Lab session 8: Group-level SPM contrasts

Andrew Bauer

03/16/16

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 estimate GLM model → **3** Generate condition contrasts (e.g. Tools – Buildings)

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

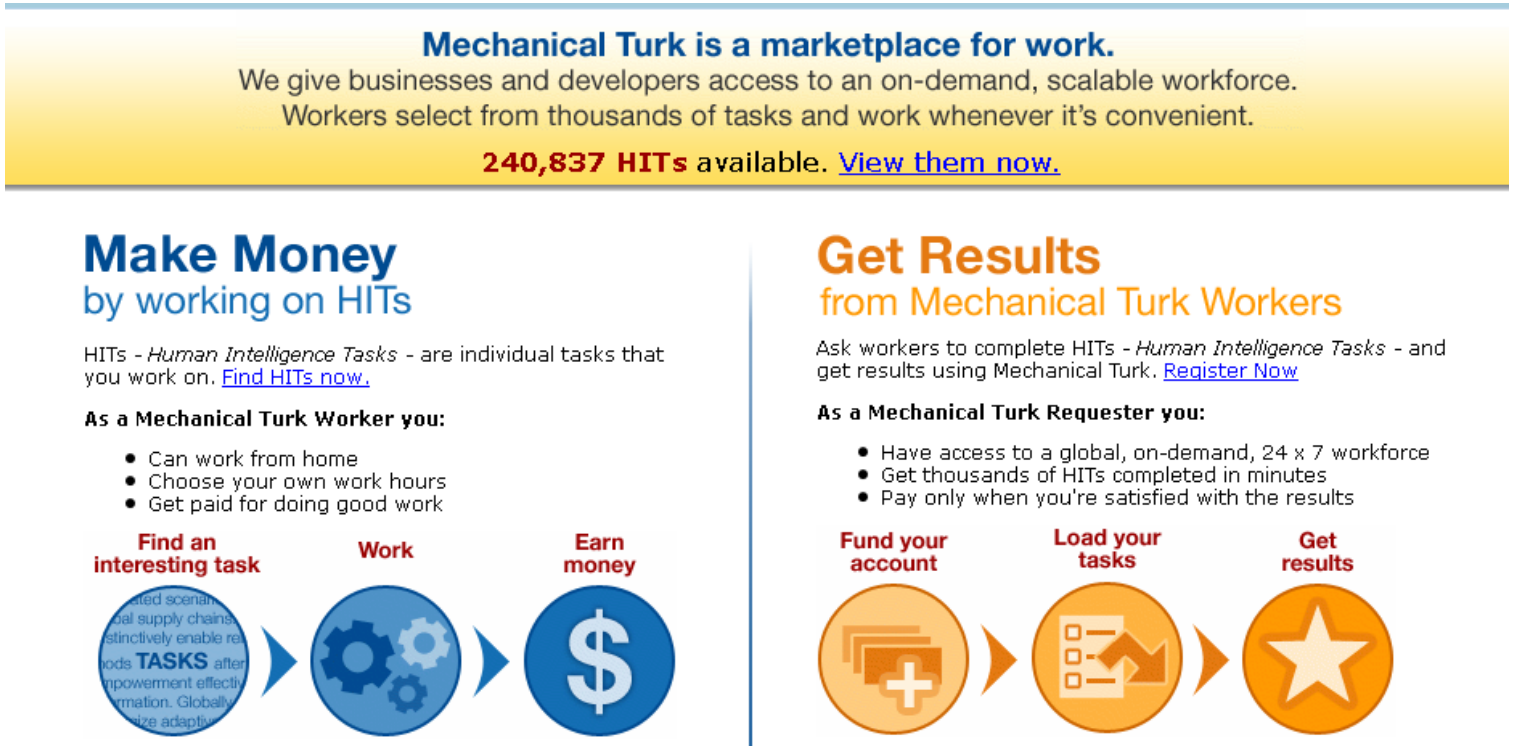
If there are multiple groups of subjects ***(in our case, no)***: → **5** Condition contrasts between two groups (e.g. Depressed – Control)

Why analyze a group of subjects?

- The goal of a psychological research study is to evaluate a falsifiable hypothesis about a *population* (whose members vary in many respects)
  - A study is conducted on a *sample* of some population…
  - … and a conclusion about that population is made by generalizing from the sample
  - The sample should be as representative of the population as possible

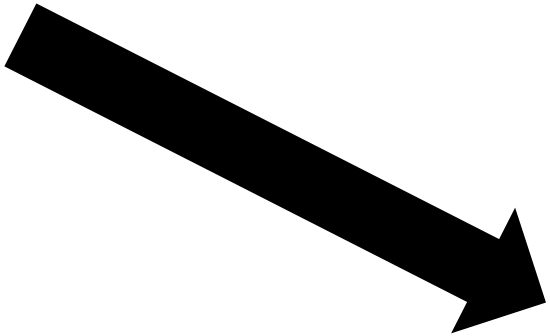
Getting a representative sample

- Can recruit subjects from different parts of the world using Amazon Mechanical Turk
  - Reference to late 18th century fake chess-playing machine (a person hid within the machine and did all the playing)



How will we go about analyzing data on the group level?

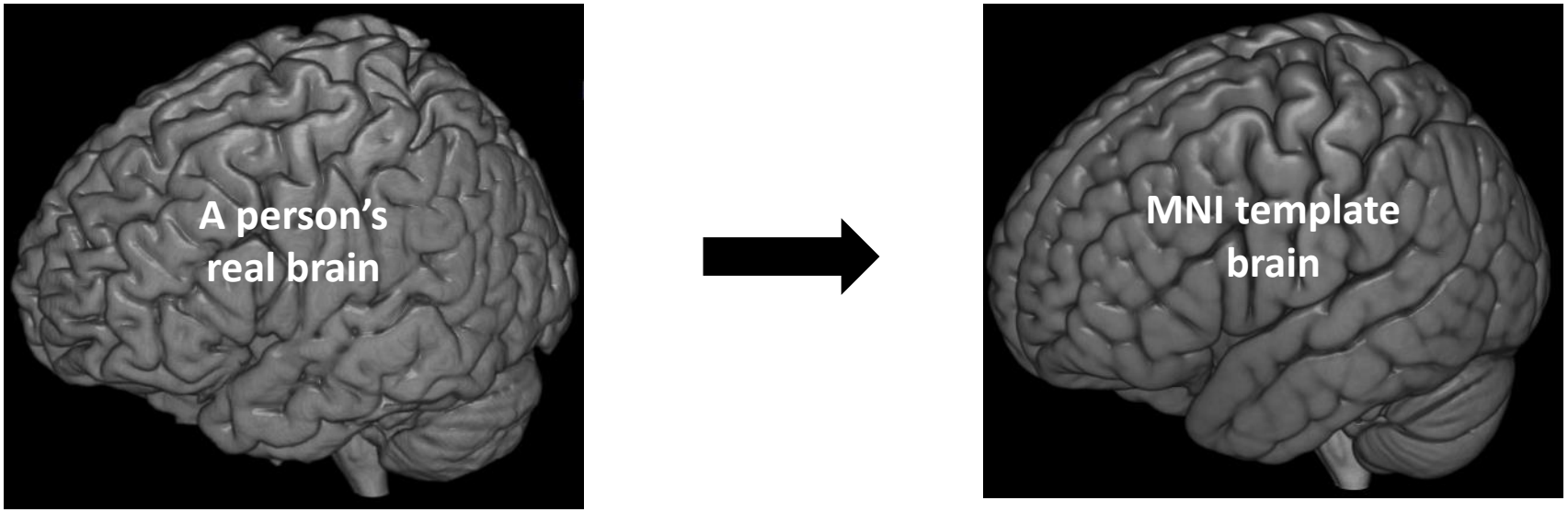
(1) Determine how to *prepare* subjects' data that allows for group-level analysis



(2) Determine how to *treat* each subject's prepared data in the analysis

How to account for neuroanatomical differences between subjects? **Use spatial normalization**

- Morphs an individual's brain to a common template
  - We are using the Montreal Neurological Institute (MNI) template, which is the average of 152 brains
- Examine activation in the *same voxels* across subjects



Instead of spatial normalization, one could also identify the same brain regions in each subject using "functional localizers"

- Use a localizer scan to identify a brain region of interest in each subject (e.g. show pictures of faces to find each subject's "face area"); the regions will be slightly different across subjects

- Then, extract activation data for different trials/conditions from this region in each subject

- *Advantage:* An individual's data are left intact; no warping of the data into a template brain, which could introduce errors and noise

- *Disadvantages:* May be difficult to ensure that the localizer reveals valid brain areas ("is this *really* the face area for subject X?"); also, you don't get nice voxel-level spatial resolution for comparing across subjects (as in spatial norm.)

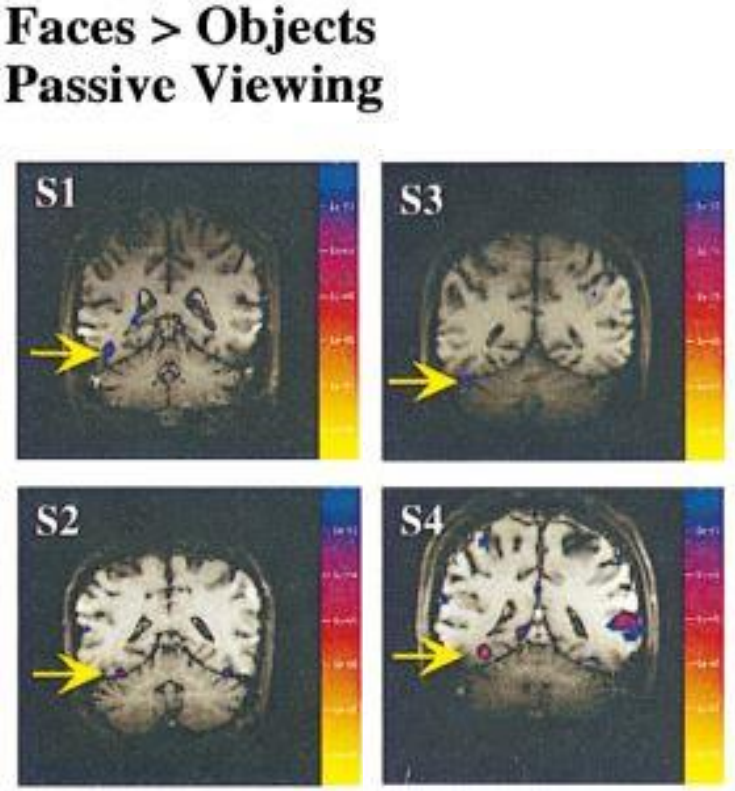
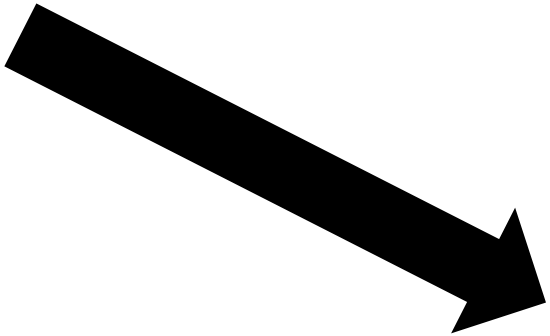


Image from Wojciulik, Kanwisher, & Driver (1998)

How will we go about analyzing data on the group level?

(1) Determine how to *prepare* subjects' data that allows for group-level analysis



(2) Determine how to *treat* each subject's prepared data in the analysis

Fixed-effects analysis (X now discouraged)

Subjects' fMRI time courses

Averaged (combined) time courses

Statistical map (from averaged time courses) (e.g. *Tools - Buildings*)

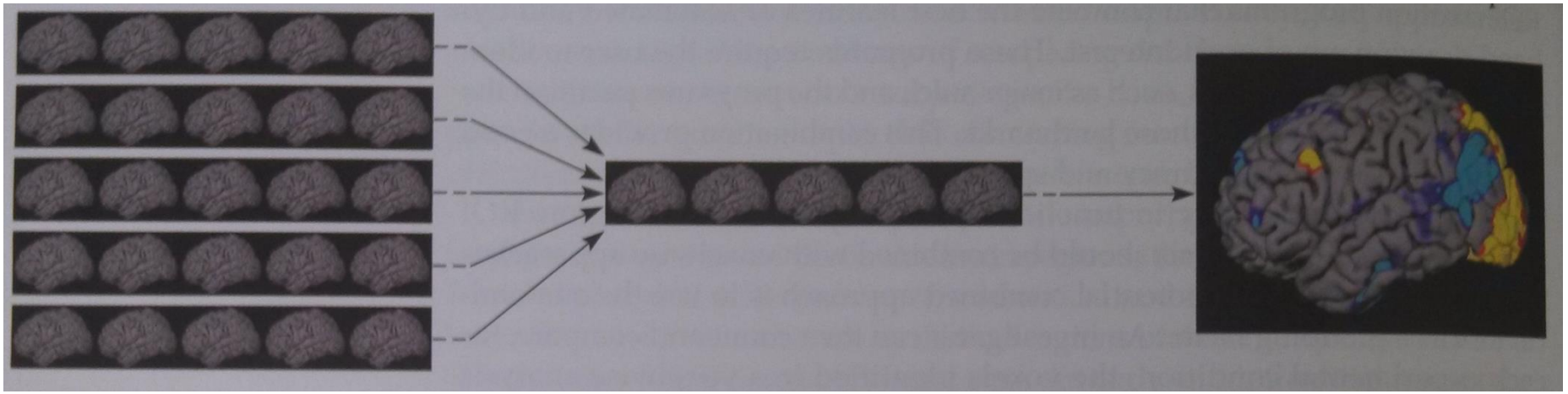


Image from Huettel, Song, & McCarthy: Functional Magnetic Resonance Imaging, 2nd ed.

- Averages subjects' data, giving equal weight to each subject; assumes that any effect is the same ("fixed") for each subject, apart from some noise
- By averaging, this analysis does **NOT** account for the *variation* of the effect across subjects, which is a defining element of a *population*
  - Thus, this analysis is heavily influenced by unrepresentative outlier subjects

Random-effects analysis (✔standard practice)

Subjects' fMRI time courses

Subjects' statistical maps (e.g. *Tools* - *Buildings*)

Combined (i.e. group-level) statistical map (e.g. *Tools* - *Buildings*)

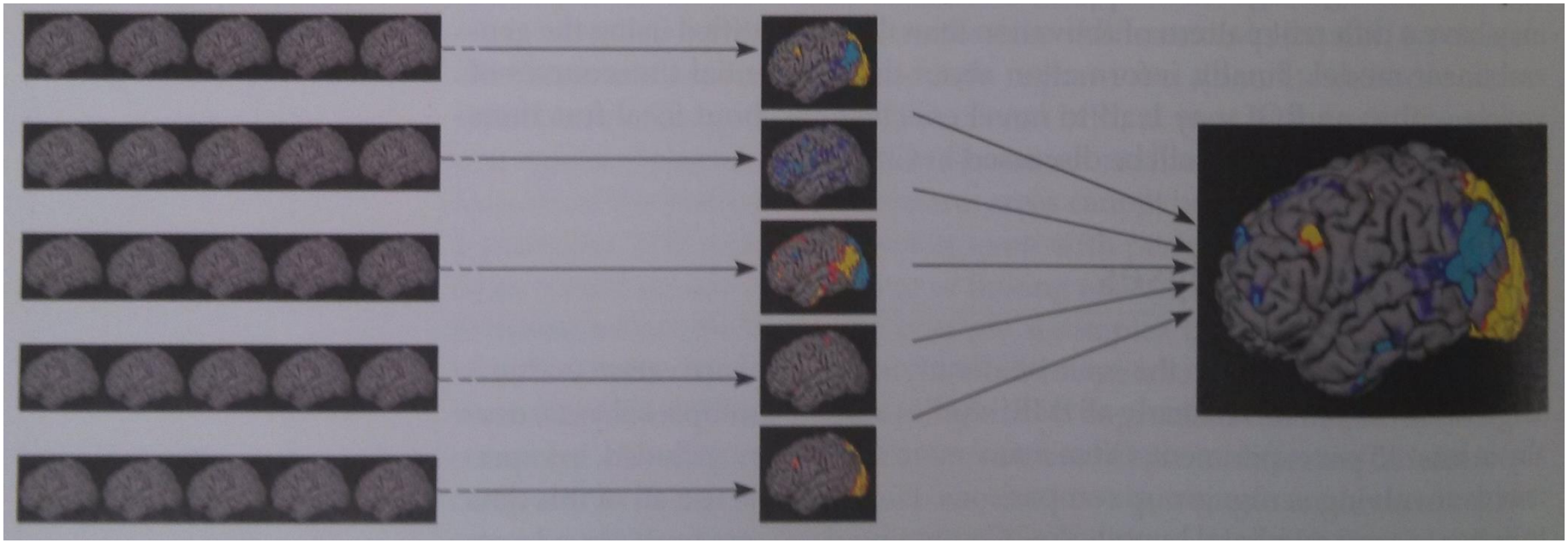
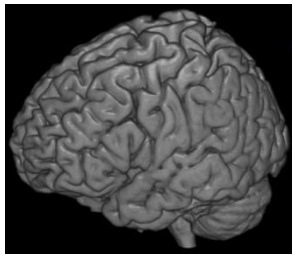


Image from Huettel, Song, & McCarthy: Functional Magnetic Resonance Imaging, 2nd ed.

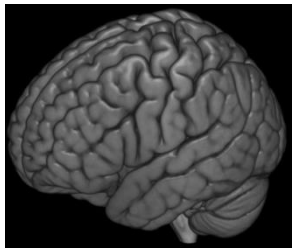
- Does **NOT** average subjects' data; treats pooled subjects as a *distribution*
- **DOES** account for the variation of the effect across subjects
  - This analysis recognizes outliers in the distribution and is less influenced by them

How we will analyze group-level data in the lab

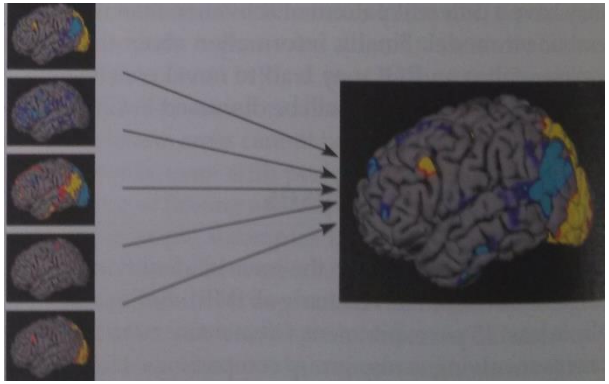
(1)



Normalization

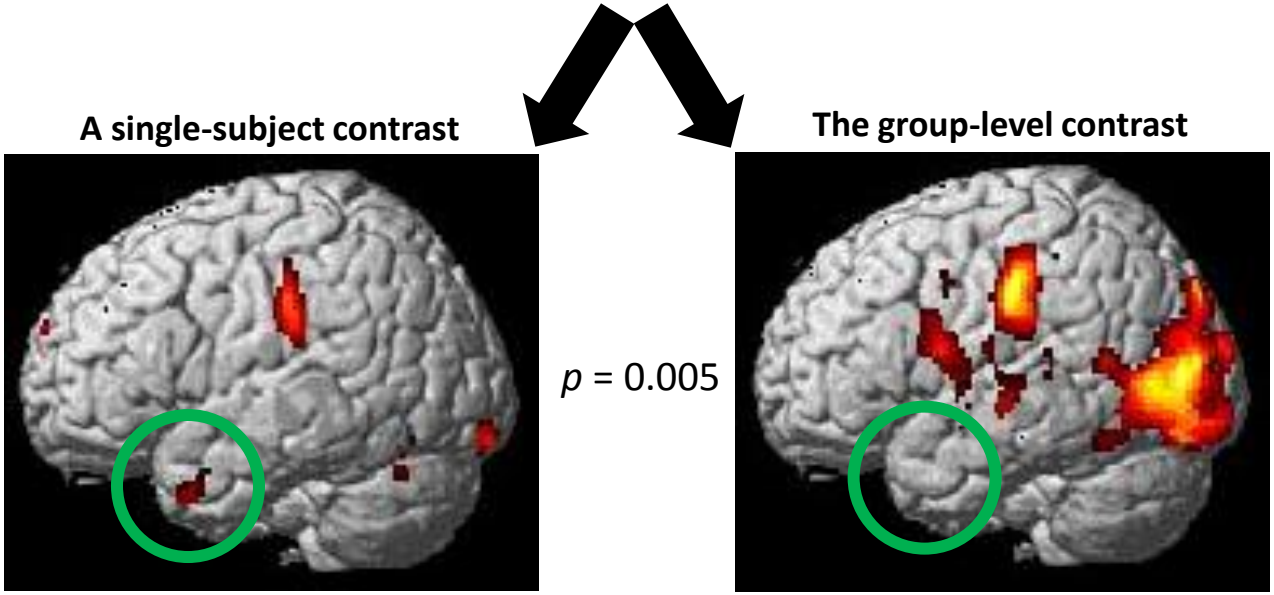


(2) *Random-effects analysis* in each voxel (in MNI space)



What are group-level results generally like?

- Stronger activation, which often means:
  - Greater number of statistically significant voxels (using the same *p*-value threshold when comparing a single-subject to a group-level contrast)



- Also, group-level results contain *common* clusters of activation
  - **Disappearance of clusters that correspond to only one or a couple subjects**
  - The less common a cluster, the less likely it will be statistically significant in the group-level analysis

Multiple comparisons problem
(Applies to *both* single-subject and group-level analysis)

- Say we set $p = 0.05$ threshold for each voxel in a contrast
  - This means we are willing to tolerate a 5% chance that a voxel is statistically significant purely due to chance
  - If 200,000 voxels tested in an analysis, then there could be 200,000 * 0.05 = **10,000 falsely significant voxels**

- Ways to combat this problem:
  - Lower the *p*-value threshold to make a statistically significant voxel less likely due to chance
  - Set a cluster size threshold (e.g. 10, 20, 30 voxels)
    - A big cluster of significant voxels is less likely to be due to chance

Now follow the slides below to generate a group-level contrast as practice for the assignment…

Animals vs. other object categories
(group level, *N* = 10 subjects)

You already have the *t*-test image of each contrast (an object category vs. average of all others) for each of 10 subjects

(Refer to this slide for the assignment)

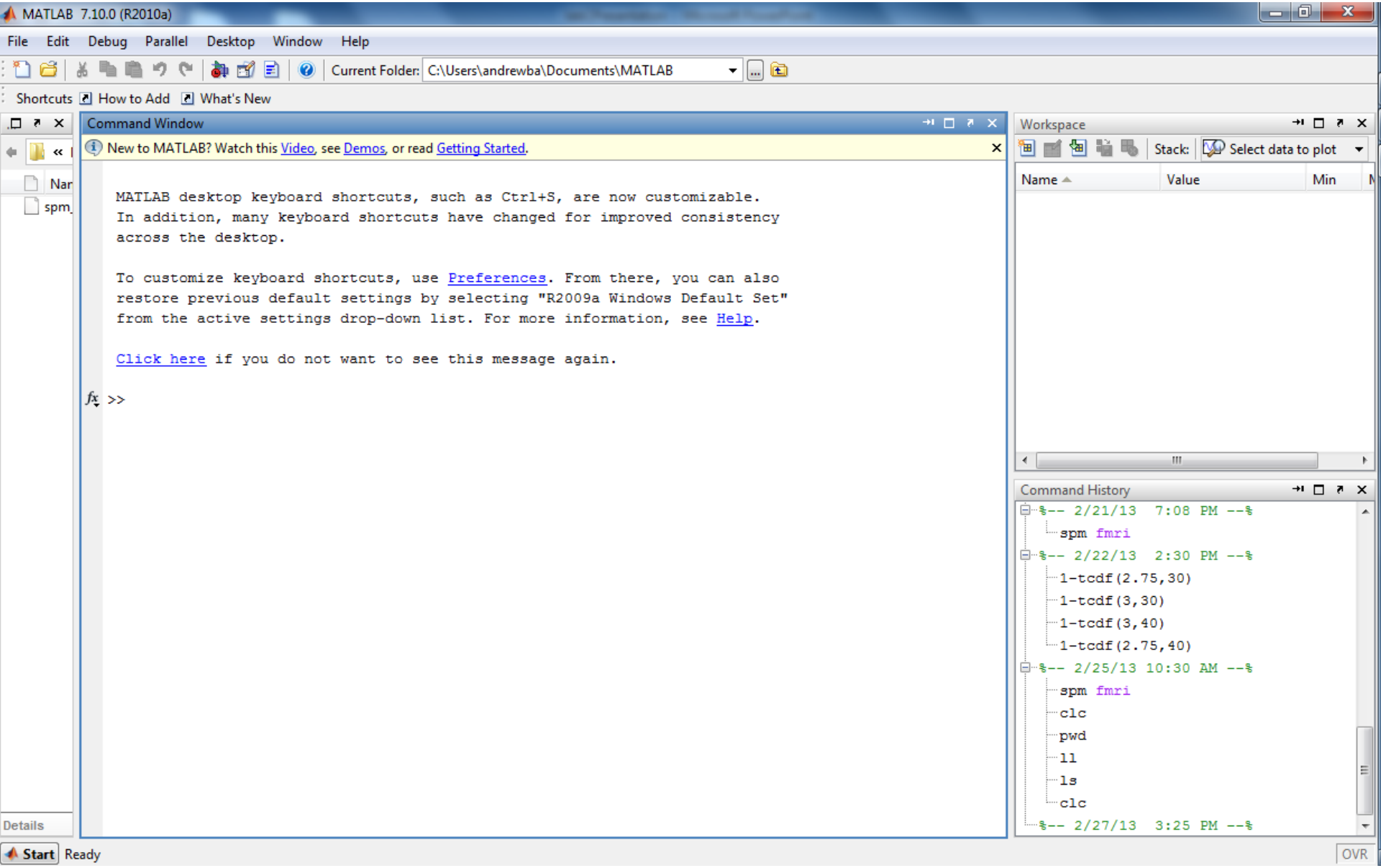
The numbered folders in the session8 folder

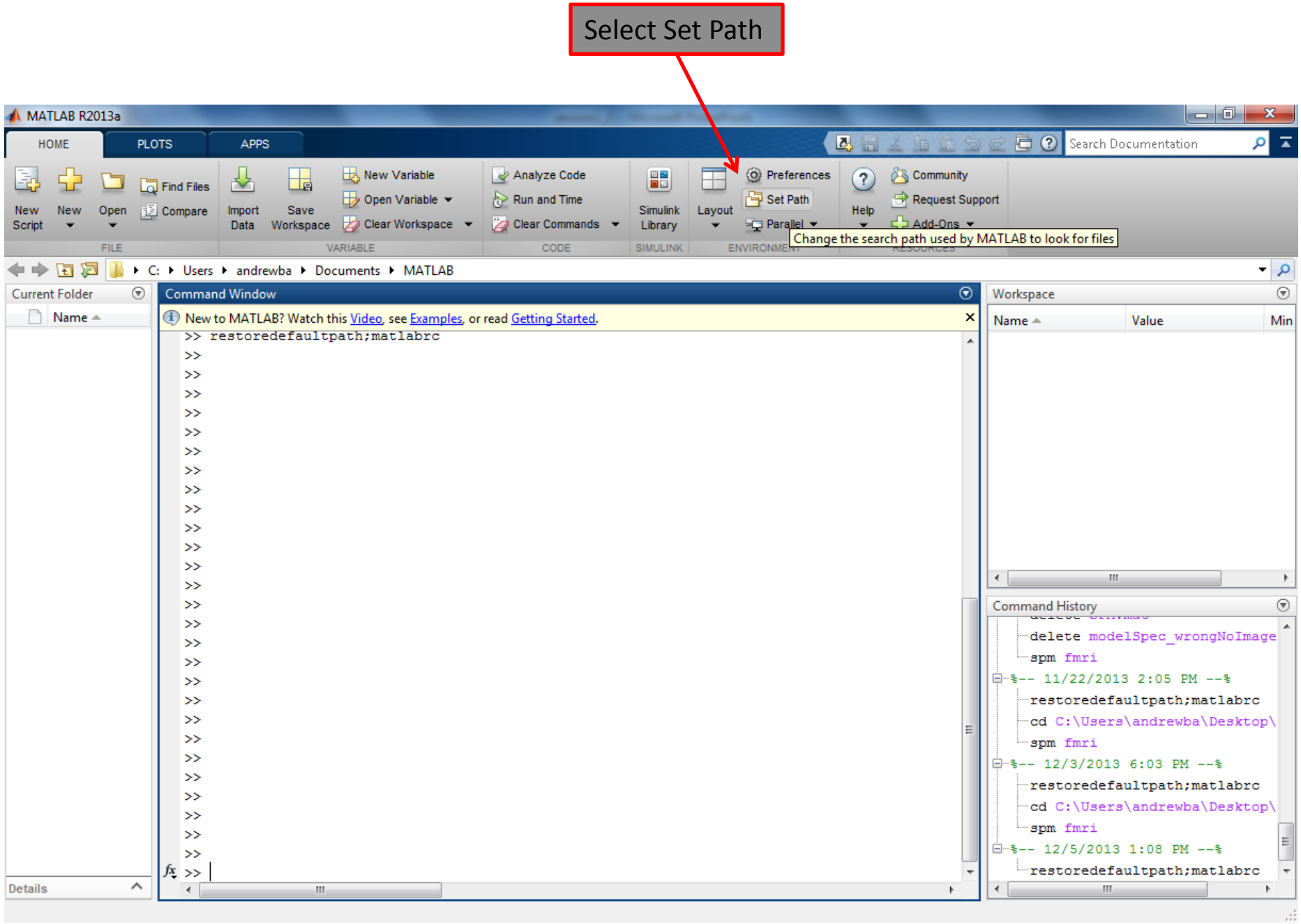
For example, one folder is: animal_0013

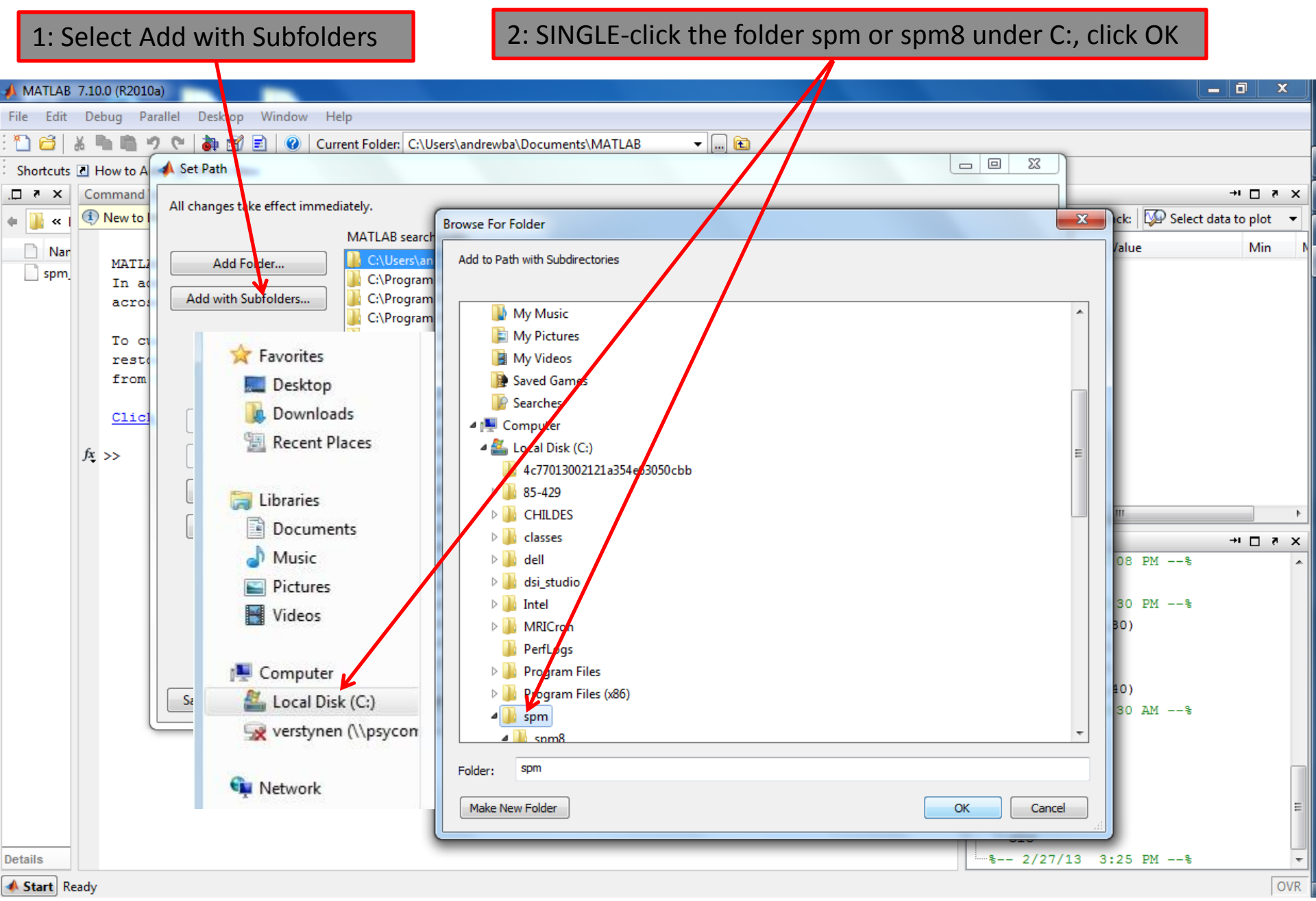
Folder no.	Contrast name	Baseline	1	2	3	4	5	6	7	8	9	10	11	12	Constant
13	Animals_vs_others	[0	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
14	Bodyparts_vs_others	[0	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
15	Buildings_vs_others	[0	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	-1	0]
16	Buildingparts_vs_others	[0	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	-1	0]
17	Clothing_vs_others	[0	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	-1	0]
18	Furniture_vs_others	[0	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	-1	0]
19	Insects_vs_others	[0	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	-1	0]
20	Kitchen_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	-1	0]
21	Manmade_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	-1	0]
22	Tools_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	-1	0]
23	Vegetables_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	-1	0]
24	Vehicles_vs_others	[0	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	11	0]

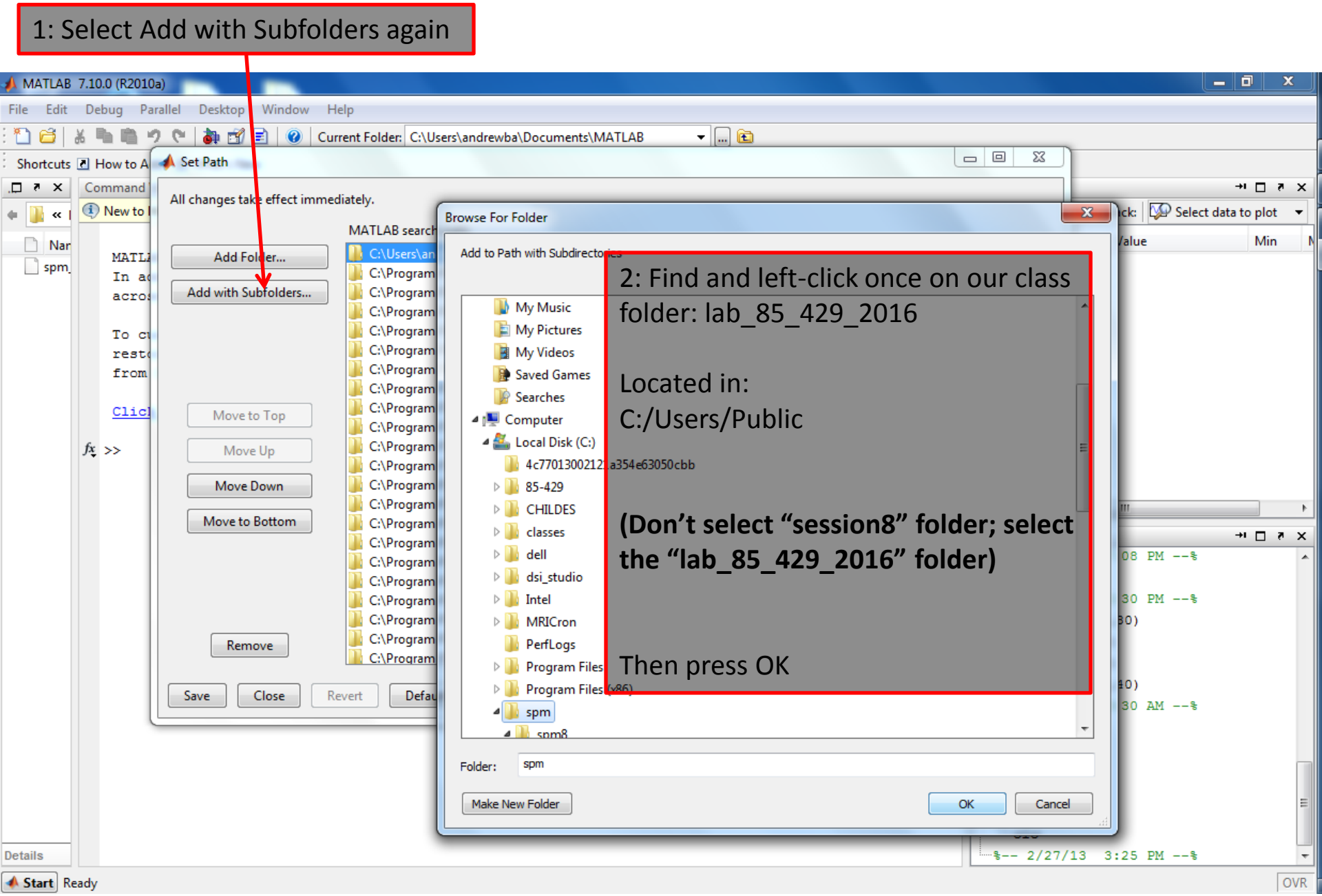
Start Matlab 2012b (on desktop, or type “matlab” in Start menu to find it)

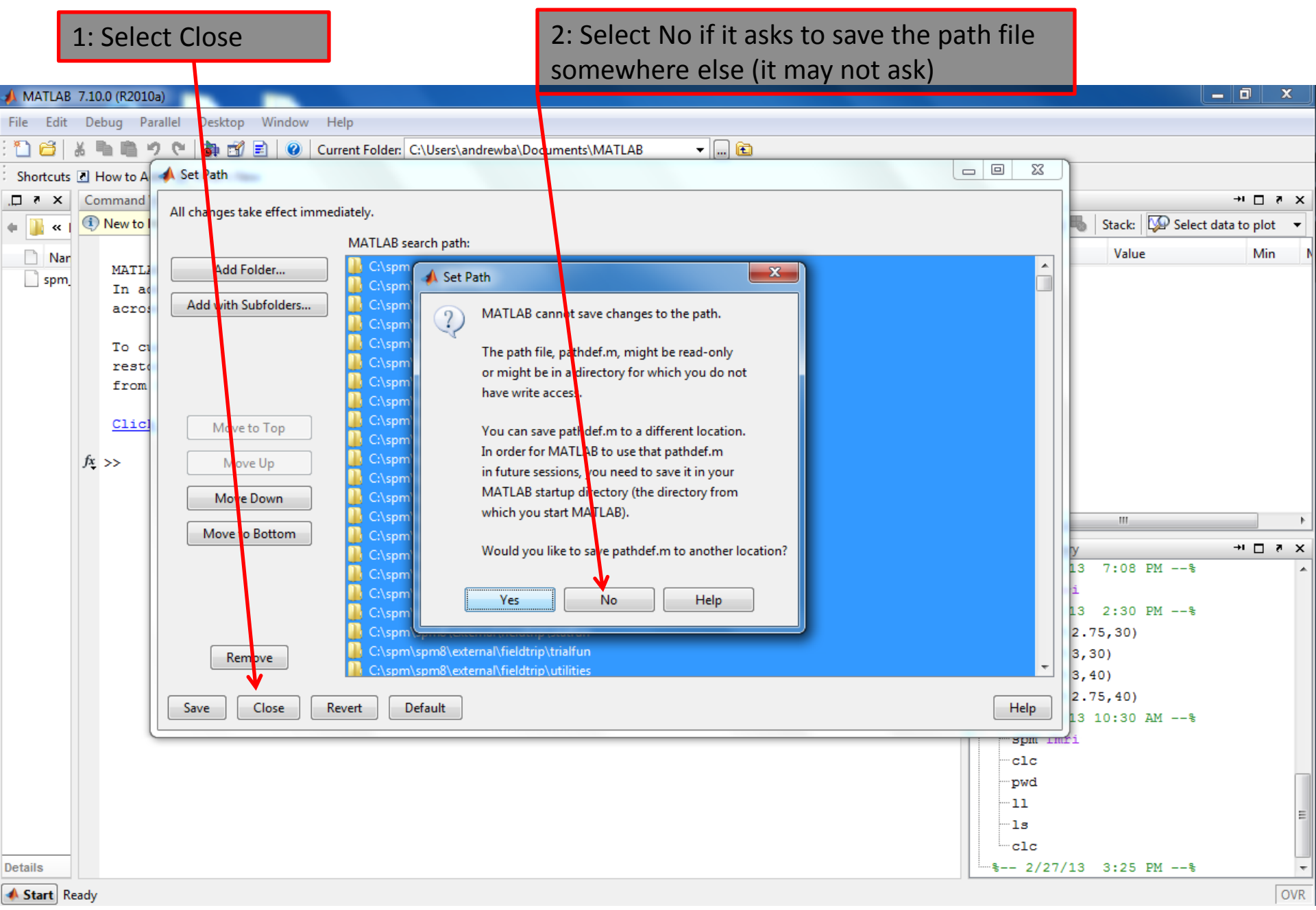
NOTE: You MUST select Matlab 2012b, do NOT select 2014b




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
Change the search path used by MATLAB to look for files
FILE
VARIABLE
CODE
SIMULINK
ENVIRONMENT
RESOURCES
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:)
4c77013002121a354e83050cbb
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 "session8" folder; select the "lab_85_429_2016" folder)
Then press OK
Start
Ready

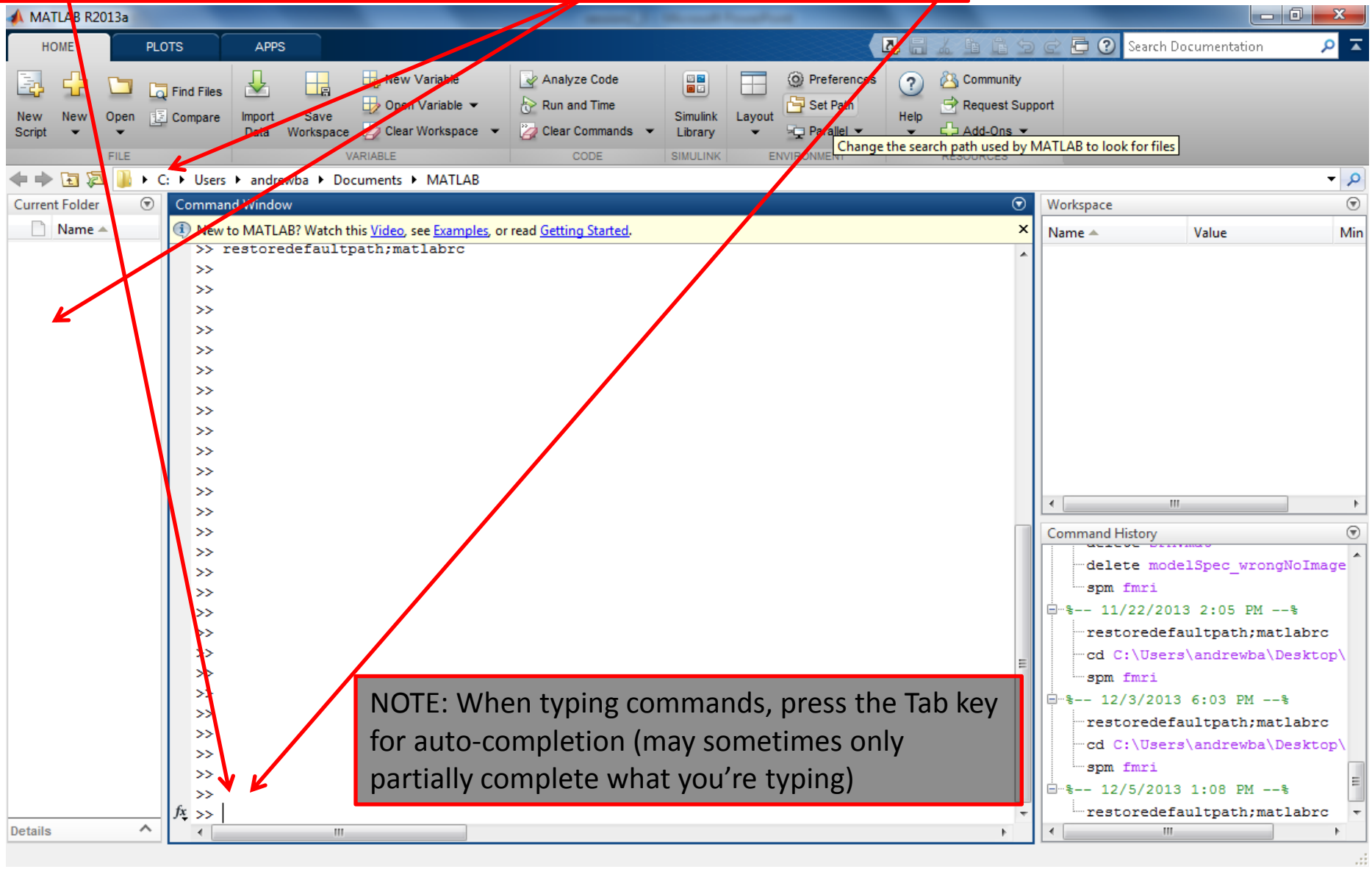

1: Select Close
2: Select No if it asks to save the path file somewhere else (it may not ask)
MATLAB 7.10.0 (R2010a)
File Edit Debug Parallel Desktop Window Help
Current Folder: C:\Users\andrewba\Documents\MATLAB
Set Path
All changes take effect immediately.
MATLAB search path:
Add Folder...
Add with 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:

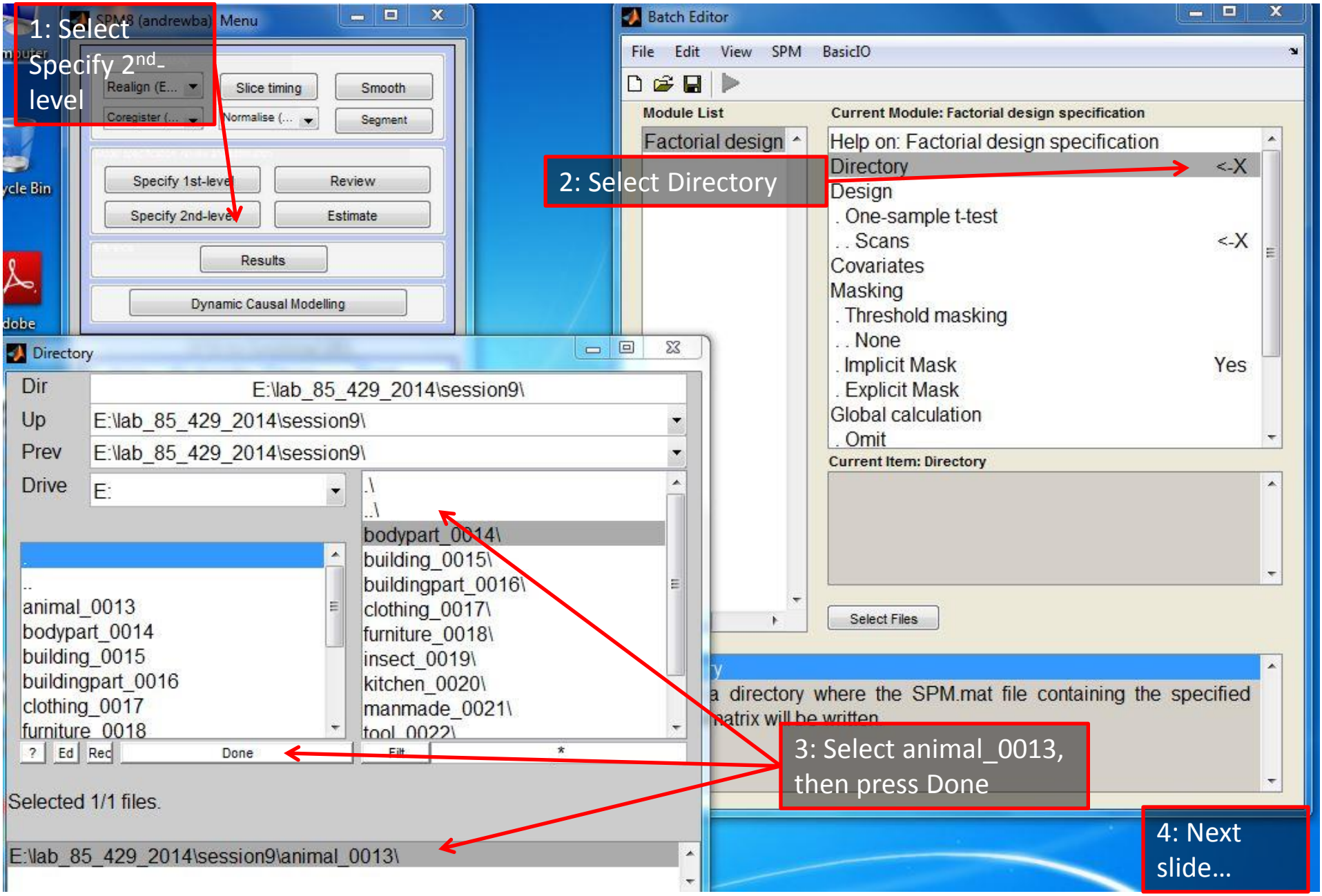
cd C:/Users/Public/lab_85_429_2016/session8

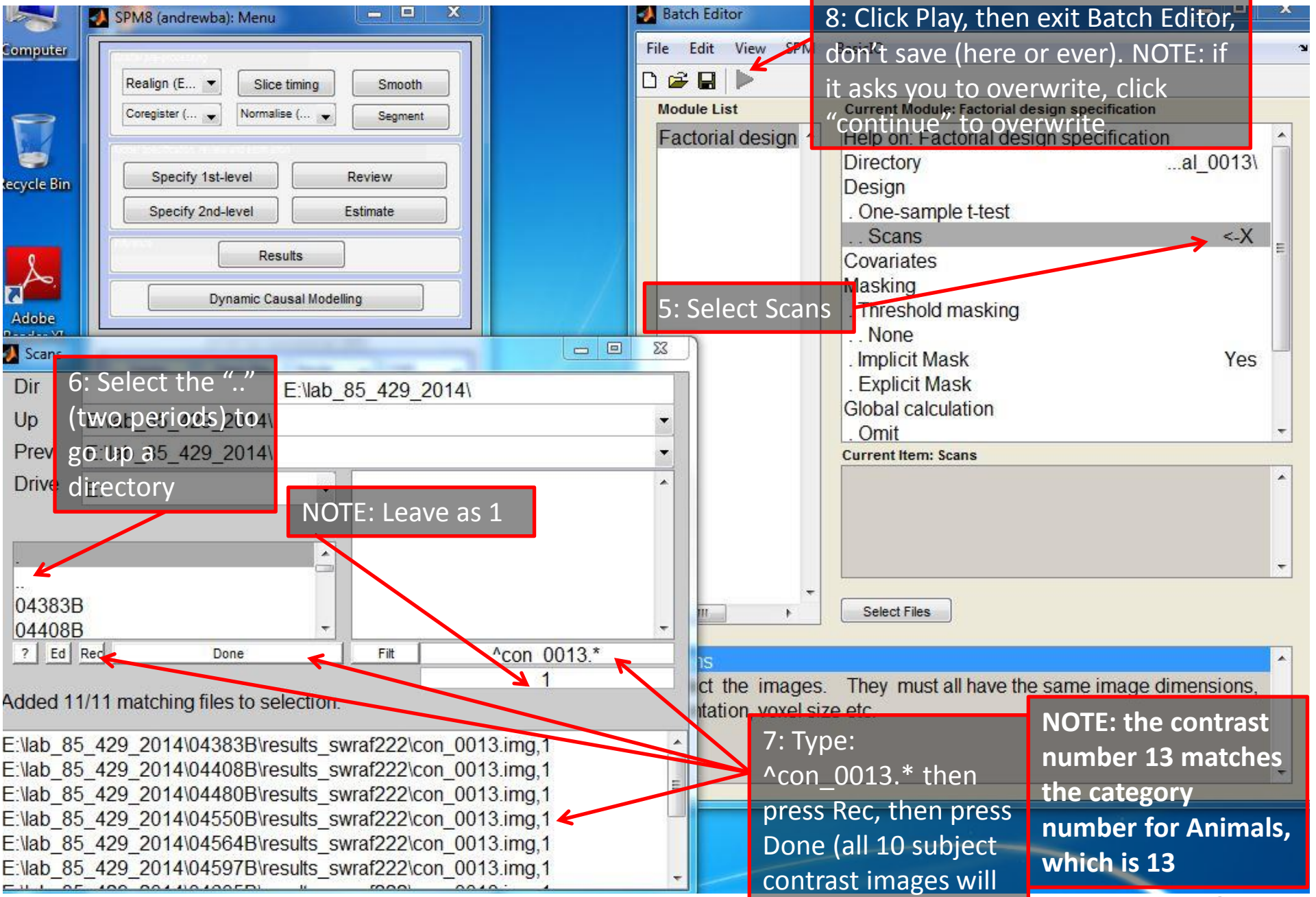
…(OR navigate there using the browser)

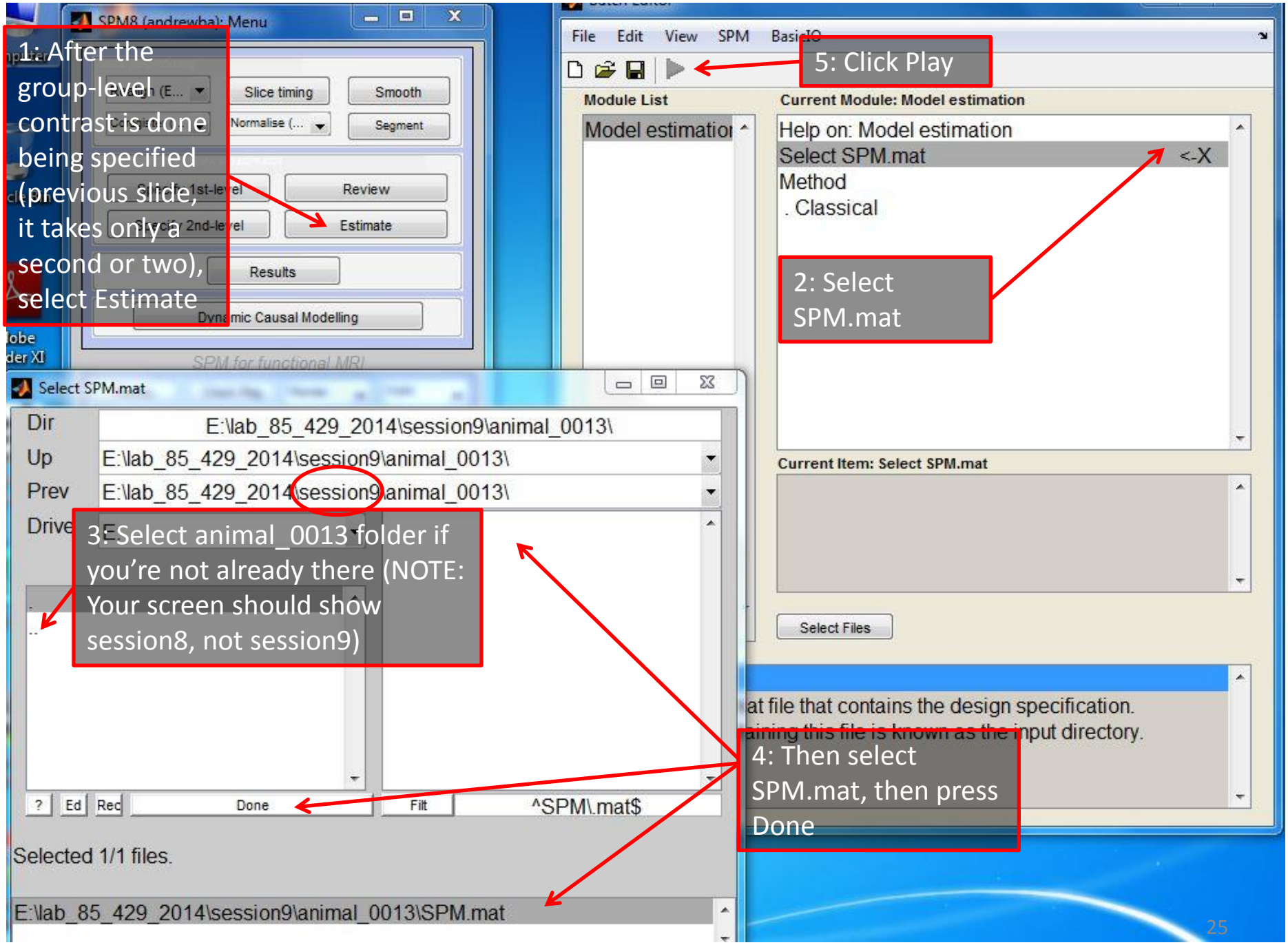
2: Then type: spm fmri

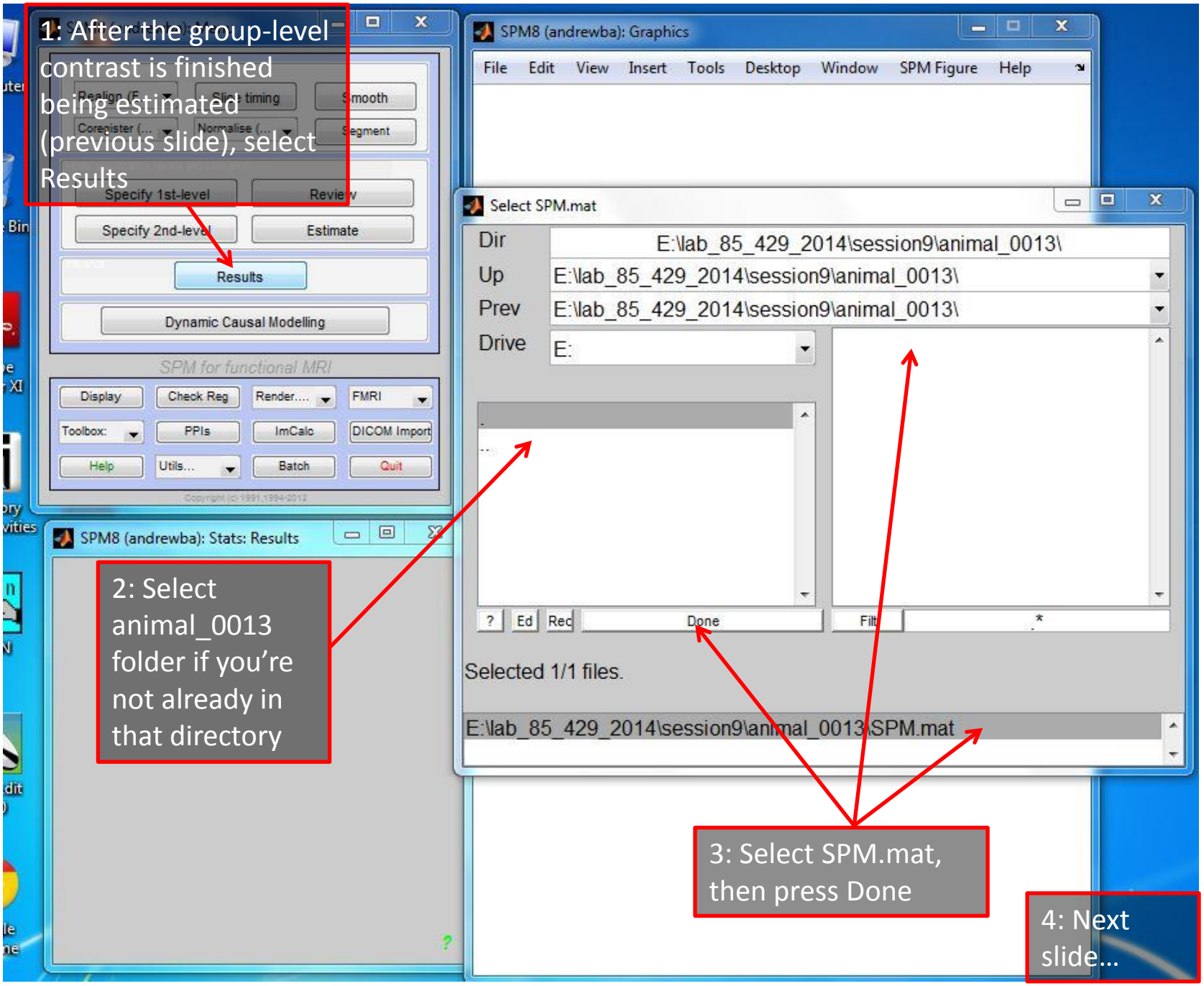


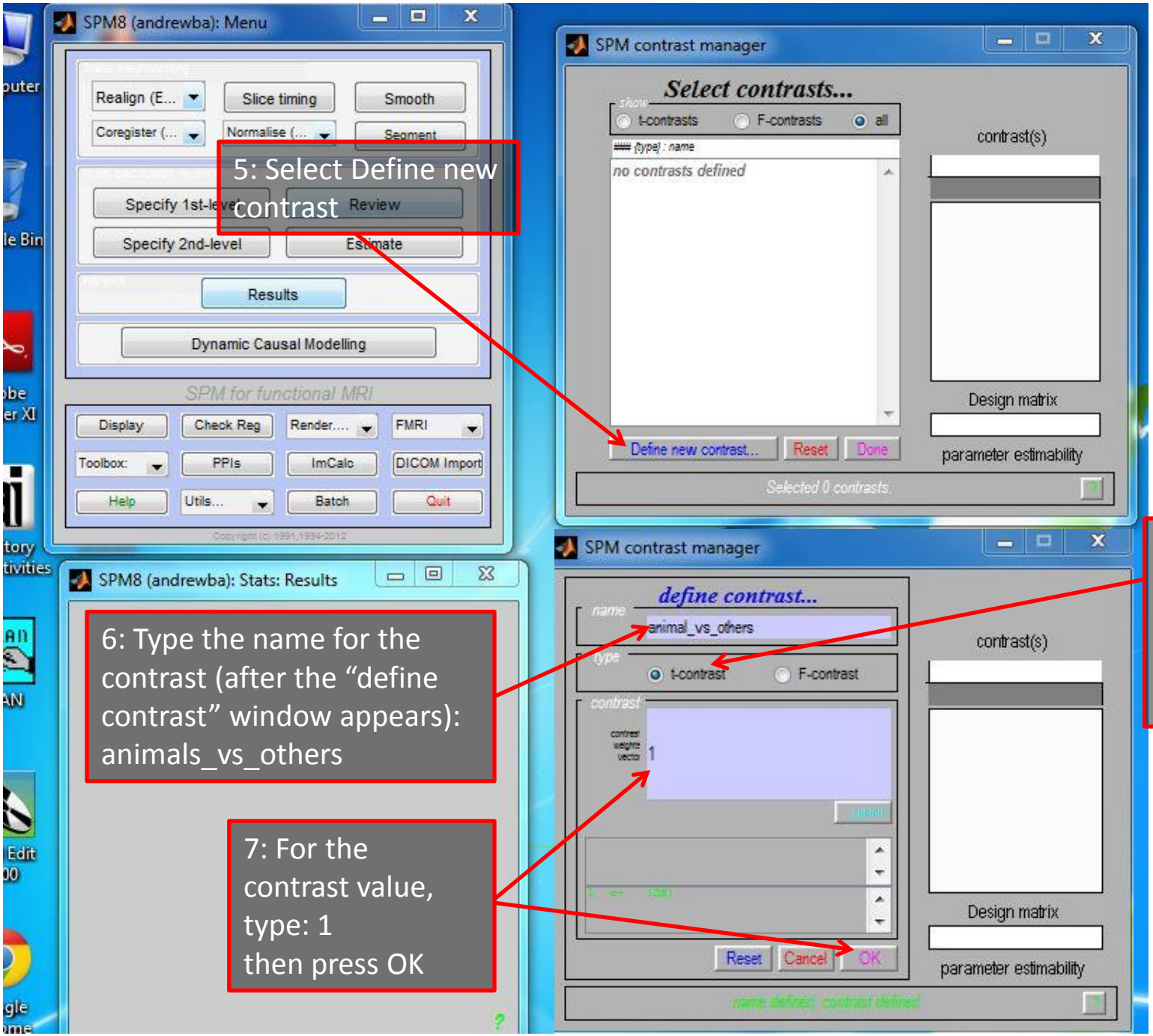
NOTE: When typing commands, press the Tab key for auto-completion (may sometimes only partially complete what you're typing)

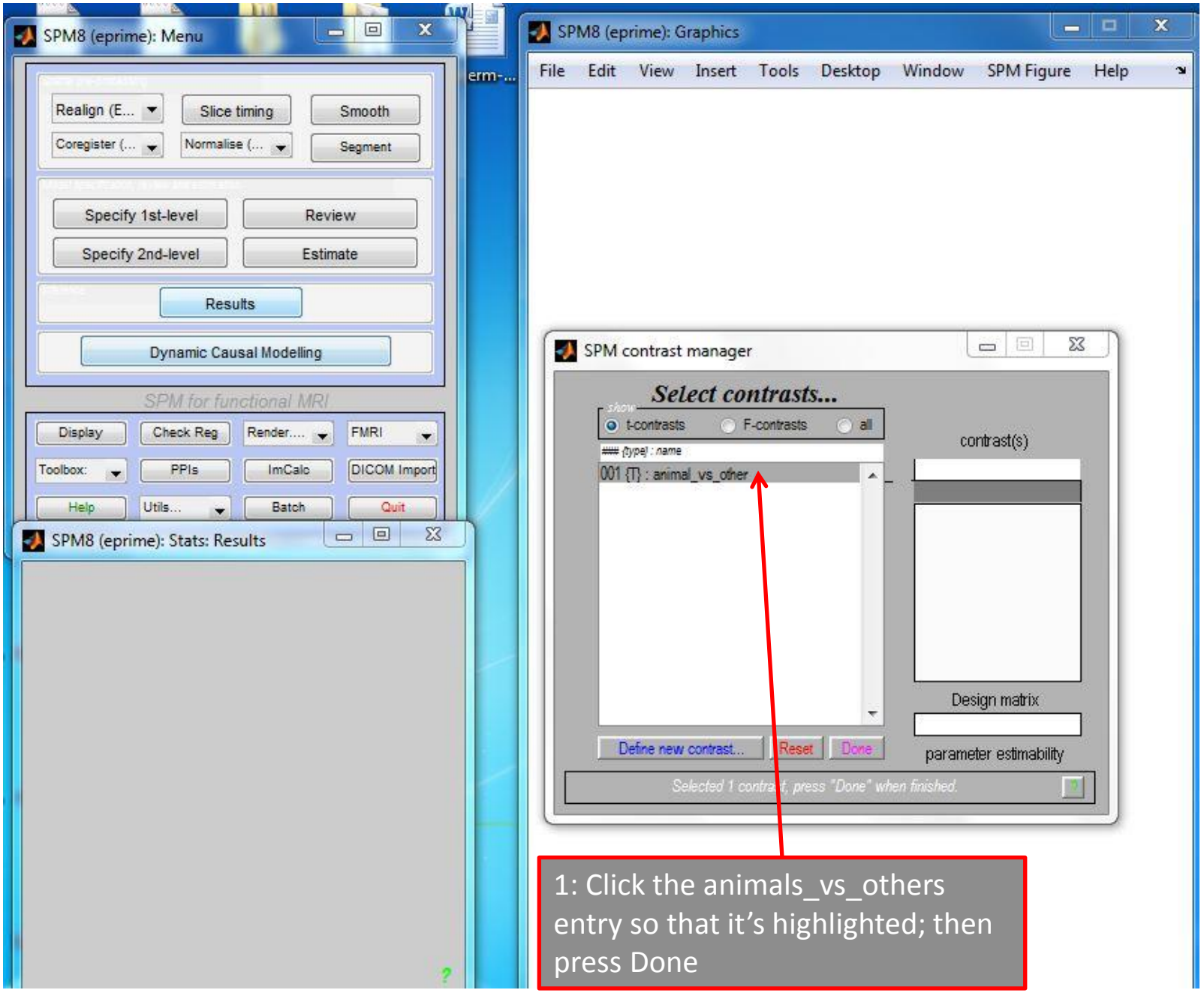

1: Select Specify 2nd-level
SPM8 (andrewba) Menu
Realign (E...
Slice timing
Smooth
Coregister (...
Normalise (...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
Batch Editor
File Edit View SPM BasicIO
Module List
Factorial design
Current Module: Factorial design specification
Help on: Factorial design specification
Directory <-X
Design
. One-sample t-test
. . Scans <-X
Covariates
Masking
. Threshold masking
. . None
. Implicit Mask Yes
. Explicit Mask
Global calculation
. Omit
2: Select Directory
Current Item: Directory
Select Files
a directory where the SPM.mat file containing the specified
Directory
Dir E:\lab_85_429_2014\session9\
Up E:\lab_85_429_2014\session9\
Prev E:\lab_85_429_2014\session9\
Drive E:
.\
..\
bodypart_0014\
building_0015\
buildingpart_0016\
clothing_0017\
furniture_0018\
insect_0019\
kitchen_0020\
manmade_0021\
tool_0022\
animal_0013
bodypart_0014
building_0015
buildingpart_0016
clothing_0017
furniture_0018
? Ed Rec Done Filt *
Selected 1/1 files.
E:\lab_85_429_2014\session9\animal_0013\
3: Select animal_0013, then press Done
4: Next slide…


SPM8 (andrewba): Menu
Realign (E...
Slice timing
Smooth
Coregister (...
Normalise (...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
Batch Editor
File Edit View
Module List
Factorial design
Current Module: Factorial design specification
Help on: Factorial design specification
Directory ...al_0013\
Design
. One-sample t-test
. . Scans <-X
Covariates
Masking
. Threshold masking
. . None
. Implicit Mask Yes
. Explicit Mask
Global calculation
. Omit
Current Item: Scans
Select Files
8: Click Play, then exit Batch Editor, don't save (here or ever). NOTE: if it asks you to overwrite, click "continue" to overwrite
5: Select Scans
6: Select the ".." (two periods) to go up a directory
NOTE: Leave as 1
Dir
Up
Prev
Drive
E:\lab_85_429_2014\
04383B
04408B
Done
Filt
^con_0013.*
1
Added 11/11 matching files to selection.
E:\lab_85_429_2014\04383B\results_swraf222\con_0013.img,1
E:\lab_85_429_2014\04408B\results_swraf222\con_0013.img,1
E:\lab_85_429_2014\04480B\results_swraf222\con_0013.img,1
E:\lab_85_429_2014\04550B\results_swraf222\con_0013.img,1
E:\lab_85_429_2014\04564B\results_swraf222\con_0013.img,1
E:\lab_85_429_2014\04597B\results_swraf222\con_0013.img,1
7: Type: ^con_0013.* then press Rec, then press Done (all 10 subject contrast images will be selected for you)
NOTE: the contrast number 13 matches the category number for Animals, which is 13


1: After the group-level contrast is done being specified (previous slide, it takes only a second or two), select Estimate
SPM8 (andrewba): Menu
Slice timing
Smooth
Segment
Review
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
File Edit View SPM BasicIO
5: Click Play
Module List
Model estimation
Current Module: Model estimation
Help on: Model estimation
Select SPM.mat <-X
Method
. Classical
2: Select SPM.mat
Current Item: Select SPM.mat
Select Files
Select SPM.mat
Dir E:\lab_85_429_2014\session9\animal_0013\
Up E:\lab_85_429_2014\session9\animal_0013\
Prev E:\lab_85_429_2014\session9\animal_0013\
3: Select animal_0013 folder if you're not already there (NOTE: Your screen should show session8, not session9)
at file that contains the design specification.
aining this file is known as the input directory.
4: Then select SPM.mat, then press Done
? Ed Rec Done Filt ^SPM\.mat$
Selected 1/1 files.
E:\lab_85_429_2014\session9\animal_0013\SPM.mat

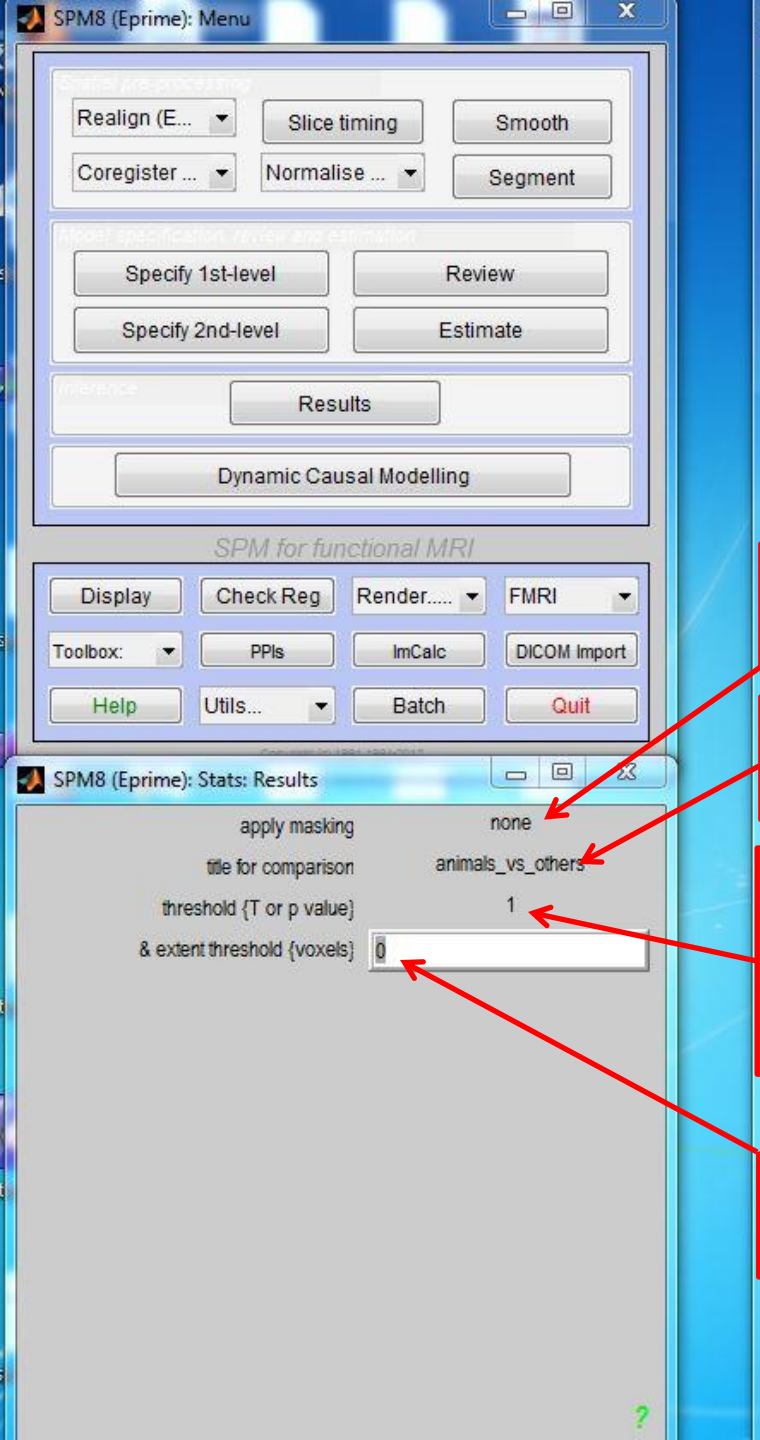

1: After the group-level contrast is finished being estimated (previous slide), select Results
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Render....
FMRI
Toolbox:
PPIs
ImCalc
DICOM Import
Help
Utils...
Batch
Quit
SPM8 (andrewba): Graphics
File Edit View Insert Tools Desktop Window SPM Figure Help
Select SPM.mat
Dir E:\lab_85_429_2014\session9\animal_0013\
Up E:\lab_85_429_2014\session9\animal_0013\
Prev E:\lab_85_429_2014\session9\animal_0013\
Drive E:
? Ed Rec Done Filt *
Selected 1/1 files.
E:\lab_85_429_2014\session9\animal_0013\SPM.mat
SPM8 (andrewba): Stats: Results
2: Select animal_0013 folder if you're not already in that directory
3: Select SPM.mat, then press Done
4: Next slide…

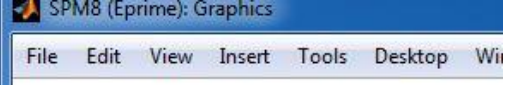

SPM8 (andrewba): Menu
Realign (E...
Slice timing
Smooth
Coregister (...
Normalise (...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Render....
FMRI
Toolbox:
PPIs
ImCalc
DICOM Import
Help
Utils...
Batch
Quit
5: Select Define new contrast
SPM contrast manager
Select contrasts...
show
t-contrasts
F-contrasts
all
(type) : name
no contrasts defined
contrast(s)
Design matrix
parameter estimability
Define new contrast...
Reset
Done
Selected 0 contrasts.
SPM8 (andrewba): Stats: Results
6: Type the name for the contrast (after the "define contrast" window appears): animals_vs_others
7: For the contrast value, type: 1 then press OK
SPM contrast manager
define contrast...
name
animal_vs_others
type
t-contrast
F-contrast
contrast
contrast weights vector
1
Reset
Cancel
OK
contrast(s)
Design matrix
parameter estimability
NOTE: Make sure that the t-contrast button is selected
8: Next slide...



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 “animals_vs_others”

5: Threshold: First choose “none” for “*p* value adjustment to control”, then type: 1

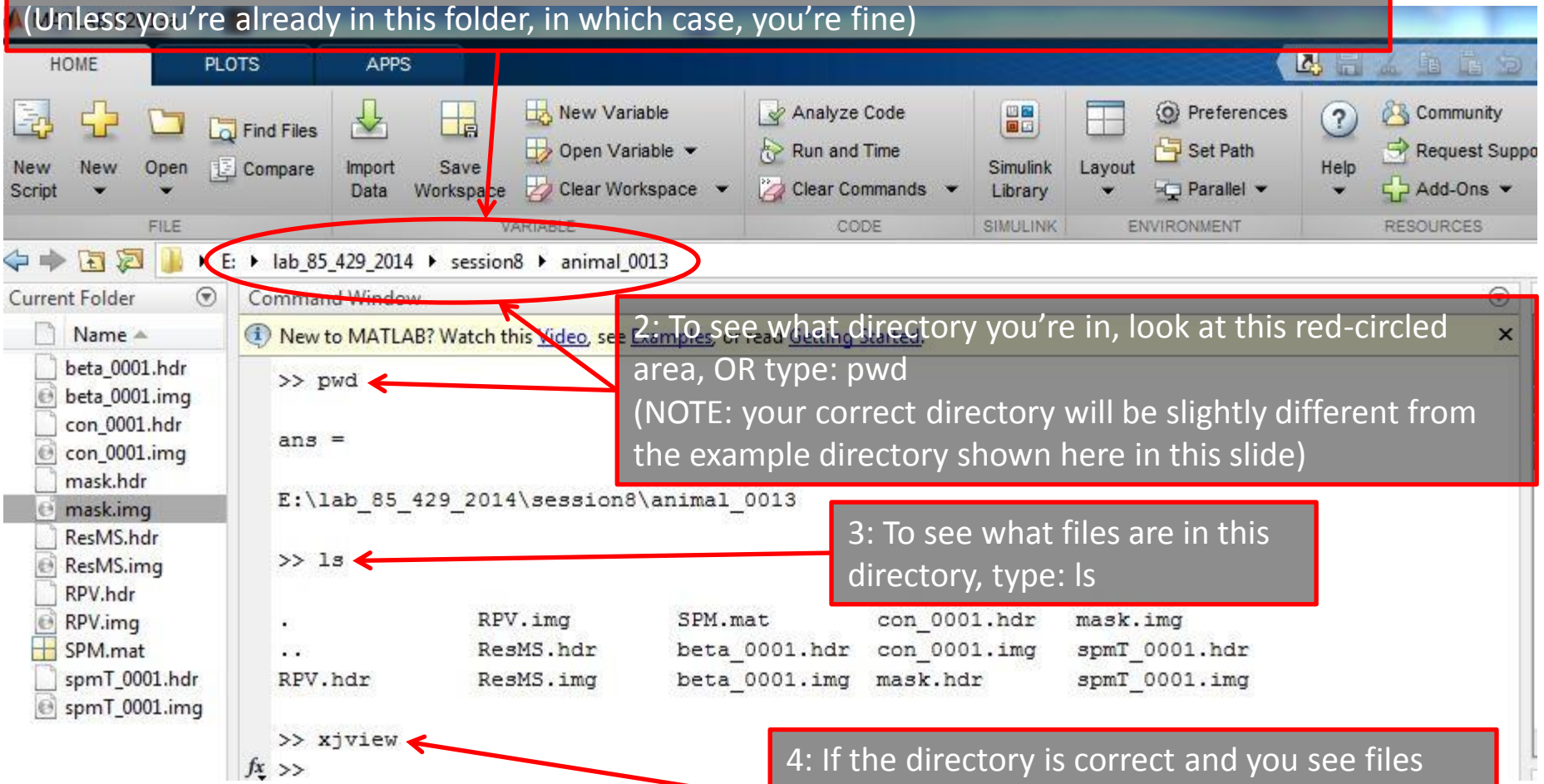
(we will view results in xjview and set the *p* threshold there)

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, as we did with single-subject spm contrasts. But don't close spm. Go back to the Matlab command window (it's already open) and cd to the directory with the results. That is, type:

cd C:/Users/Public/lab_85_429_2016/session8/animal_0013

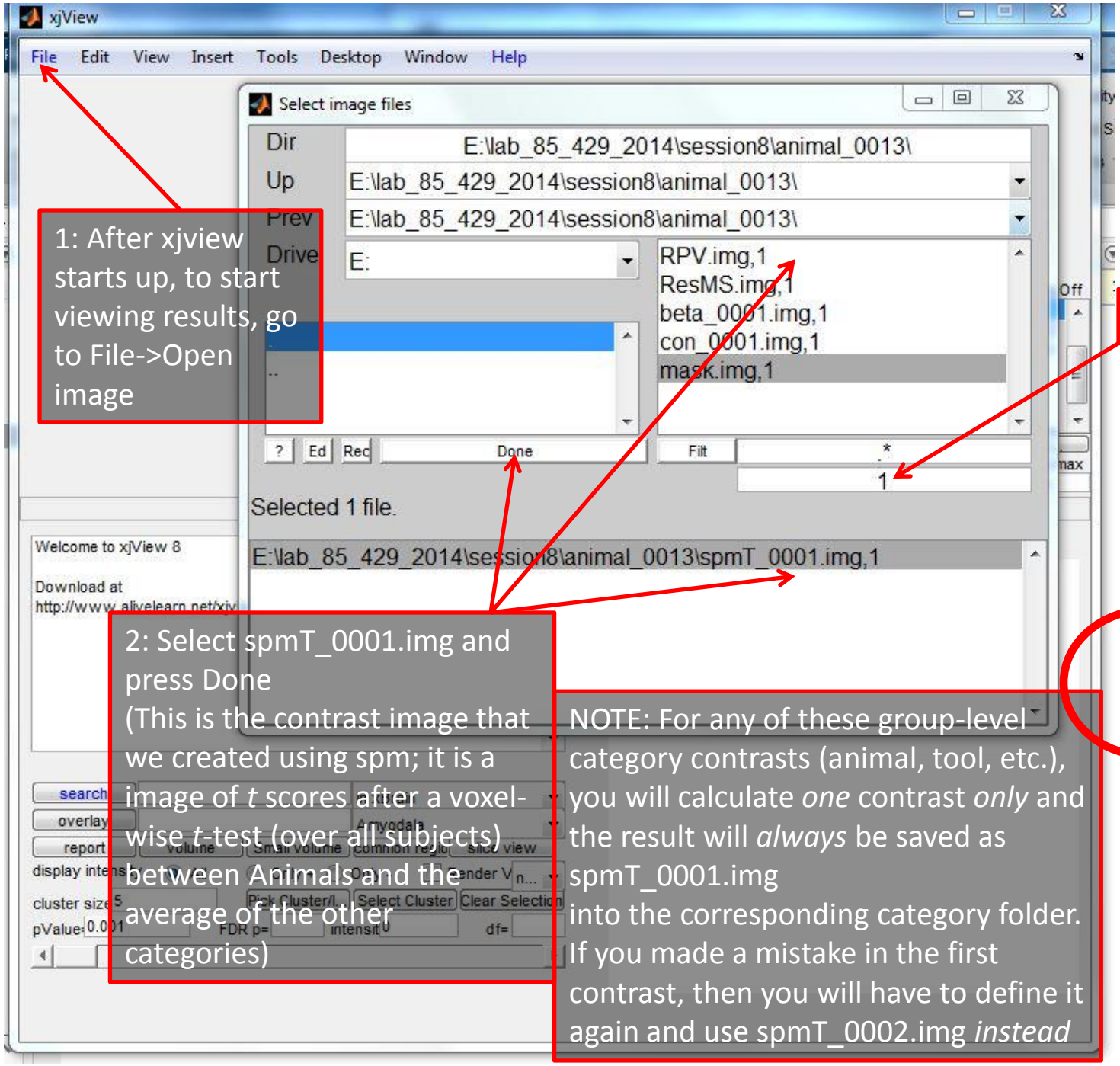
(Unless you're already in this folder, in which case, you're fine)

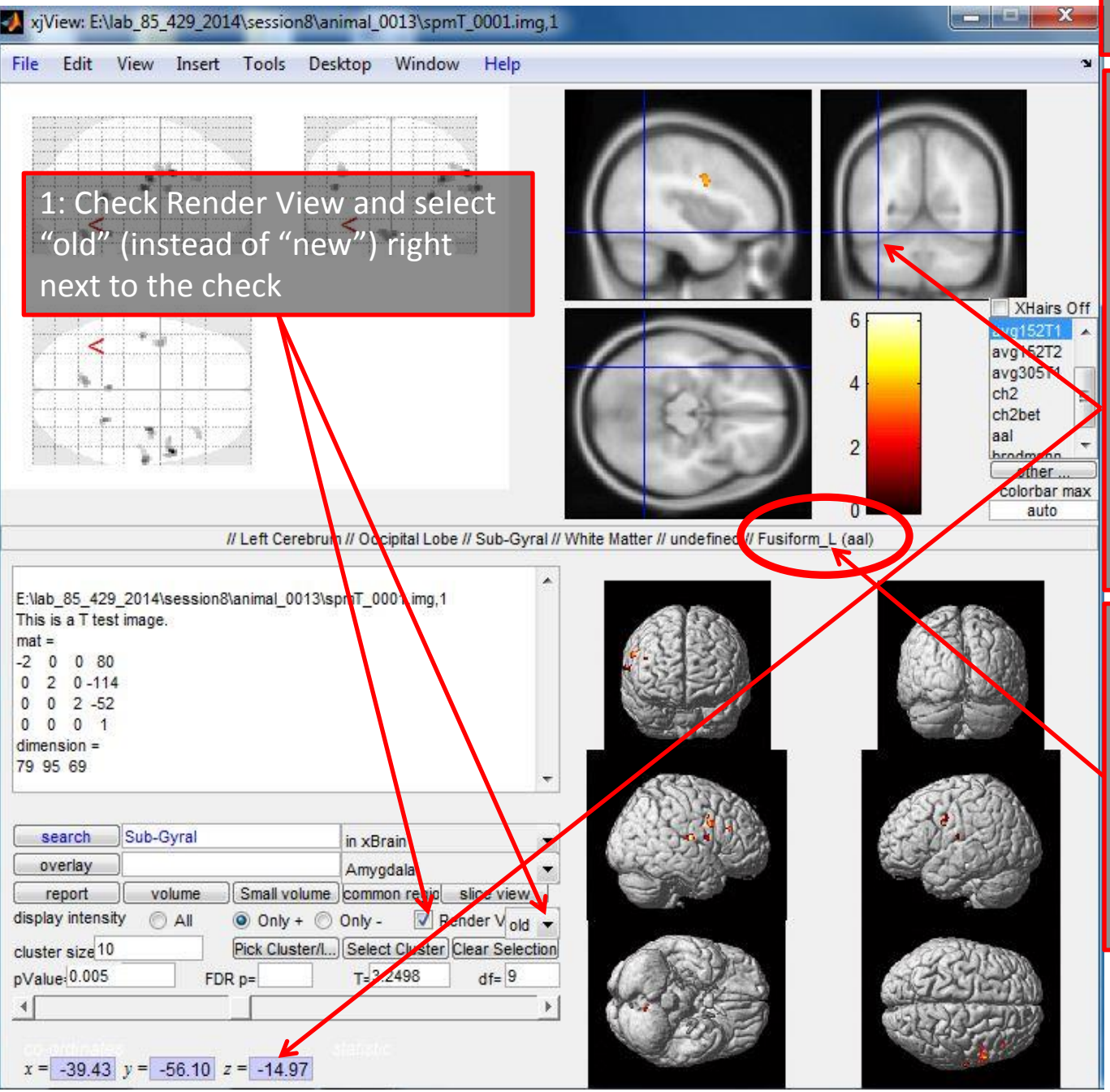


2: To see what directory you're in, look at this red-circled area, OR type: pwd
(NOTE: your correct directory will be slightly different from the example directory shown here in this slide)

3: To see what files are in this directory, type: ls

4: If the directory is correct and you see files such as "spmT_0001.img", then next type: xjview


xjView
File Edit View Insert Tools Desktop Window Help
Select image files
Dir
E:\lab_85_429_2014\session8\animal_0013\
Up
E:\lab_85_429_2014\session8\animal_0013\
Prev
E:\lab_85_429_2014\session8\animal_0013\
Drive
E:
RPV.img,1
ResMS.img,1
beta_0001.img,1
con_0001.img,1
mask.img,1
? Ed Rec Done Filt
.
1
Selected 1 file.
E:\lab_85_429_2014\session8\animal_0013\spmT_0001.img,1
Welcome to xjView 8
Download at
search
overlay
report
cluster size
pValue
FDR p=
df=
Select Cluster
Clear Selection
1: After xjview starts up, to start viewing results, go to File->Open image
2: Select spmT_0001.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 (over all subjects) between Animals and the average of the other categories)
NOTE: Leave as 1
NOTE: For any of these group-level category contrasts (animal, tool, etc.), you will calculate *one* contrast *only* and the result will *always* be saved as spmT_0001.img
into the corresponding category folder.
If you made a mistake in the first contrast, then you will have to define it again and use spmT_0002.img *instead*
3: Next slide…

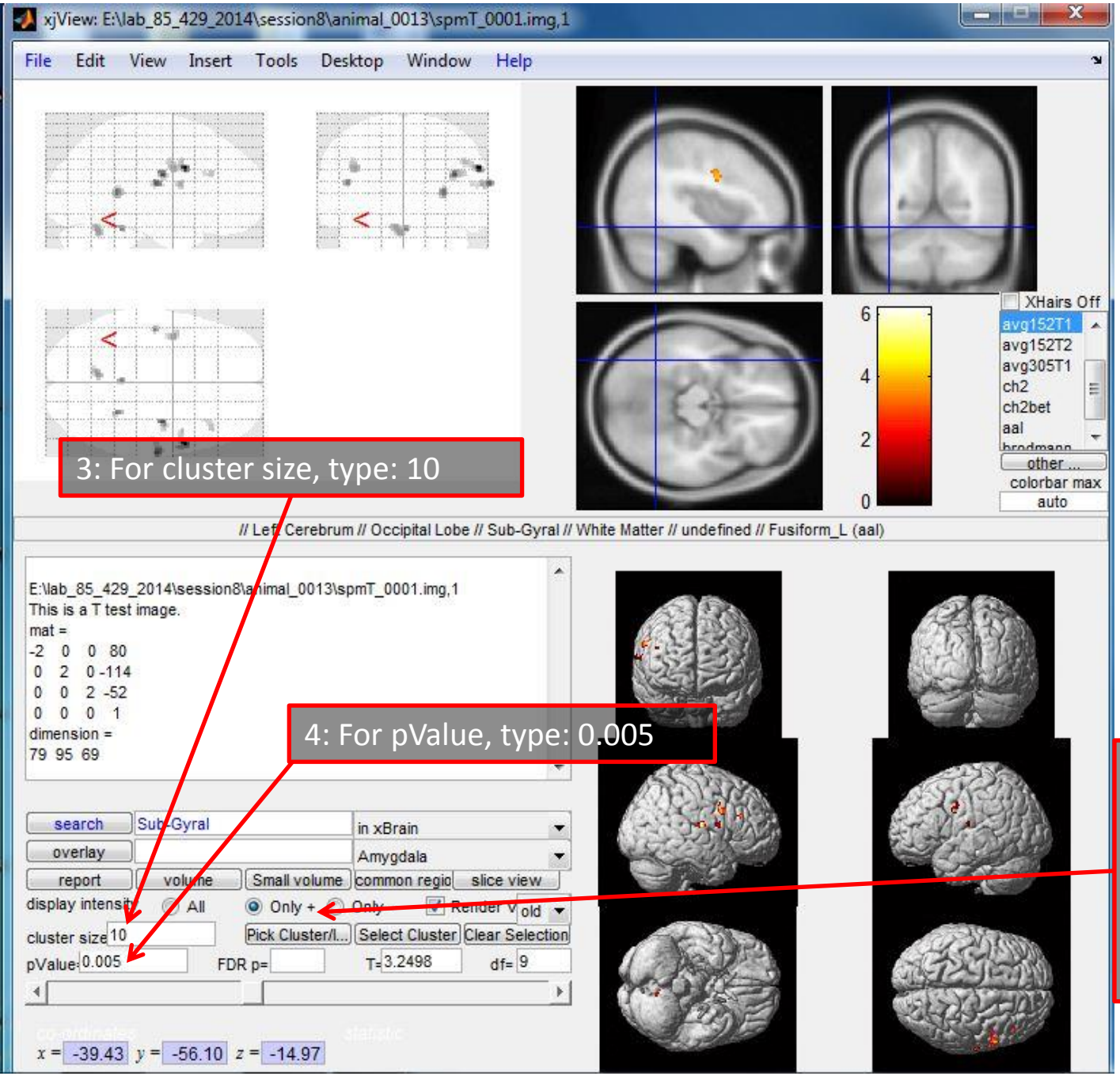


NOTE: The window won't maximize on our computers

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

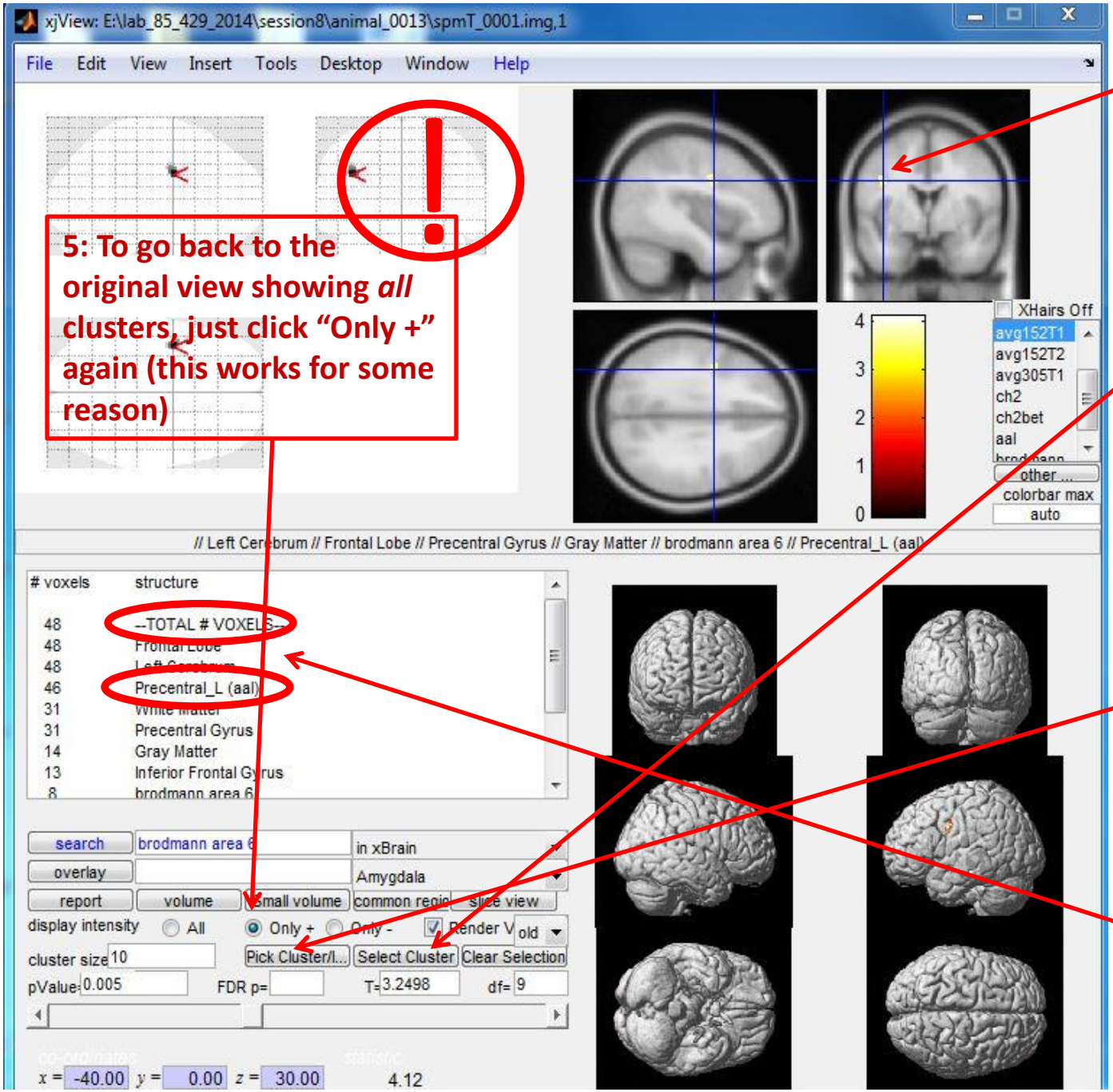
2: Next slide…



3: For cluster size, type: 10

4: For pValue, type: 0.005

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



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

1: To show a single cluster and display its anatomical information, first click within *any* cluster on the screen

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: Pay attention *only* to the AAL brain areas and the TOTAL # VOXELS value

Important notes for assignment

- *Always...*
  - Load the file spmT_0001.img in xjview for a given category group contrast, found in that category folder
    - Unless you made a mistake and had to create the contrast a second time, in which case use spmT_000***2***.img, etc.
  - Display *positive* activation (toggle the "Only +" button)
  - Use a cluster size threshold of 10 voxels
    - Unless stated otherwise
  - Use a *p*-value threshold of 0.005
    - Unless stated otherwise

- This is all the guidance that you should need to do this session's assignment

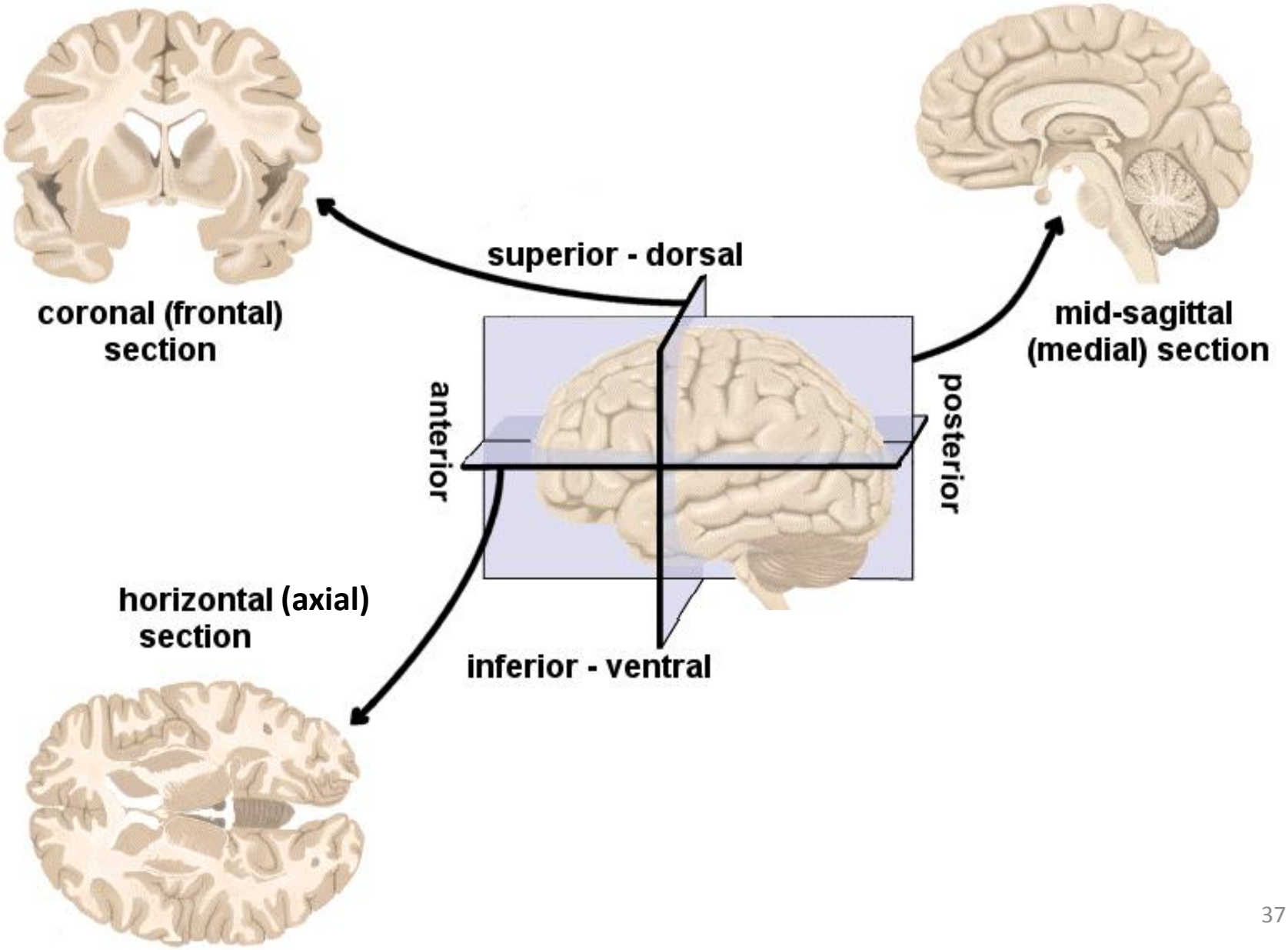
- If you haven't already, you are free to download the xjview manual off Blackboard for further help

- 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 the paths again and cd to the directory of whatever category contrast you are working on*

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

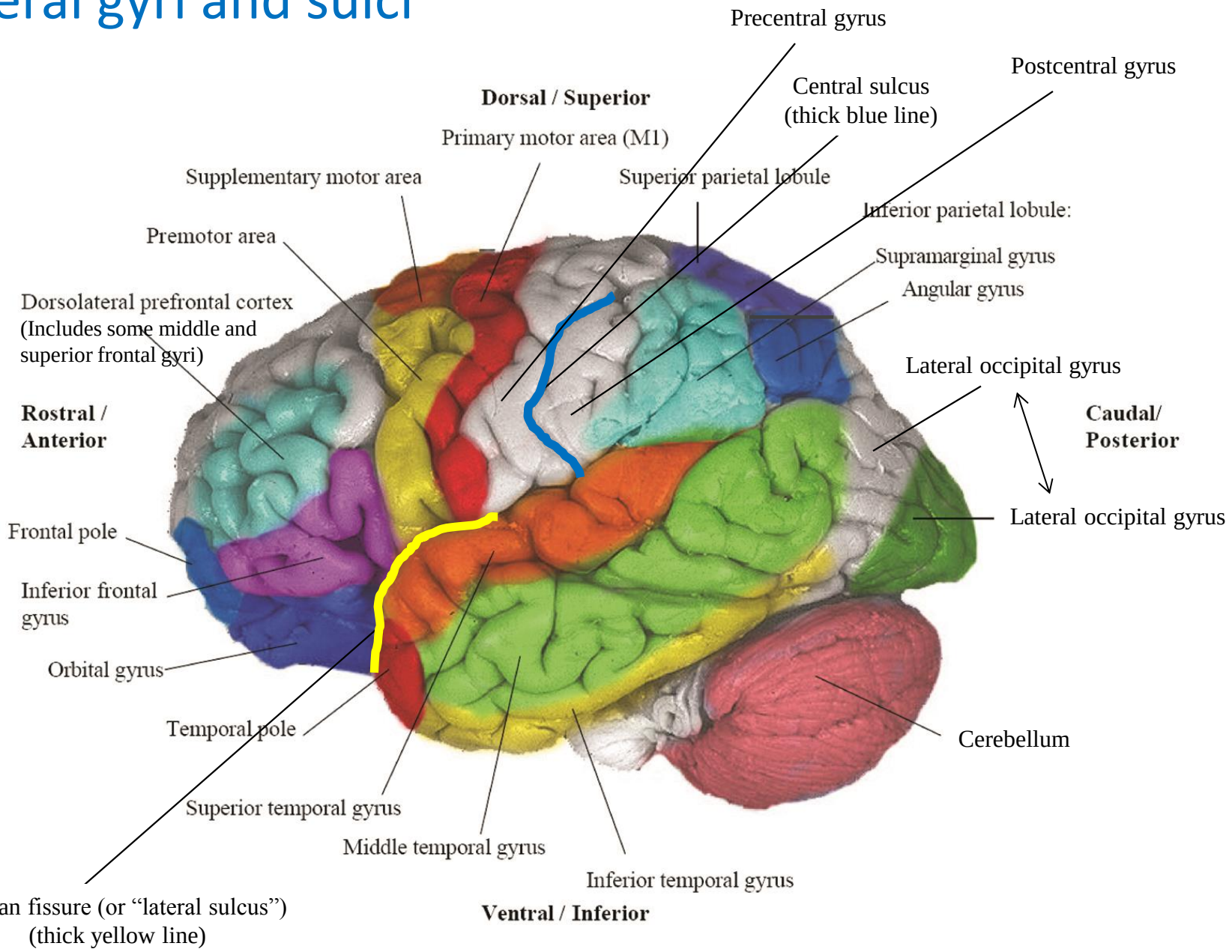
Orientation terms and planes



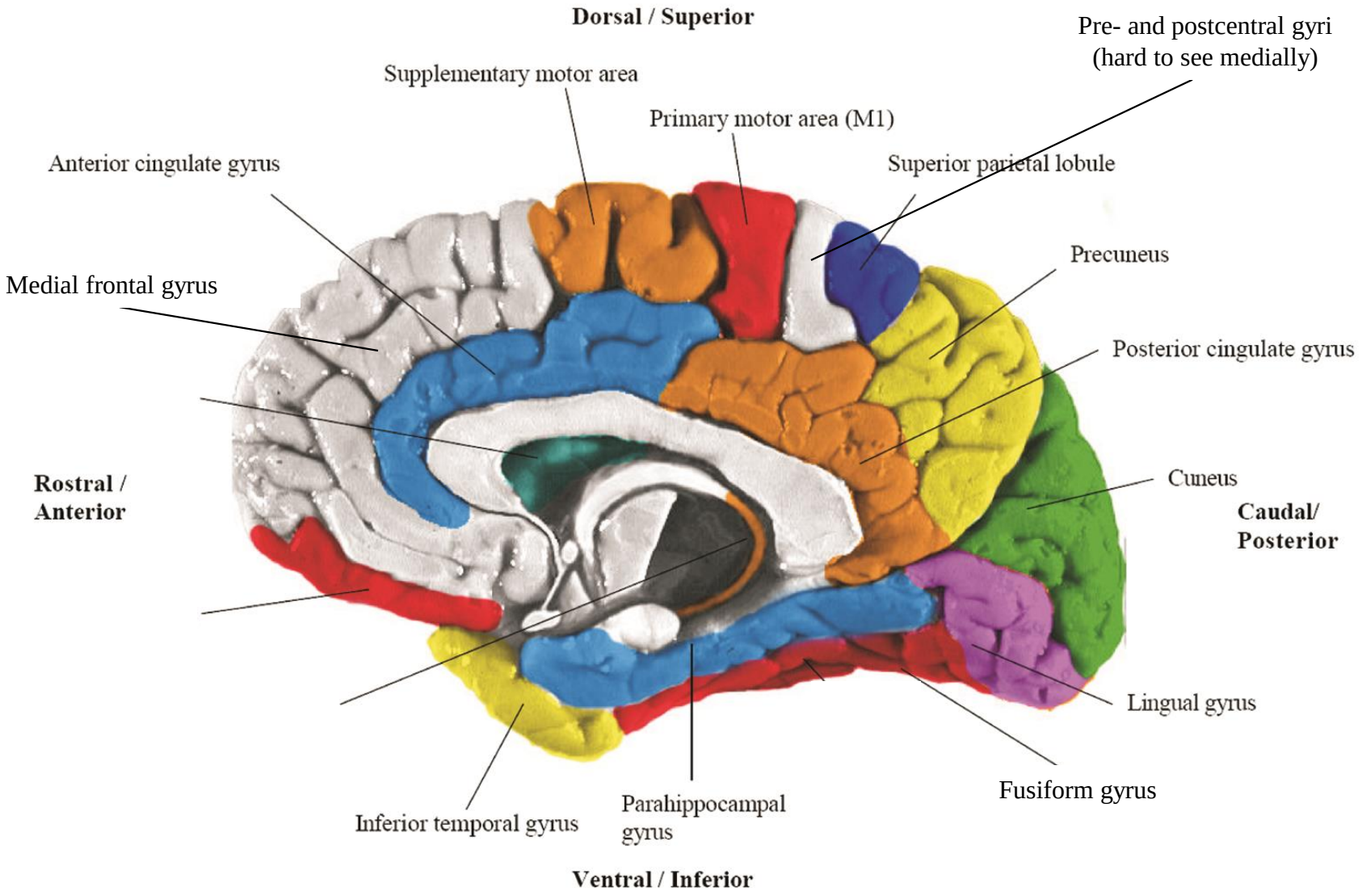
We are using the Automated Anatomical Labeling (AAL) atlas in this lab (very similar to the atlases of your two quizzes)

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