Lab session 5:

Single-subject Statistical Parametric Mapping (SPM) contrasts

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02/10/16

Session no.	Date (all Wednesday)	Topic/activity	Topic of quiz that day	Topic of lab write-up (assignment) due that day
1	13-Jan	Lab overview		
2	20-Jan	Brain anatomy		
3	27-Jan	Data preprocessing	Brain anatomy (no. 1)	
4	3-Feb	Set up GLM model	Functional brain anatomy (no. 2)	
5	10-Feb	Single-subject SPM contrasts	Data preprocessing and GLM model (no. 3)	Brain anatomy (no. 1)
6	17-Feb	Within-subject MVPA		Single-subject SPM contrasts (no. 2)
7	24-Feb	SIBR tour and review for mid-term exam		Within-subject MVPA (no. 3)
No lab	2-Mar	No lab (mid-term exam)		
No lab	9-Mar	No lab (spring break)		
8	16-Mar	Group-level SPM contrasts		
9	23-Mar	Between-subjects MVPA		Group-level SPM contrasts (no. 4)
10	30-Mar	Voxel-wise modeling		Between-subjects MVPA (no. 5)
11	6-Apr	Functional connectivity analysis (*no assignment*)		
12	13-Apr	Review for final exam		Voxel-wise modeling (no. 6)
No lab	20-Apr	No lab		
No lab	27-Apr	No lab (final exam)		

General sequence of data preprocessing and GLM analysis

For each individual subject: → **1** Data preprocessing → **2** Set up (specify conditions) and run GLM model → **3** Generate condition contrasts (e.g. Tools – Buildings)

Across **all subjects in a group:** → **4** Generate condition contrasts (e.g. Tools – Buildings)

If there are multiple groups of subjects ***(in our case, no)***: → **5** Generate condition contrasts between two groups (e.g. Depressed – Control)

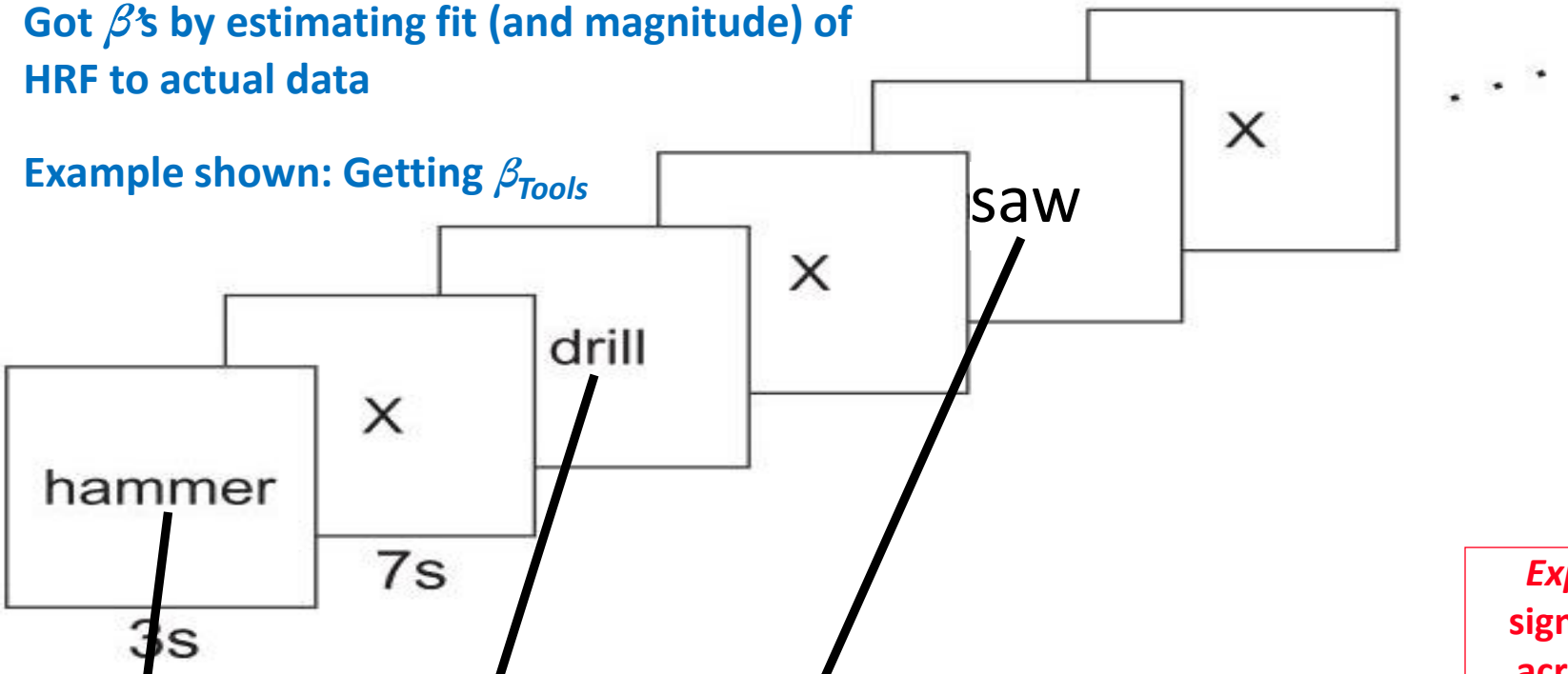
Programming statistical β contrasts to compare…

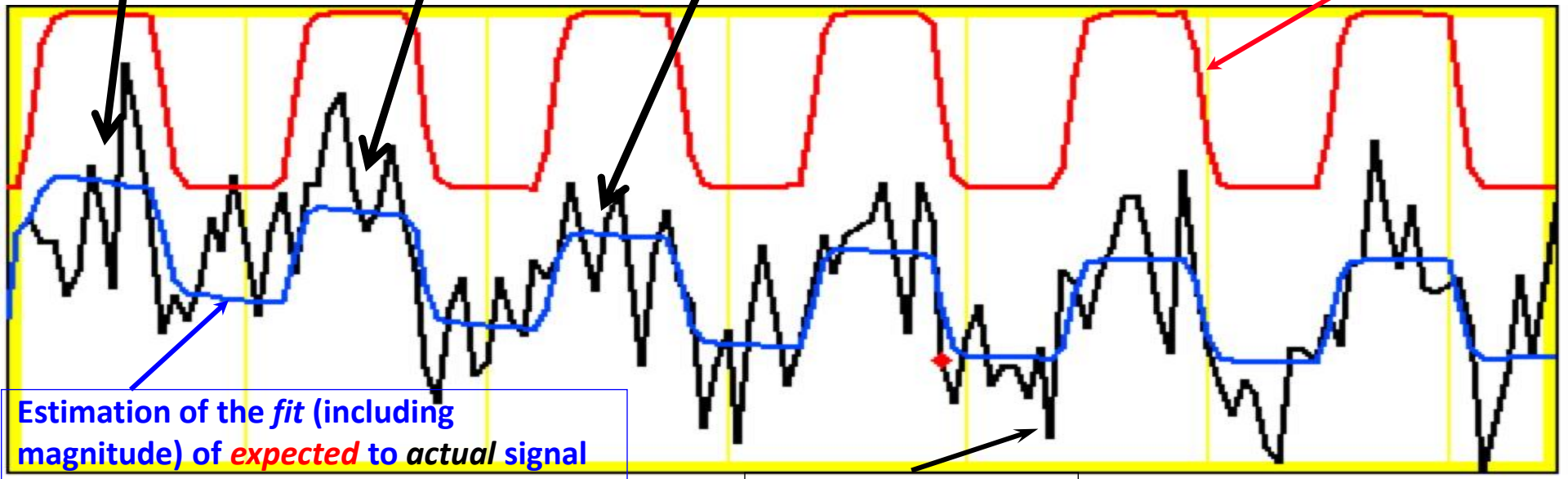
- Activation of one condition vs. Baseline ("Resting")
- Activation between two different conditions
  - Baseline cancels out (see below)

Contrast	Baseline multiplier	Tools multiplier	Buildings multiplier	Statistical result (*t-stat and p-value*) in <u>each</u> voxel
$\beta_{Tools} - \beta_{Baseline}$	-1	1	0	***Tools activation that is > "Resting"***
$\beta_{Buildings} - \beta_{Baseline}$	-1	0	1	***Buildings activation that is > "Resting"***
$\beta_{Tools} - \beta_{Buildings}$ *i.e. (Tools - Baseline) - (Buildings - Baseline)*	0	1	-1	***(Tools > "Resting") that is > (Buildings > "Resting")***
$\beta_{Buildings} - \beta_{Tools}$ *i.e. (Buildings - Baseline) - (Tools - Baseline)*	0	-1	1	***(Buildings > "Resting") that is > (Tools > "Resting")***

Got β's by estimating fit (and magnitude) of HRF to actual data

Example shown: Getting β_{Tools}





Expected **MRI signal (the HRF) across all trials**

Estimation of the *fit* (including magnitude) of *expected* to *actual* signal

(Determines the value of β_{Tools})

Actual **MRI signal across all trials**

Waveform image from AFNI web site

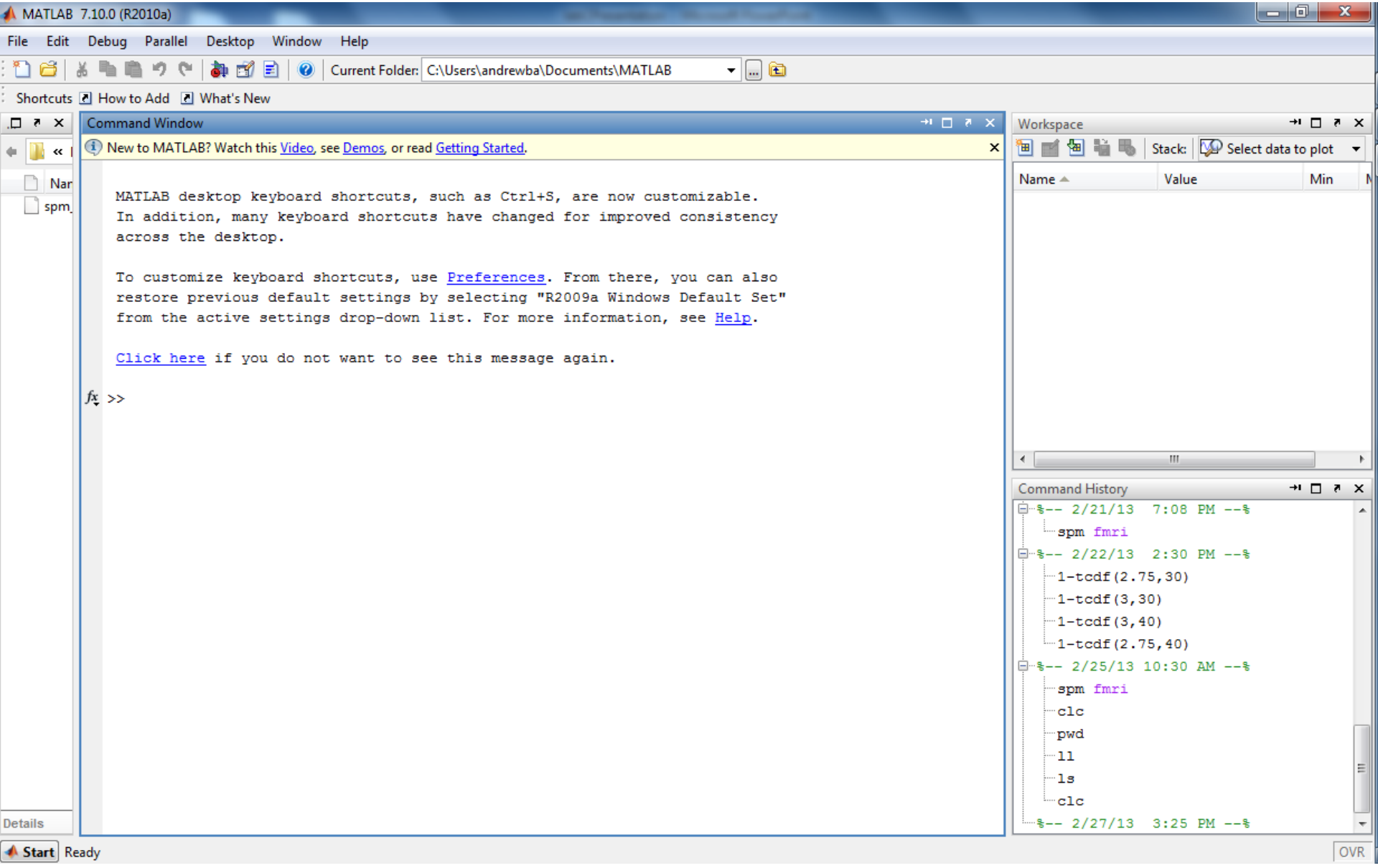
Multiplier vectors for β contrasts
Each category vs. average of others

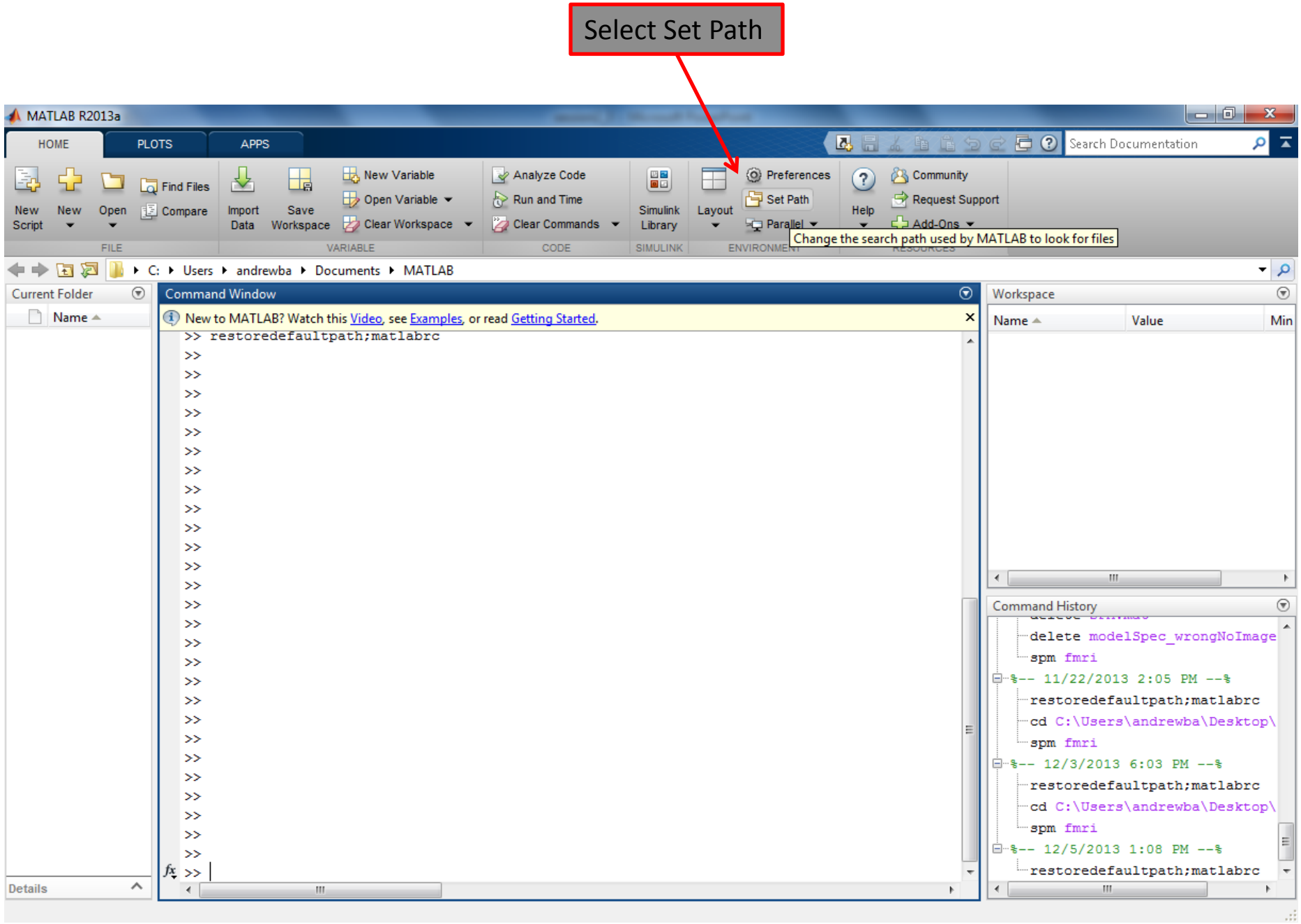
(For the assignment, you will need to download an Excel file called "session5 companion betaMultis" off Blackboard. You will need to save it to the computer and open it in Excel)

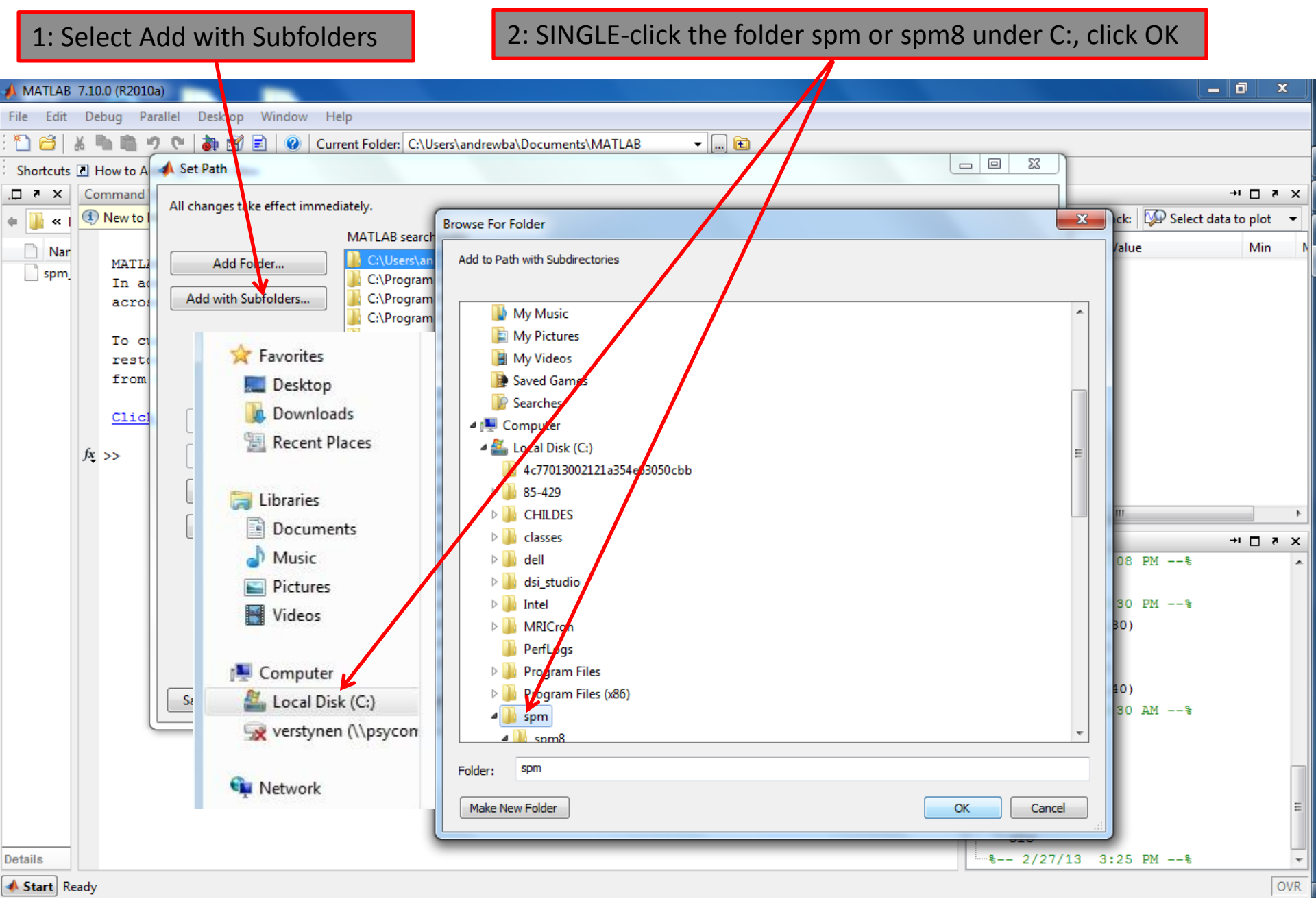
Category no.	Contrast name	Baseline	1	2	3	4	5	6	7	8	9	10	11	12	Constant
1	Animals_vs_others	[0	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
2	Bodyparts_vs_others	[0	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
3	Buildings_vs_others	[0	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
4	Buildingparts_vs_others	[0	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	0]
5	Clothing_vs_others	[0	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	0]
6	Furniture_vs_others	[0	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	0]
7	Insects_vs_others	[0	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	0]
8	Kitchen_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	0]
9	Manmade_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	0]
10	Tools_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	0]
11	Vegetables_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	0]
12	Vehicles_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	0]

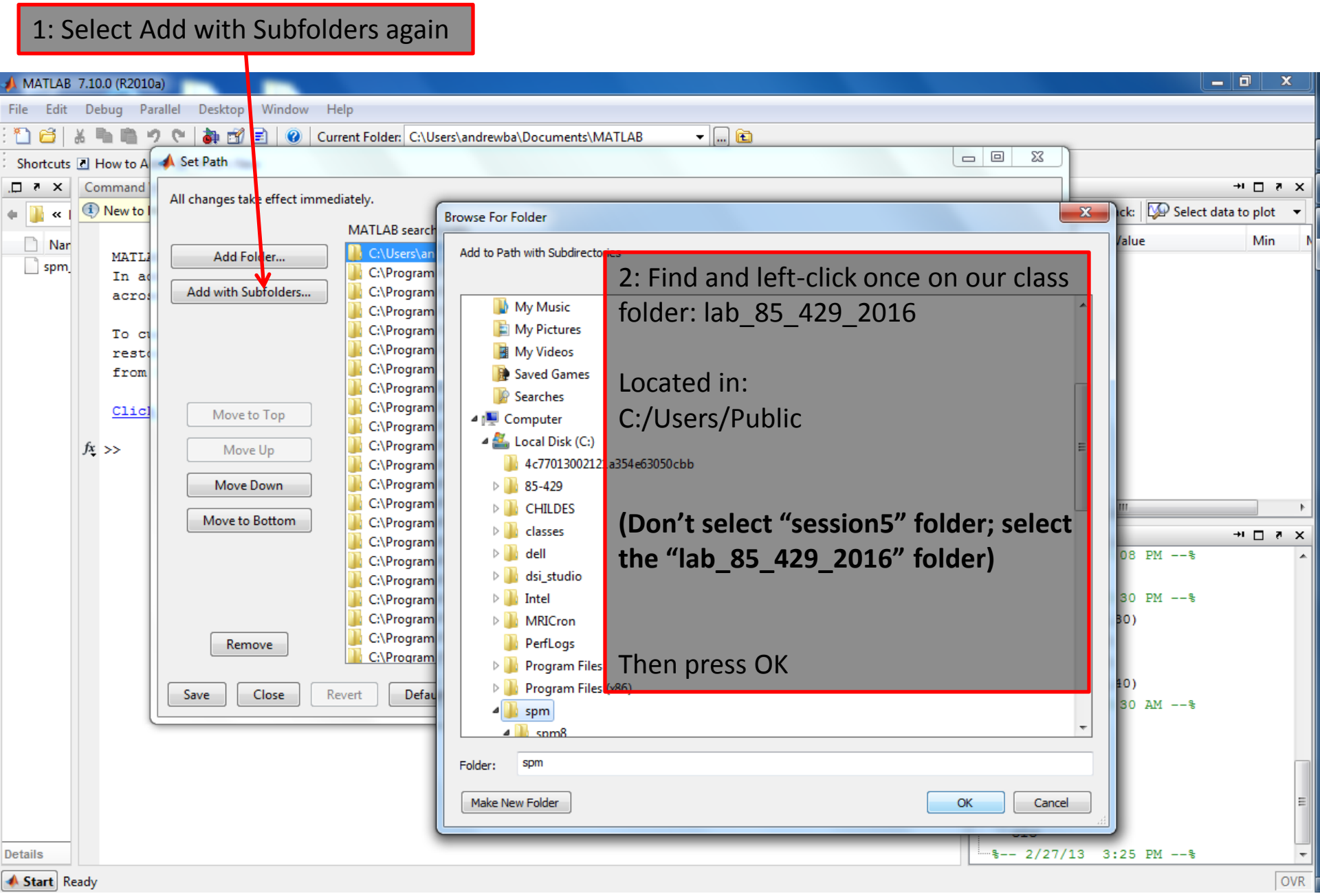
Start Matlab 2012b (on desktop, or type “matlab” in Start menu to find it)

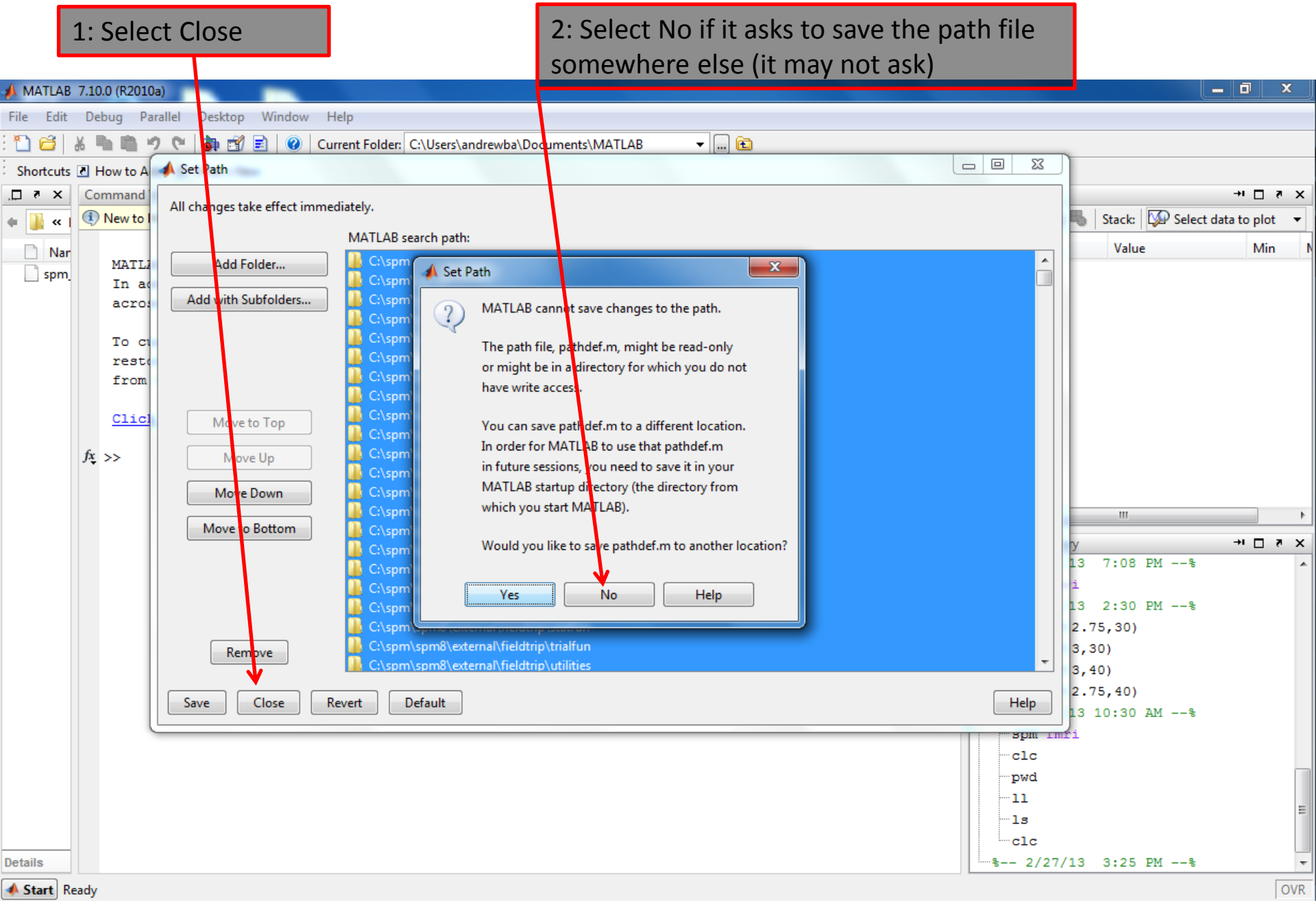
NOTE: You MUST select Matlab 2012b, do NOT select 2014b




Select Set Path
MATLAB R2013a
HOME
PLOTS
APPS
Search Documentation
New Script
New
Open
Find Files
Compare
Import Data
Save Workspace
New Variable
Open Variable
Clear Workspace
Analyze Code
Run and Time
Clear Commands
Simulink Library
Layout
Preferences
Set Path
Parallel
Help
Community
Request Support
Add-Ons
FILE
VARIABLE
CODE
SIMULINK
ENVIRONMENT
RESOURCES
Change the search path used by MATLAB to look for files
C: ▸ Users ▸ andrewba ▸ Documents ▸ MATLAB
Current Folder
Name
Command Window
New to MATLAB? Watch this Video, see Examples, or read Getting Started.
>> restoredefaultpath;matlabrc
Workspace
Name
Value
Min
Command History
delete modelSpec_wrongNoImage
spm fmri
%-- 11/22/2013 2:05 PM --%
restoredefaultpath;matlabrc
cd C:\Users\andrewba\Desktop\
spm fmri
%-- 12/3/2013 6:03 PM --%
restoredefaultpath;matlabrc
cd C:\Users\andrewba\Desktop\
spm fmri
%-- 12/5/2013 1:08 PM --%
restoredefaultpath;matlabrc
Details


1: Select Add with Subfolders
2: SINGLE-click the folder spm or spm8 under C:, click OK
MATLAB 7.10.0 (R2010a)
File Edit Debug Parallel Desktop Window Help
Current Folder: C:\Users\andrewba\Documents\MATLAB
Set Path
All changes take effect immediately.
Add Folder...
Add with Subfolders...
MATLAB search
Browse For Folder
Add to Path with Subdirectories
My Music
My Pictures
My Videos
Saved Games
Searches
Computer
Local Disk (C:)
4c77013002121a354e63050cbb
85-429
CHILDES
classes
dell
dsi_studio
Intel
MRICron
PerfLogs
Program Files
Program Files (x86)
spm
spm8
Favorites
Desktop
Downloads
Recent Places
Libraries
Documents
Music
Pictures
Videos
Computer
Local Disk (C:)
verstynen (\\psycon
Network
Folder: spm
Make New Folder
OK
Cancel
Select data to plot
Start
Ready
OVR


1: Select Add with Subfolders again
MATLAB 7.10.0 (R2010a)
File Edit Debug Parallel Desktop Window Help
Current Folder: C:\Users\andrewba\Documents\MATLAB
Set Path
All changes take effect immediately.
Add Folder...
Add with Subfolders...
Move to Top
Move Up
Move Down
Move to Bottom
Remove
Save
Close
Revert
MATLAB search
Browse For Folder
Add to Path with Subdirectories
My Music
My Pictures
My Videos
Saved Games
Searches
Computer
Local Disk (C:)
85-429
CHILDES
classes
dell
dsi_studio
Intel
MRICron
PerfLogs
Program Files
spm
Folder:
Make New Folder
OK
Cancel
2: Find and left-click once on our class folder: lab_85_429_2016
Located in:
C:/Users/Public
(Don't select "session5" folder; select the "lab_85_429_2016" folder)
Then press OK
Start
Ready

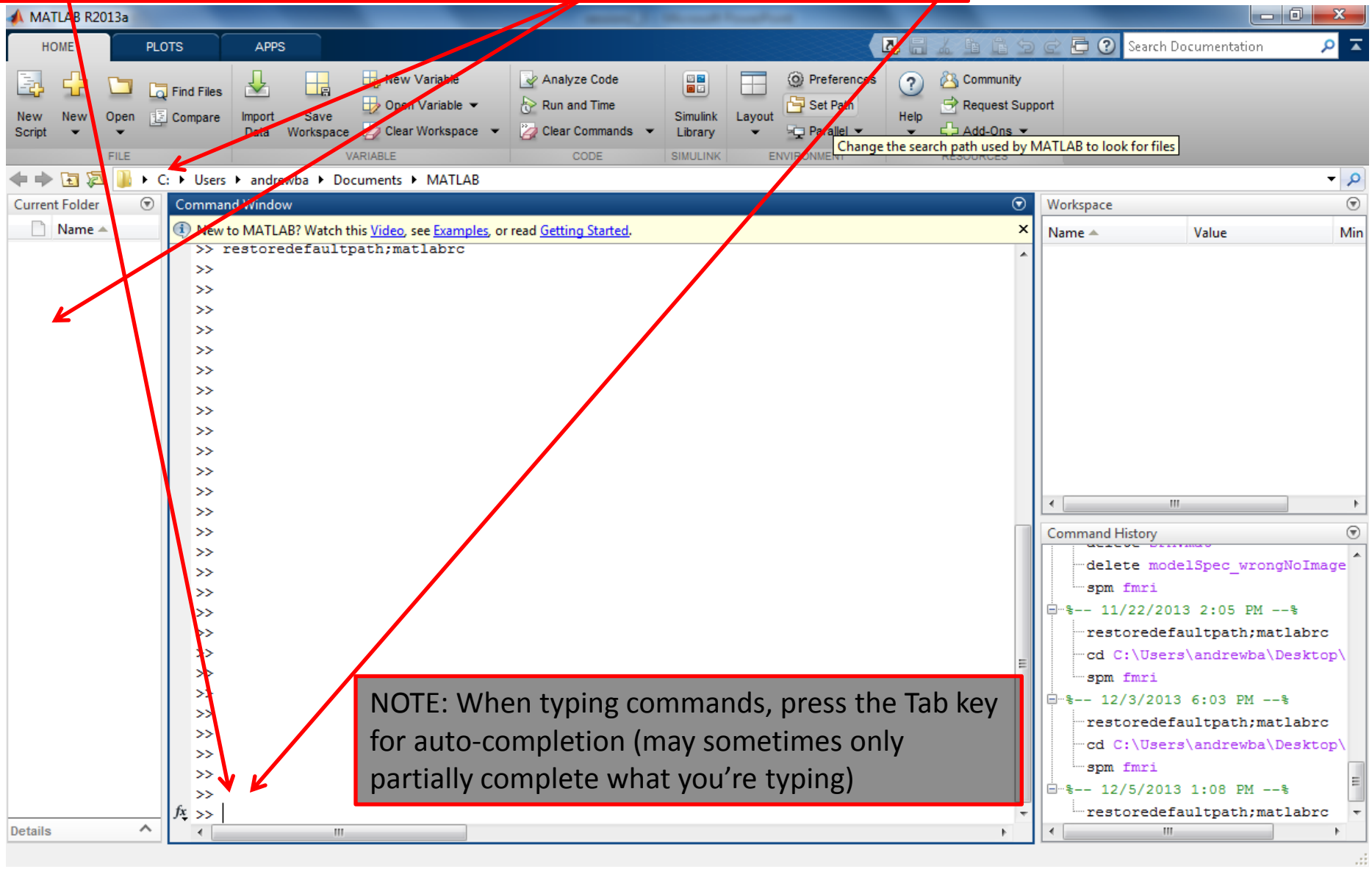

1: Select Close
2: Select No if it asks to save the path file somewhere else (it may not ask)
MATLAB 7.10.0 (R2010a)
File Edit Debug Parallel Desktop Window Help
Current Folder: C:\Users\andrewba\Documents\MATLAB
Set Path
All changes take effect immediately.
MATLAB search path:
Add Folder...
Add with Subfolders...
Move to Top
Move Up
Move Down
Move to Bottom
Remove
Save
Close
Revert
Default
Help
Set Path
MATLAB cannot save changes to the path.
The path file, pathdef.m, might be read-only or might be in a directory for which you do not have write access.
You can save pathdef.m to a different location. In order for MATLAB to use that pathdef.m in future sessions, you need to save it in your MATLAB startup directory (the directory from which you start MATLAB).
Would you like to save pathdef.m to another location?
Yes
No
Help
C:\spm\spm8\external\fieldtrip\trialfun
C:\spm\spm8\external\fieldtrip\utilities
Stack:
Select data to plot
Value
Min
clc
pwd
ll
ls
clc
Start
Ready
OVR

1: Go to the Matlab Command Window and type:

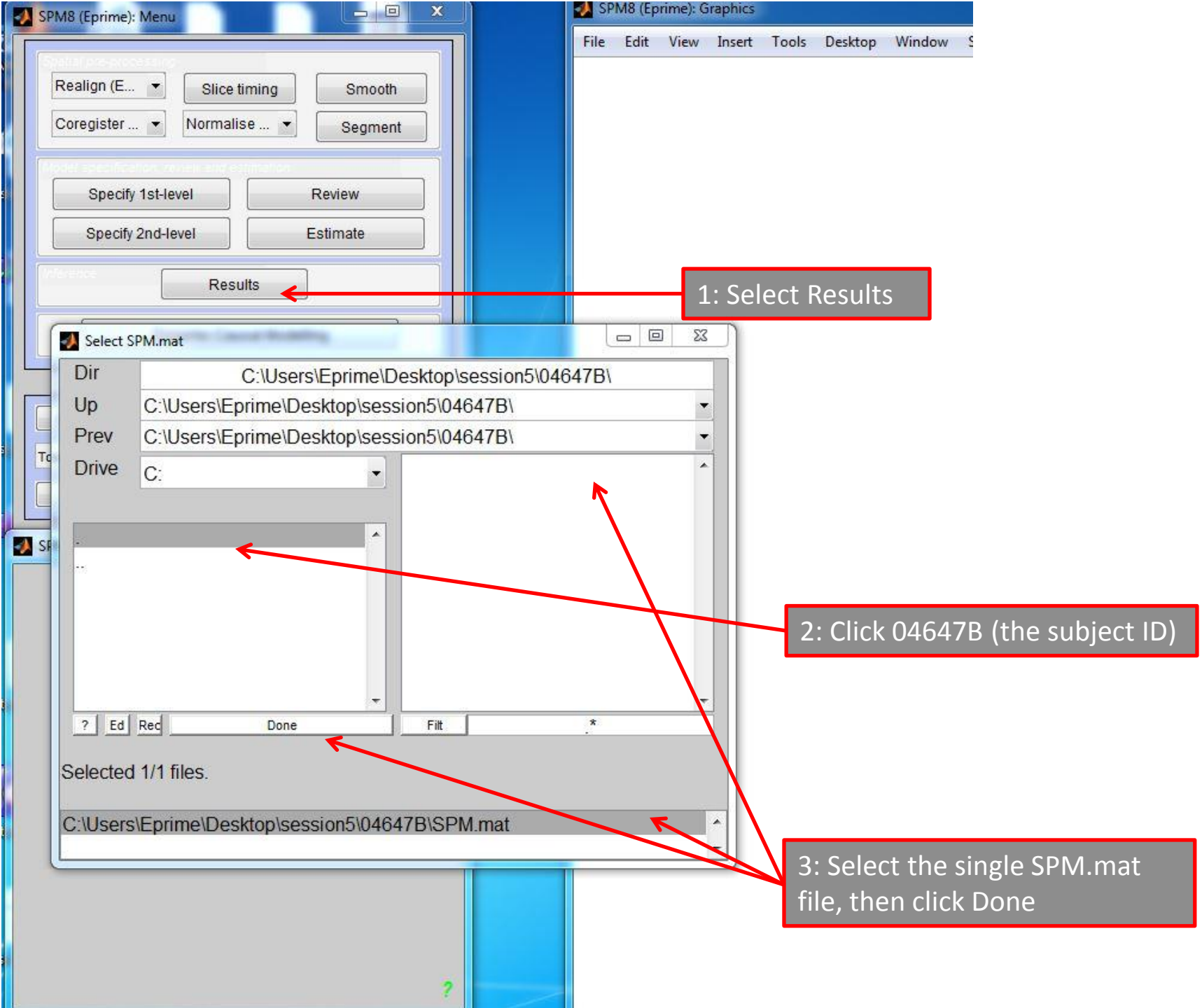
cd C:/Users/Public/lab_85_429_2016/session5

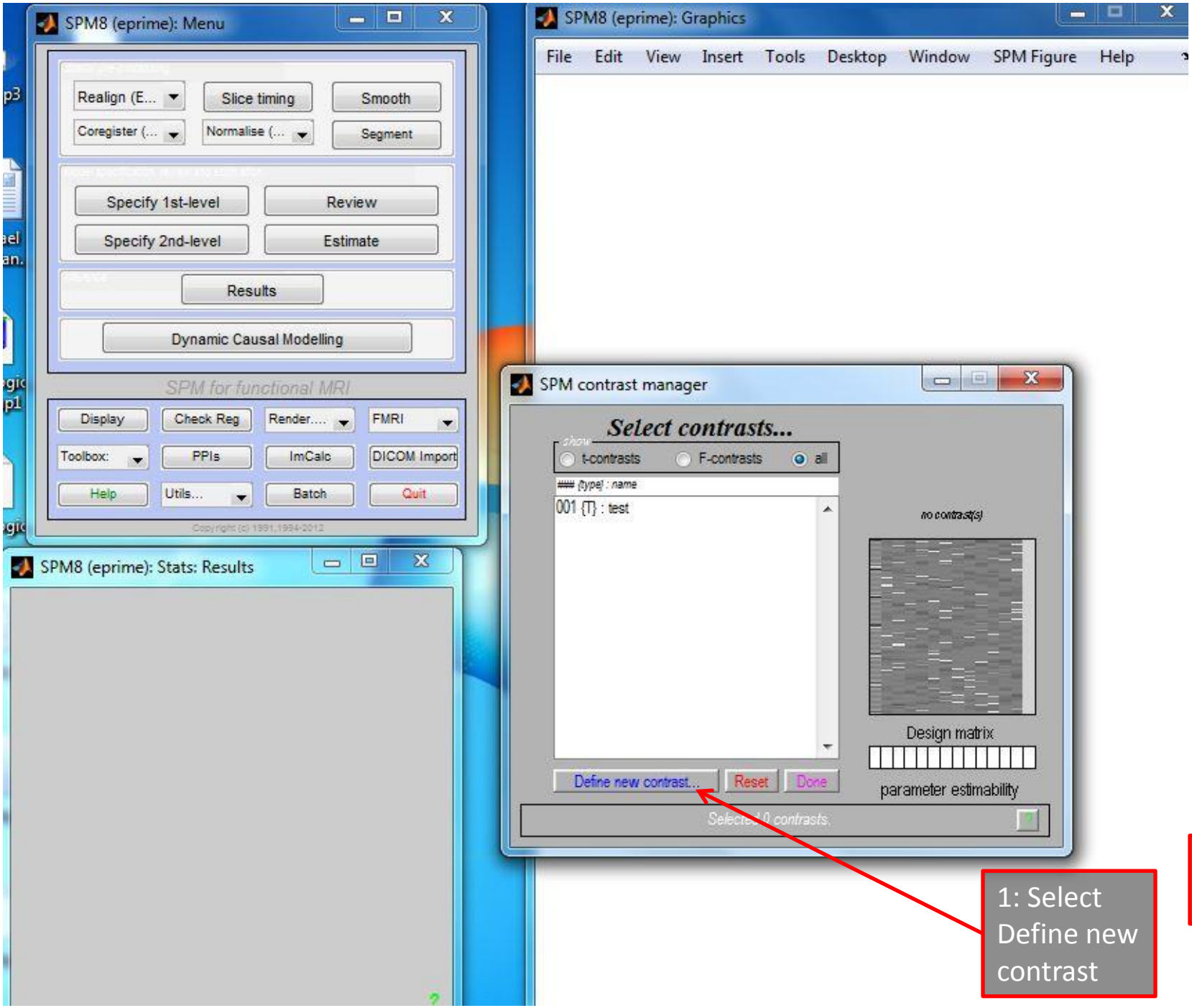
…(OR navigate there using the browser)

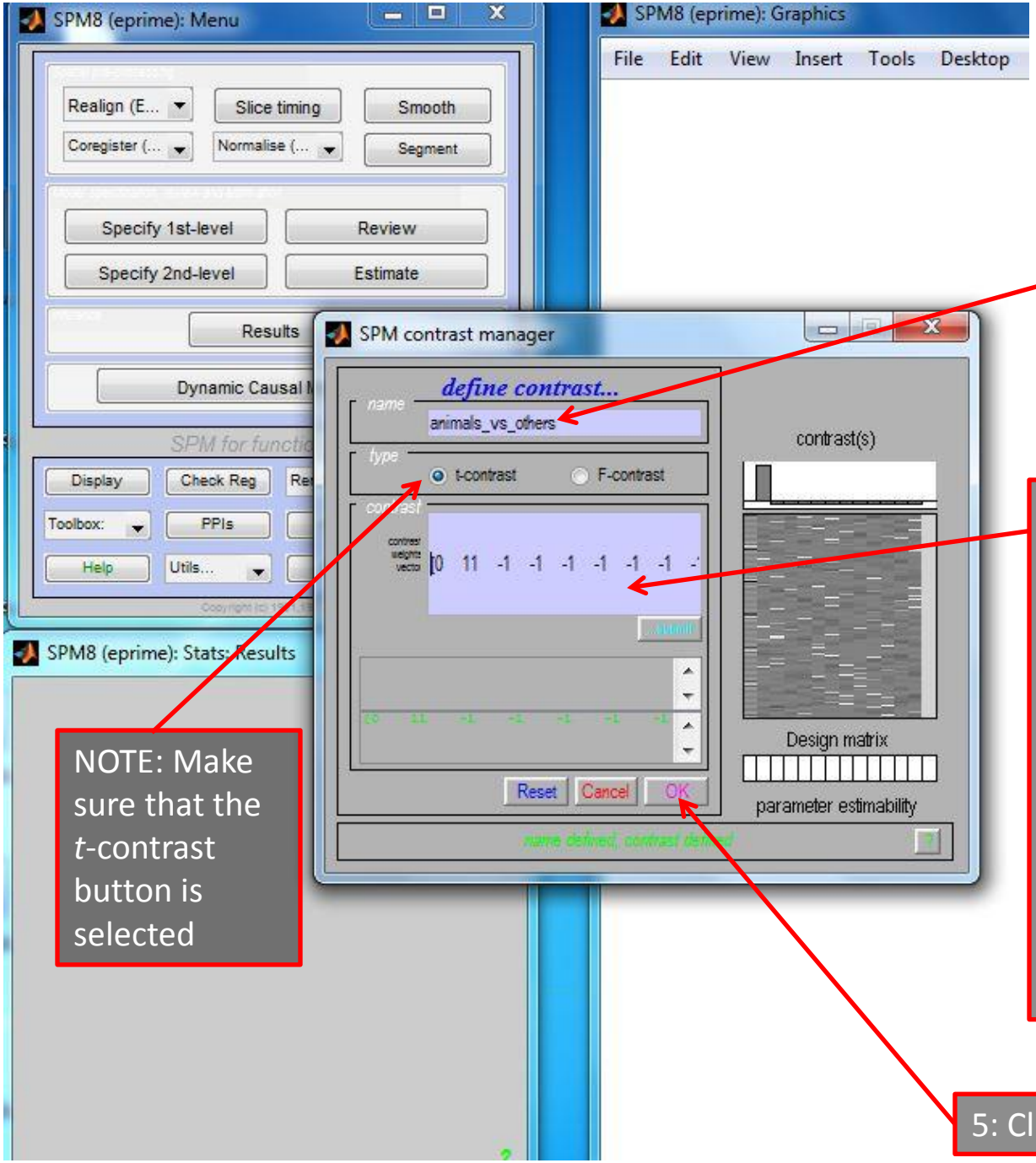
2: Then type: spm fmri



NOTE: When typing commands, press the Tab key for auto-completion (may sometimes only partially complete what you're typing)


SPM8 (Eprime): Menu
Realign (E...
Slice timing
Smooth
Coregister ...
Normalise ...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
SPM8 (Eprime): Graphics
File Edit View Insert Tools Desktop Window
Select SPM.mat
Dir C:\Users\Eprime\Desktop\session5\04647B\
Up C:\Users\Eprime\Desktop\session5\04647B\
Prev C:\Users\Eprime\Desktop\session5\04647B\
Drive C:
? Ed Rec Done Filt *.*
Selected 1/1 files.
C:\Users\Eprime\Desktop\session5\04647B\SPM.mat
1: Select Results
2: Click 04647B (the subject ID)
3: Select the single SPM.mat file, then click Done


SPM8 (eprime): Menu
Realign (E...
Slice timing
Smooth
Coregister (...
Normalise (...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Render....
FMRI
Toolbox:
PPIs
ImCalc
DICOM Import
Help
Utils...
Batch
Quit
SPM8 (eprime): Graphics
File
Edit
View
Insert
Tools
Desktop
Window
SPM Figure
Help
SPM8 (eprime): Stats: Results
SPM contrast manager
Select contrasts...
t-contrasts
F-contrasts
all
(type) : name
001 {T} : test
no contrast(s)
Design matrix
parameter estimability
Define new contrast...
Reset
Done
1: Select Define new contrast
2: Next slide…



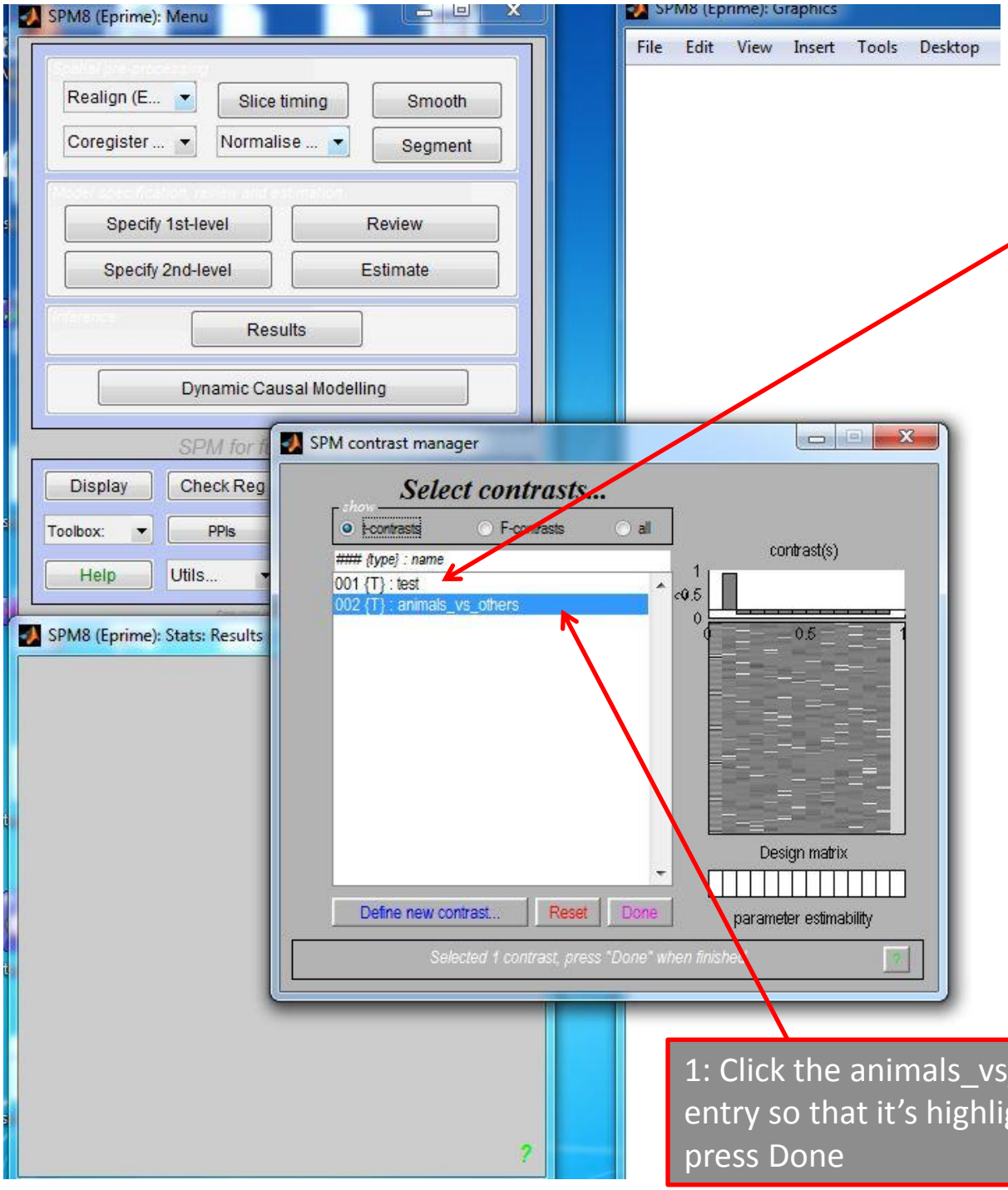
3: For Name, type: animals_vs_others

NOTE: For your assignment, you will create different contrasts and you should name them differently

4: This is where you input the condition multipliers for a contrast. For Animals, we give it the multiplier "11", and for each of the remaining categories (11 left), we put "-1". This sums to 0. **Use the file from Blackboard called "session5 companion betaMultis" to copy (ctrl+c) the vector of multipliers for Animals, and paste (ctrl+v) it here (include the brackets!)**

NOTE: Make sure that the *t*-contrast button is selected

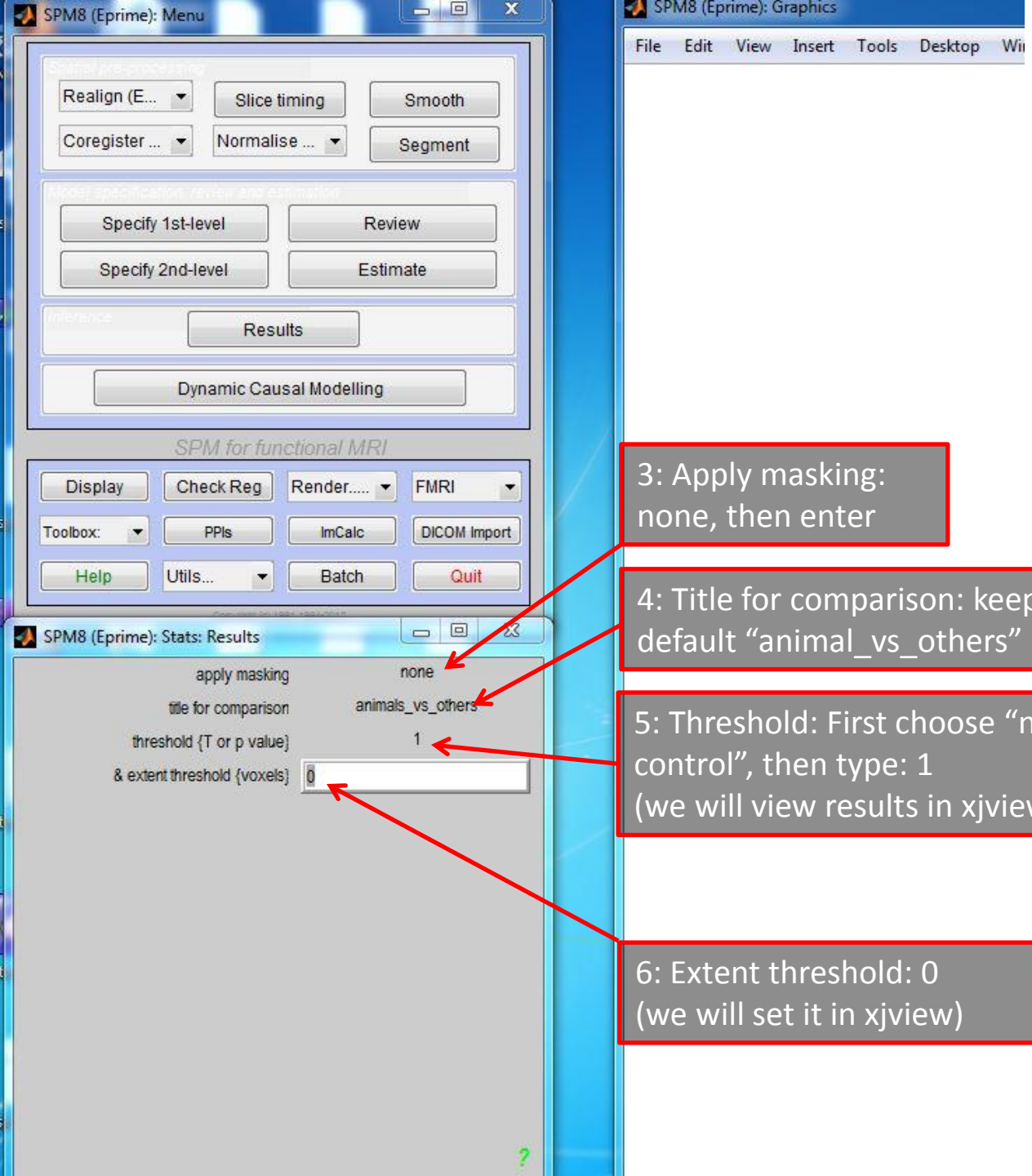
5: Click OK



NOTE: I created "test" earlier, don't click this ever

1: Click the animals_vs_others entry so that it's highlighted; then press Done

2: Next slide…



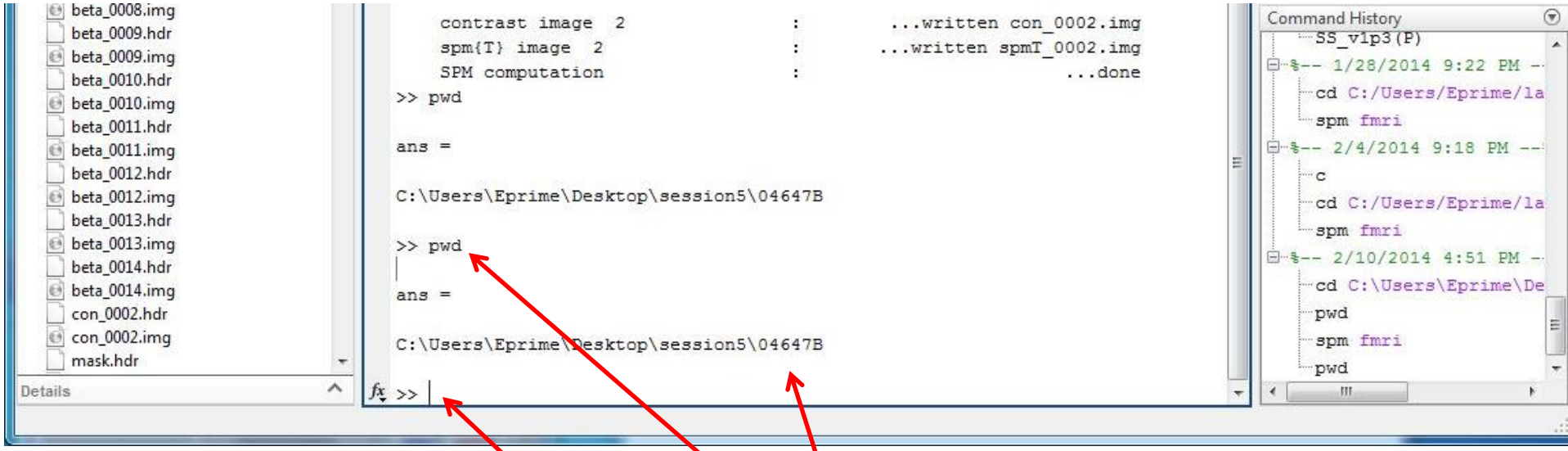
3: Apply masking:
none, then enter

4: Title for comparison: keep at default “animal_vs_others”

5: Threshold: First choose “none” for “*p* value adjustment to control”, then type: 1
(we will view results in xjview and set the *p* threshold there)

6: Extent threshold: 0
(we will set it in xjview)

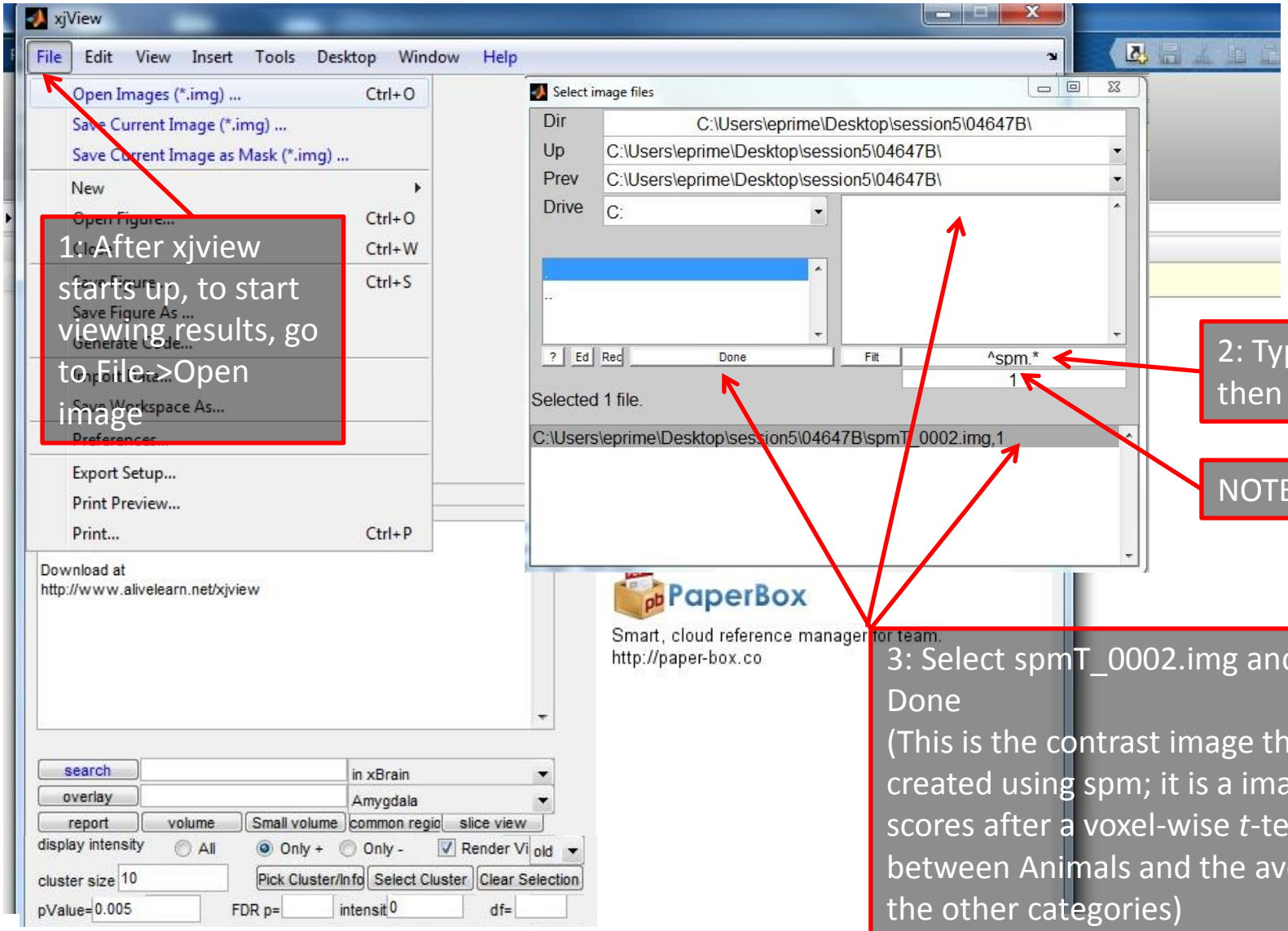
1: After defining the contrast parameters in the previous slide, spm will display a window of results. However, we will ignore this and instead view results using xjview. But don't close spm. Go back to the Matlab command window (it's already open)



2: To see what directory you're in, type: pwd

3: If the directory includes the subject ID, which is 04647B, then start xjview by typing: *xjview*

If you're not in that directory, then cd to it



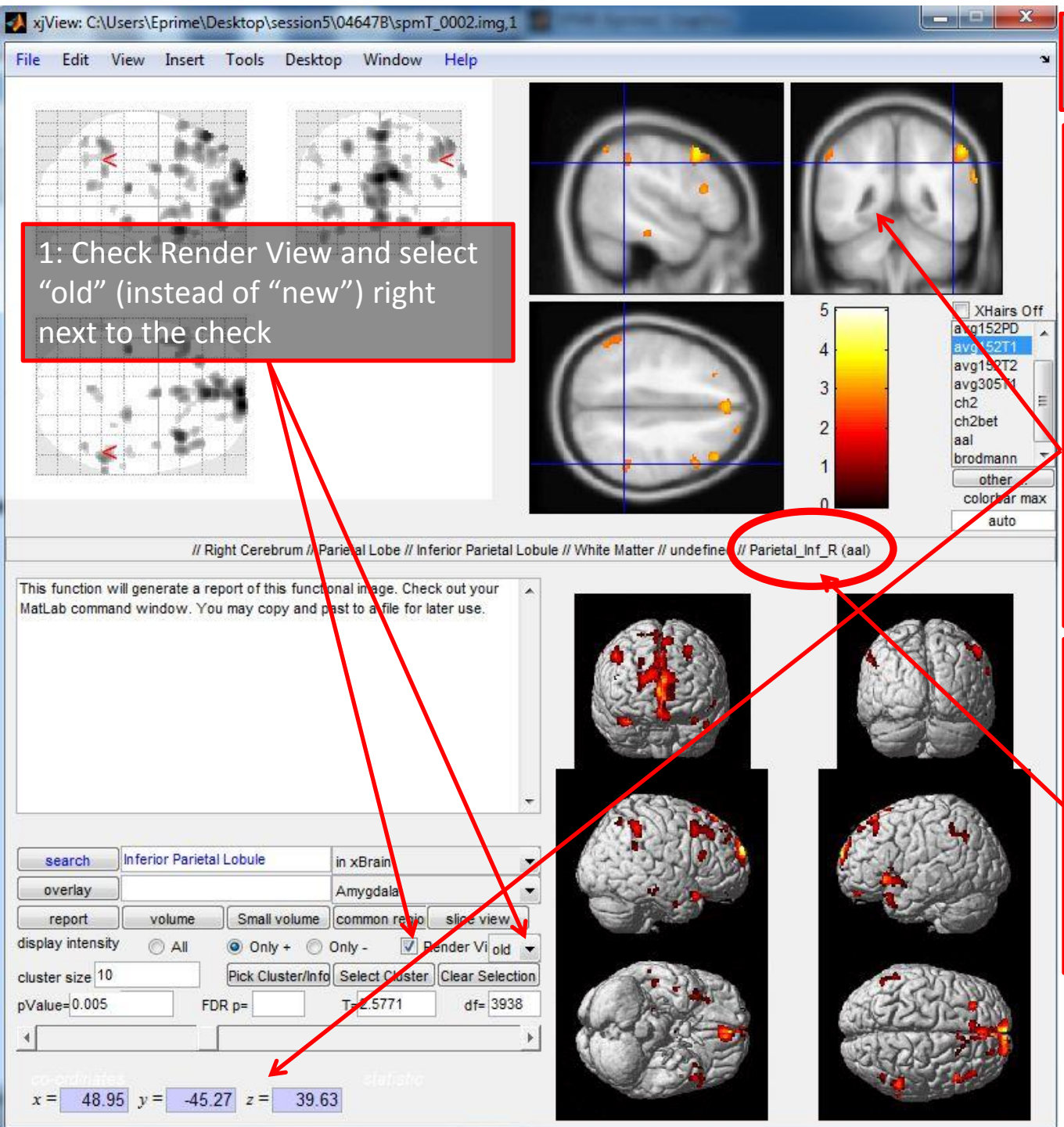
1: After xjview starts up, to start viewing results, go to File->Open image

2: Type ^spm.* then press enter

NOTE: Leave as 1

3: Select spmT_0002.img and press Done
(This is the contrast image that we created using spm; it is a image of *t* scores after a voxel-wise *t*-test between Animals and the average of the other categories)

NOTE: For your assignment, you will open different files that you created, which will be named differently

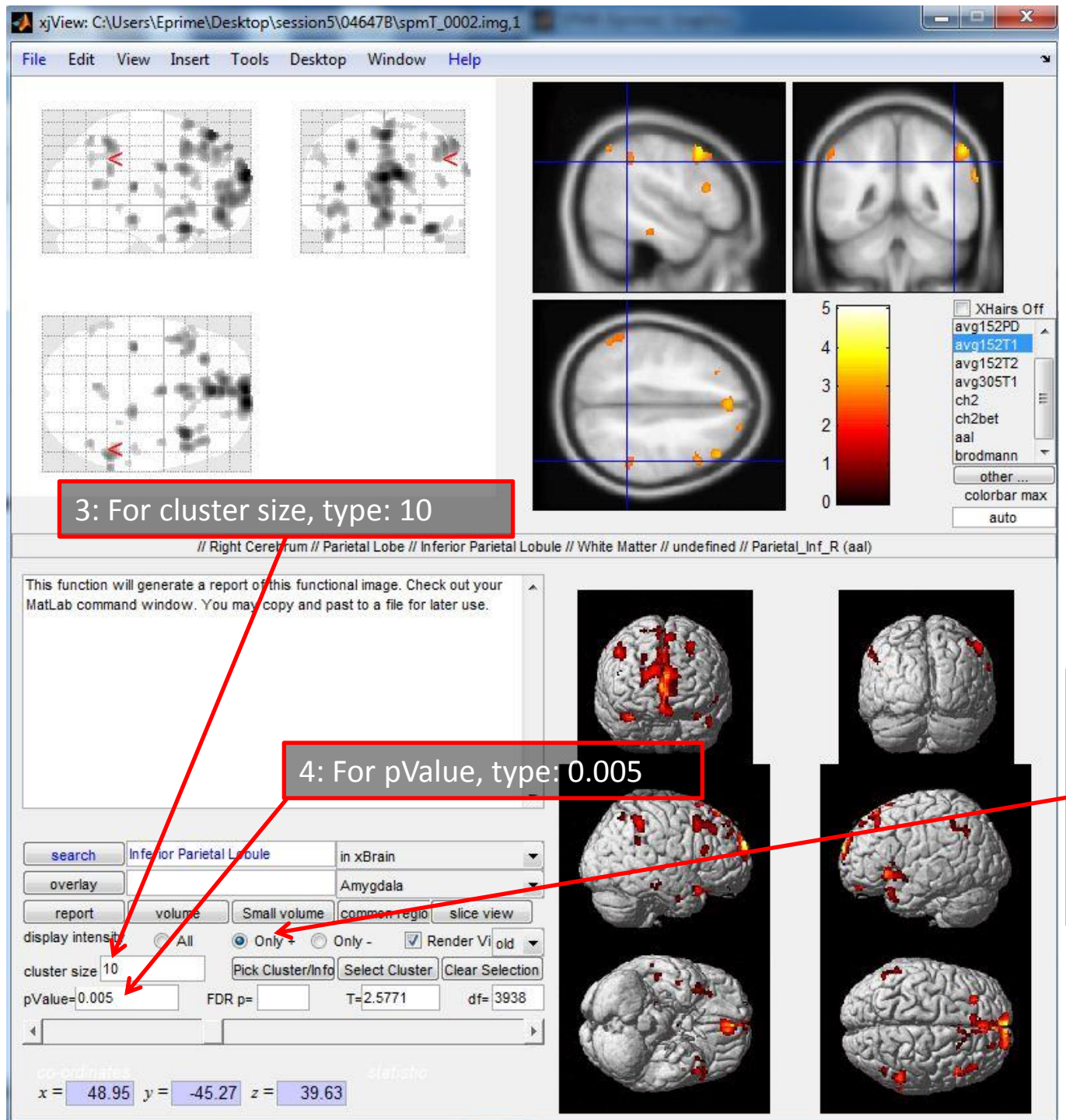


NOTE: The window will not maximize on these computers

NOTE: Wherever you click in the brain (in one of the three slice views), the MNI coordinates will adjust themselves accordingly. You can also manually enter coordinates into these fields and your cursor will go to that point (although the coordinates may change slightly, but that's okay – don't worry about it)

NOTE: The AAL brain region name will appear in this circled area whenever your cursor is within the grey matter of the brain. Sometimes the AAL name won't appear; it means that that point isn't defined there, and your cursor is probably in white matter or on/outside the skull

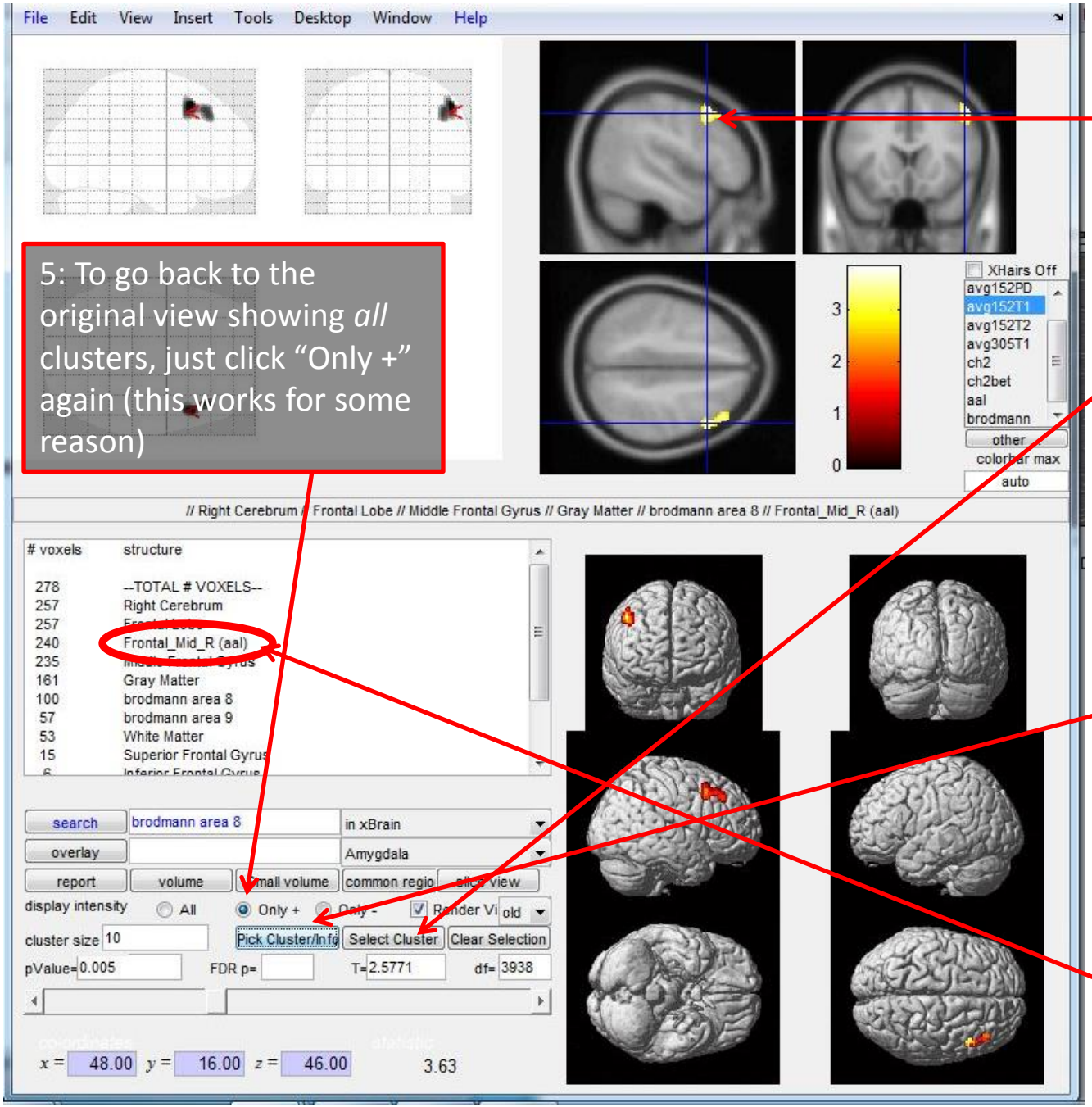
2: Next slide…



3: For cluster size, type: 10

4: For pValue, type: 0.005

5: Select: Only +
(We are viewing only positive brain activation here, or in other words, where activation is greater for Animals vs. the others)



1: To show a single cluster and display its anatomical information, first click within a desired cluster on the screen (doesn't have to be the one displayed here)

2: Click Select Cluster. It should say that there is one cluster selected in the white space to the left. (If you must de-select a cluster ever, click Clear Selection to the right)

3: Click Pick Cluster/Info. Now you should see # voxels per brain area in the white space to the left

4: That is all that you'll need to do to display this information. The assignment will ask you identify the AAL region with the most voxels. Here, it's Frontal_Mid_R

5: To go back to the original view showing *all* clusters, just click "Only +" again (this works for some reason)

- We created the *Animals vs. others* contrast as practice. You will create other contrasts for the assignment. This is all the guidance/information that you should need to do the assignment

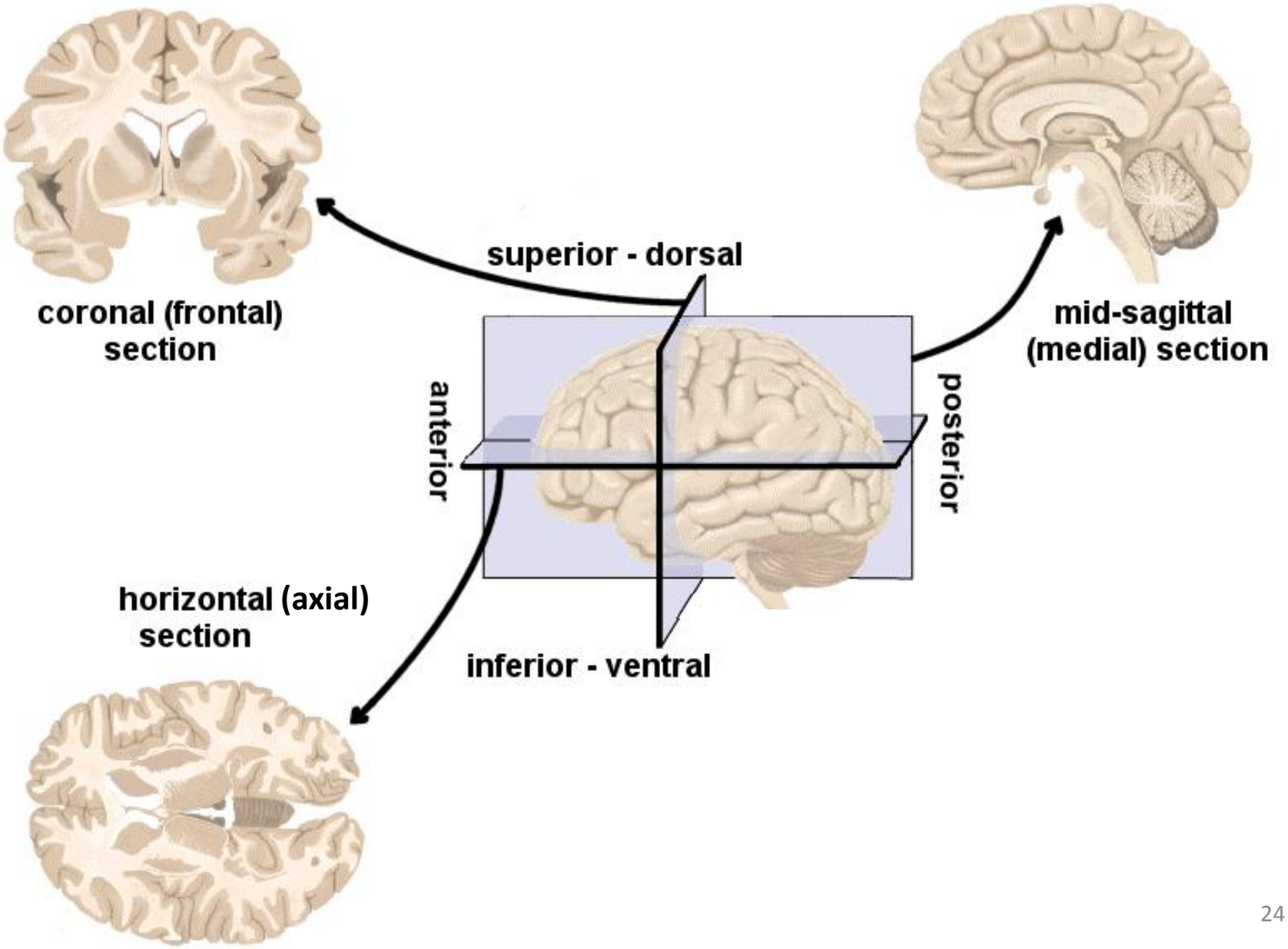
- See the slides below for help with orientation terms, planes, and brain anatomy and functions

- You are free to download the xjview manual off Blackboard for further help

- If something goes wrong with spm or xjview, just exit the program and restart it from Matlab as usual. You don't have to exit out of Matlab to restart spm or xjview

- If you must restart Matlab for whatever reason, after you start Matlab up be sure to set both paths again and cd back to the "session5" directory

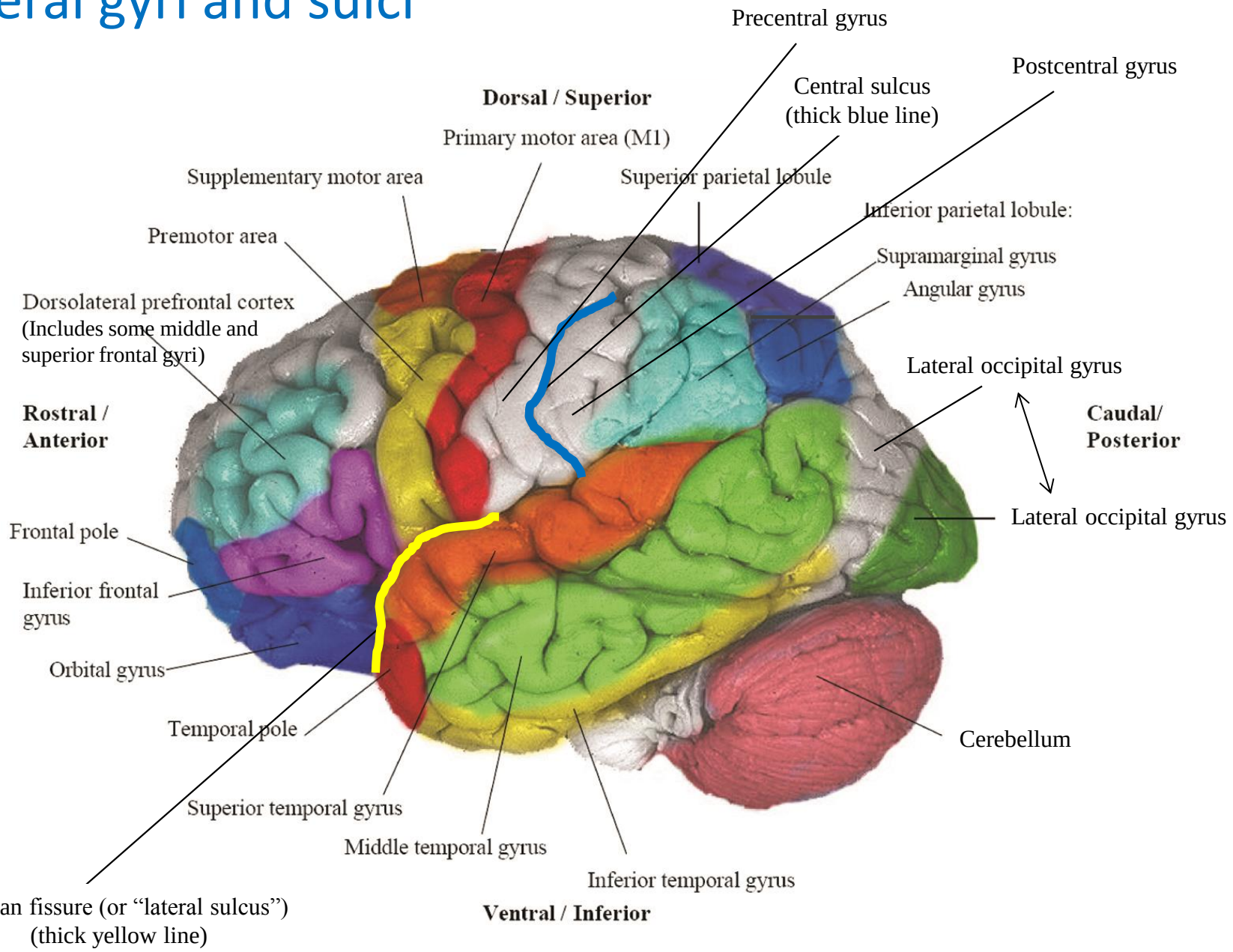
Orientation terms and planes



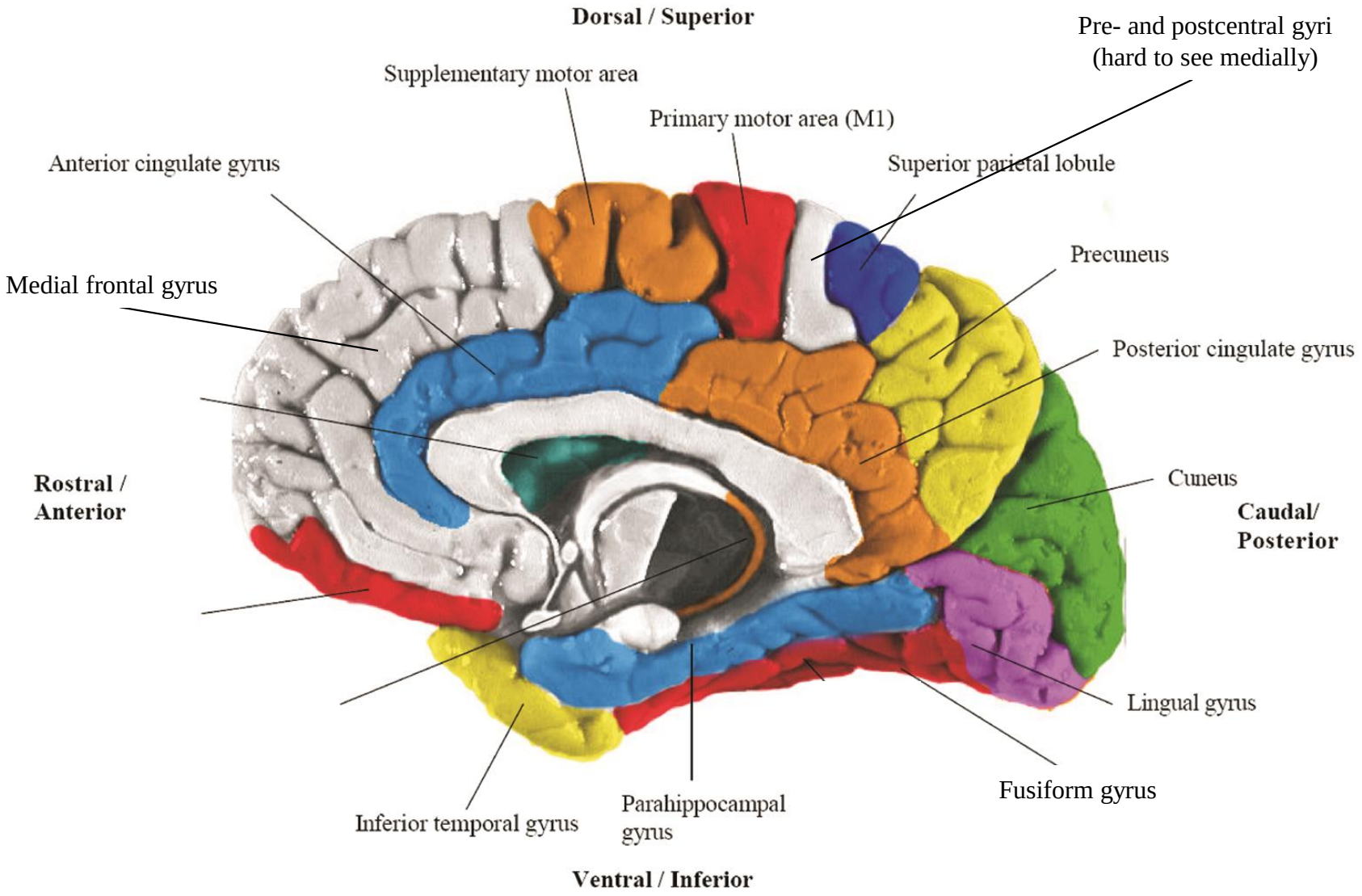
We are using the Automated Anatomical Labeling (AAL) atlas in this lab (very similar to the atlases of your two quizzes)

Images: http://www.frontiersin.org/Journal/10.3389/fnhum.2013.00845/full

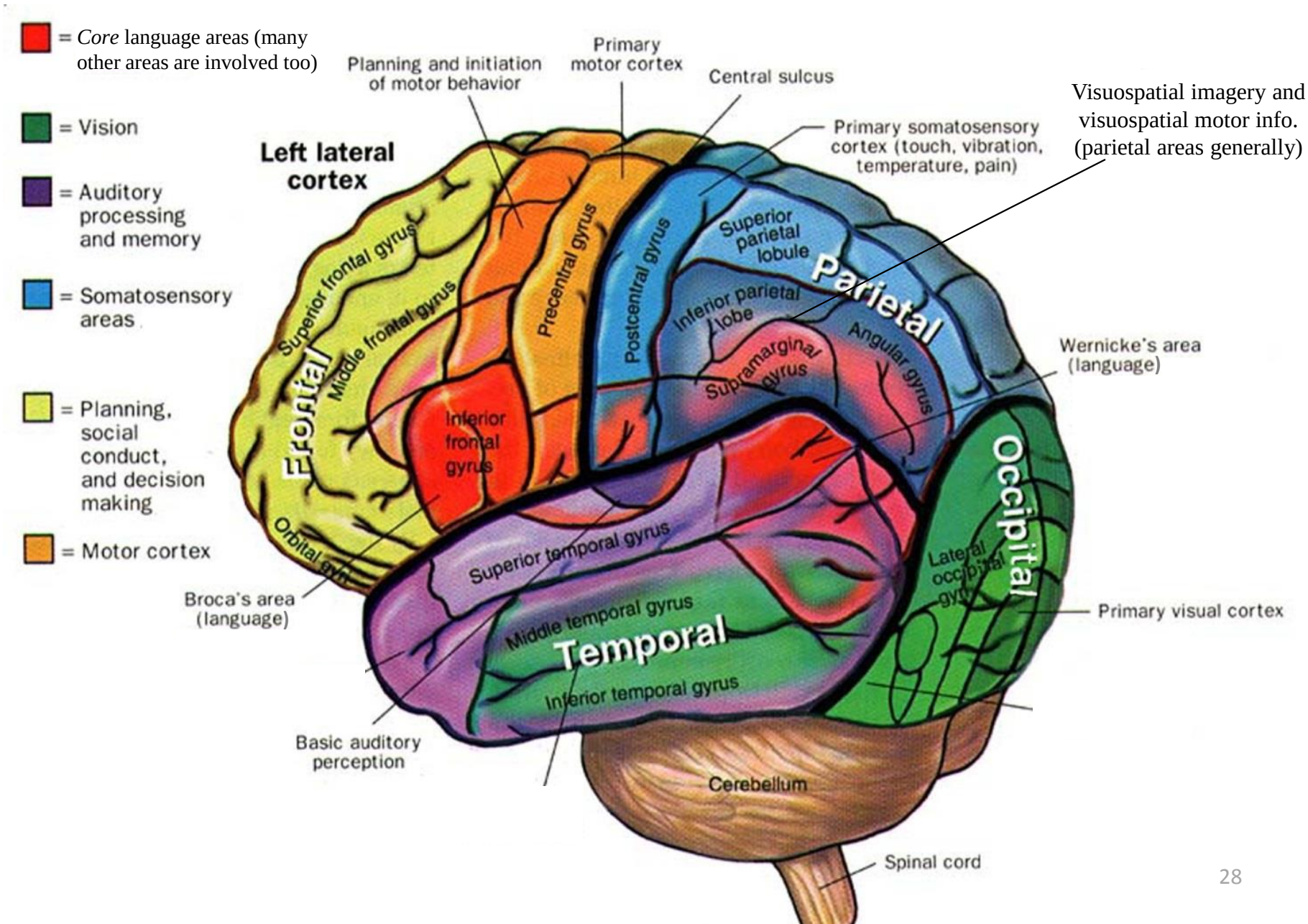
Lateral gyri and sulci



Medial gyri (some redundancy w/previous slide)



General functional neuroanatomy



References

Ferstl, E. C., Neumann, J., Bogler, C., & von Cramon, D. Y. (2008). The extended language network: a meta-analysis of neuroimaging studies on text comprehension. Human Brain Mapping, 29(5), 581–93. doi:10.1002/hbm.20422

Just, M. A., Cherkassky, V. L., Aryal, S., & Mitchell, T. M. (2010). A neurosemantic theory of concrete noun representation based on the underlying brain codes. PLoS One, 5(1), e8622. doi:10.1371/journal.pone.0008622

Patterson, K., Nestor, P. J., & Rogers, T. T. (2007). Where do you know what you know? The representation of semantic knowledge in the human brain. Nature Reviews. Neuroscience, 8(12), 976–87. doi:10.1038/nrn2277