



Data Visualization for MRI

Cyril Pernet

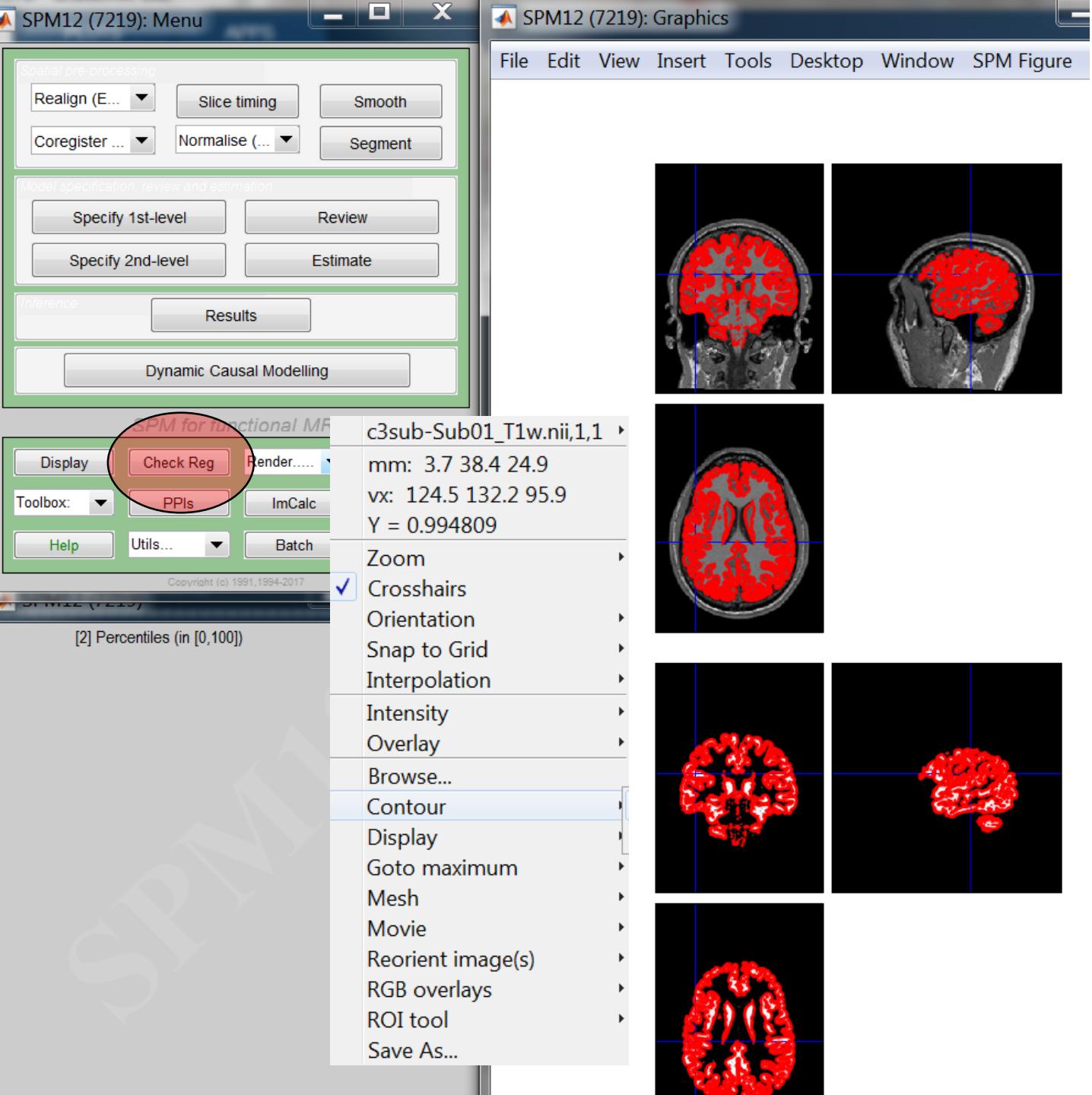
Centre for Clinical Brain Sciences (CCBS)
Neuroimaging Sciences

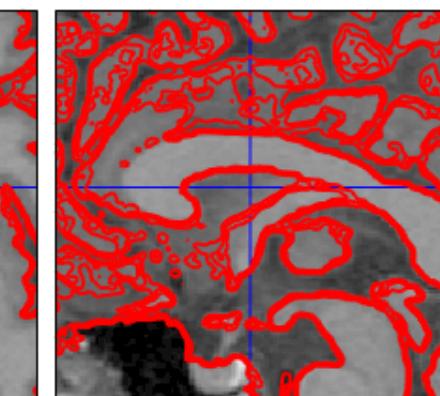
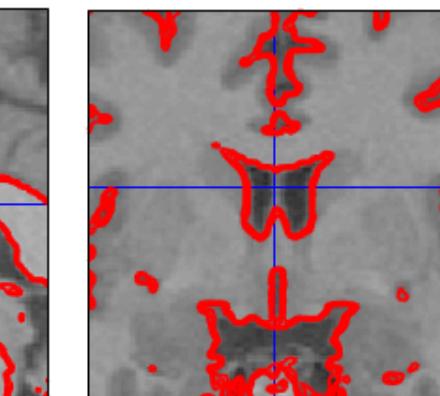
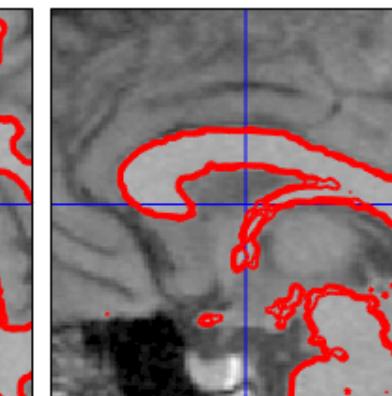
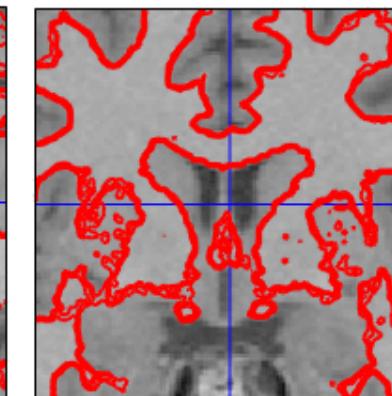
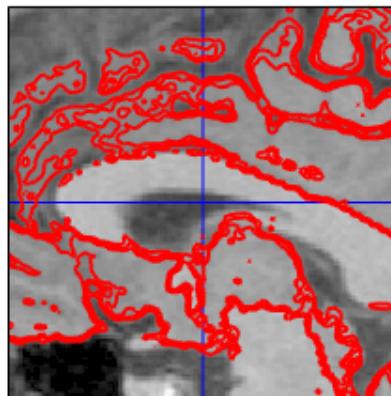
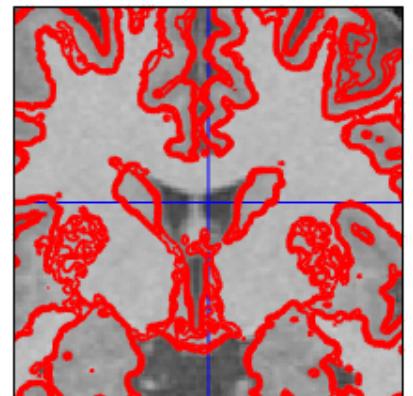
What to visualize?

- Brain and tissues / Brains and blobs
 - Activation patterns
 - Activation levels
 - Differences in activations
-
- The diagram illustrates the types of visualizations. It features two main groups of items, each enclosed in a brace and followed by a label. The first group, which includes 'Brain and tissues / Brains and blobs' and 'Activation patterns', is grouped under the label 'Maps'. The second group, which includes 'Activation levels' and 'Differences in activations', is grouped under the label '& Plots'.

Brain and Tissue

- Accuracy in realignment, segmentation and normalization is important to any analysis
- *Check Reg → anat + c1*
- *Right click c1, show contour / zoom / etc*

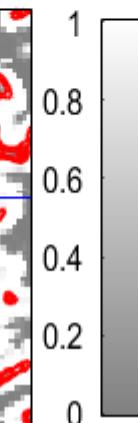
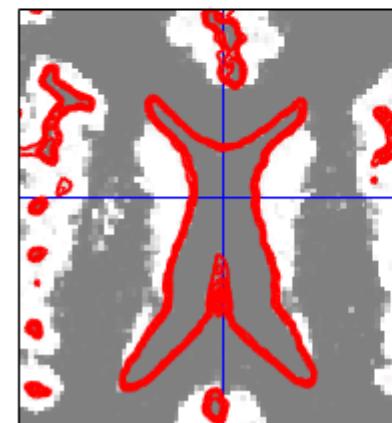
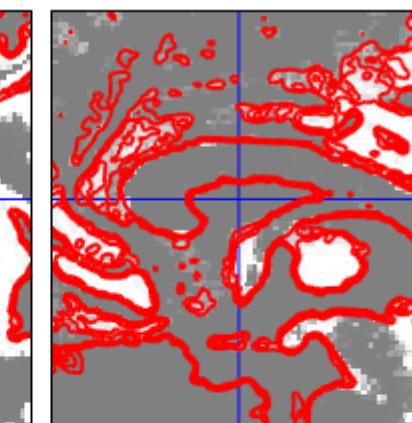
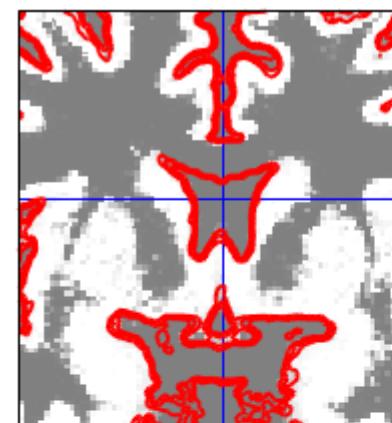




C1 (GM)

C2 (WM)

C3 (CSF)



T1w with C3 border + GM map

Brains and Blobs

- single subject vs. group vs. template



ELSEVIER

Target Article

In praise of tedious anatomy

Joseph T. Devlin^{a,*} and Russell A. Poldrack^b

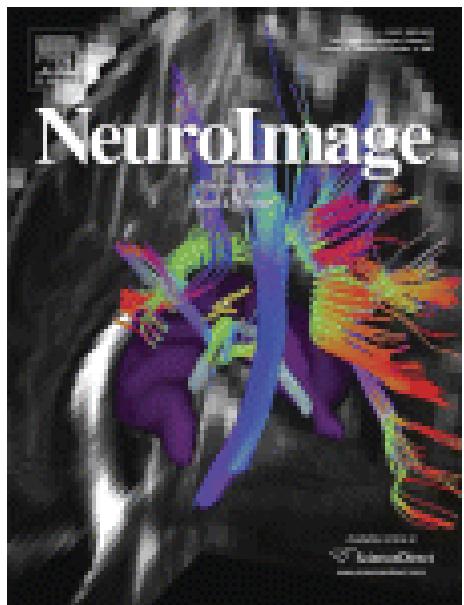
^aCentre for Functional Magnetic Resonance of the Brain, University of Oxford, UK

^bDepartment of Psychology and Brain Research Institute, UCLA, USA

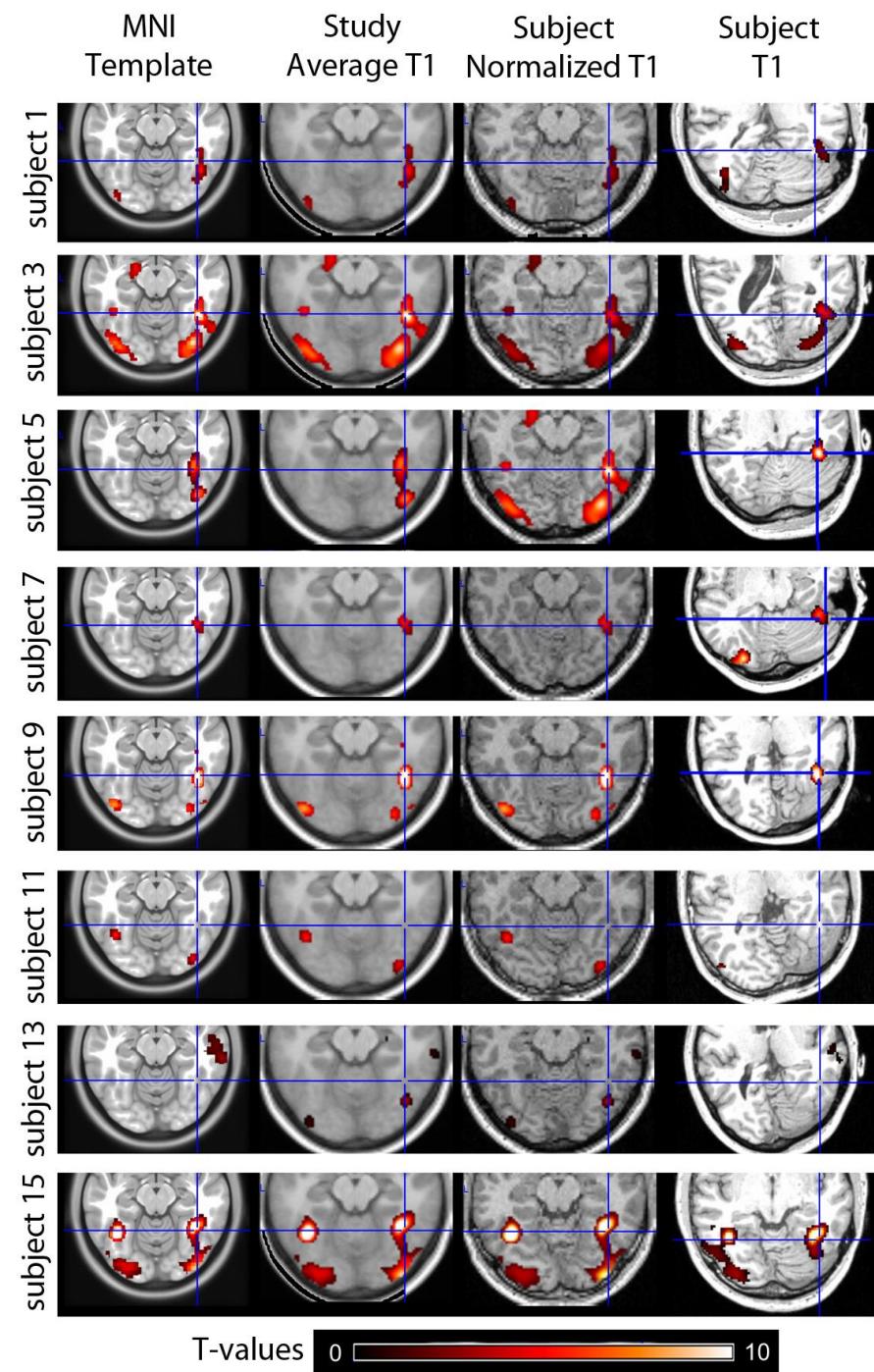
Received 9 August 2006; accepted 27 September 2006

NeuroImage

www.elsevier.com/locate/ynimng
NeuroImage 37 (2007) 1033–1041

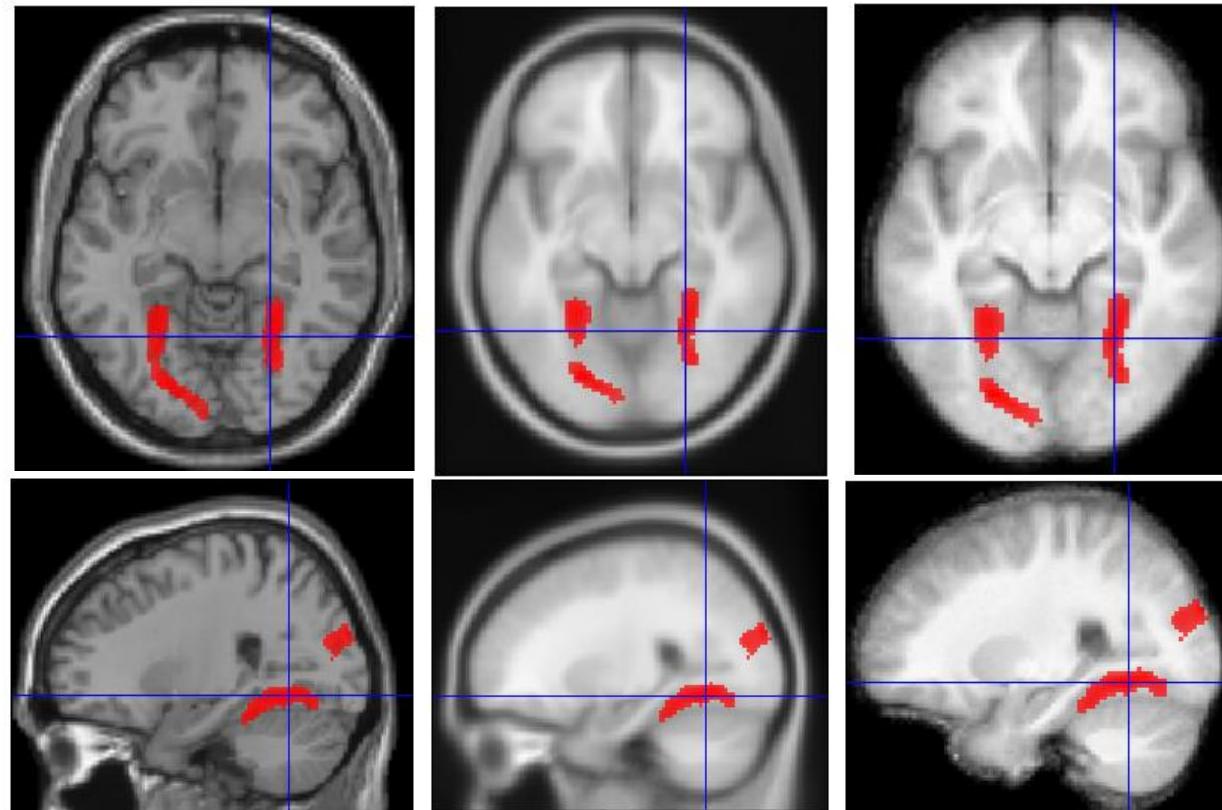


Issue 37(4) 2007



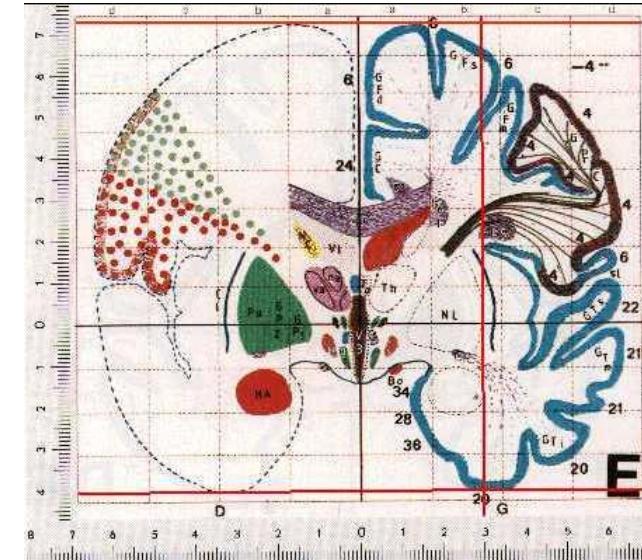
Brains and Blobs

- Displaying results on the MNI template can be misleading
→ Using the group average wT1 reflects more closely the underlying data



Blobs and Labels

Talairach atlas ?



Coarse sampling (up to 4 mm gap between slices)

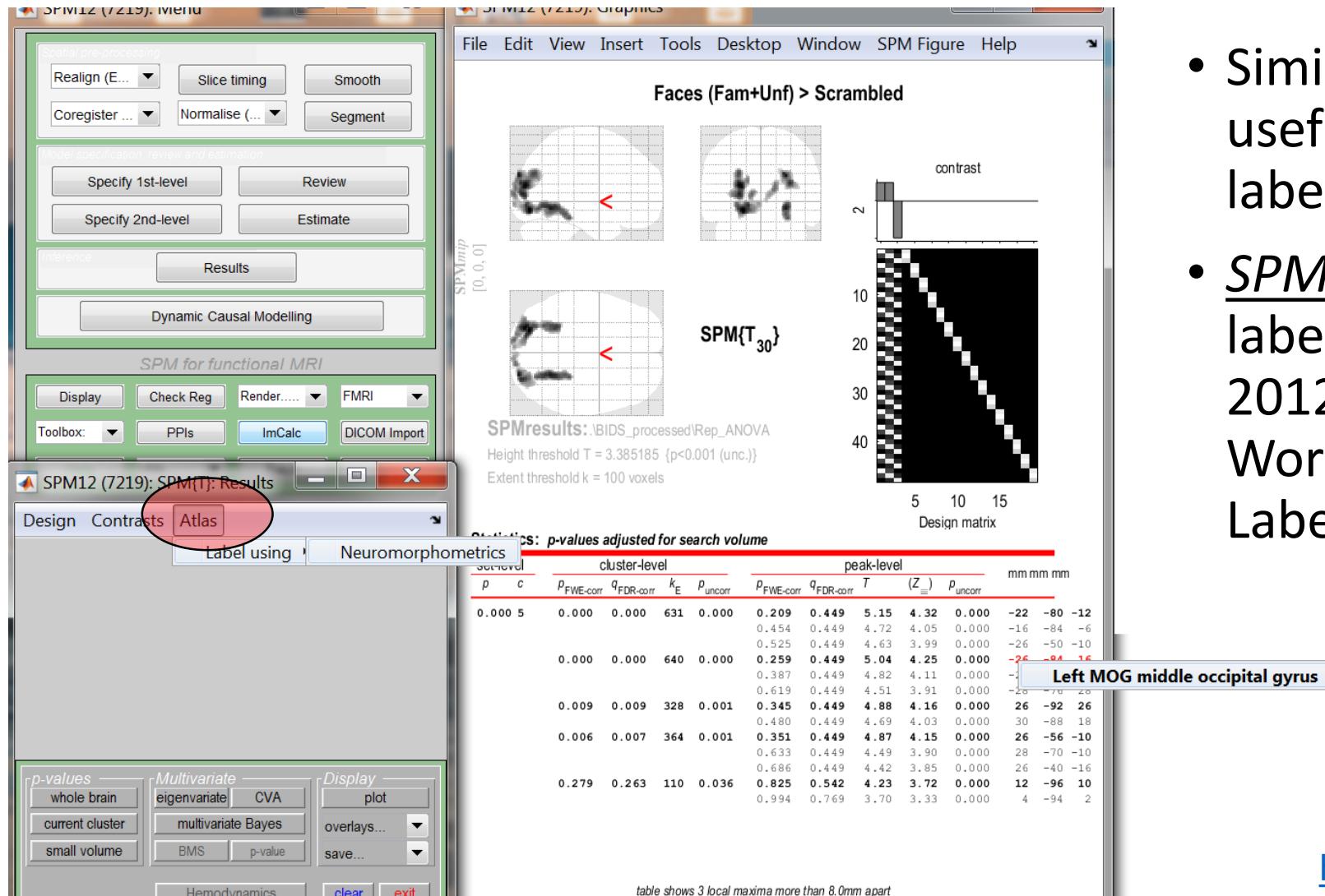
Sparse indication of areal borders

No information on interindividual variability

Not in MNI space

Histological labels are approximate estimates

Blobs and Labels



- Similarly, while extremely useful, be careful of automated labelling
- SPM neuromorphometric:*** labels derived from the MICCAI 2012 Grand Challenge and Workshop on Multi-Atlas Labeling (consistency of label)

<https://en.wikibooks.org/wiki/SPM/Atlases>

Blobs and Labels

- Microstructural areas represent functional modules¹, and are thus the most appropriate topographical reference for regionally specific activations
- Macroanatomy and stereotaxic location are not sufficient for the anatomical interpretation of functional imaging results
- Lobular and gyral anatomy can, however, provide an intuitive description where an activation is located

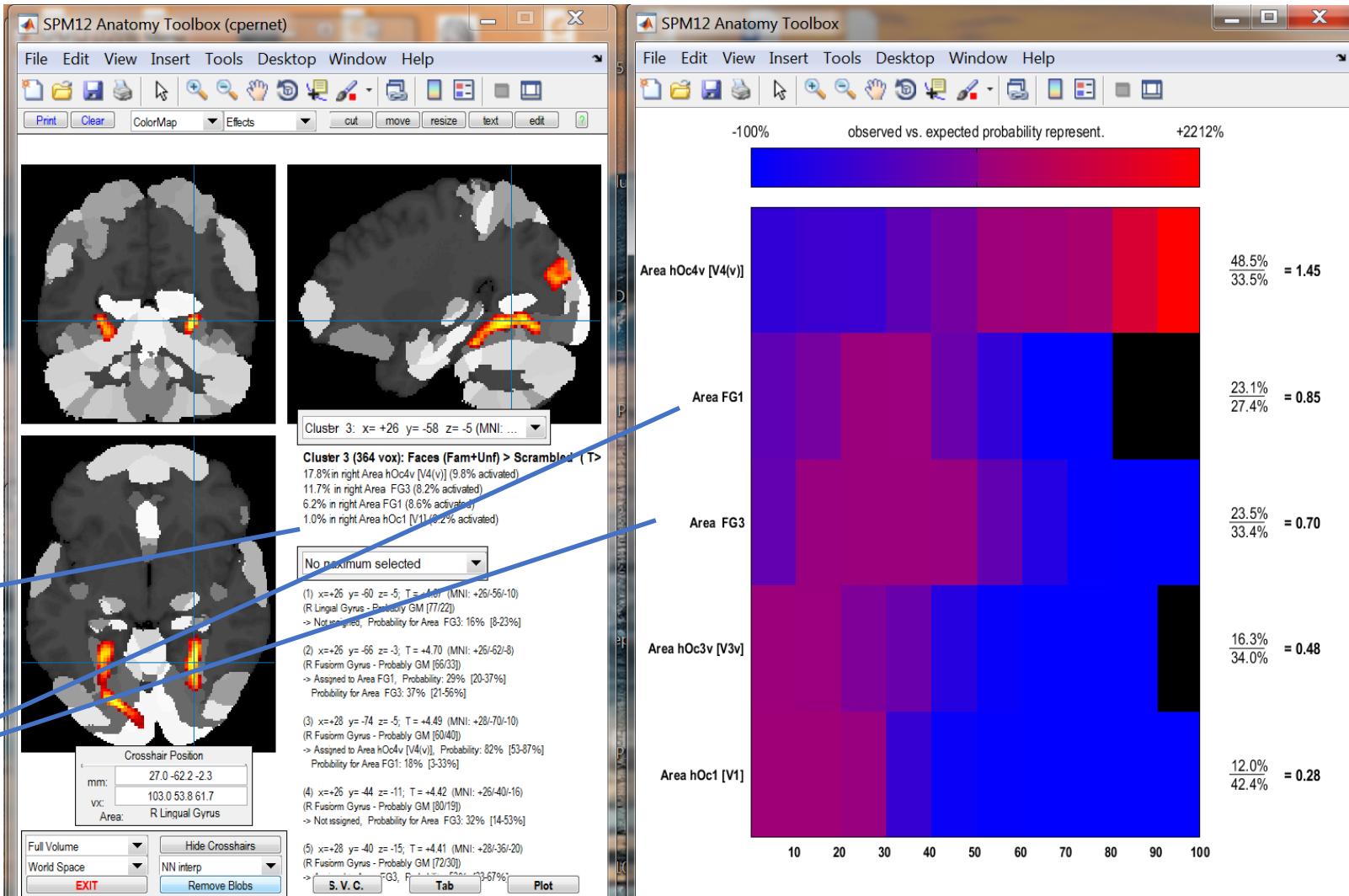
¹ Passingham 2002. *Nat Rev Neurosci*

Blobs and Labels

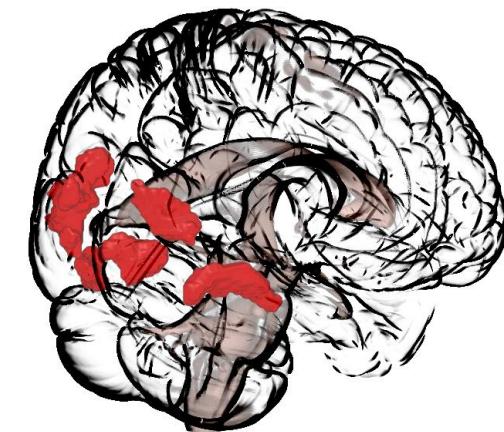
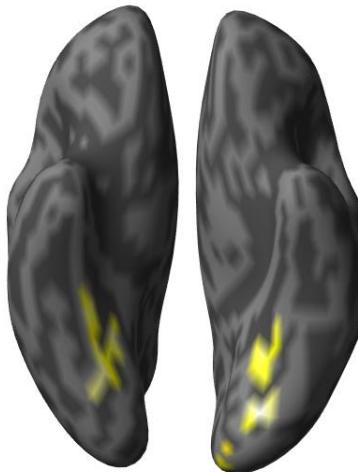
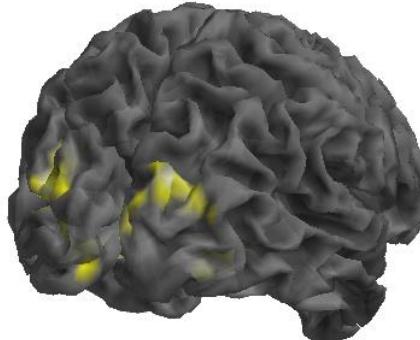
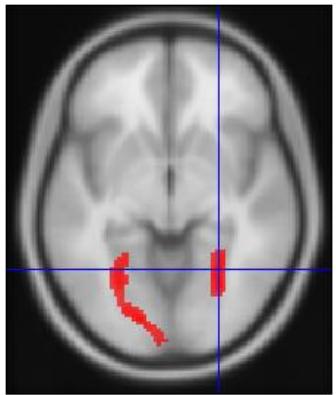
- **Anatomy Toolbox:** assign probabilities based on
 - (i) blobs location given anatomical labels
 - (ii) probabilistic cytoarchitecture

Face = fusiform right?
17.6 % fusiform
17.8 % occipital

Prob(FG | all voxels) < 1
= more next to fusiform



Brains and Blobs



INTERPRETATION

PRECISION

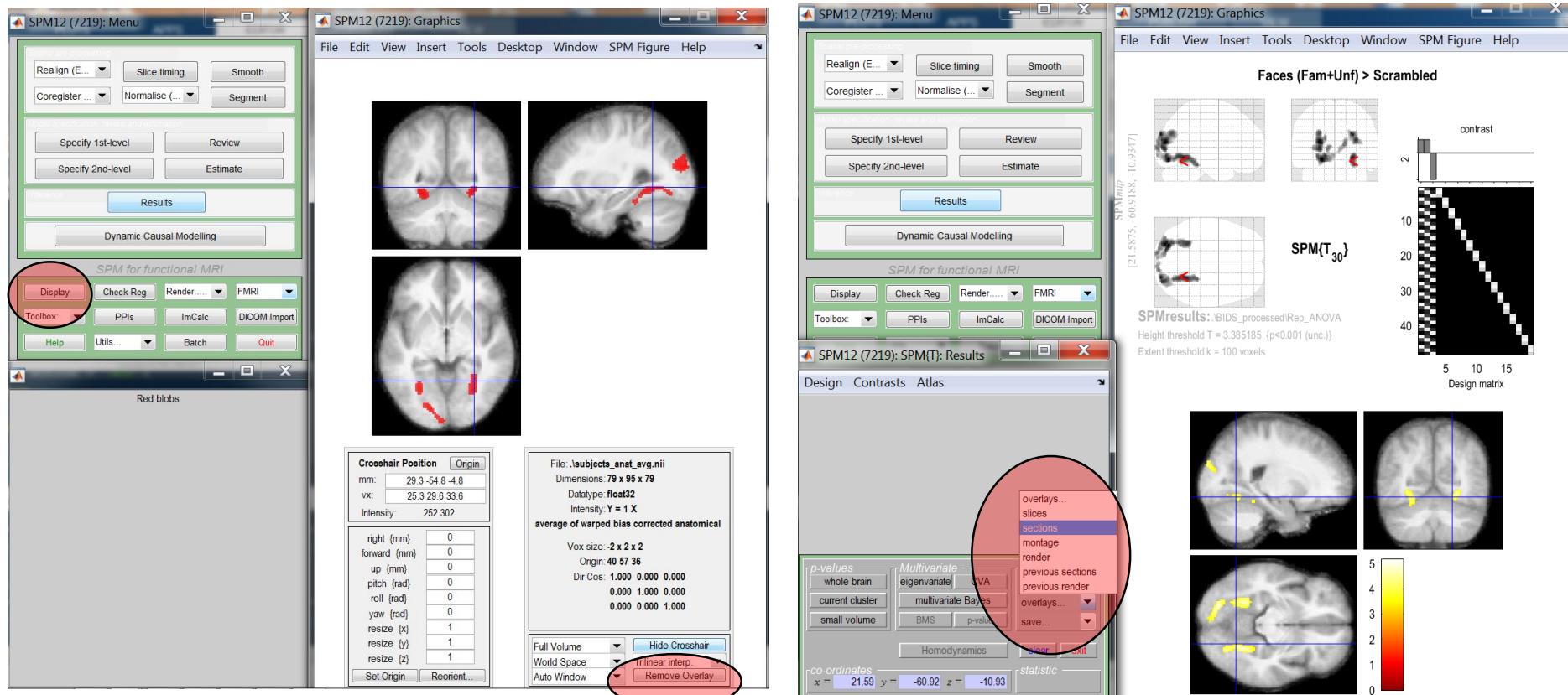
SLICES TO SPECIFY
A LOCAL EFFECT

RENDER and SURFACES
(no deep structures, use cut-outs)

GLASS BRAIN TO
SHOW IT ALL

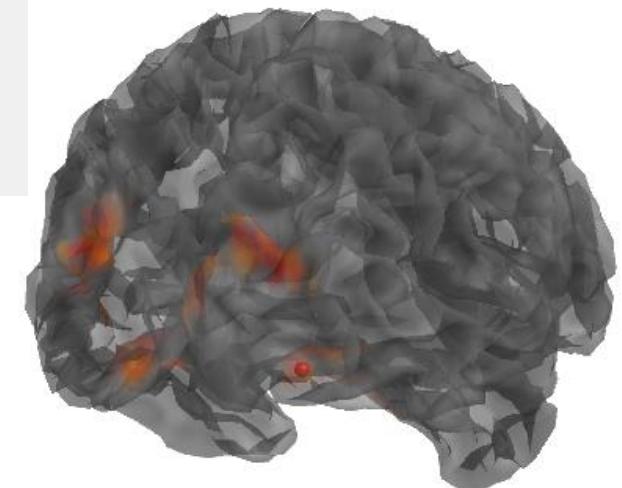
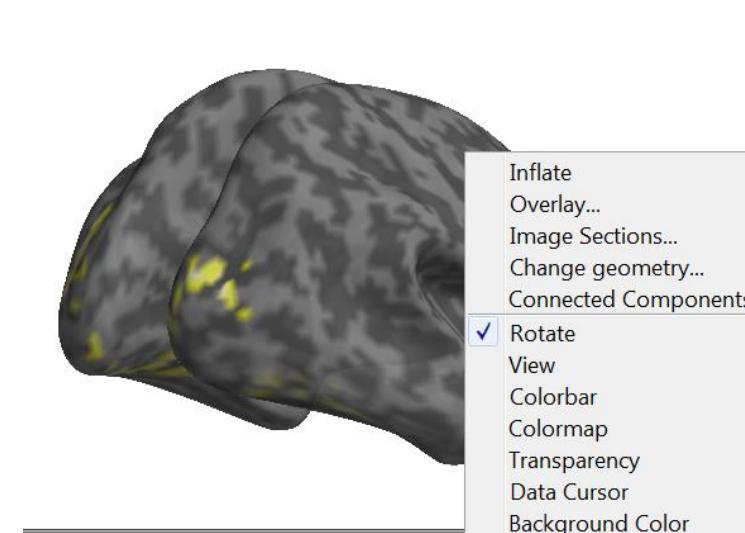
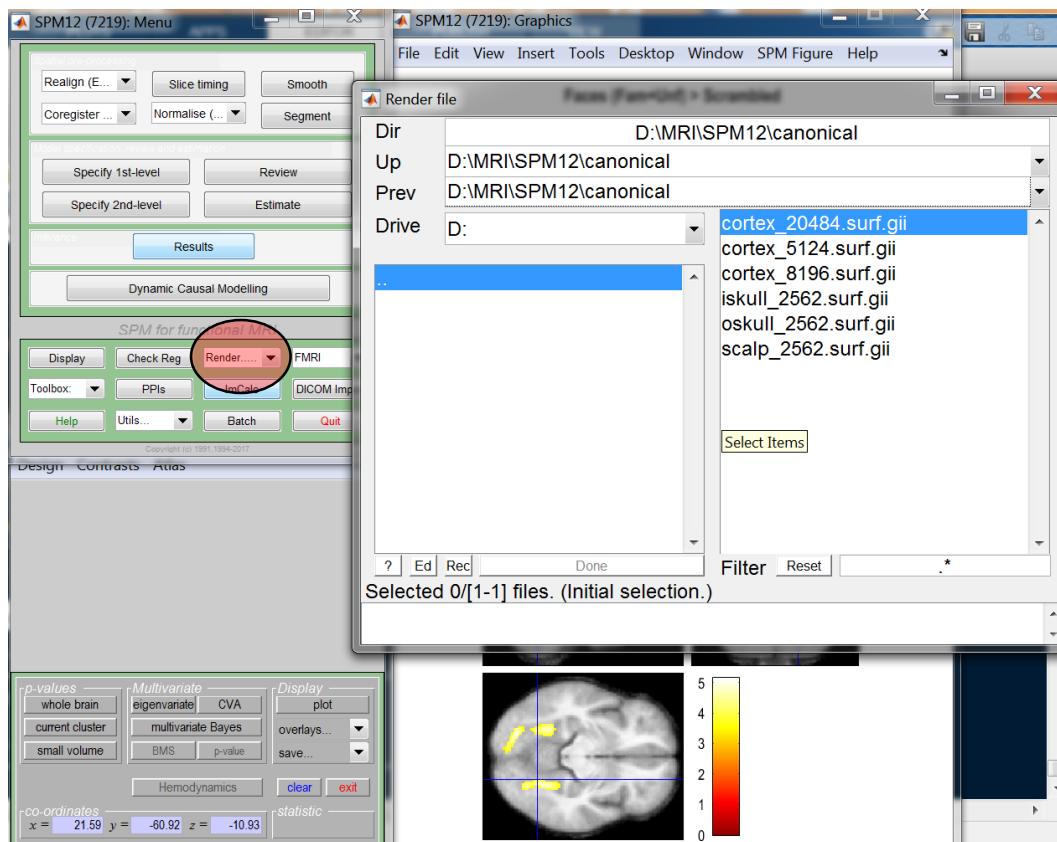
Brains and Blobs

- SPM has good tools for slices



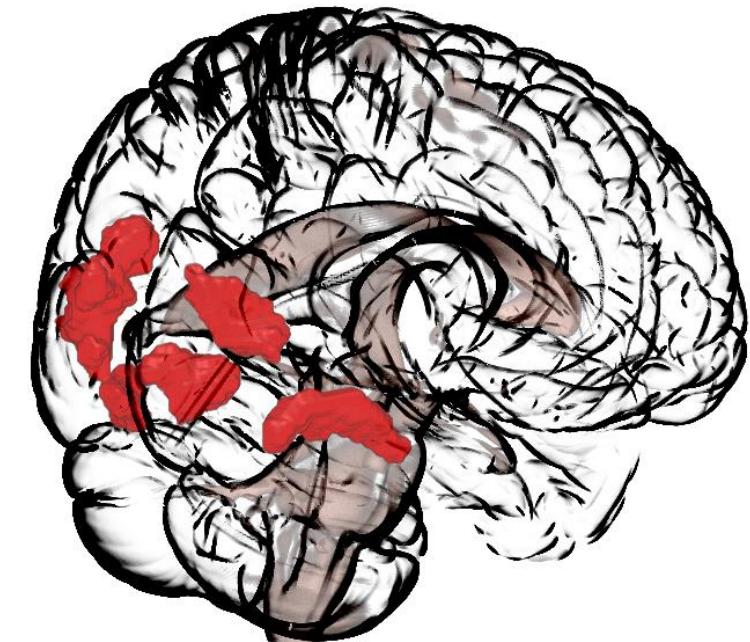
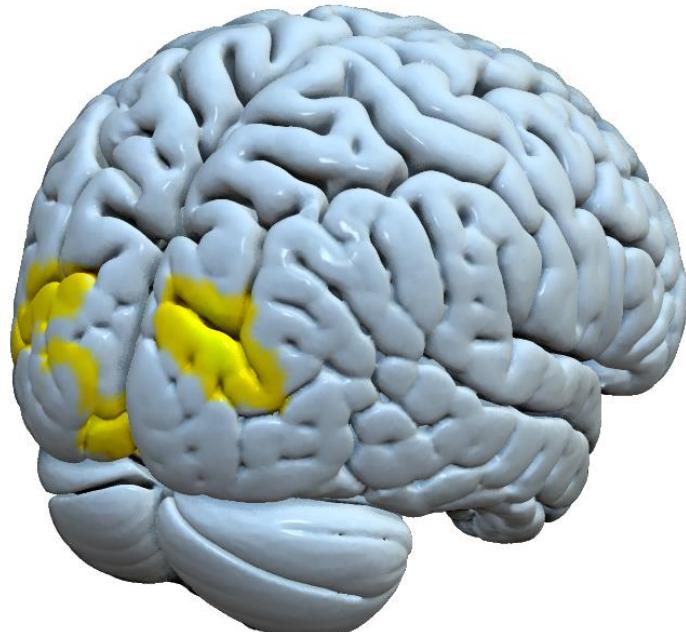
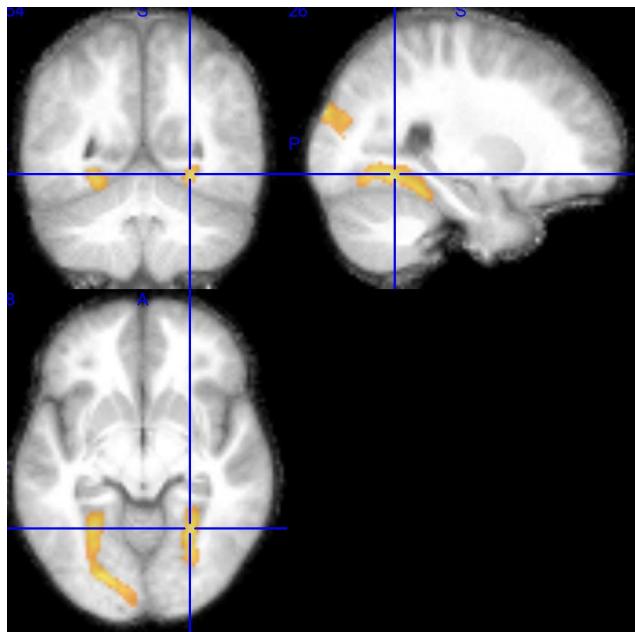
Brains and Blobs

- SPM has different rendering options (including inflated brain)



Brains and Blobs

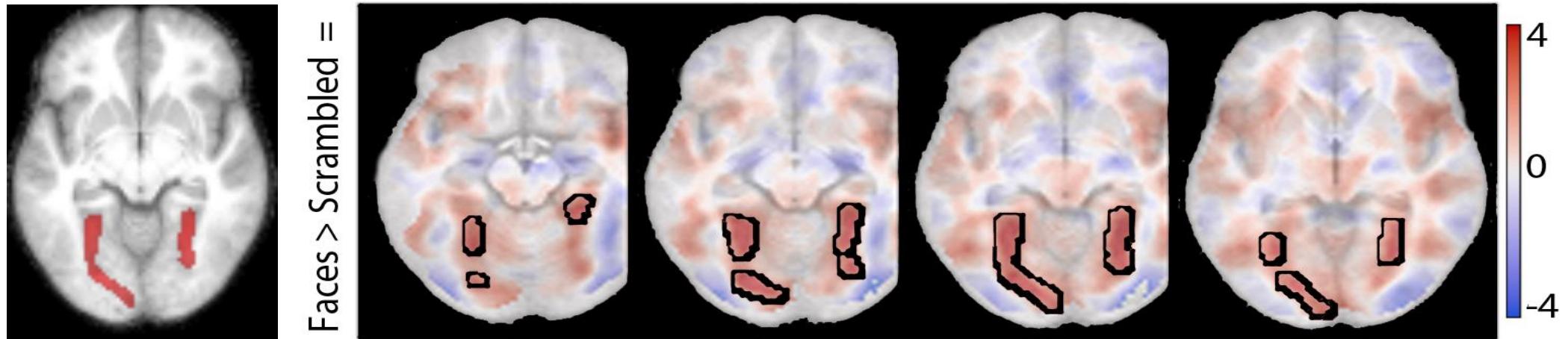
- MRICRoN, MRIcroGL and Surface are ideal companions
→ save thresholded map (result section) and use as overlay



Summary 1

- **What is your message?** *Local effect* = slice vs. *Global pattern* = ‘glass’ brain
- **Local effect:** use an underlay image that reflects the data, e.g. avg wT1
- **Global pattern:** renders don’t show deep structures and deep activations are best shown using cut-offs and slices.
- Use **automated labelling**, but be careful and do check the underlying anatomy: (1) if inference about a cluster then all regions are ‘active’ not just the hot spot in the gyrus you want it to be (2) how many voxels of your cluster of interest are in each gyri/cytoarchitectonic area?

Activation patterns

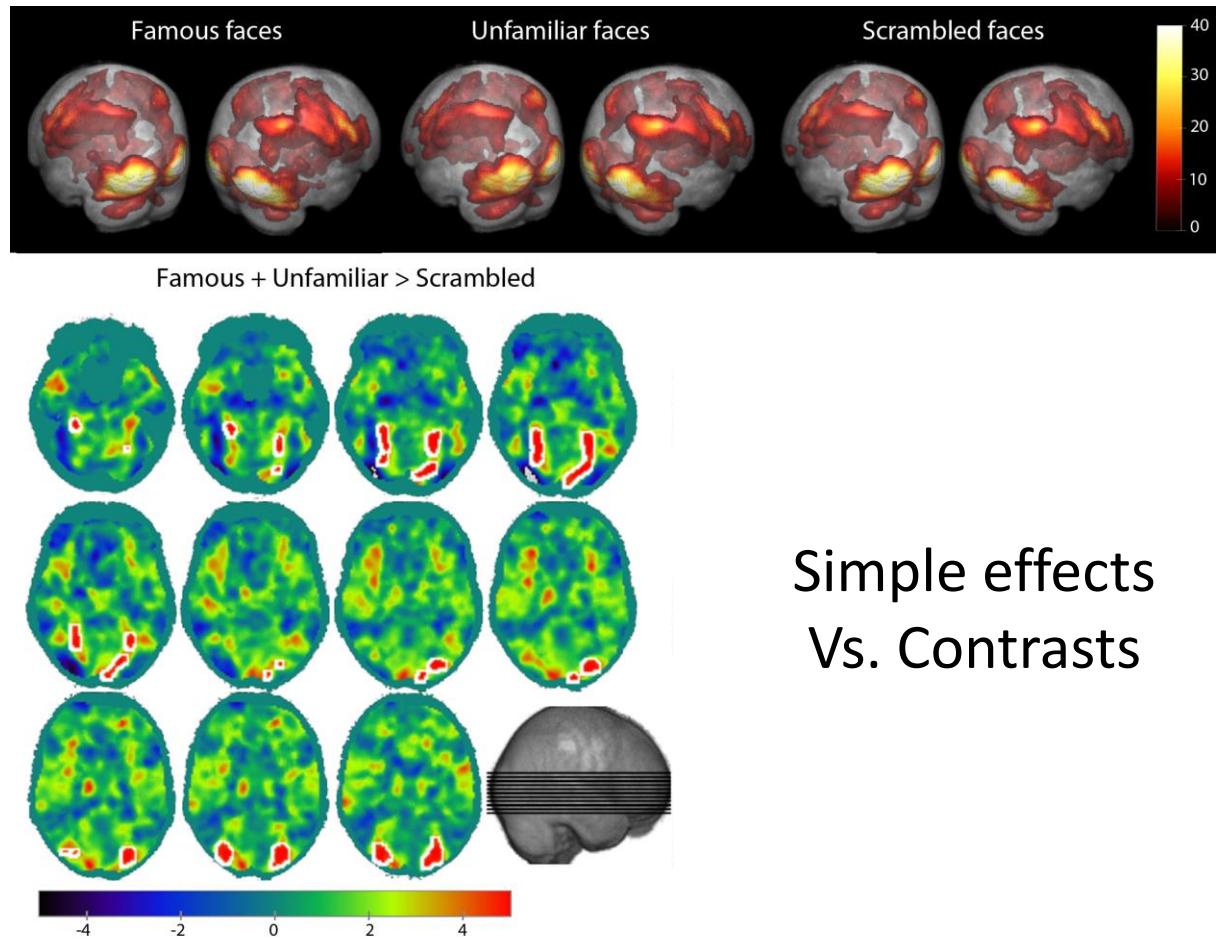


THRESHOLD

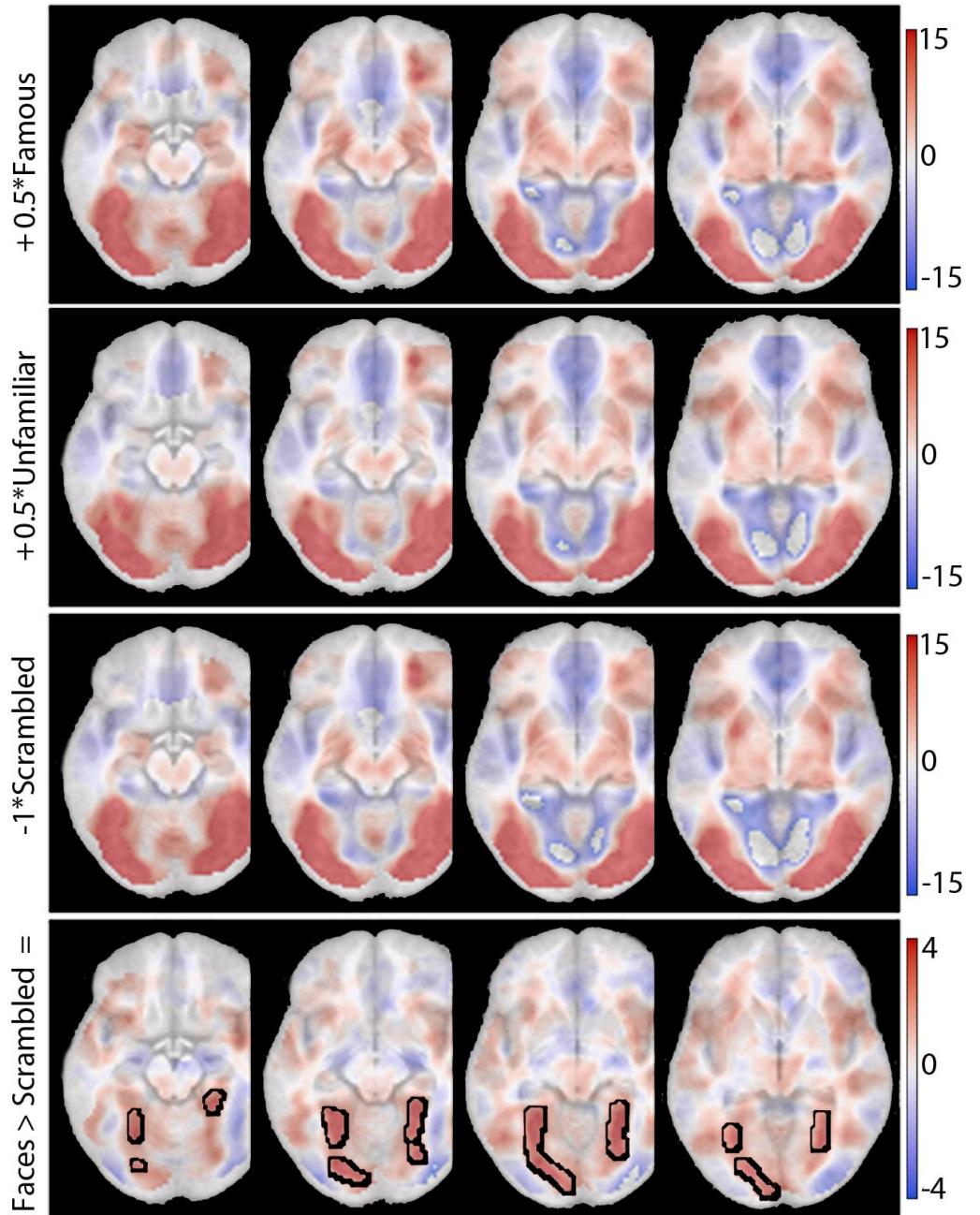
FALSE ANATOMICAL SPECIFICITY

TRULY FOCAL EFFECT SHOWS
ON UNTRESHOLDED MAPS

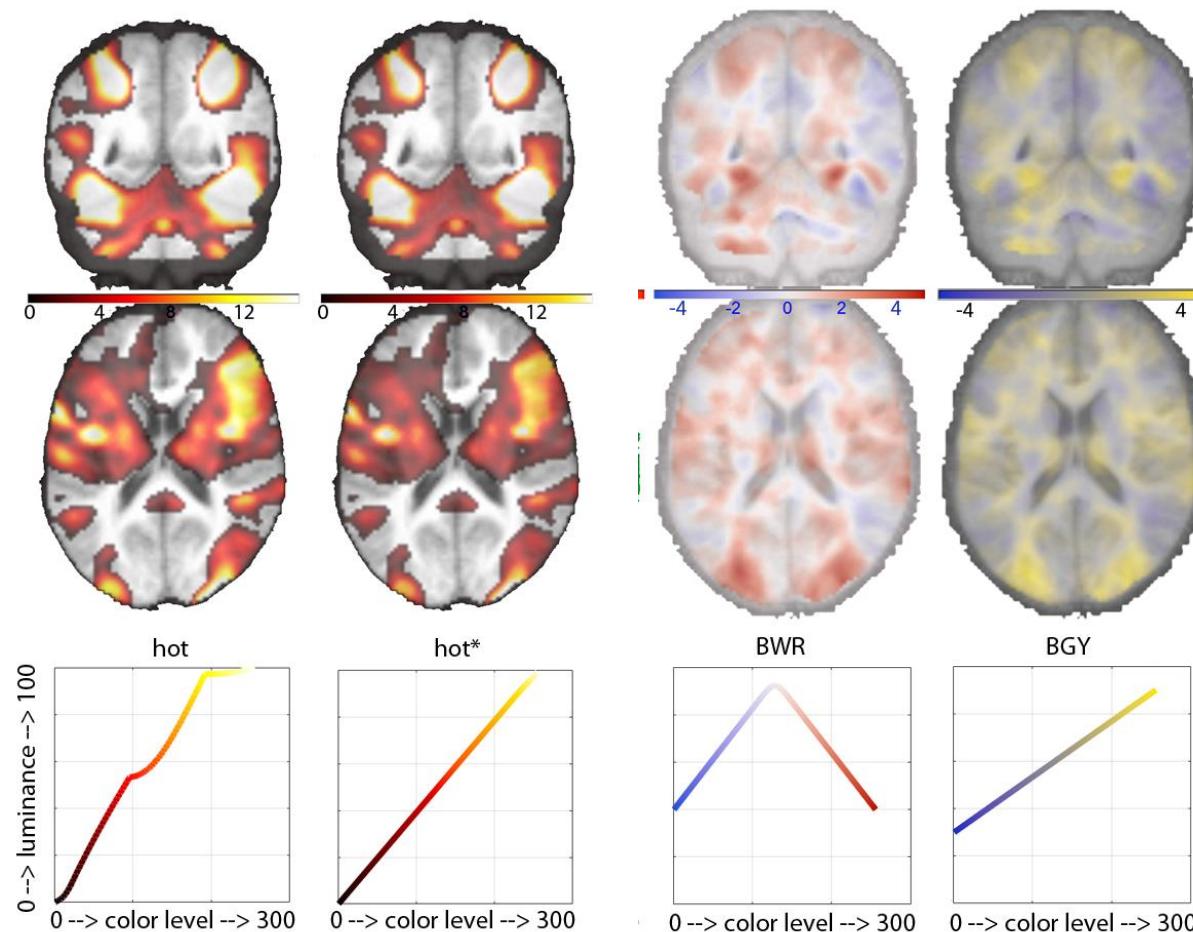
Activation patterns



Simple effects
Vs. Contrasts



Activation patterns



Humans do not perceive RGB → averaging
RGB values does not linearly correspond to
changes in luminance while luminance
changes are better perceived than hue to
reflect magnitude.

CIELAB → Commission Internationale de
l'Eclairage defined a color space
perceptually uniform that relies on
luminance (L^*), red-green (A^* , ~550–700
nm wavelength), and blue-yellow
(B^* , ~400–550 nm wavelength) colours.

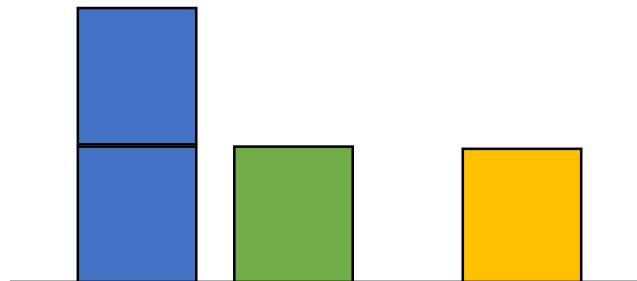
spm_colourmap.m
https://github.com/CPernet/brain_colours

Summary 2

- **Think of what want to show?**
- No activation and specific anatomical activations are better shown on **unthresholded maps!**
- Display **simple effects** (patterns = render) and **contrasts** of interest (local effects - slices)
- **Choose your colour map** based on the data: linear (hot / cool) for (+ / -) contrasts and divergent for unthresholded maps (! Defaults are not (yet) luminance equalized, needs updates, expect for FSL eyes)

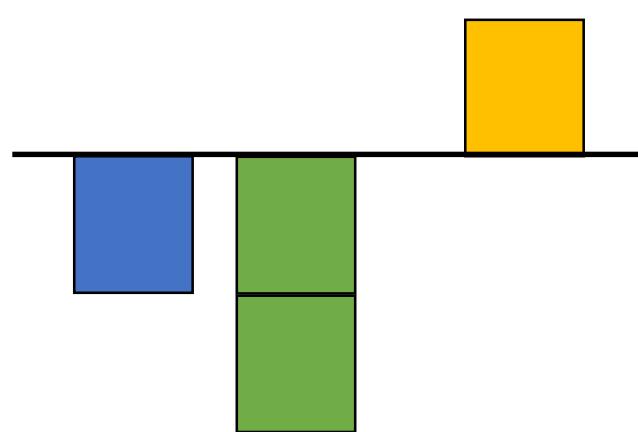
Plotting effects

- Look for each conditions and how this leads to your contrasts
→ physiological / cognitive interpretation depends on this

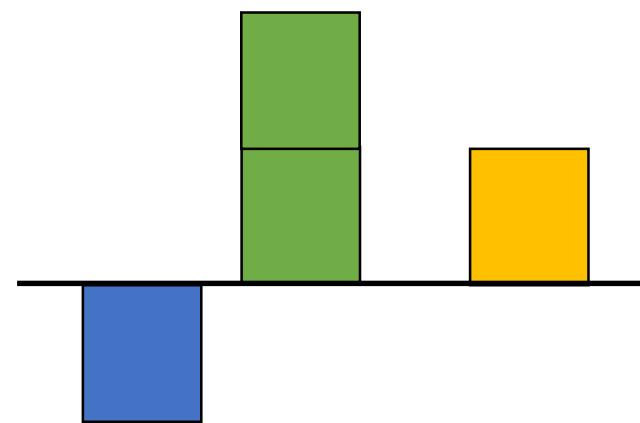


Test A (=2) > B (=1) = C (1)

Contrast [1 -1] ≠ 0



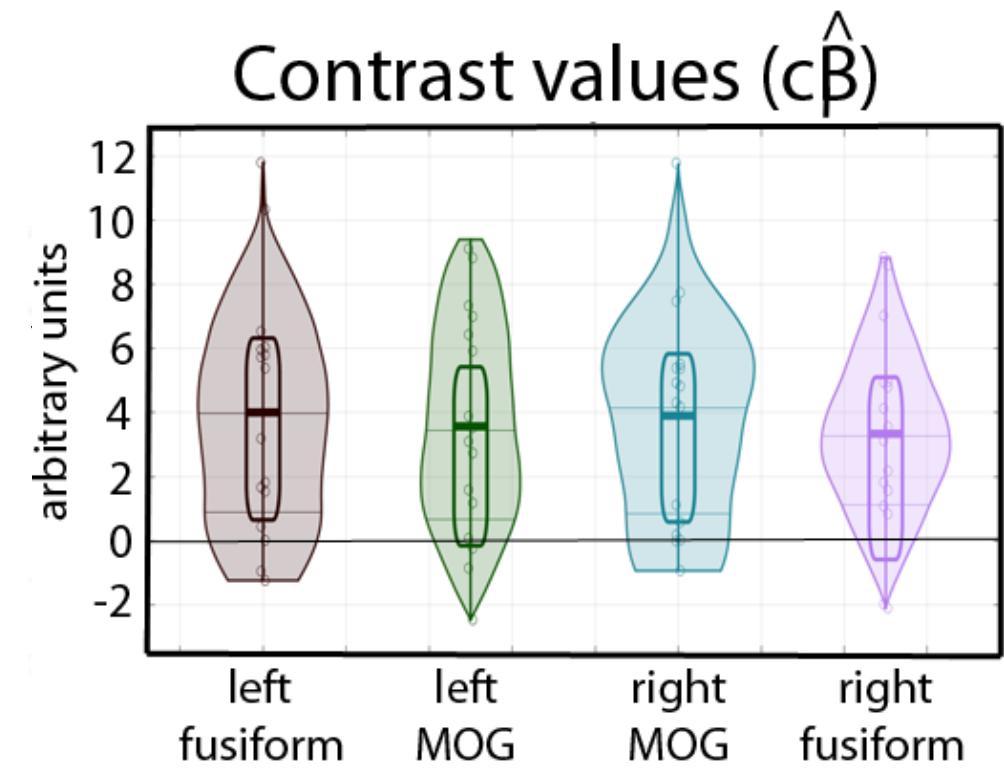
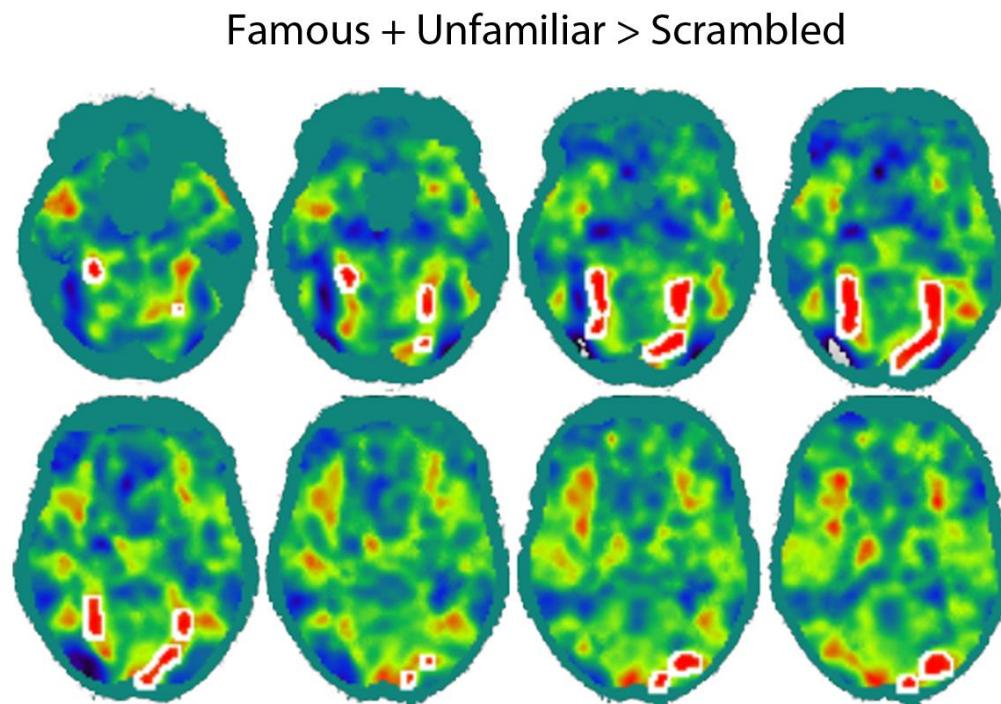
Test A (=−1) > B (−2) = C (1)



Test A (=−1) > B (2) = C (1)

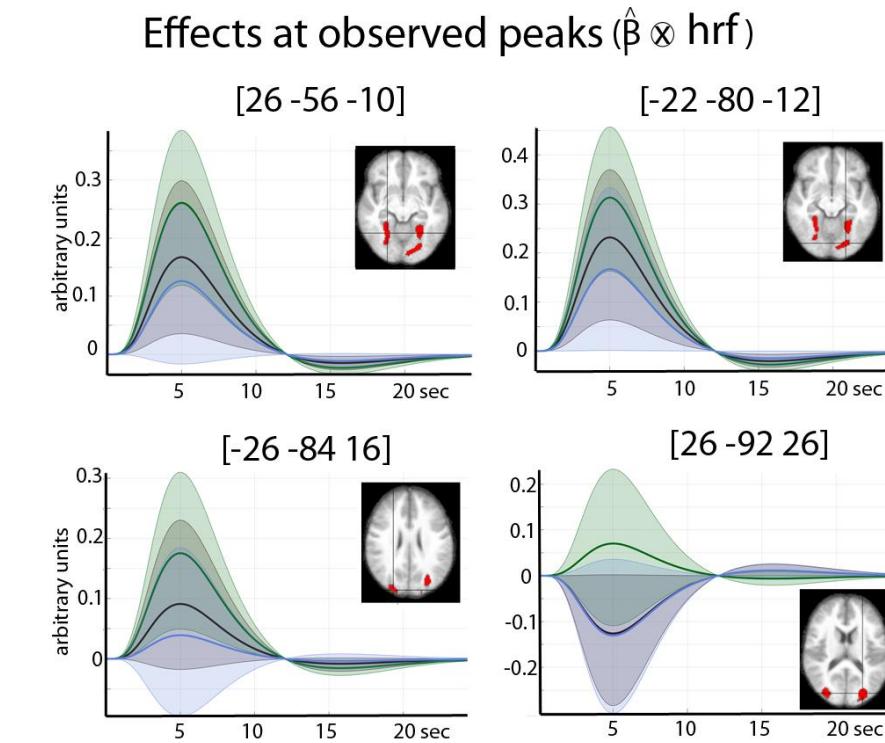
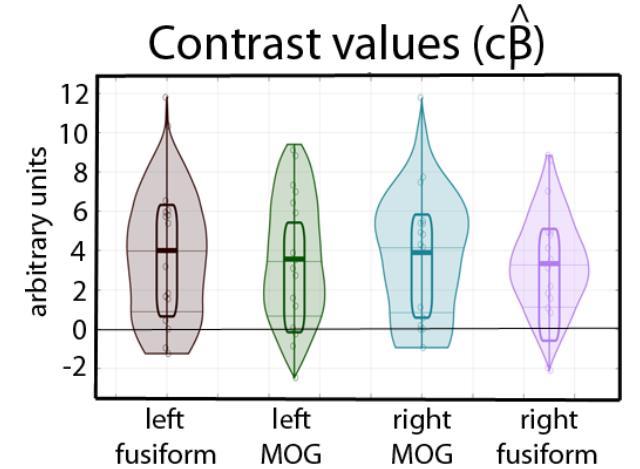
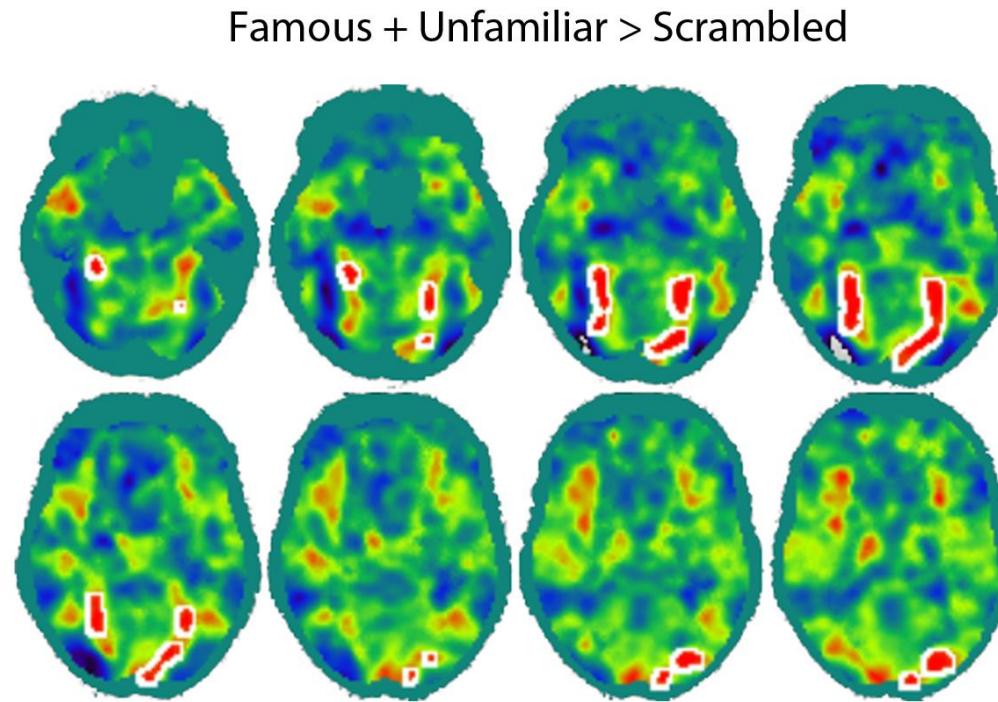
Plotting effects

- Check all blobs!



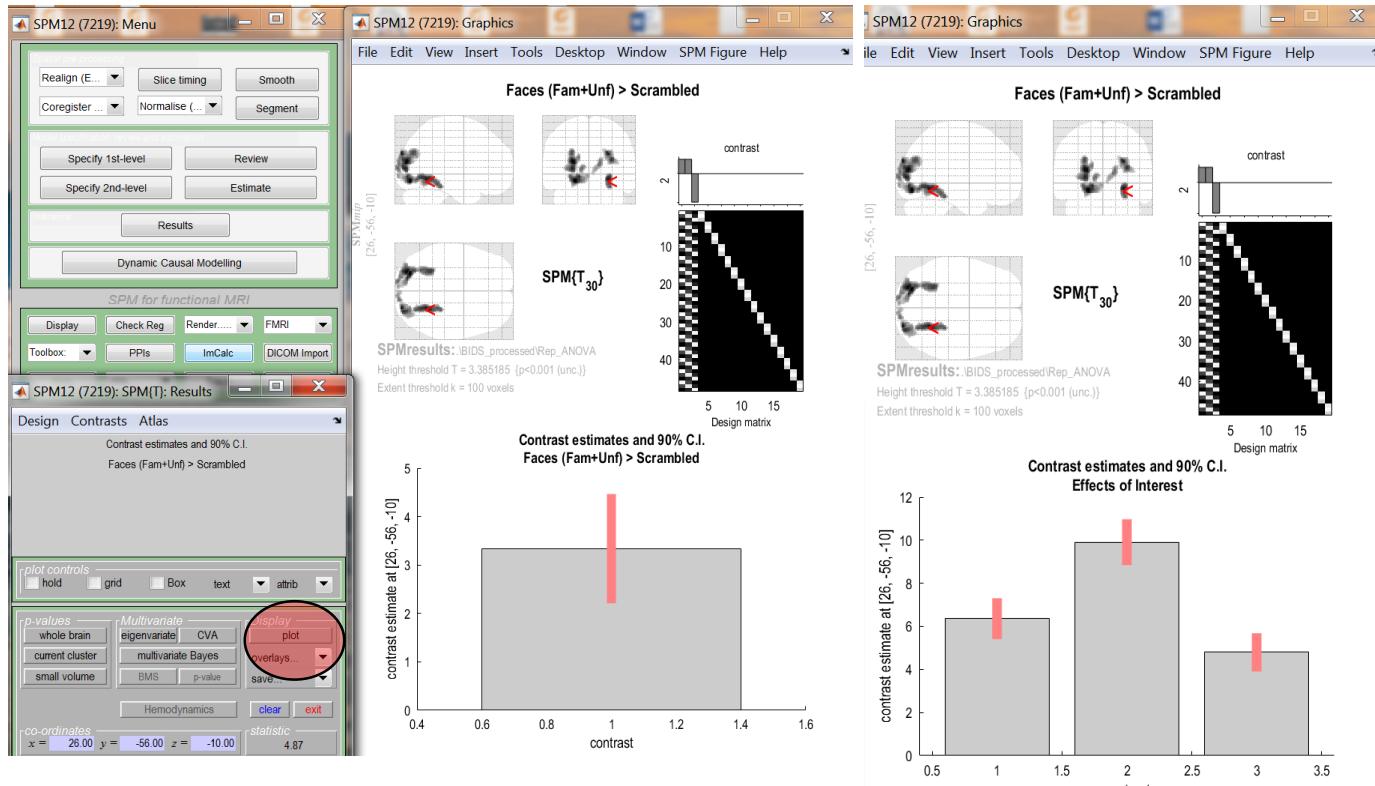
Plotting effects

- Check all blobs!



Plotting effects

- SPM offers a quick way to check effects in each blobs
- Data are returned in workspace

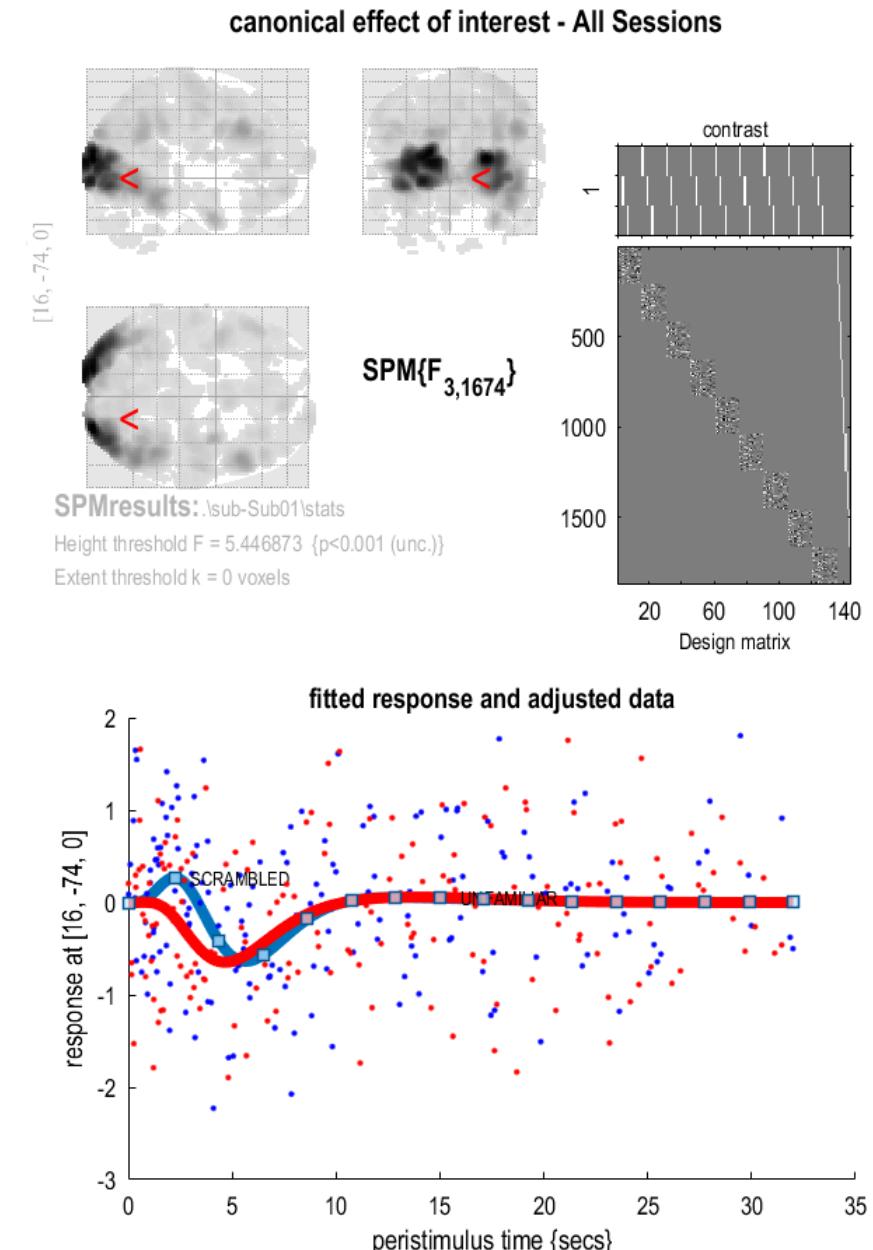


Useful contrast: 'effect of interest' a F-test that spans all columns of the design matrix

```
contrast =  
contrast: [3×1 double]  
standarderror: [3×1 double]  
interval: [3×1 double]  
Y: []  
y: []  
beta: [19×1 double]  
Bcov: [19×19 double]
```

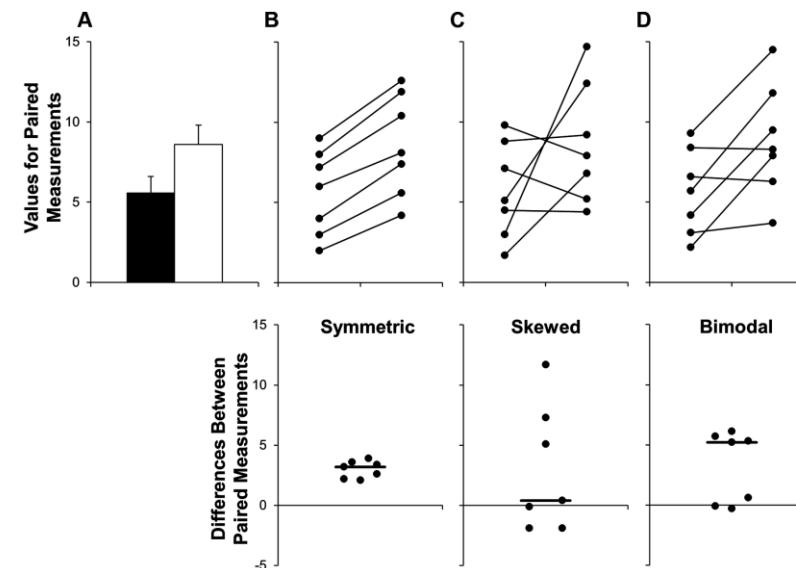
Plotting effects

- Data, predicted data and adjusted data ??
- $Y = XB + e \rightarrow XB$ are the predicted data
 $\rightarrow Y - X(:,[])B$ are adjusted data
- but could be predicted for or adjusted by any column of X , in SPM the data are adjusted for confound (filter at 1st level, sphericity at 2nd level)



Plotting effects

- In general (1) plot the data used at the group level, i.e. beta/con and (2) plot for all simple effects (3) and the contrast
- **spm_summarize** is your go to function to read data from any images in ROI/coordinates
- Plot design → **no bar graph**



Summary 3

- **Show the data**
- Plot the simple effects used to create the contrast of interest
- Each blob need to be looked at! (make csv files and add them as supplementary material / post on an archive)
- Interpret based on simple effects, not based on contrast sign
- No bar graph (quick an easy in SPM to check)

- Pernet and Madan (2019). Data visualization for inference in tomographic brain imaging. EJN <https://psyarxiv.com/egc6q>
- Heickhoff et al. (2007). Assignment of functional activations to probabilistic cytoarchitectonic areas revisited. [NeuroImage, 36, 511-521](#)
- Jernigan TL, et al (2003). More "mapping" in brain mapping: statistical comparison of effects. [Hum Brain Mapp. 19\(2\):90-5](#)
- Weissgerber et al. (2015). Beyond Bar and Line Graph [PLOS One](#)