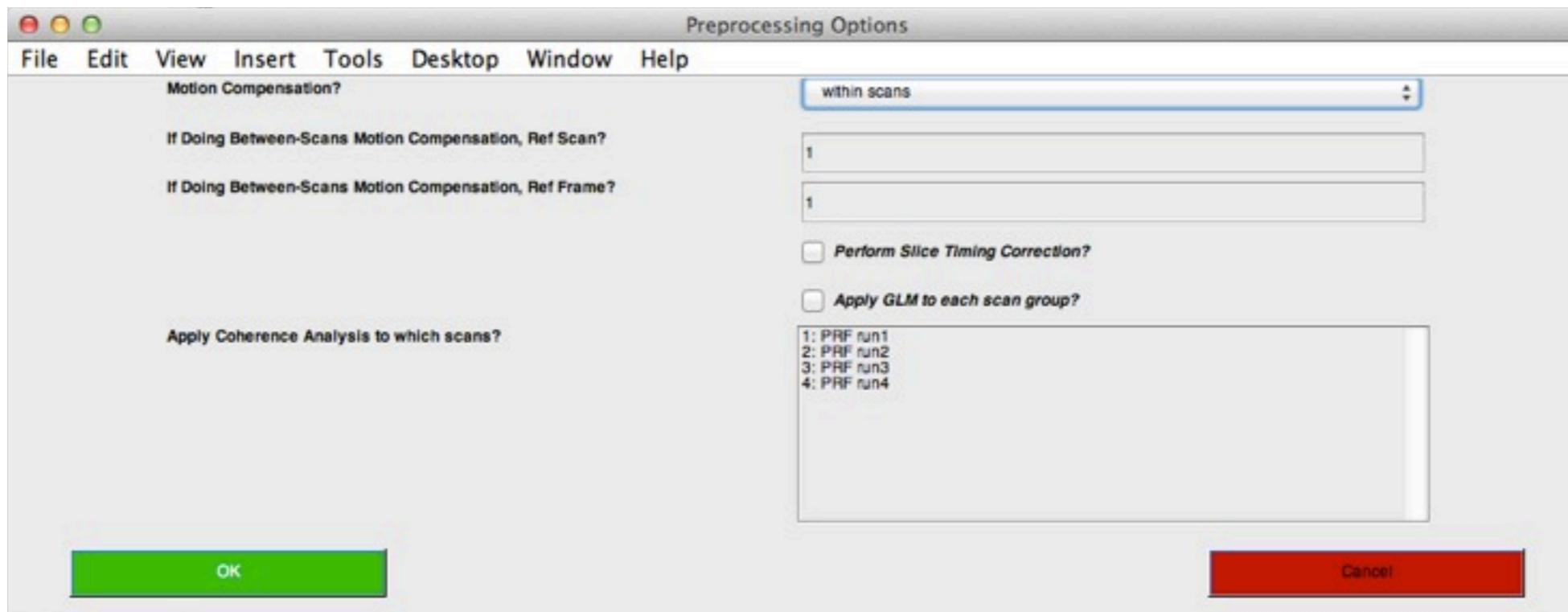


click OK

# Initialize and preprocess functional data

---

*select within scans*

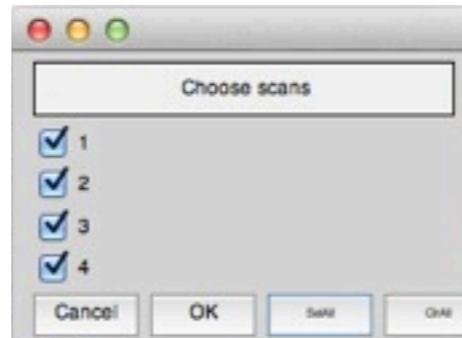


click OK

# Initialize and preprocess functional data

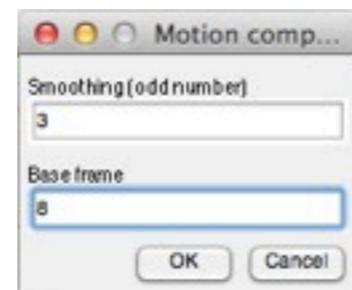
---

*select all scans*



*click OK*

*enter default parameters*

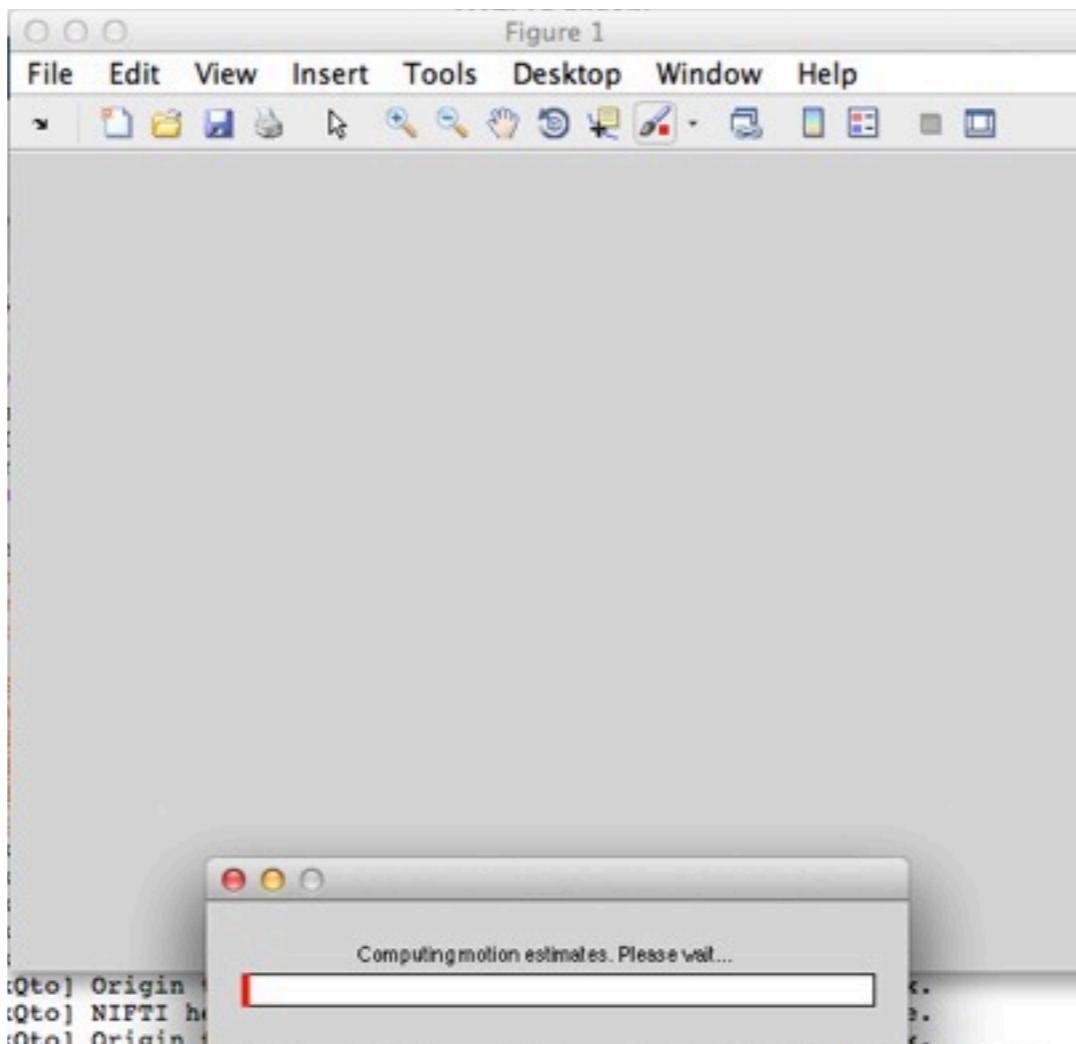


*click OK*

# Initialize and preprocess functional data

---

*wait...*

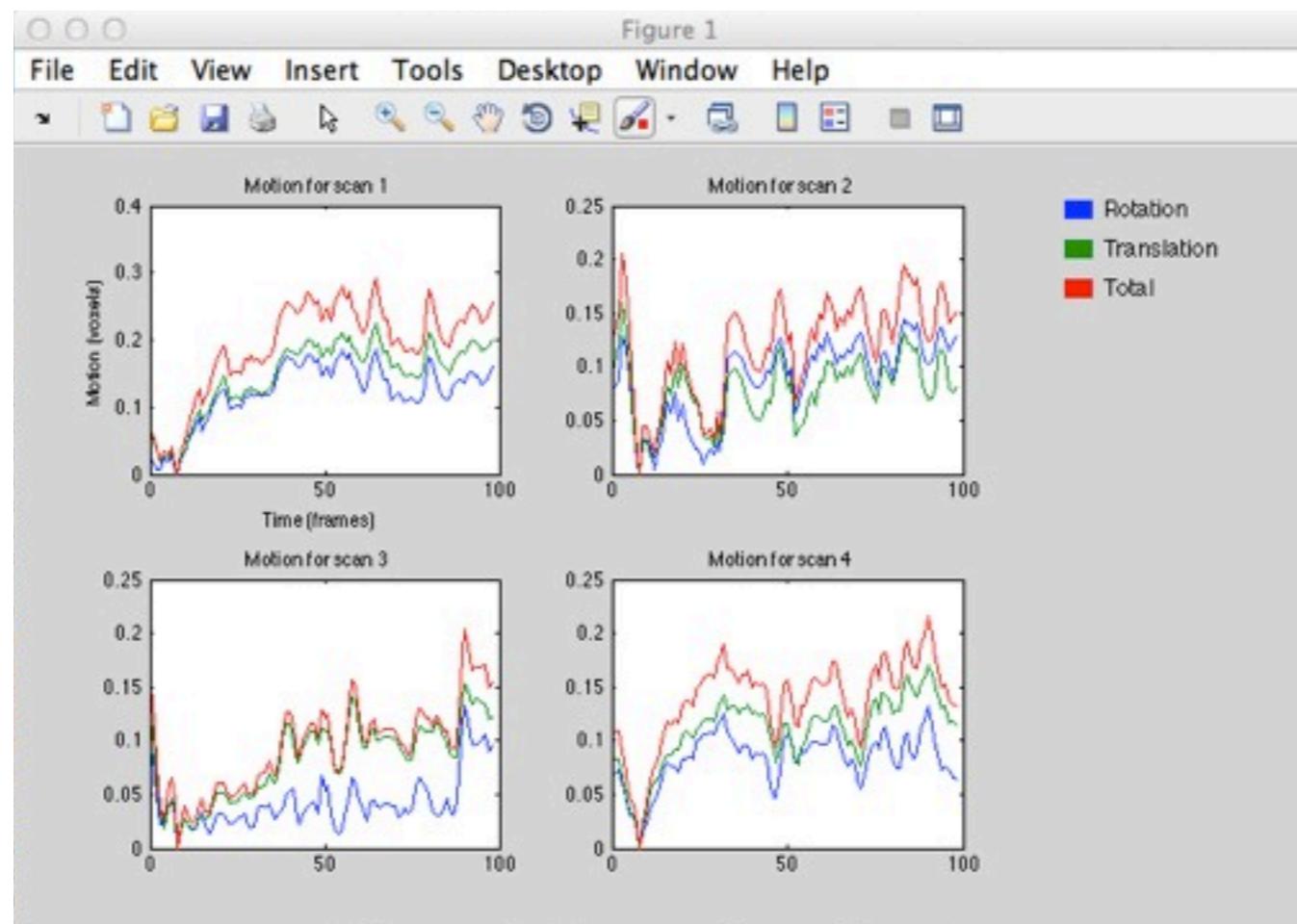


*this will take 5-10 min per run*

# Initialize and preprocess functional data

---

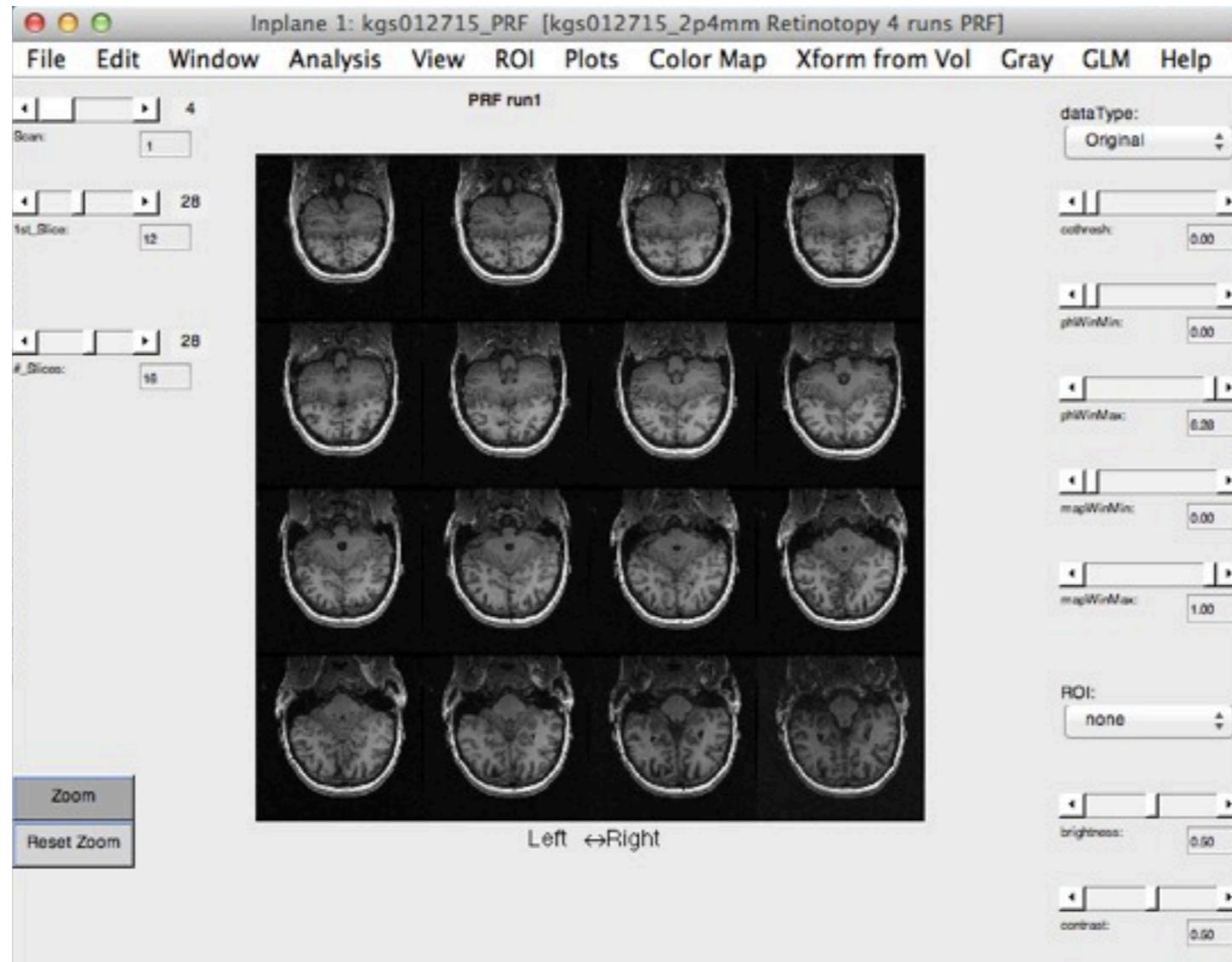
*check within scans motion*



*should be < 1 voxel per scan*

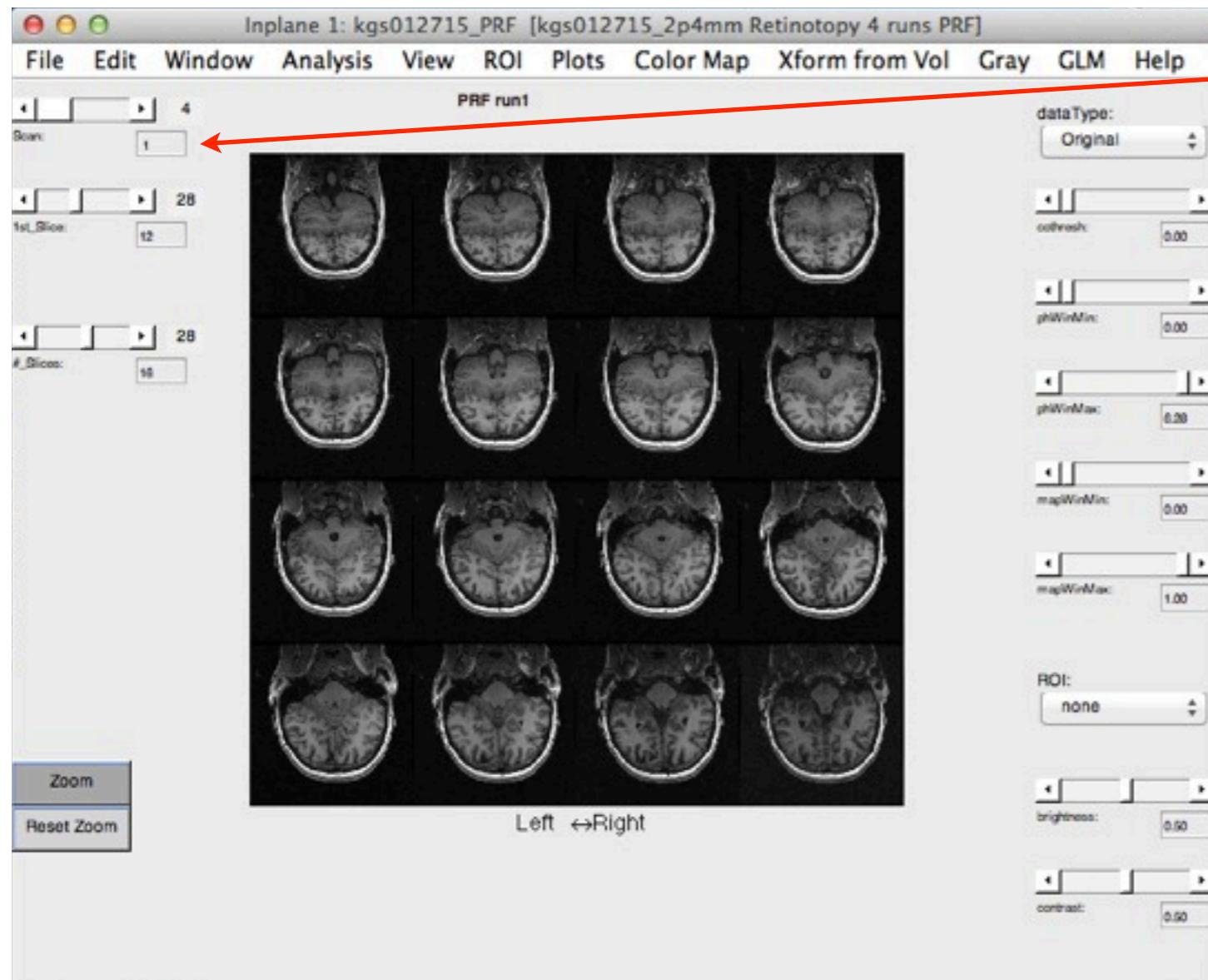
## **Part 2: Introduction to mrVista inplane view**

# Introduction to mrVista inplane view



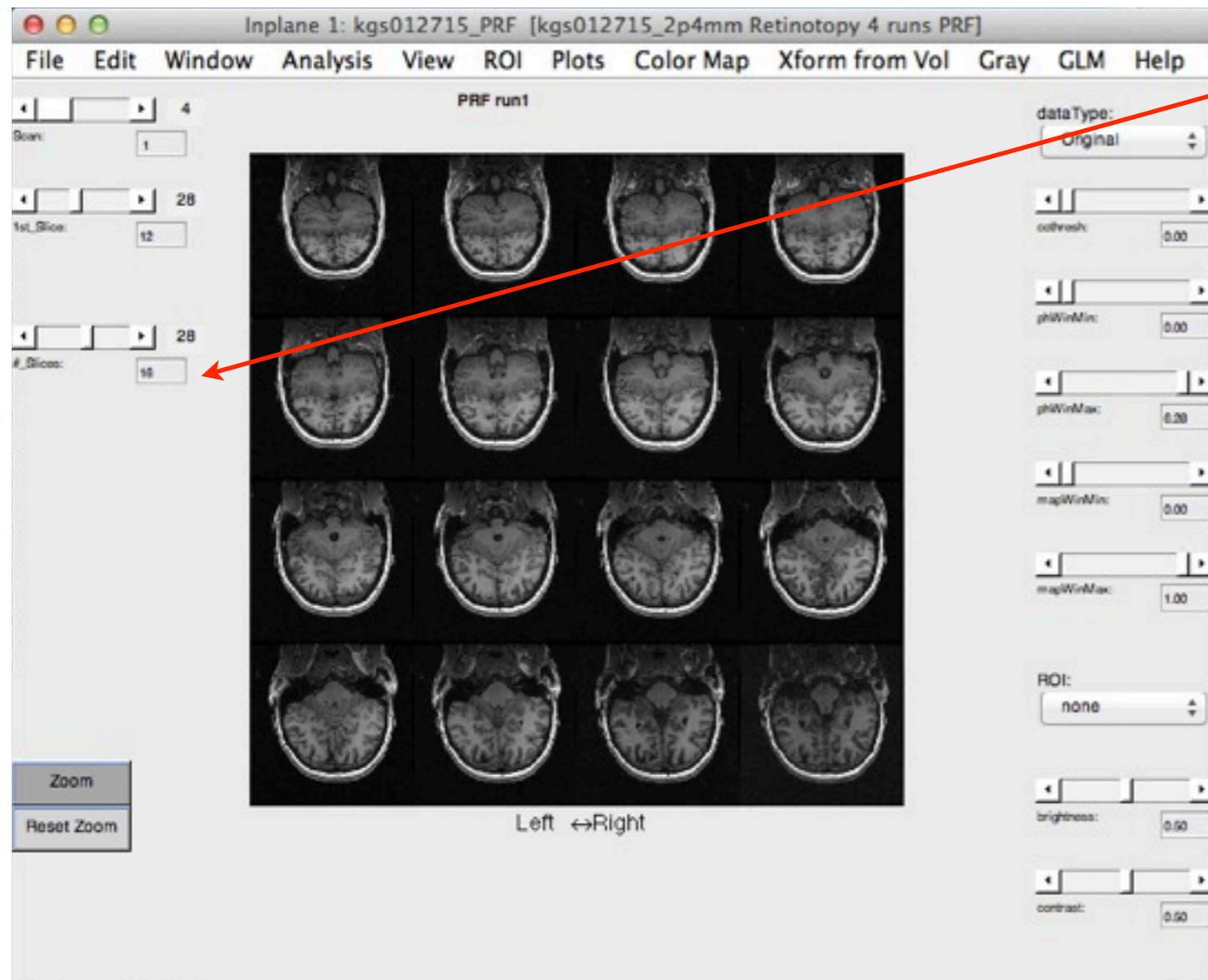
- Navigate to initialized session and launch mrVista inplane view GUI by typing `mrVista` in the MATLAB command line

# Introduction to mrVista inplane view



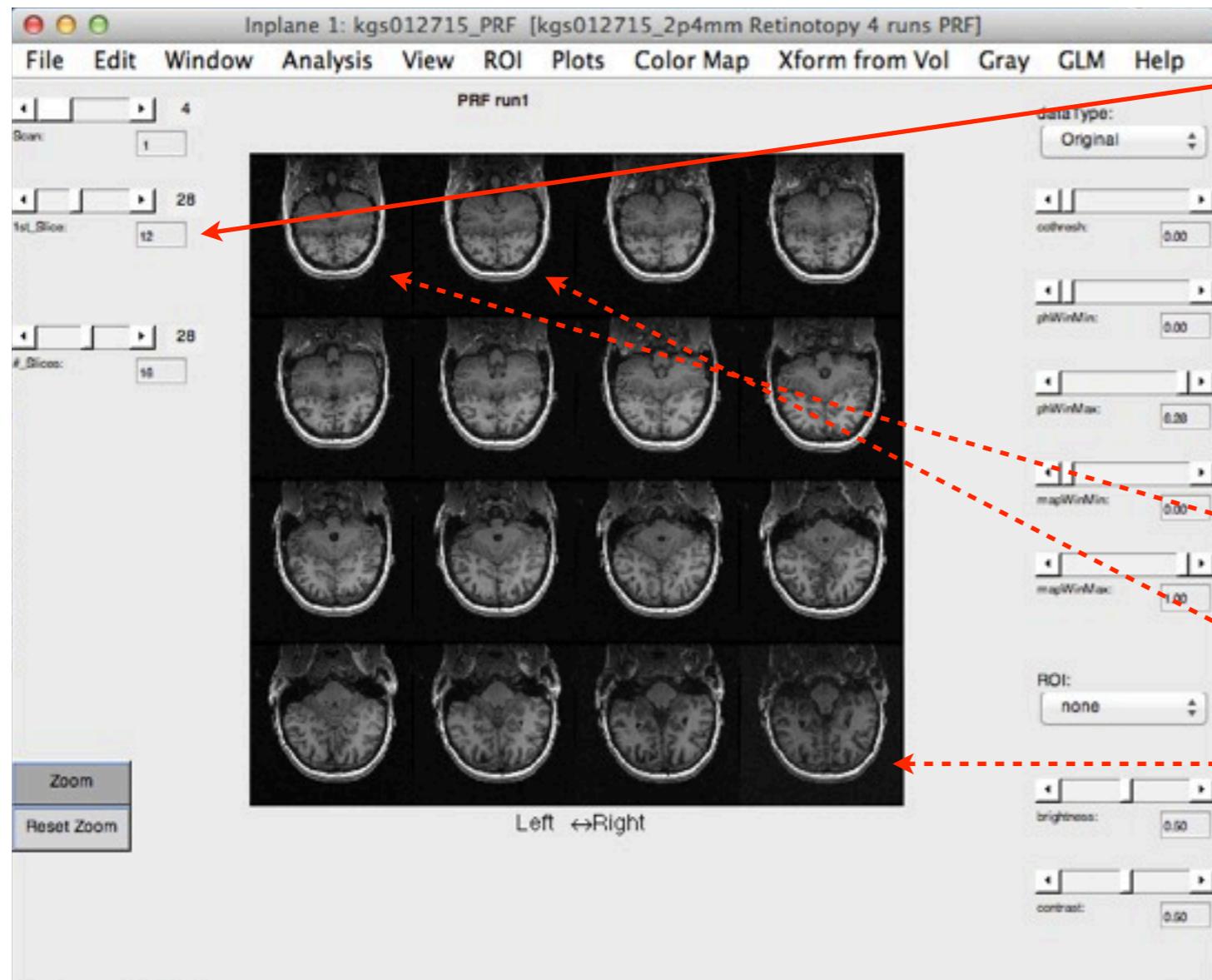
**Scan:**  
corresponds to  
number of runs

# Introduction to mrVista inplane view



**#\_Slices:**  
how many of the  
28 inplane slices  
to show in GUI

# Introduction to mrVista inplane view

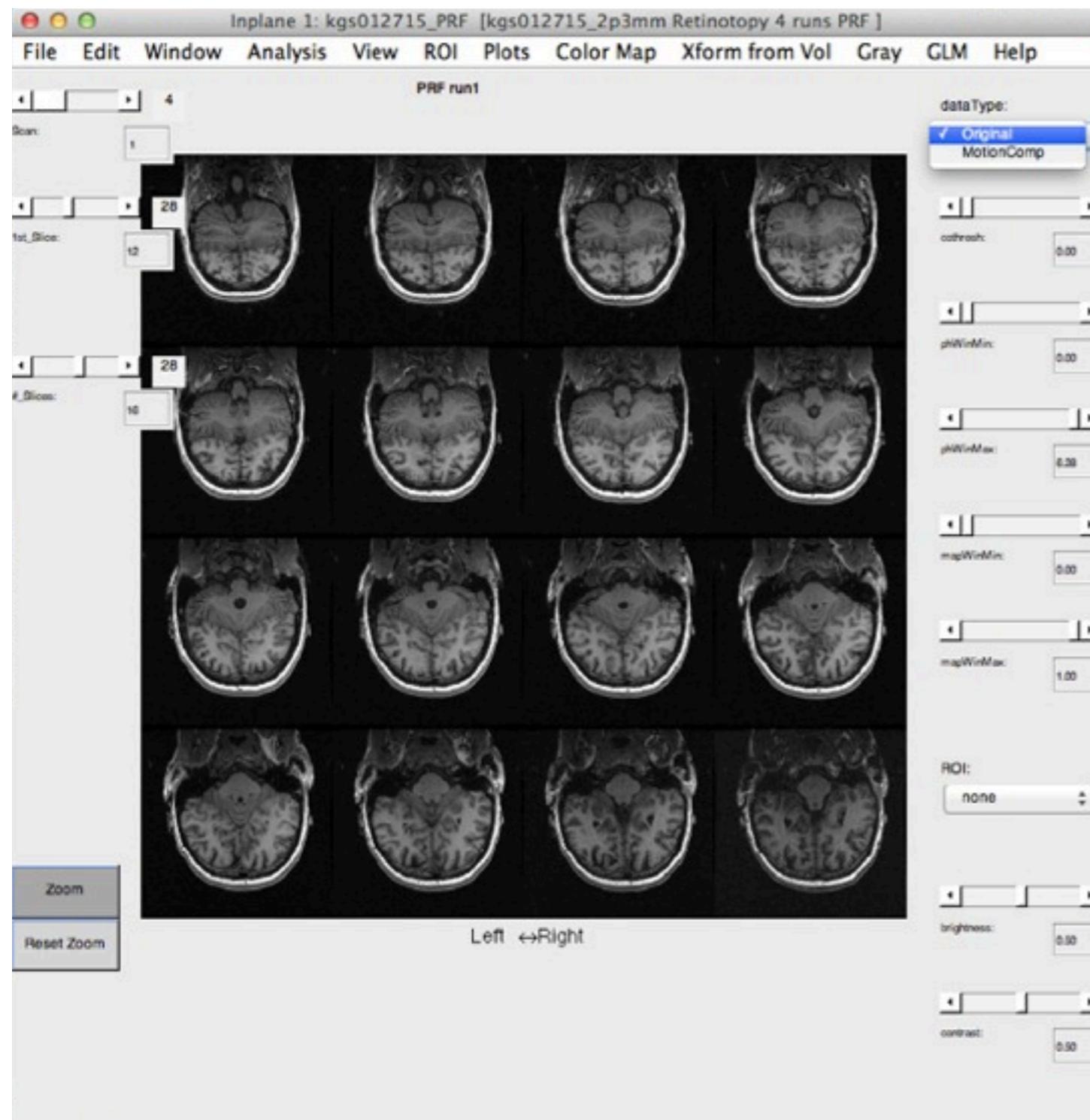


**1st\_Slice:**  
which slice to  
show in upper left

*slice 12*  
*slice 13*  
*slice 27*

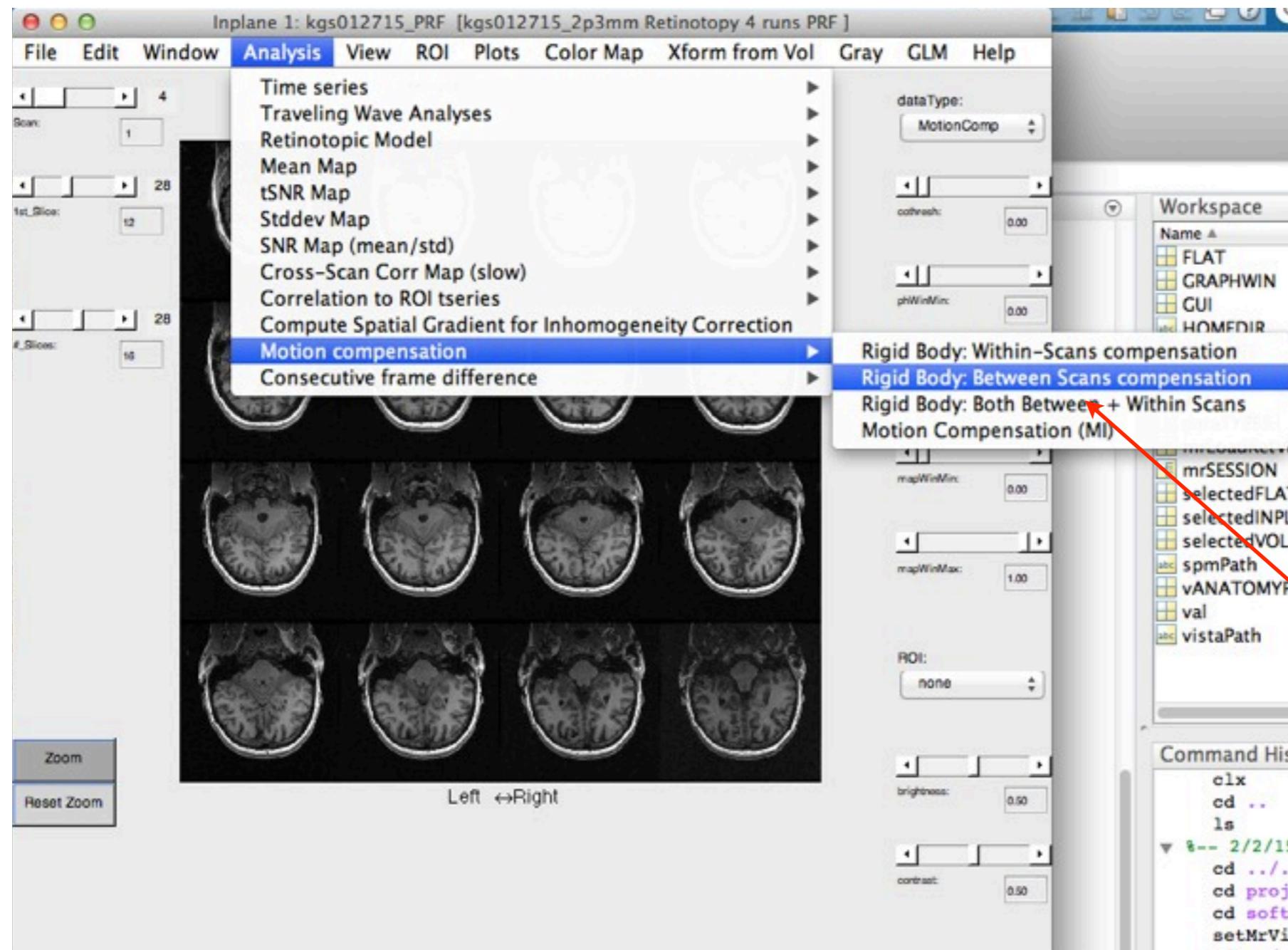
## Part 3: **Between scans motion correction**

# Between scans motion correction



**Data Type:**  
change from  
Original (raw data)  
to MotionComp  
(within scan  
motion corrected  
data) to perform  
between scans  
motion correction

# Between scans motion correction



make sure  
data type is  
**MotionComp**

initiate  
between  
scans motion  
correction

# Between scans motion correction

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*select first scan as base scan*



*click OK*

# Between scans motion correction

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*select all scans for correction*

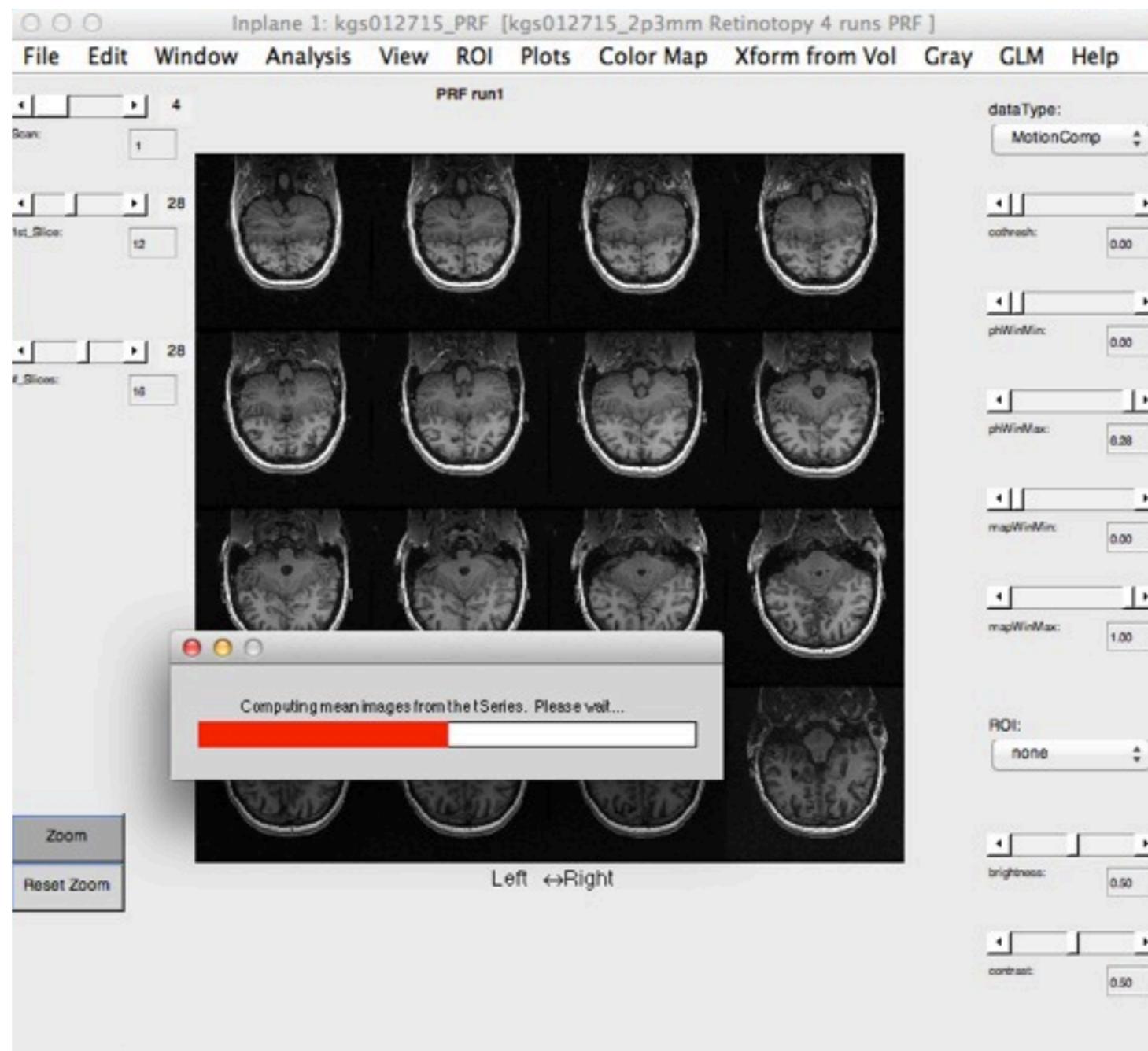


*click OK*

# Between scans motion correction

---

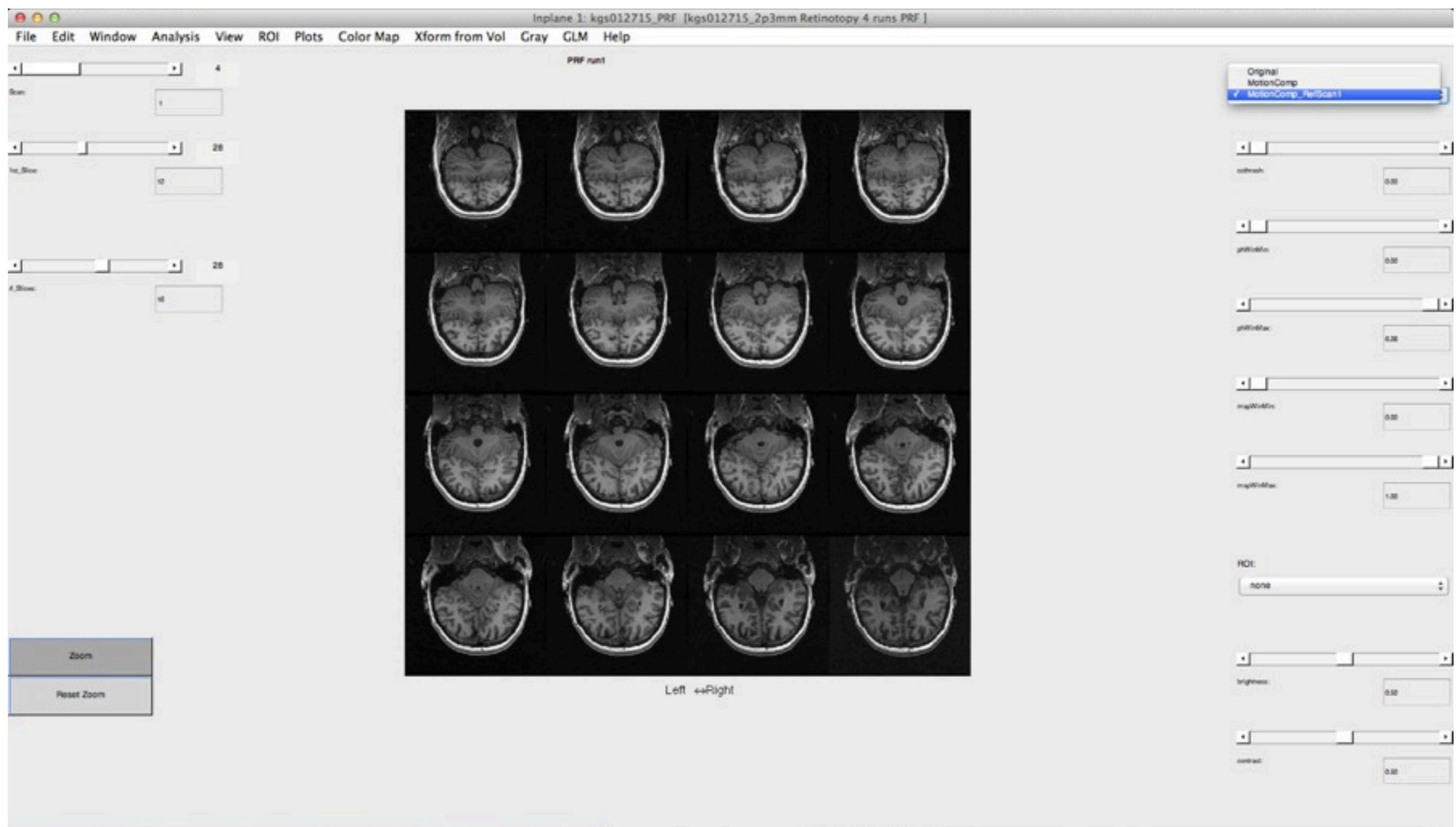
*wait...*



# Between scans motion correction

---

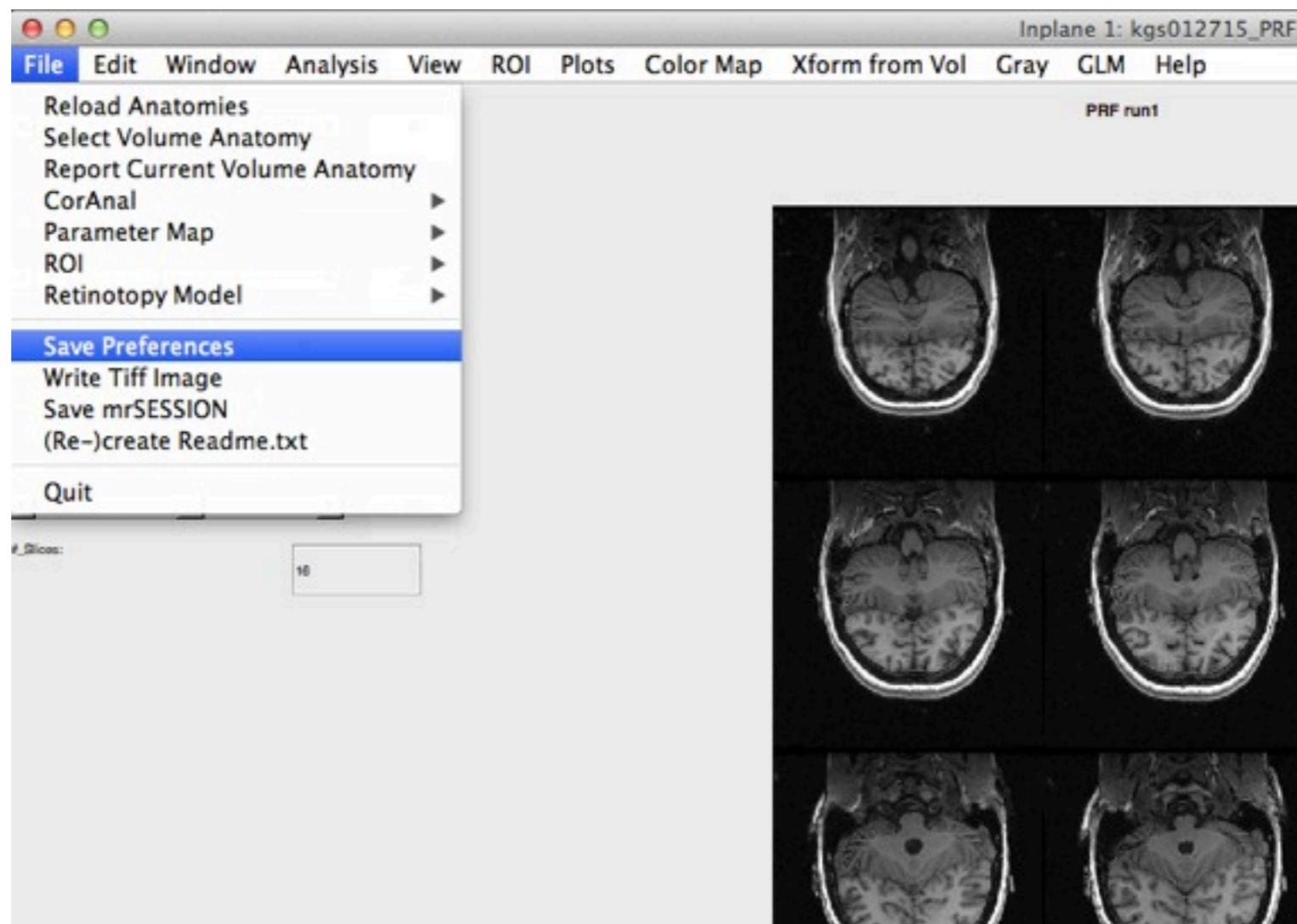
*set Data Type to MotionComp\_RefScan1*



# Between scans motion correction

---

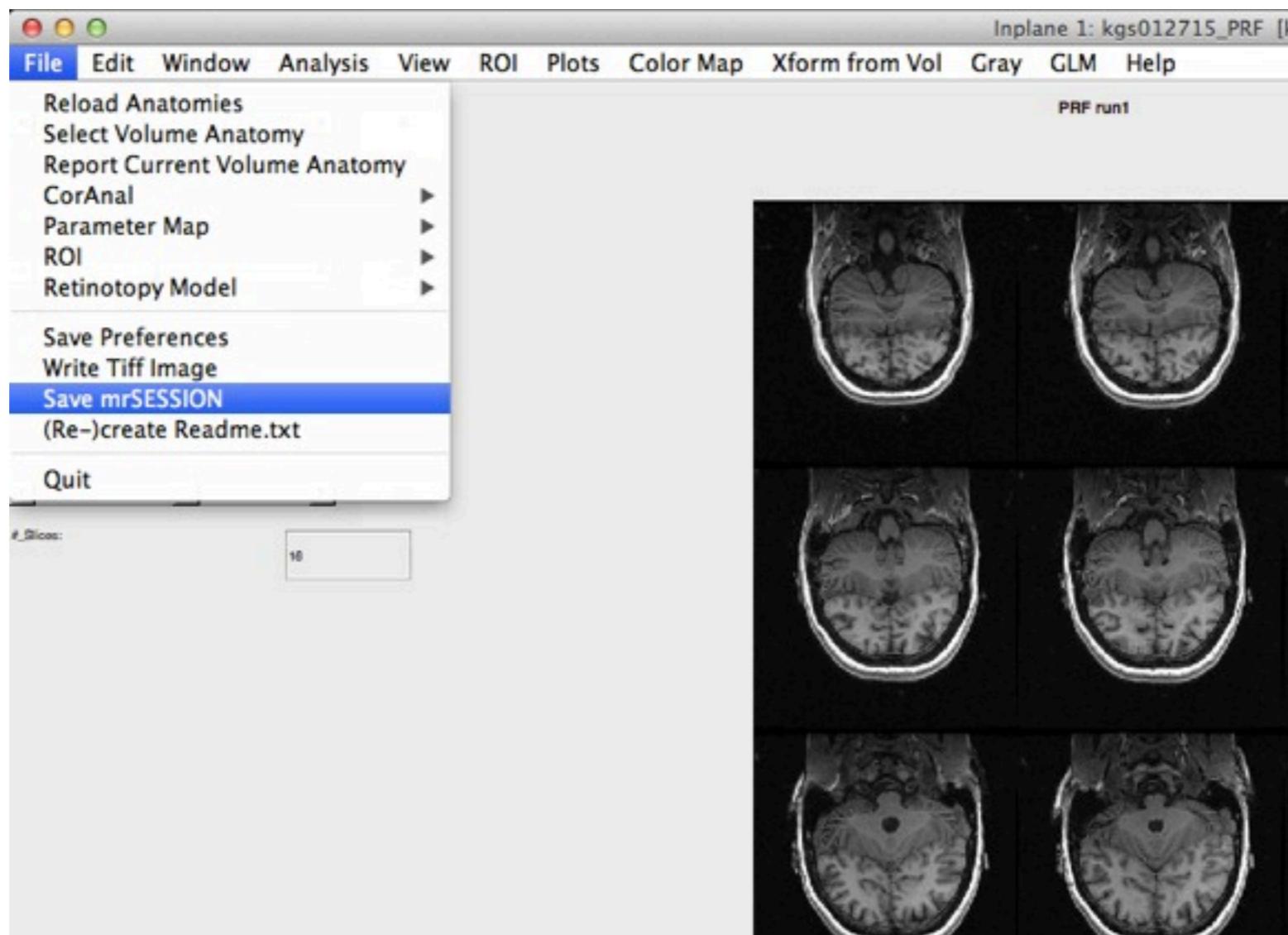
*save preferences*



# Between scans motion correction

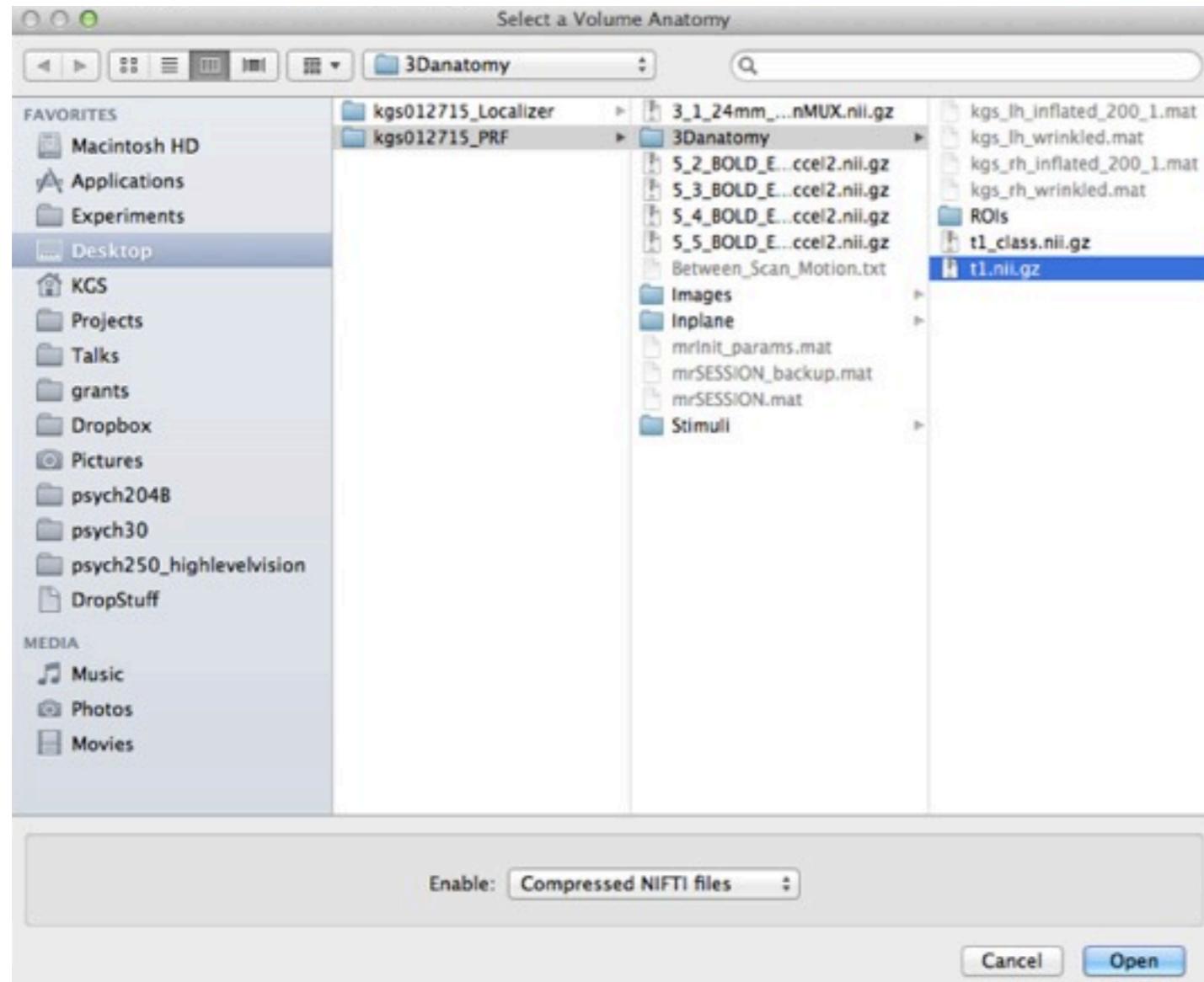
---

*save mrSESSION*



## **Part 4: Align functional data to anatomy**

# Align functional data to anatomy

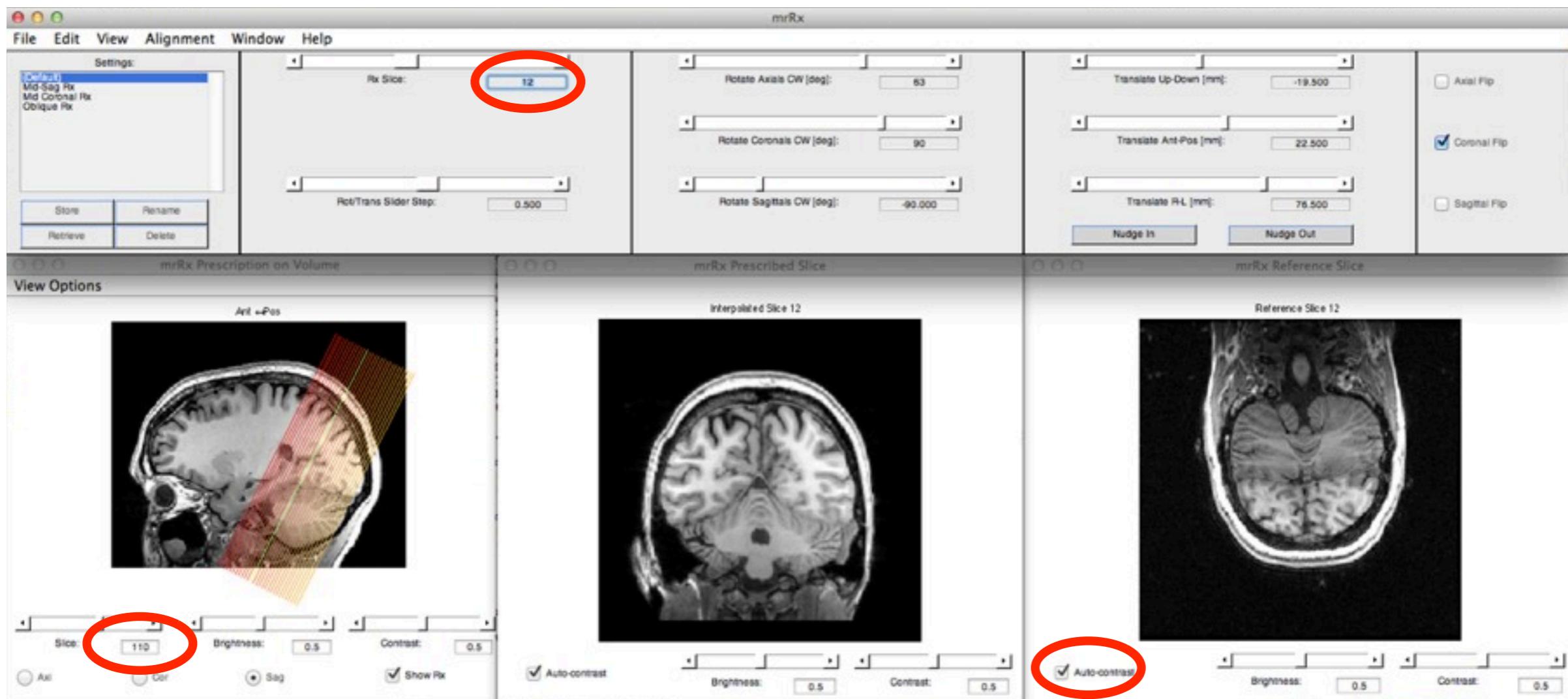


*choose t1.nii.gz  
when asked to  
select a volume  
anatomy*

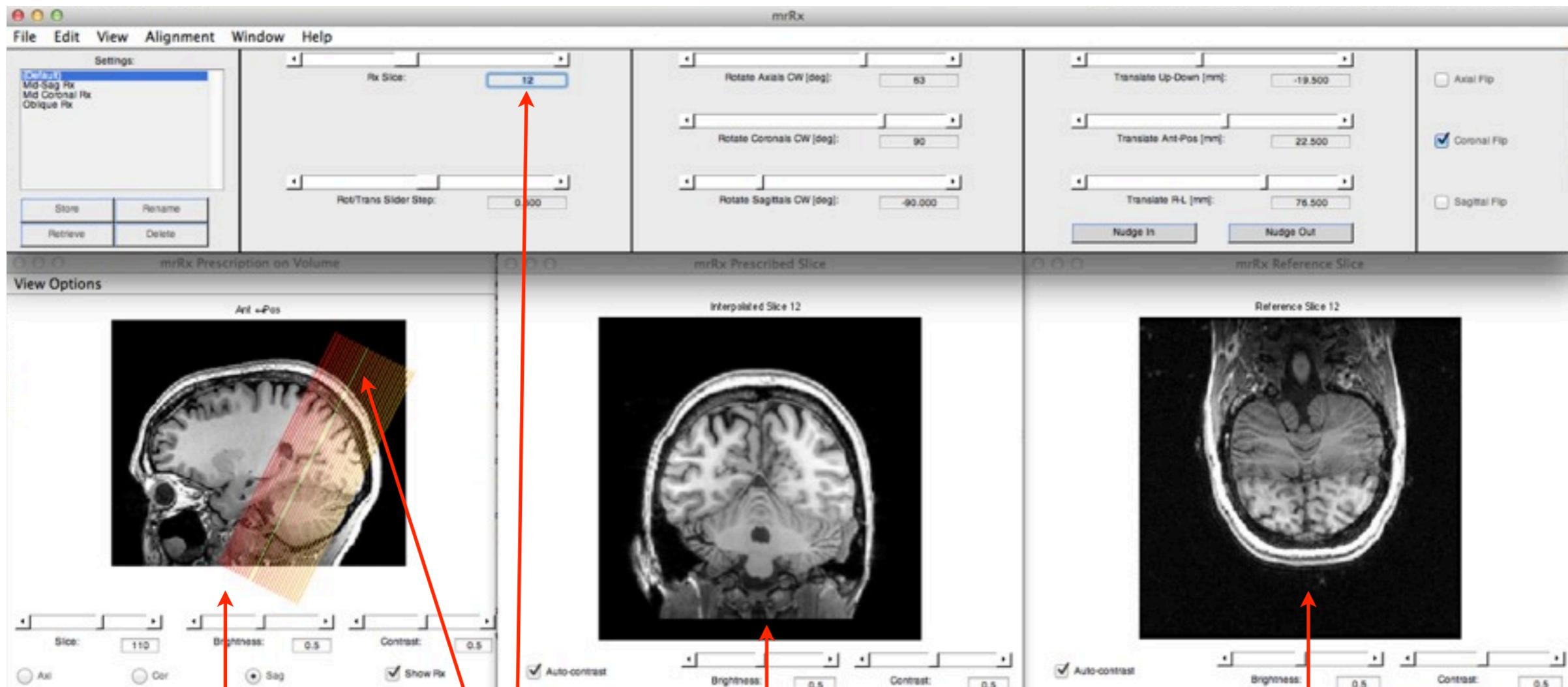
- Navigate to session directory and open alignment GUI by typing `rxAlign` in the MATLAB command line

# Align functional data to anatomy

*apply some presets*



# Align functional data to anatomy



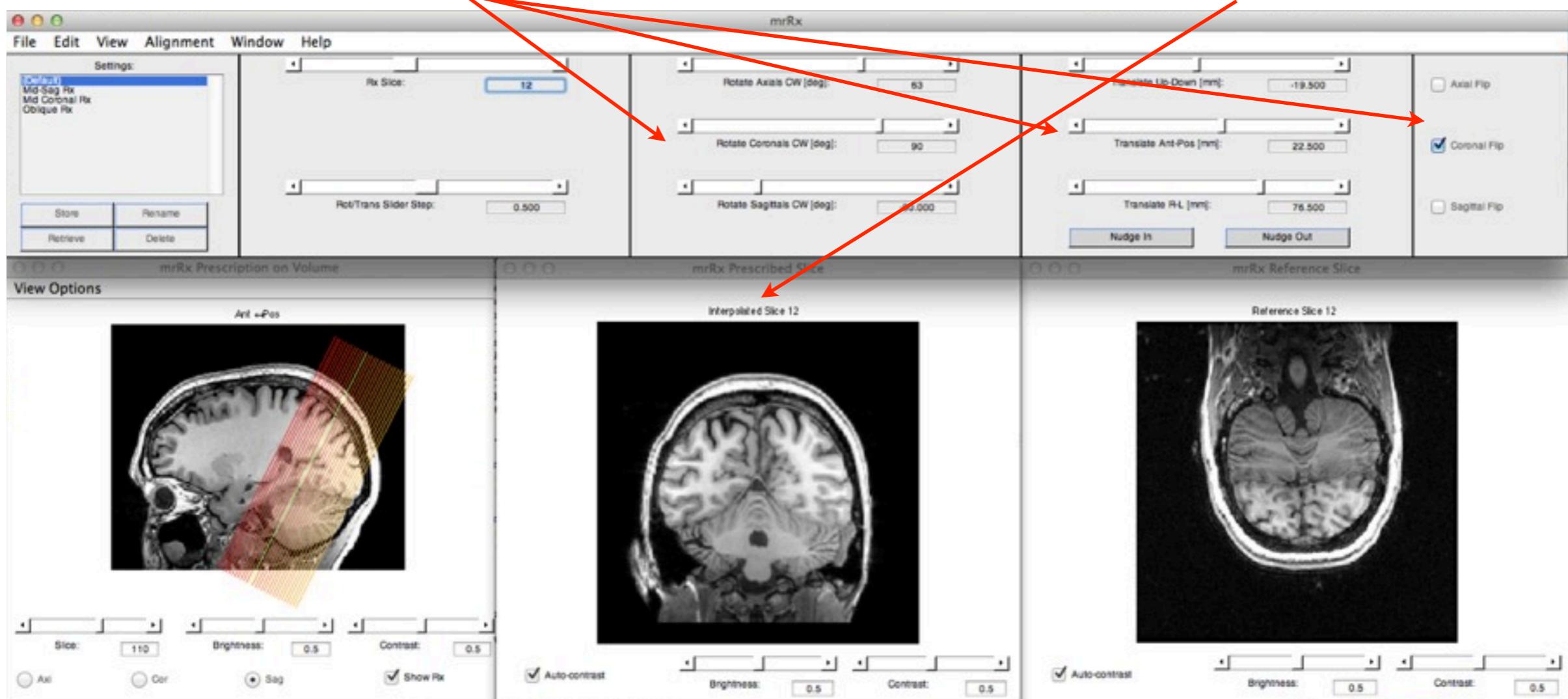
t1.nii.gz

interpolation of  
yellow slice (12)  
given current Rx

inplanes

# Align functional data to anatomy

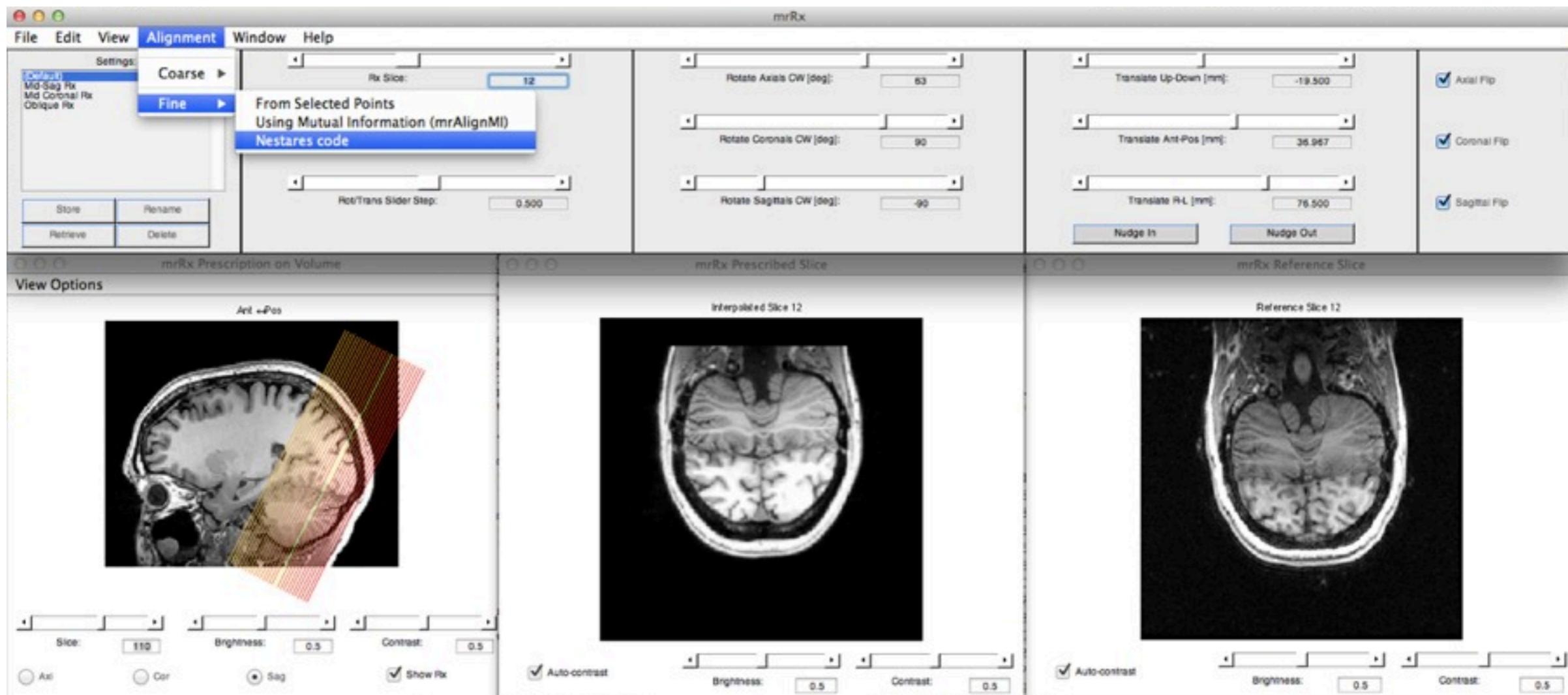
*changing Rx parameters only affects interpolation*



*try to roughly match interpolation and inplanes*

# Align functional data to anatomy

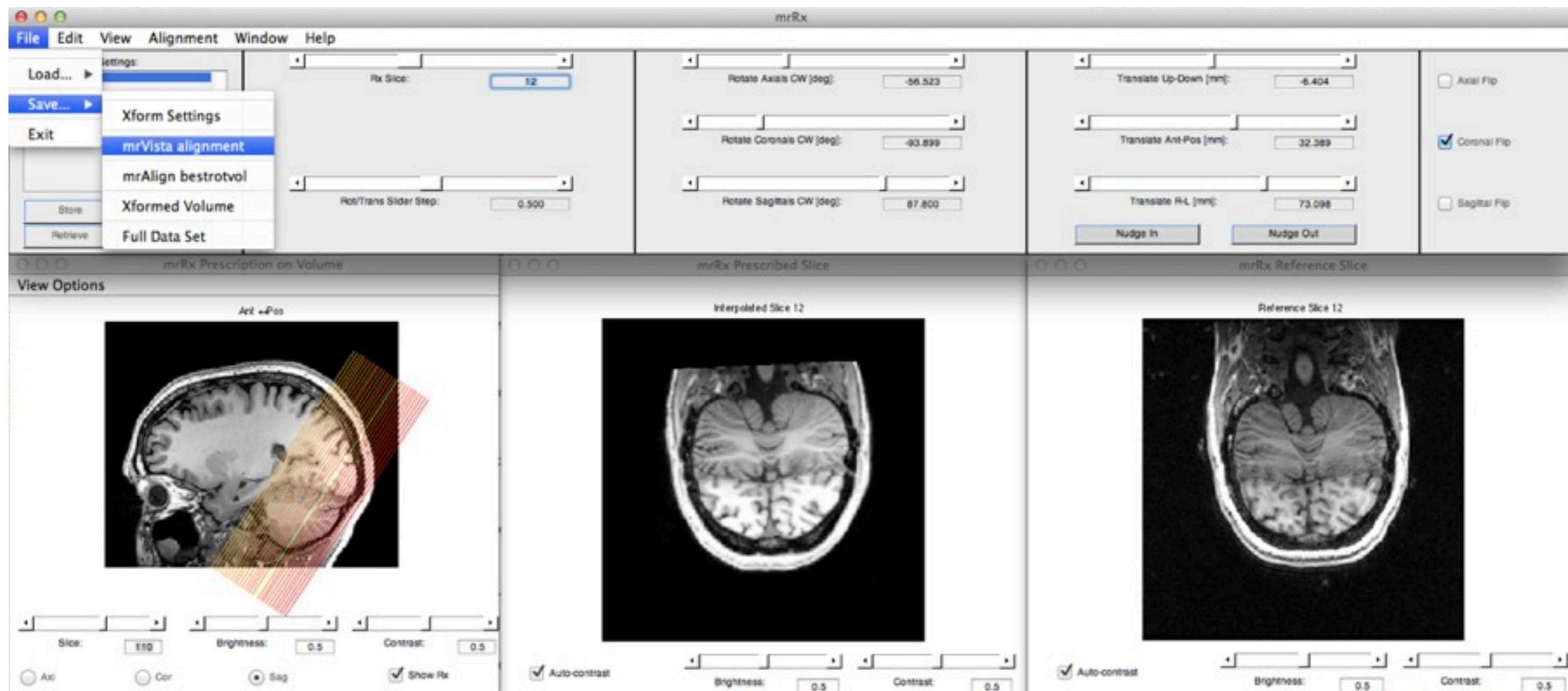
*then use Nestares code to fine-tune alignment*



*interpolation and inplanes should be the same*

# Align functional data to anatomy

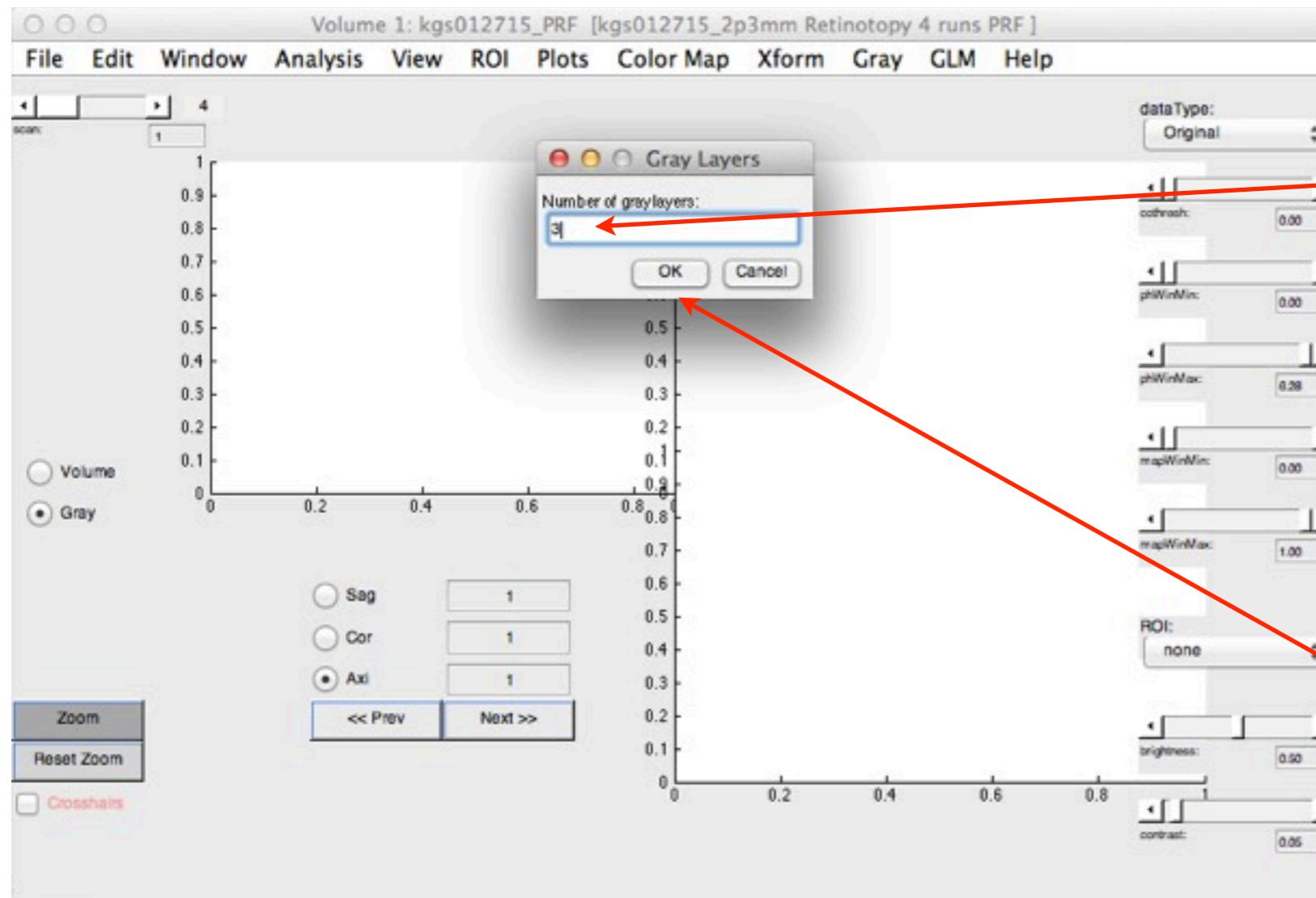
*save mrVista alignment*



*delete existing alignment if prompted*

# **Part 5: Install gray matter segmentation**

# Install gray matter segmentation

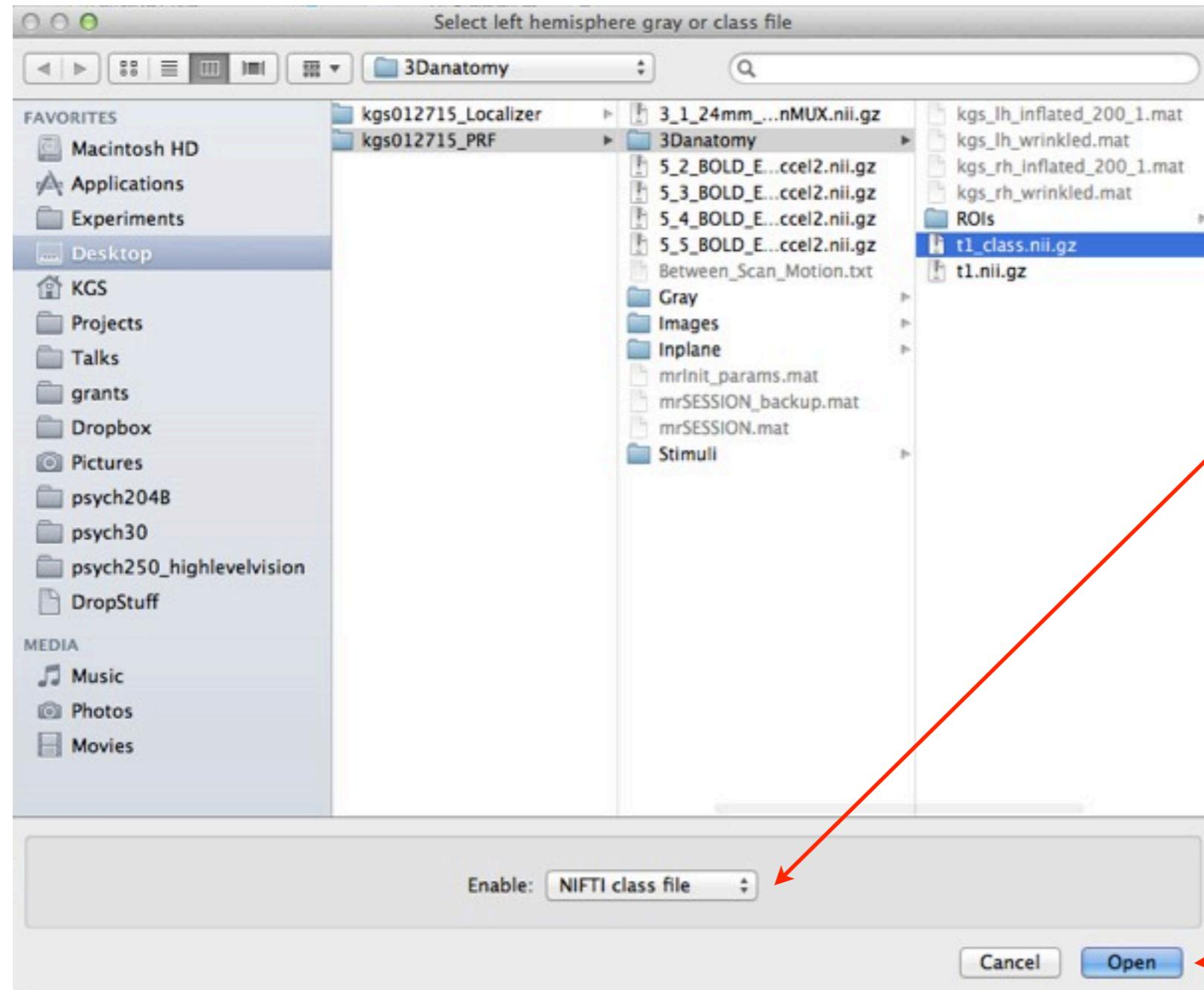


*install 3 gray layers for the left hemisphere*

*click OK*

- With the alignment saved, navigate to session directory and install segmentation by typing `mrVista 3` in the MATLAB command line

# Install gray matter segmentation

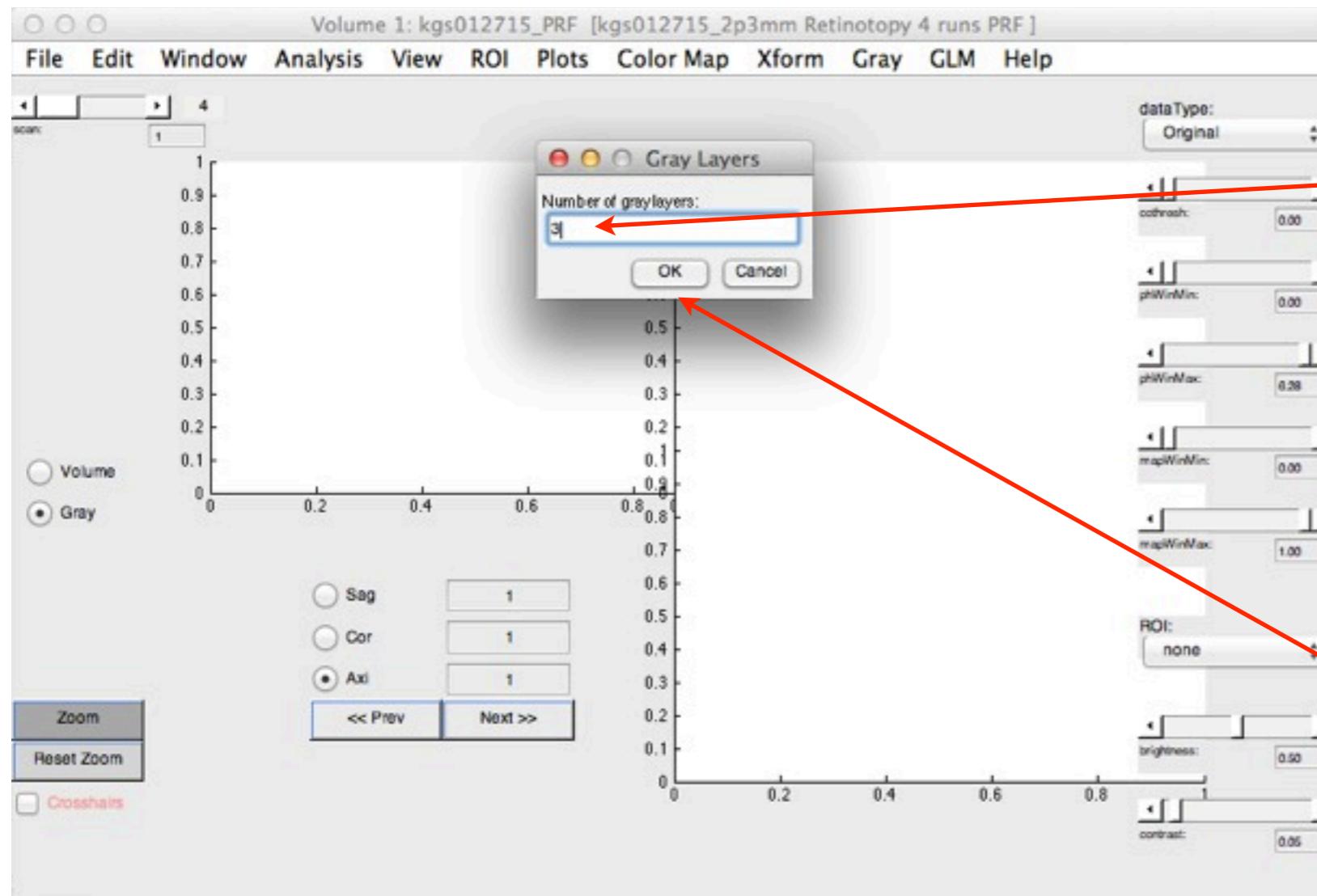


select class file  
*t1\_class.nii.gz*

make sure class  
file is enabled

click Open

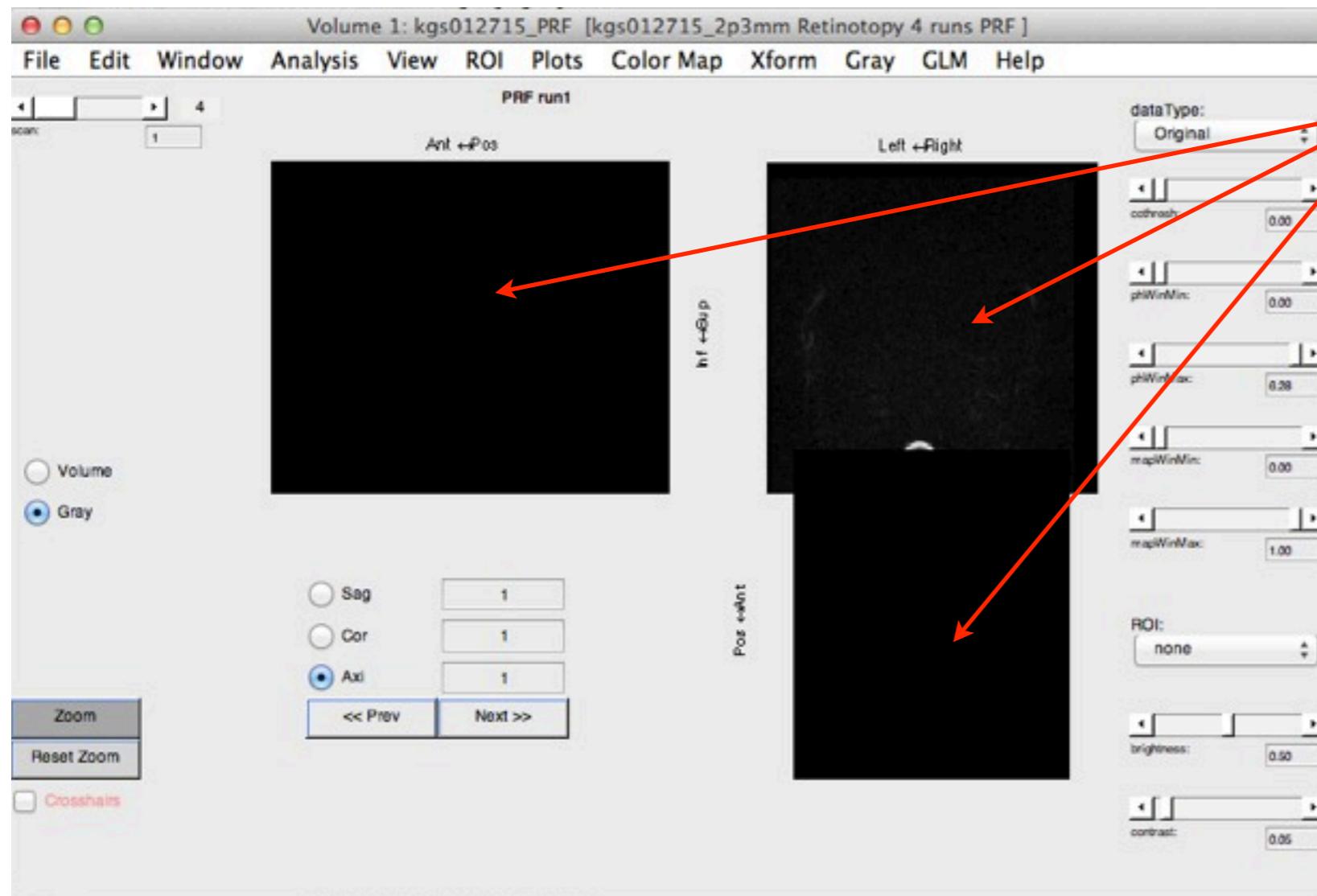
# Install gray matter segmentation



*install 3 gray layers for the right hemisphere*

*click OK*

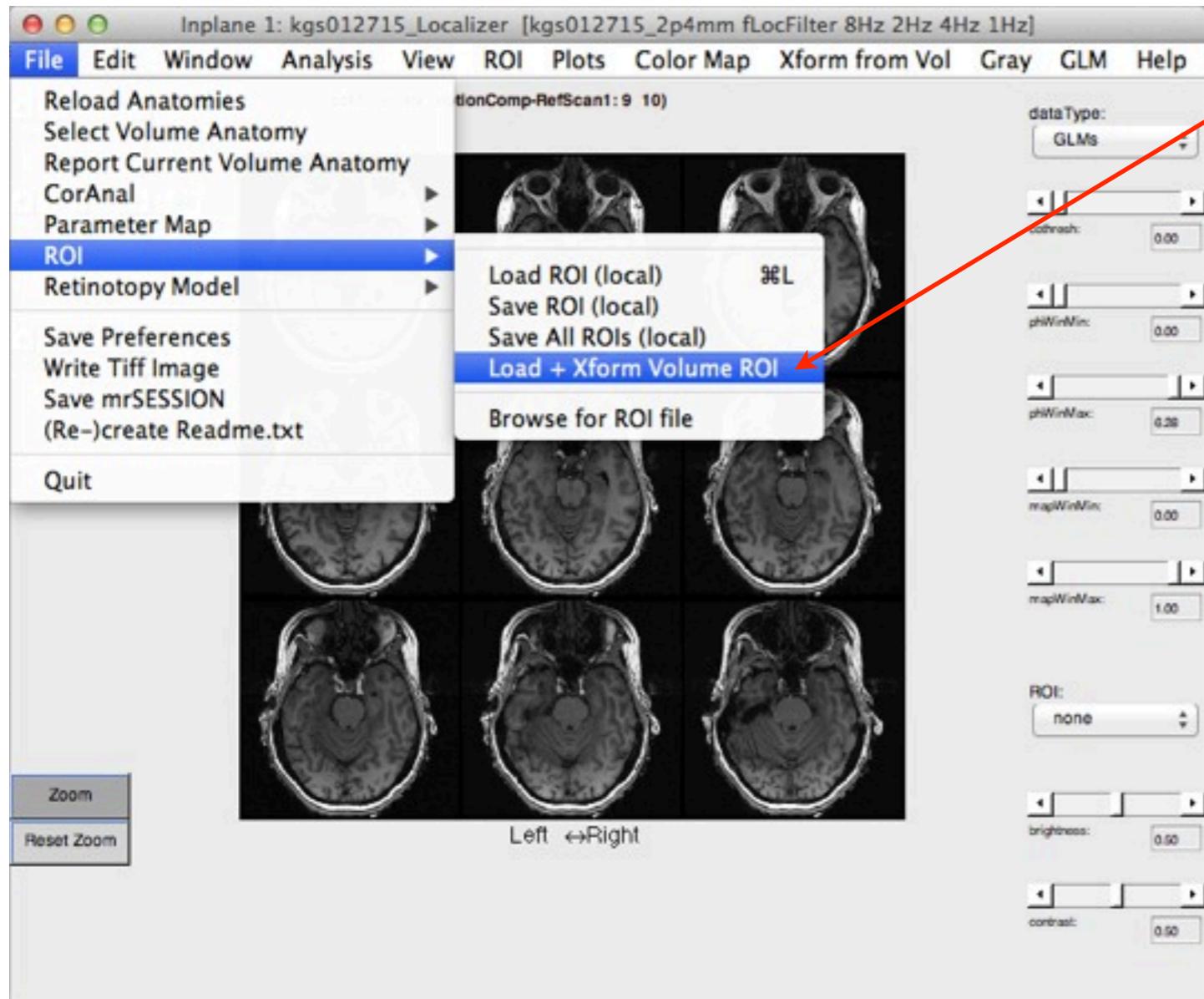
# Install gray matter segmentation



*click anywhere  
in the middle of  
the 3 planes to  
locate brain*

*set Data Type and save preferences/mrSESSION*

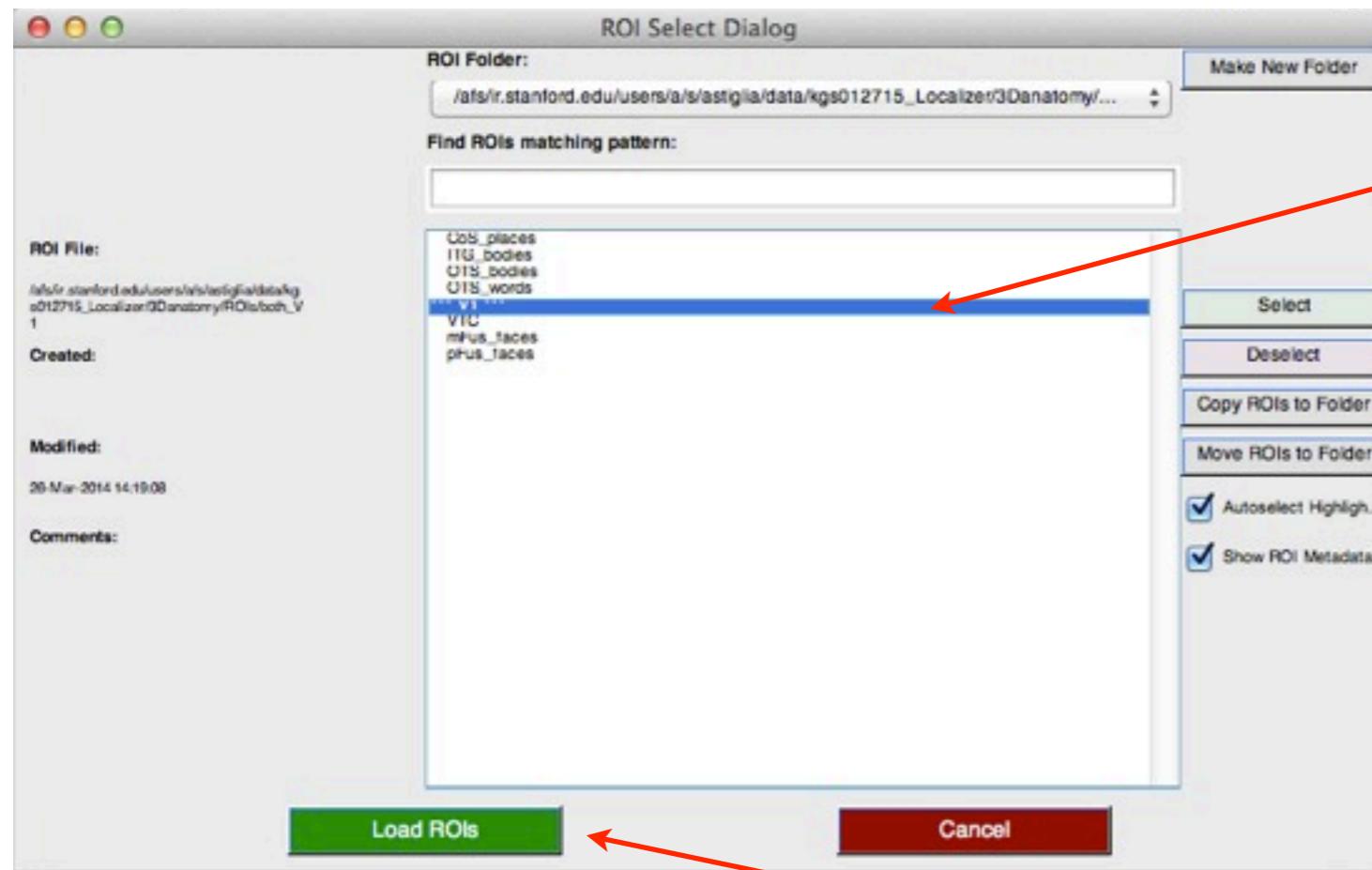
# Install gray matter segmentation



*you can now load  
a volume ROI in  
the inplane view by  
transforming the  
from the gray view*

- With the segmentation installed, navigate to initialized session and launch mrVista inplane view GUI by typing `mrVista` in the MATLAB command line

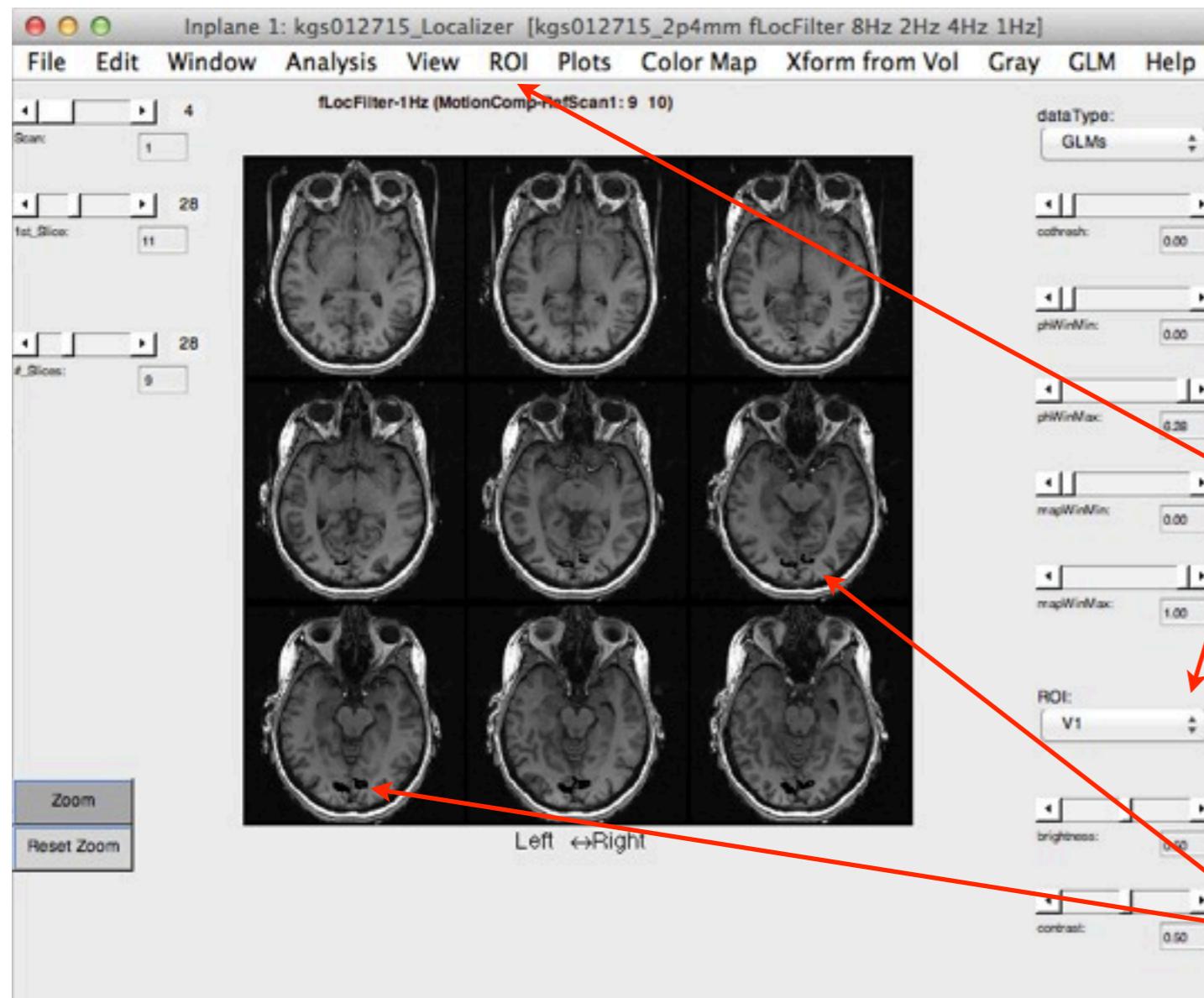
# Install gray matter segmentation



*select ROIs you would like to load*

*click load ROIs*

# Install gray matter segmentation



*loaded ROIs are listed in ROI field*

*you can change the color of the ROI here*

*V1 is colored black*

# Future directions

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- Your data is now fully preprocessed
- All processing steps shown so far are common to all types of analysis
- The next step is running your main analyses:
  - Population receptive field (pRF) model
  - General linear model (GLM)
  - Multi-voxel pattern (MVP) analysis