

Resources for “Power and Meta-Analysis” Practical SPM Course 2014, Zurich

<http://www.translationalneuromodeling.org/practical-sessions/>

Preliminary

- Get this file: <http://warwick.ac.uk/tenichols/zurich.pdf>
- Create a Practical directory on your machine
- Create a DATA subdirectory
- Create a RESULTS subdirectory

Nonparametric Inference

SnPM13 Setup

- Download <http://warwick.ac.uk/snpm/ZurichSnPM13.zip> (Course use only)
- Expand ZIP file, move SnPM13 into your spm8/toolbox directory; if open, quit SPM.
- Download Faces group data http://www.fil.ion.ucl.ac.uk/spm/data/face_rfx/ getting [face_rfx.zip](#). (If slow, grab just [cons_can.zip](#))
- Expand, move face_rfx into your DATA directory

STOP... wait for short slide presentation (or help your neighbor with setup)

SnPM13 Practical

- First analyze Faces canonical data with SPM
 1. In your RESULTS directory, create a new directory, Canonical-P
 2. “Specify 2nd-level”
 - a. “Directory”: Canonical-P
 - b. “Scans”: all 12 images in DATA/face_rfx/cons_can
 3. Save configuration, “File” -> “Save Batch”, e.g. Canonical-P/batch.mat
 4. Run! (Green arrow)
 5. “Estimate” -> “Select SPM.mat” -> Run
 6. “Results” -> “Select SPM.mat”
 7. Click “t-contrast”, “define new t-contrast”;
“name”: Faces > Baseline
“contrast”: 1
OK... Done
 8. “apply masking”: none
title: Faces > Baseline (*accept*)
“p-value adjustment to control”: FWE
“p value (FWE)”: 0.05 (*accept*)
“& extent threshold [voxels]”: 0 (*accept*)
 9. Click “whole brain” under “p-values”

10. From results window menu, “SPM Figure” -> “Save Figure” -> “Default File”
(Or make a screen snapshot, for later comparison)
- Now analyze Faces canonical data with SnPM
 1. In your RESULTS directory, create a new directory, Canonical-nP
 2. Start SnPM: “toolbox” -> “SnPM13”
 3. Interactive window,
“SnPM13” -> “Specify” -> “MultiSub: One Sample T test on diffs/contrasts”
 4. Batch window,
 - a. “Analysis Directory”: Canonical-nP
 - b. “Images to Analyze”: all 12 images in DATA/face_rfx/cons_can
 5. Save config., “File” -> “Save Batch”, e.g. Canonical-nP/batch.mat
 6. Run! (Green arrow)
 7. (Start SnPM again: “toolbox” -> “SnPM13”; [bug, will be fixed])
 8. Interactive window,
“SnPM13” -> “Compute”
 9. Select “SnPMcfg.mat configuration file”
 10. Run! (Green arrow)
 11. (Start SnPM again: “toolbox” -> “SnPM13”; [bug, will be fixed])
 12. Interactive window,
“SnPM13” -> “Inference”
 13. Select “SnPM.mat results file”
Review other options... ask questions.
 14. Run! (Green arrow)
Compare with parametric.

 - Now analyze Faces canonical data with SnPM **with** variance smoothing
 1. In your RESULTS directory, create a new directory, Canonical-nPs
 2. Start SnPM: “toolbox” -> “SnPM13”
 3. Interactive window,
“SnPM13” -> “Specify” -> “MultiSub: One Sample T test on diffs/contrasts”
 4. Batch window,
 - a. “Analysis Directory”: Canonical-nPs
 - b. “Images to Analyze”: all 12 images in DATA/face_rfx/cons_can
 - c. “Variance Smoothing”: set to 6 6 6
 - d. *(Try adding cluster inference if you want... slows it down a little)*
 5. Save config., “File” -> “Save Batch”, e.g. Canonical-nPs/batch.mat
 6. Run! (Green arrow)
 7. (Start SnPM again: “toolbox” -> “SnPM13”; [bug, will be fixed])
 8. Interactive window,
“SnPM13” -> “Compute”
 9. Select “SnPMcfg.mat configuration file”
 10. Run! (Green arrow)
 11. (Start SnPM again: “toolbox” -> “SnPM13”; [bug, will be fixed])

12. Interactive window,
“SnPM13” -> “Inference”
13. Select “SnPM.mat results file”
Review other options... ask questions.
14. Run! (Green arrow)
Compare this nonparametric smoothed-variance t with parametric & nonparametric t -test.

Power Analysis

Set up... Create a `Power` subdirectory in your `Practical` directory

WFU PickAtlas set up

- Download: <http://fmri.wfubmc.edu/software/PickAtlas> (Download, at bottom)
You will need to give name email address and receive link via email.
Click on link emailed, then select “WFU_PickAtlas 3.0” & your OS.
- Expand the download; inside the `WFU_PickAtlas_3.0.4` directory, move the following into your `spm8/toolbox` directory:
 - `wfu_pickatlas`
 - `wfu_results`
 - `wfu_tbx_common`If open, close SPM.

FSL set up (for Atlas Data)

- Download FSL: <http://www.fmrib.ox.ac.uk/fsl>
(*Actually don't!* It's way too large; see me if you don't already have FSL)
- All atlases are in `$FSLDIR/data/atlases`

G*Power set up

- Download, for Mac or PC, from: <http://www.gpower.hhu.de/en.html>

STOP... wait for short slide presentation (or help your neighbor with setup)

Practical...

Creating ROI Masks with WFU PickAtlas

- “Toolbox” -> “wfupickatlas” -> “Human Atlas”
- Atlas options
 - TD = Talairach Daemon, atlas of Talairach & Tournoux, first atlas, based on **one** elderly French woman, dead; 55 labeled regions; 74 Brodmann Areas
 - AAL = Automated Anatomical Labelling; based on **just 1** manually segmented brain (young Canadian man, living); 116 regions
 - IBASPM; derived from AAL; 71 & 116 regions
- Select “TD Labels” (“TD” = Talairach Daemon, Talairach labels)
- Choose a region(s) to measure power in Face data
 1. Double-click on a region (or select and click “ADD ->” button).

Let's all do something different! Select some subset of:

 - Inferior Occipital Gyrus
 - Middle Occipital Gyrus
 - Superior Occipital Gyrus
 - Cuneus
 2. When ready, save image with “SAVE MASK” button, putting image in your Power directory
 3. Click “DONE” to close the PickAtlas.

Creating ROI Masks by hand

- Atlases in FSL
 - “Harvard-Oxford” cortical and sub-cortical atlas, **average of 37** manually segmented brains, 69 regions.
 - “Juelich” atlas, histologically defined on **multiple (post-mortem) subjects**, 62 regions.
 - Others... (white matter tracks, etc)
- Each atlas has “maxprob” image, giving most likely label for a voxel;
 - maxprob-thr0: All voxels with any data
 - maxprob-thr25: Filters out voxels with (maximum) probability < 0.25
 - maxprob-thr50: Filters out voxels with (maximum) probability < 0.5
- Examine “Juelich.xml”; you’ll find labels and “index” values

```
<label index="88" x="132" y="52" z="76">GM Visual cortex V5 L</label>
<label index="89" x="41" y="60" z="78">GM Visual cortex V5 R</label>
```
- But (!!!) these index values are one-minus the values that define the region; i.e. voxels with value 89 and 90 define V5/MT. On Matlab command line

```
% Creating Juelich-V5.nii
Atlas='.../fsl/data/Atlases/Juelich/Juelich-maxprob-thr25-2mm.nii';
AtlasV5='Juelich-V5.nii';
spm_imcalc_ui(Atlas,AtlasV5,'i1==89|i1==90')
```

Using ROI Masks to Extract Mean & Standard Deviation

- Open standard (parametric) Faces results
- “Results” -> “Select SPM.mat”
- Contrast manager: Select contrast (Faces > Baseline), “done”

- “apply masking”: none
- “ROI analysis”: “no” (Note, this is a WFUpickatlas modification)
title: Faces > Baseline (*accept*)
- “p-value adjustment to control”: **none** (*Crucial*)
- “Threshold {T or p value}”: **1** (*P ≤ 1 means give me all data*)
- “& extent threshold [voxels]”: 0 (*accept*)
- Click “eigenvariate”
- “name of region”: VOI_V5 (or some name that reflects **your** region)
- “VOI definition...”: “mask”
- Select your ROI mask (e.g. VOI_V5.nii)
- Find Matlab command window...
- xY structure, xY.y has one row for each subject, one column for each voxel


```
mn_vx = mean(xY.y);      % Mean, over subjects, at each voxel
sd_vx = std(xY.y);      % Standard deviation, over subjects, at each voxel
mn = mean(mn_vx)        % Effect in region (mean over voxels)
sd = mean(sd_vx)        % SD of effect in region (mean over voxels)
ES = mn/sd              % Effect size (unitless)
```
- I got 1.5974 (1.0 is considered large... this is a huge effect).

*Must include **all** voxels to prevent circularity*

G*Power Power Tool

- Menu -> “Tests” -> “Means” -> “One group: Difference from constant”
- Set “Effect size d” (here 1.5974)
- Leave “alpha” set to 0.05
- Set “Power” to 0.8
- Click “Calculate”
- Try “X-Y plot for a range of values”
- Change “Plot (on y axis)” to “Power (1-β err prob)”
- Click “Draw plot”
- Try changing it to “Plot (on y axis)” to “Total sample size”
- Click “Draw plot”

Meta-Analysis

Set up...

Get BrainMap meta-analysis tools

- “Sleuth”, tool for finding, selecting and downloading studies:
<http://www.brainmap.org/sleuth/>
- “GingerALE”, to for computing meta-analysis maps
<http://www.brainmap.org/ale/>
- For both you need to supply an email and await a link. You’ll need to specify a password... *remember it!* You’ll need it each time you run Sleuth!

While waiting for your downloads listen to the slide presentation on meta-analysis...

Practical...

Create a Meta directory in your Practical directory

Extracting studies with Sleuth

- Run “Sleuth”
- Set first selector: “Experiments” – “Paradigm” is “Stroop”
- Search
- Select some of the papers (pick, say, 3 you like) -> Download checked
- Menu: “Export” -> “Locations (GingerALE text)”
- Save to your Meta directory, e.g. `Stroop3.txt`
- Run “GingerAle”
- File -> “Open Foci”, select .txt file (e.g. `Stroop3.txt`)
- “Compute”
- Output files

<code>Stroop3_ALE.nii</code>	ALE map
<code>Stroop3_ALE_pN01.nii</code>	ALE map, FDR 0.01 thresholded
<code>Stroop3_P.nii</code>	Uncorrected P-values
<code>Stroop3_clust.nii</code>	Cluster ID map
<code>Stroop3_clust.txt</code>	Data history file
<code>Stroop3_clust.xls</code>	Cluster spreadsheet

Try downloading more studies.