



Introduction to MRI data processing

MaRBEL educational
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Who am I?



- ▶ Master in Electrical Engineering, then PhD. in Engineering
- ▶ Now FRS-FNRS Research Director & Professor
- ▶ Research and interest in “neuroimaging methods”
→ data processing of brain images (MRI and PET) and
electro-physiological data (M/EEG)
- ▶ Linked to:
 - “GIGA CRC human imaging” research units
 - “GIGA in vivo imaging” technical platform.
 - Department of Electrical Engineering & Computer Science



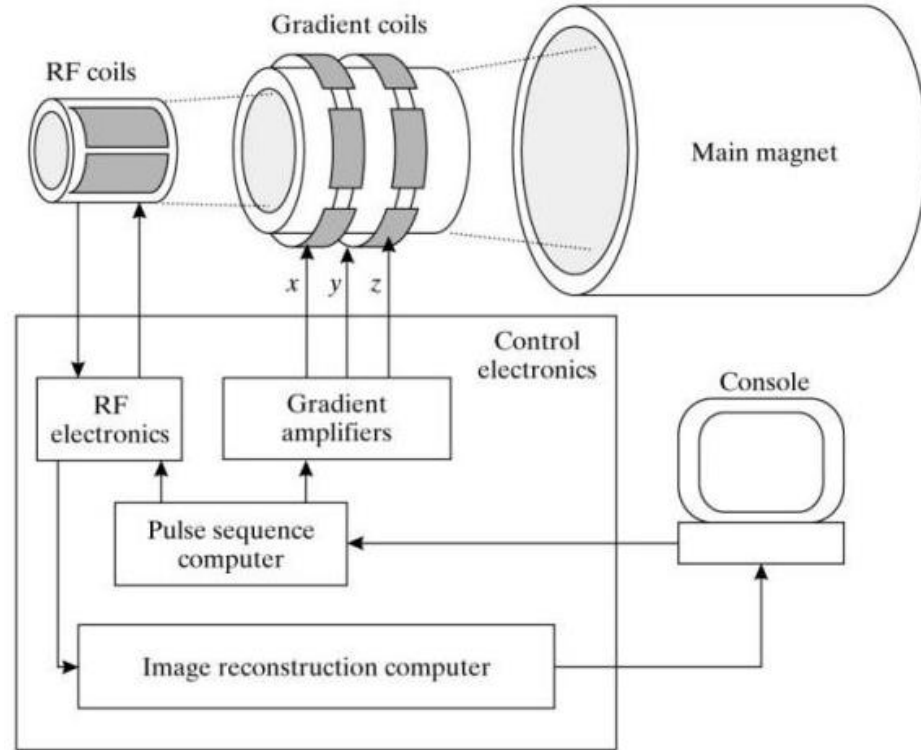
Program

- ▶ MRI “flavours”
- ▶ MRI data processing
 - Within-/between-subject processing
 - Subject-/reference-space
 - Statistical inference
- ▶ “Vanilla fMRI protocol” example
- ▶ Take home message

MR scanner



- ▶ big magnet
→ e.g. 1.5, 3 or 7T
- ▶ antenna, aka. RF coil
→ emit/receive RF signal
- ▶ gradient coils
→ small linear changes
- ▶ electronics & computer
→ control & image reconstruction



MR imaging



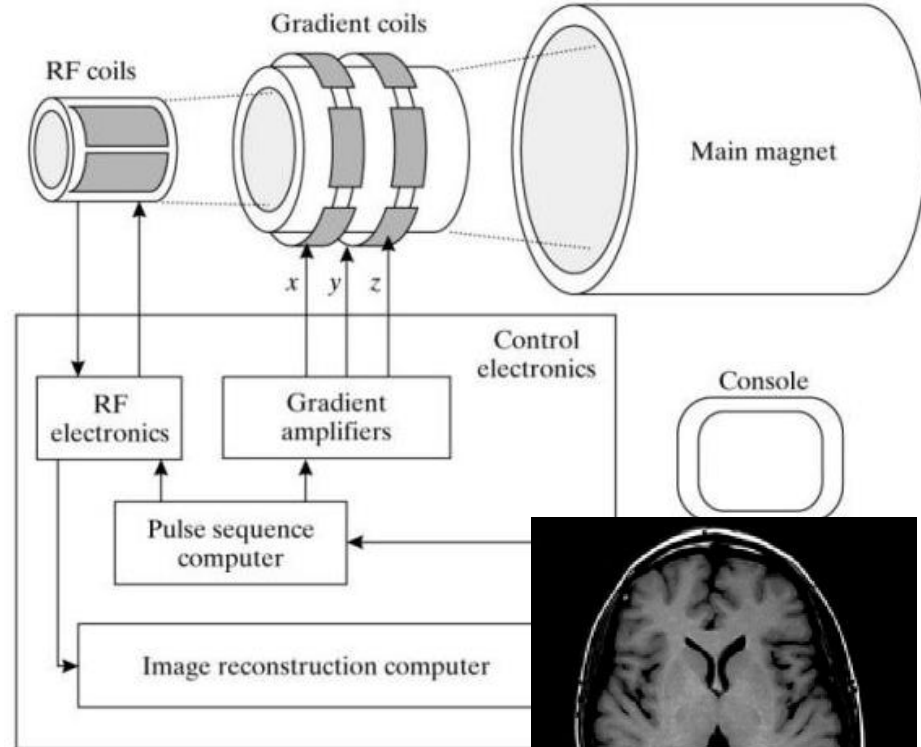
Image obtained according to

► *Pulse sequence*

- RF emission & reception
→ *signal weighting*
- linear magnetic gradient (in mT/m)
→ local variation of *frequency & phase*
→ spatial encoding

► *Image reconstruction*

→ images with “different flavours” & properties



MRI “flavours”



Signal intensity “linked” to tissue properties

- ▶ Anatomical MRI
- ▶ Functional MRI
- ▶ Diffusion-weighted MRI
- ▶ Quantitative MRI
- ▶ CEST/QSM/spectroscopy/...

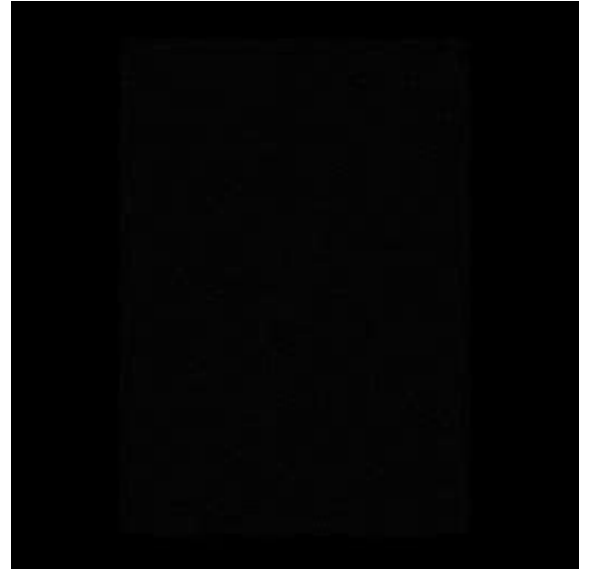
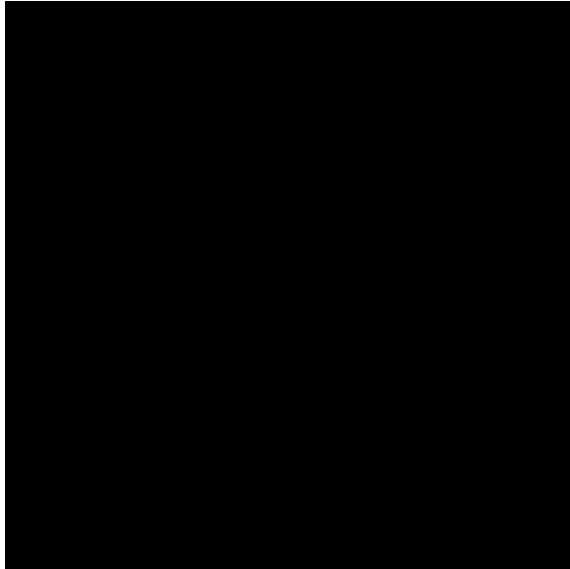
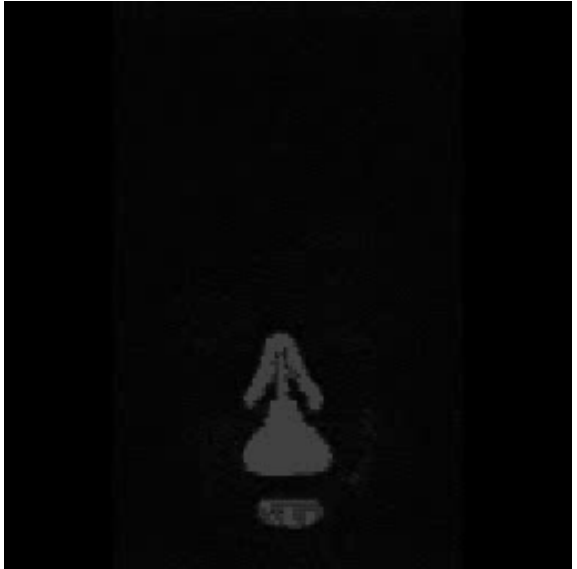
Anatomical MRI



Characteristics (typical)

- ▶ Voxel size,
 - at 3T, 1mm → 1mm³
 - at 7T, .5-.8mm → .25-.5mm³
- ▶ Acquisition time:
a few minutes
- ▶ Contrast between GM, WM, CSF, “other tissues”

Anatomical MRI





Characteristics (typical)

- ▶ Voxel size,
 - at 3T, $\sim 1\text{mm} \rightarrow \sim 1\text{mm}^3$
 - at 7T, $.5\text{-}.8\text{mm} \rightarrow .25\text{-}.5\text{mm}^3$
- ▶ Acquisition time:
a few minutes
- ▶ Contrast between GM, WM, CSF, “other tissues”

Applications

- ▶ Morphometric study
- ▶ Lesion detection
- ▶ Anatomical reference
- ▶ Inter-subject anatomical alignment
- ▶ ...

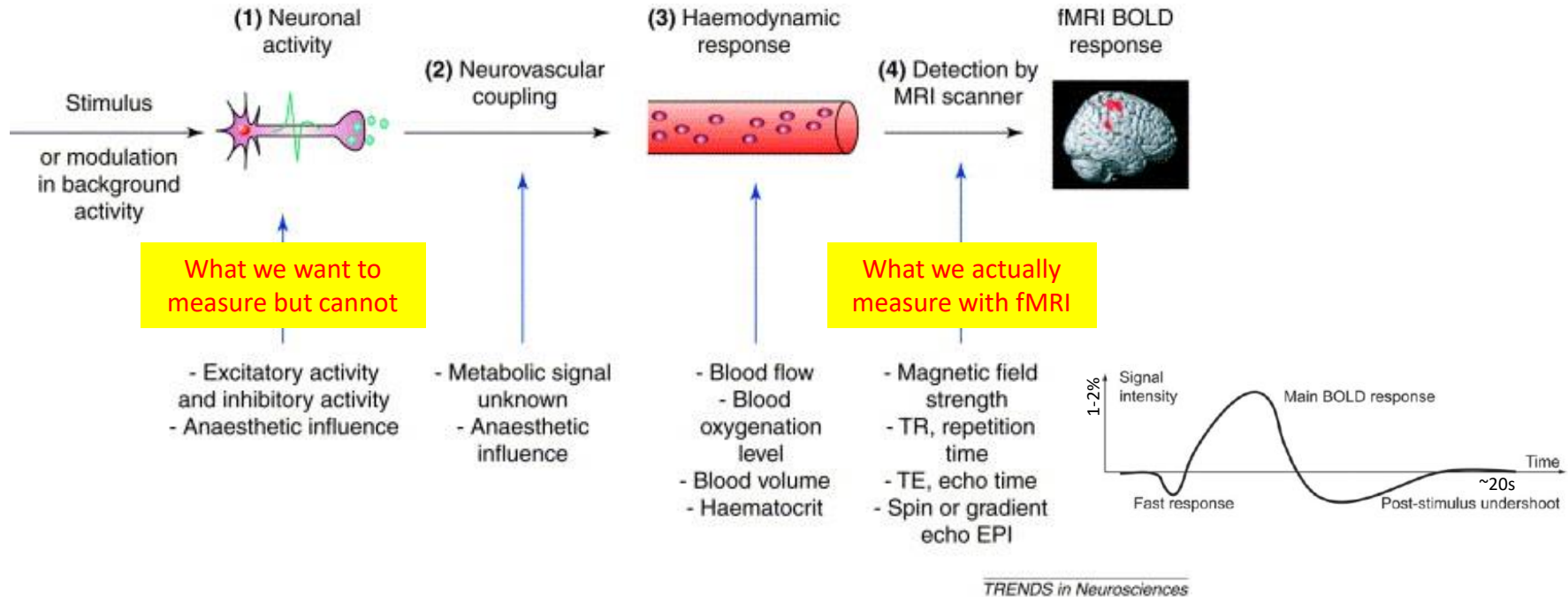
Functional MRI



Characteristics (typical)

- ▶ Voxel size,
 - at 3T, 2-3mm \rightarrow 8-27mm³
 - at 7T, 1-2mm \rightarrow 1-8mm³
- ▶ Acquisition time, from 1 to 3 seconds/image (but continuous acquisition over 5-30 minutes)
- ▶ Signal intensity variation according to neuronal activation time course

Of neurons, blood & haemoglobin



Interpretation:

Image (slightly) brighter where & when (but delay!) neurons are active.



Characteristics (typical)

- ▶ Voxel size,
 - at 3T, 2-3mm \rightarrow 8-27mm³
 - at 7T, 1-2mm \rightarrow 1-8mm³
- ▶ Acquisition time, from 1 to 3 seconds/image (but continuous acquisition over 5-10 minutes)
- ▶ Signal intensity variation according to neuronal activation time course

Applications

- ▶ Activation localisation
- ▶ Experimental manipulation of activation (age, fatigue, learning,...)
- ▶ Functional/effective connectivity analysis
- ▶ Brain activity decoding
- ▶ ...

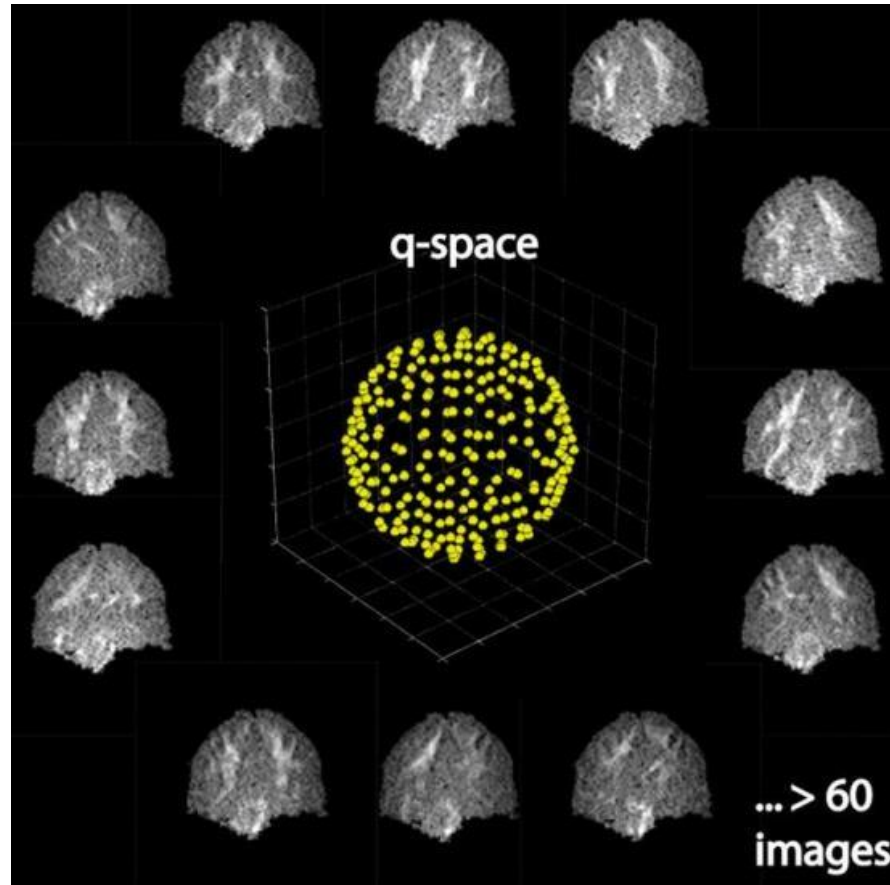
Diffusion-weighted MRI



Characteristics (typical)

- ▶ Voxel size,
at 3T & 7T, 2-3mm \rightarrow 8-27mm³
- ▶ Acquisition time, from 1 to 3
seconds/image (but need 20+
images)
- ▶ Signal intensity decrease
according to diffusion of (free)
water in direction “poked”

Diffusion-weighted MRI



Diffusion-weighted MRI



Characteristics (typical)

- ▶ Voxel size,
at 3T & 7T, 2-3mm \rightarrow 8-27mm³
- ▶ Acquisition time, from 1 to 3
seconds/image (but need 20+
images)
- ▶ Signal intensity variation
according to diffusion of (free)
water in direction “poked”

Applications

- ▶ Model water diffusion,
i.e. proxy to axon orientation & density
- ▶ WM properties, e.g. tissue
integrity
- ▶ Anatomical WM connectivity
- ▶ Correlation and group
comparison analysis
- ▶ ...

Quantitative MRI



Characteristics (typical)

- ▶ Voxel size,
 - at 3T, .8-1mm \rightarrow .5-1mm³
 - at 7T, .5-.8mm \rightarrow .13-.5mm³
 - ▶ Acquisition time: 10 to 30 minutes (for whole protocol)
 - ▶ Multiple series of
 - T1-/PD-/MT-weighted images
 - B0/B1 maps
- ➔ quantification of tissue properties

Quantitative MRI interpretation



Water
Content

Water Content;
Macromolecules,
e.g. myelin; Iron

Macromolecules
e.g. myelin

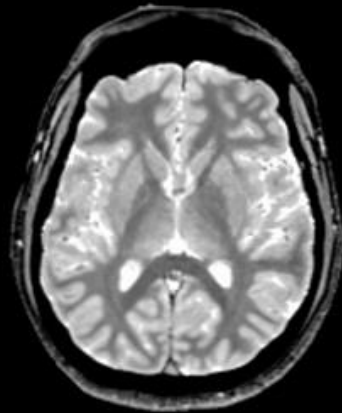
Iron

40p.u. 100p.u.

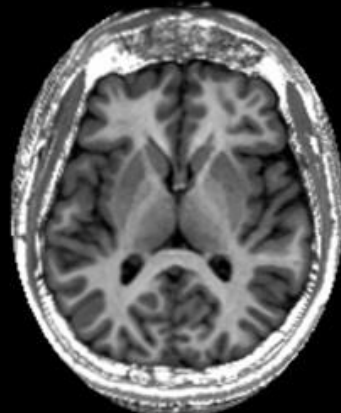
0.2s⁻¹ 1.5s⁻¹

0.2p.u. 2.2p.u.

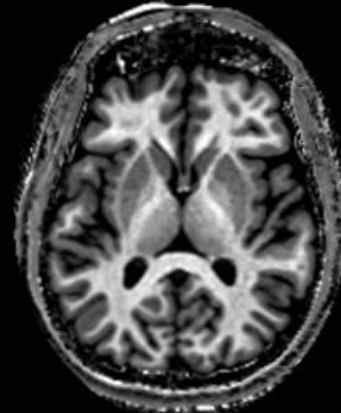
0s⁻¹ 50s⁻¹



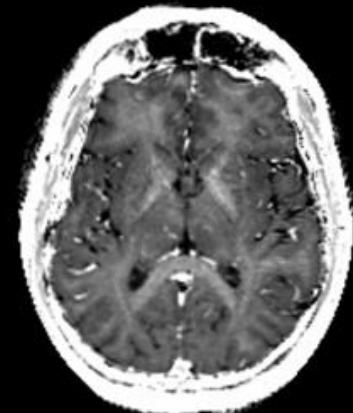
PD*



R1



MT



R2*

Quantitative MRI



Characteristics (typical)

- ▶ Voxel size,
 - at 3T, .8-1mm \rightarrow .5-1mm³
 - at 7T, .5-.8mm \rightarrow .13-.5mm³
- ▶ Acquisition time: 10 to 30 minutes (for whole protocol)
- ▶ Multiple series of
 - T1-/PD-/MT-weighted images
 - B0/B1 maps
- ➔ quantification of tissue properties

Applications

- ▶ Tissue property analysis, e.g. correlation, difference, longitudinal changes,...
- ▶ Lesion detection & characterization
- ▶ Morphometric study
- ▶ Multi-scanner/centre study
- ▶ ...



Other sequences...

- ▶ Chemical Exchange Saturation Transfer (CEST) MRI
 - ➔ molecular/metabolite concentration mapping
- ▶ Quantitative Susceptibility Mapping (QSM) MRI
 - ➔ iron deposit & calcification mapping
- ▶ MRI Spectroscopy
 - ➔ (chemical) metabolism & other nuclei mapping
- ▶ ...



Program

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- ▶ MRI data processing
 - Within- /between-subject processing
 - Subject-/reference-space
 - Statistical inference
- ▶ “Vanilla fMRI protocol” example
- ▶ Take home message

Research in neuroscience



Neuroscientific question about the brain

- ▶ Acquire data from “many” subjects
- ▶ Grouping
 - single group ?
 - ➔ within group activation, regression with continuous variable,...
 - 2 or more groups ? ➔ group comparisons, regression, interaction,...
- ▶ Sessions
 - 1 session ➔ cross-sectional study
 - sessions at t_0, t_1, t_2, \dots ➔ longitudinal study

Within AND between subject processing

Within-/between-subject



Within-subject, i.e. using data from a single-subject

▶ Spatial processing:

- Image alignment & “coregistration” SS
- Artifacts detection & correction
- Segmentation & “spatial normalisation” (=warp into reference space)

- smoothing SS or RS

▶ Modelling

- Create parametric “map of interest”
- Statistical inference

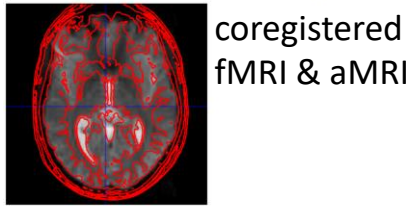
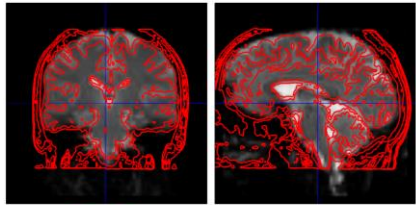
▶ In subject-space (SS), reference-space (RS) or either one.

Spatial processing: within-subject

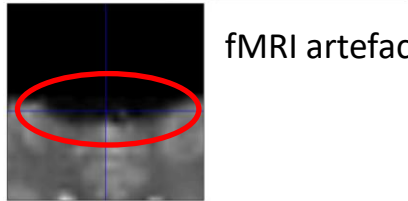
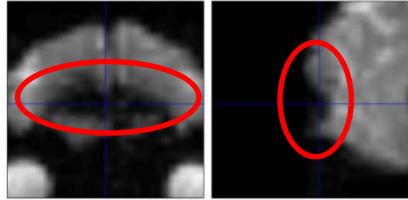
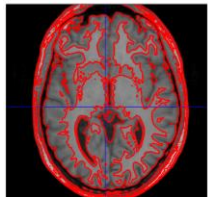
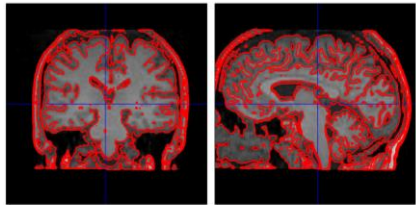


- ▶ “Rigid-body” transformation
 - Intra-modality, e.g. fMRI series, *realignment*
 - Inter-modality, e.g. (mean) fMRI and aMRI, *coregistration*
- ▶ Elastic transformation
 - Segmentation & “spatial normalisation” → typically aMRI
 - Image deformation correction, i.e. “unwarping” → fMRI & DW-MRI (“Field mapping” or “Top-Up” but needs extra data!)
- ▶ Smoothing, i.e. reduce variability → maps for statistical analysis

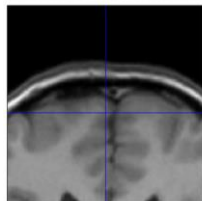
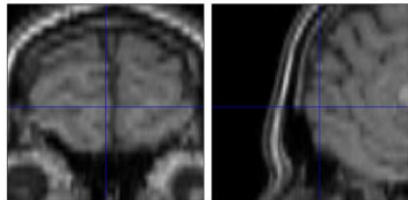
Spatial processing: within-subject



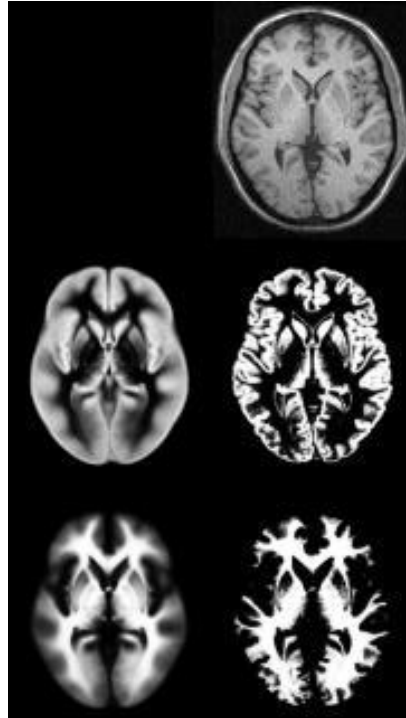
coregistered
fMRI & aMRI



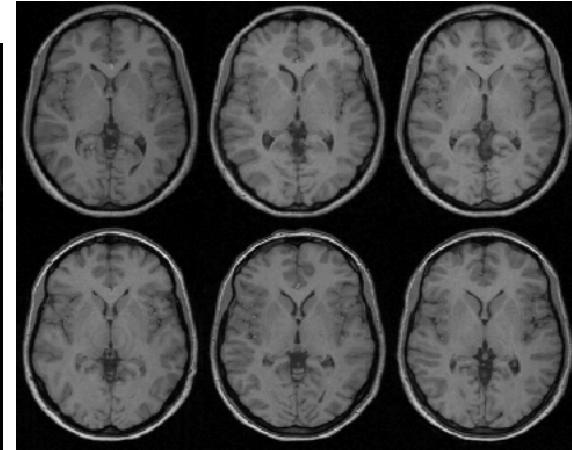
fMRI artefact



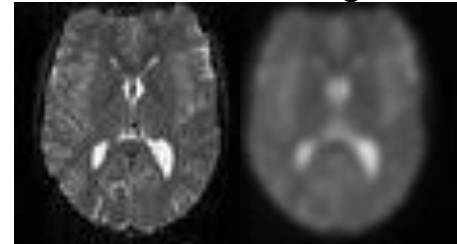
1 subject's normalized &
segmented aMRI + TPMs



6 subjects' normalized aMRI



fMRI smoothing



Within-/between-subject



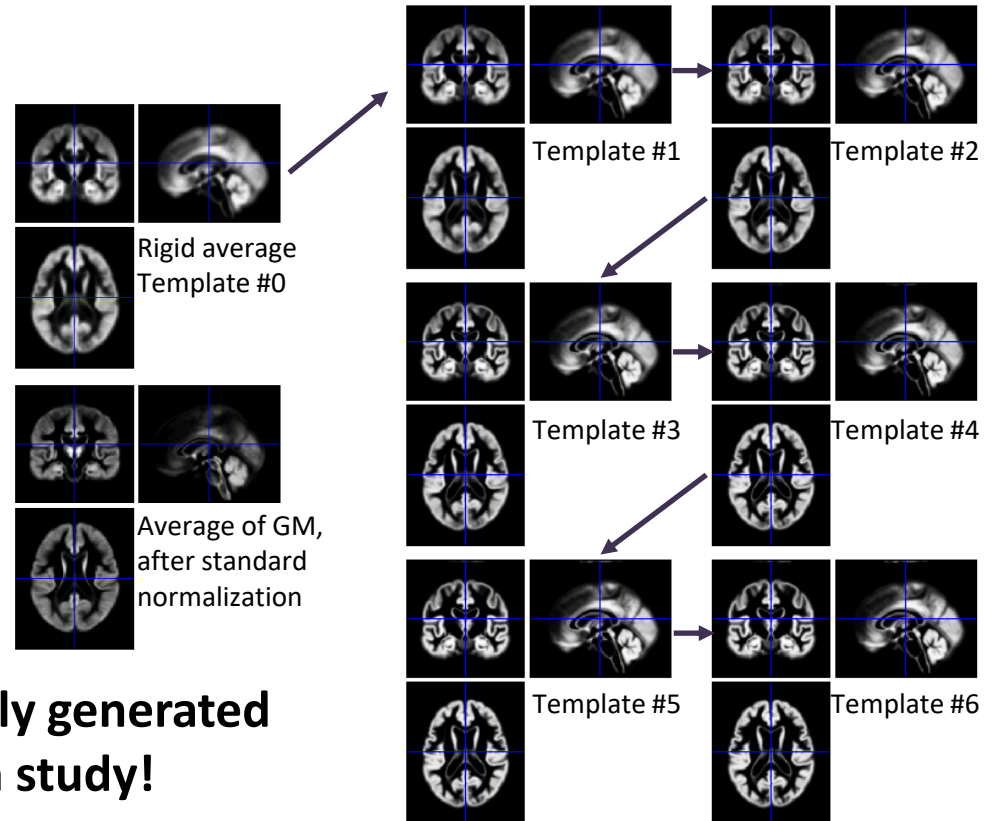
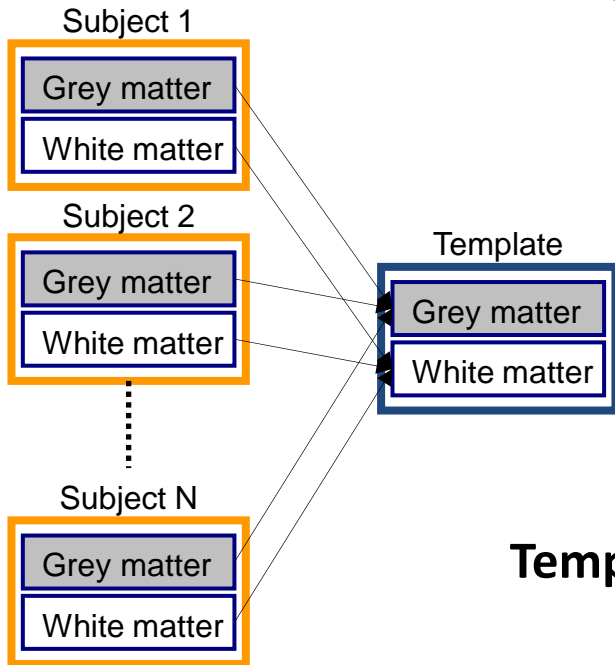
Between-subject, i.e. using data from all subjects

- ▶ Spatial processing
 - Warping individual maps into “group average” reference space
- ▶ Modelling
 - Group-level model
 - Statistical inference
- ▶ **In reference-space (RS)**
 - ➔ Atlas and standardized coordinates
 - ➔ Multi-subject analysis

Spatial processing: between-subject



- ▶ More flexible elastic, i.e. diffeomorphic, transformation
→ typically segmented aMRI for *VBM analysis*



Template implicitly generated from data in study!

Modelling: within-subject fMRI



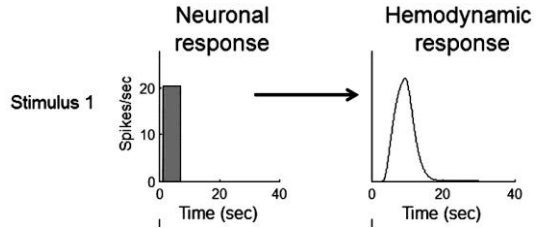
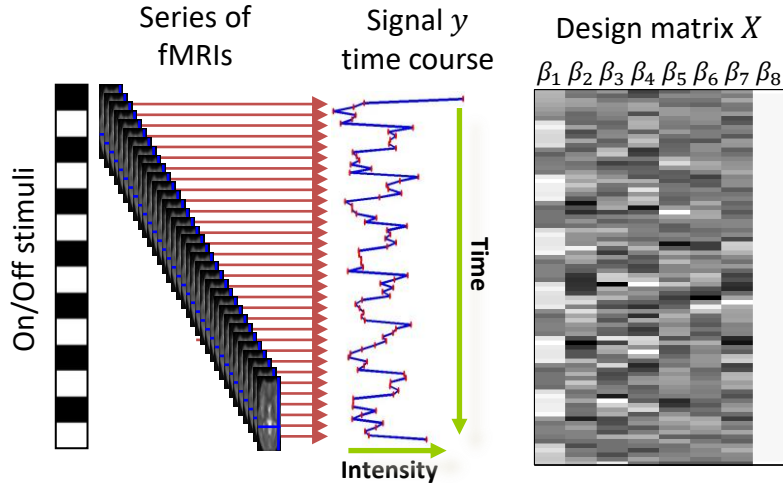
fMRI time-series modelling, i.e. General Linear Model (GLM)

- ▶ Model the signal (variance) based on $y = X\beta + e$
 - experimental protocol, e.g. stimuli, conditions, actions,...
 - confounding effects, e.g. haemodynamic response, movement,...
- ▶ Model the noise distribution C_i : noise level + autocorrelation signal
- ▶ Estimate the model parameters $\hat{\beta}$ $e_i \sim N(0, C_i)$
- ▶ Build **effect of interest** \rightarrow linear contrast of parameters $c^T \hat{\beta}$
- ▶ Statistical inference of contrast value, with t-/F-test \rightarrow **objectively detect “effect of interest”**

Modelling: within-subject fMRI

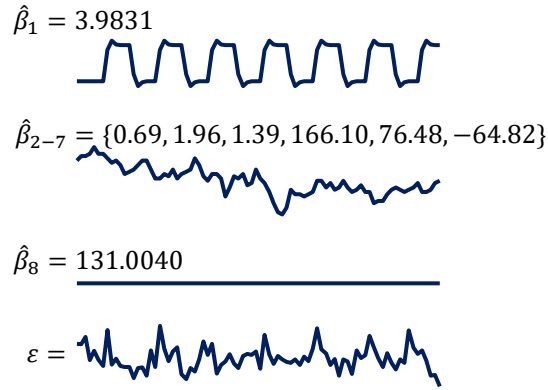
$$y = X\beta + e$$

$$e_i \sim N(0, C_i)$$



$$\hat{\beta} = (X^T C^{-1} X)^{-1} X^T C^{-1} y$$

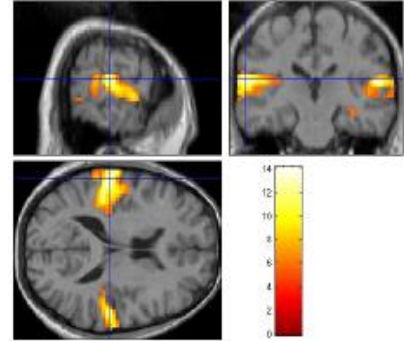
$$\hat{\beta} \sim N(\beta, \sigma^2 (X^T C^{-1} X)^{-1})$$



T-test on effect of interest

$$t = \frac{c^T \hat{\beta}}{\sqrt{\text{var}(c^T \hat{\beta})}}$$

Height threshold $T = 3.2057$ $\{p < 0.001\}$

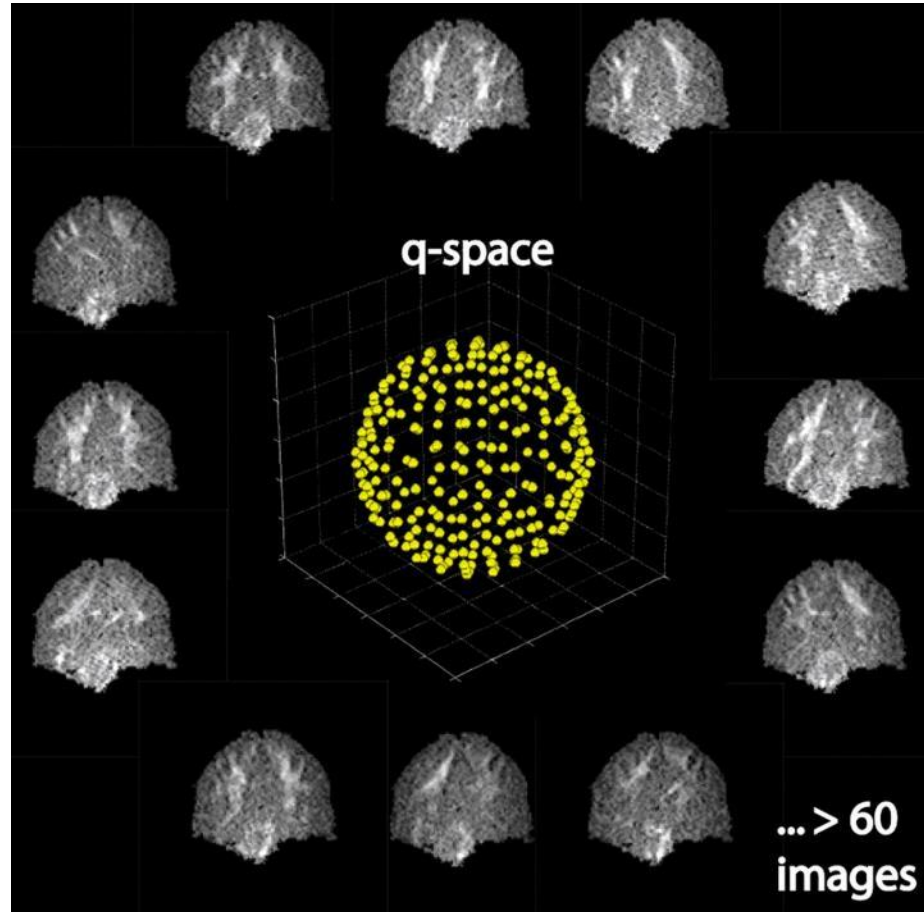


Diffusion-weighted MRI



20+ images acquired

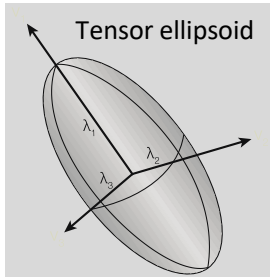
- ▶ No gradient = reference signal
- ▶ With gradient to dephase-rephase signal
→ signal loss due to water-diffusion
- ▶ 1 image = 1 diffusion direction 'poked'



Modelling: within-subject DW-MRI

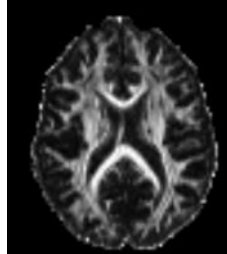
Fit tensor model to DWI data, i.e. **DTI**

- ▶ 6 parameters per voxel, i.e. 3D ellipsoid



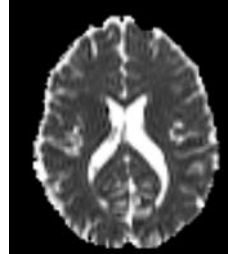
$$\begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{xy} & D_{yy} & D_{yz} \\ D_{xz} & D_{yz} & D_{zz} \end{bmatrix}$$

Fractional anisotropy

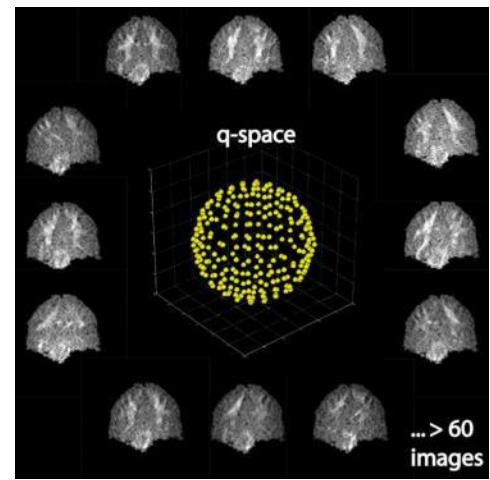


Reflects directionality of diffusion

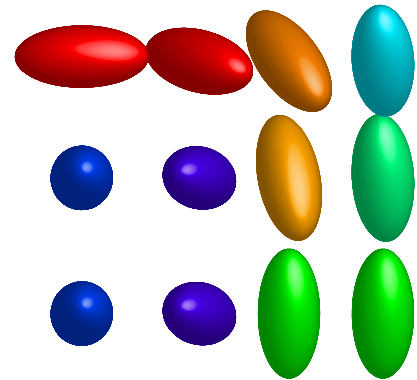
Mean diffusivity



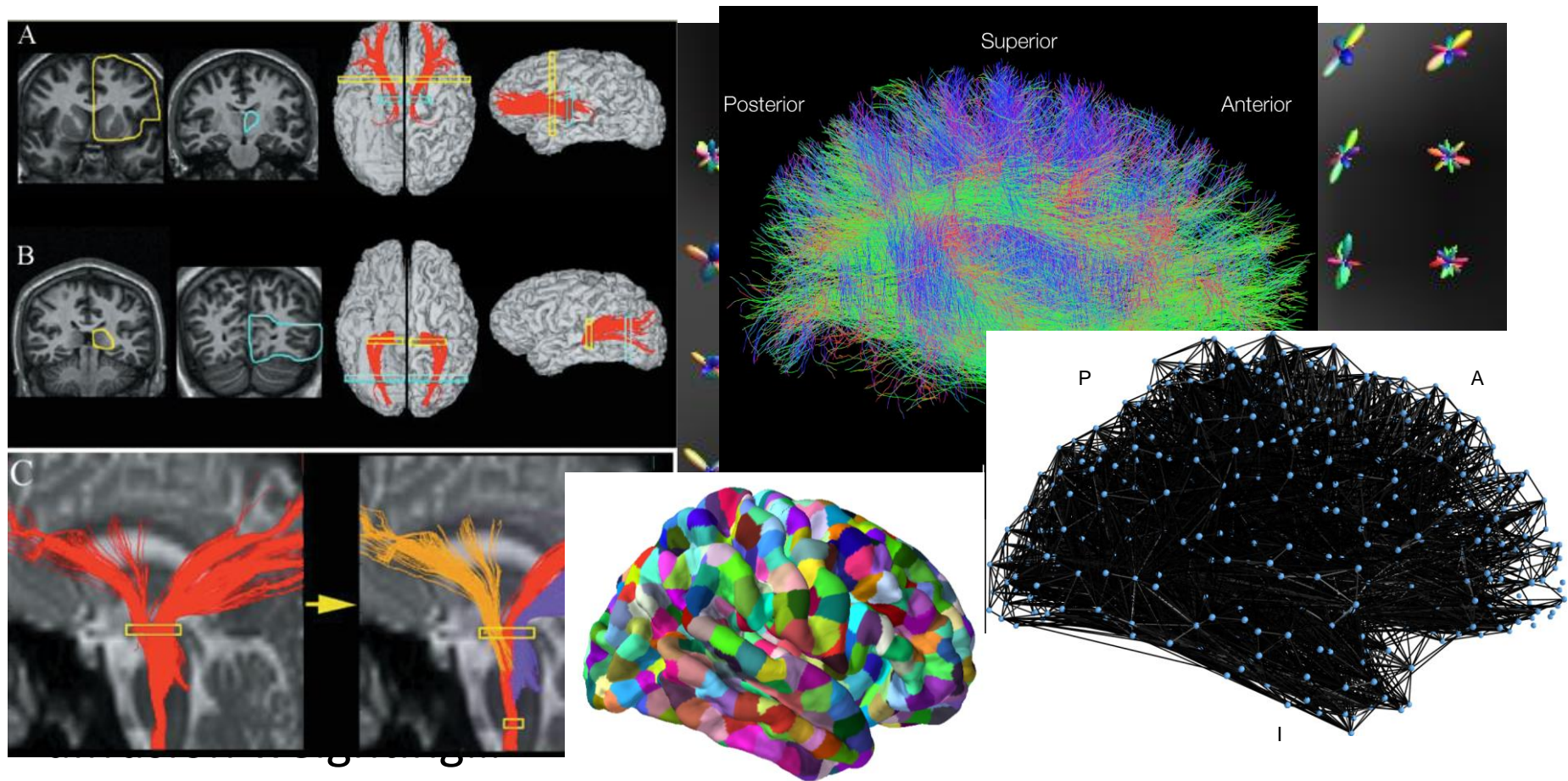
Reflects strength of diffusion



- ▶ Derive scalar map(s)
➔ “interpretable” values
- ▶ Fiber tracking



Fiber orientation distributions & connectomics



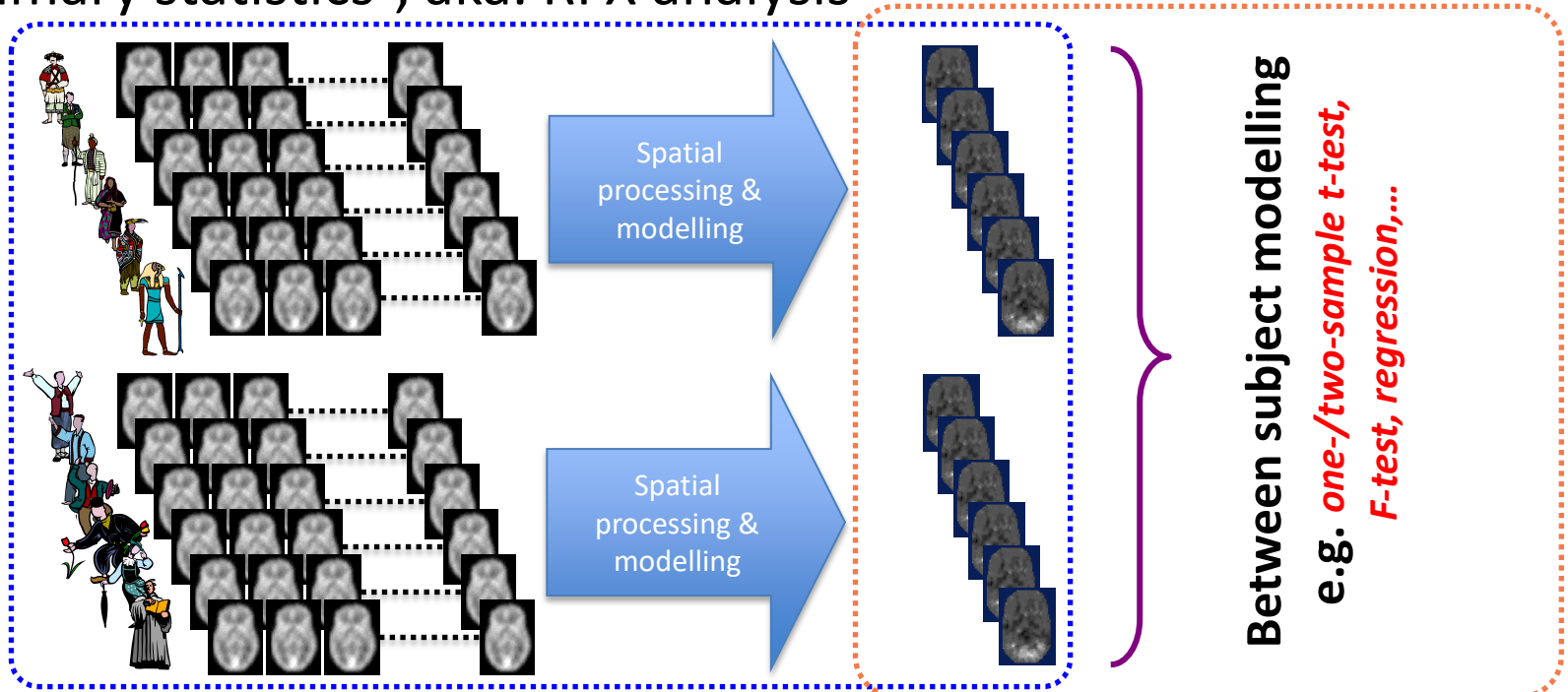
Modelling: between-subject analysis



“Summary statistics”, aka. RFX analysis



vs.



N subjects
per group

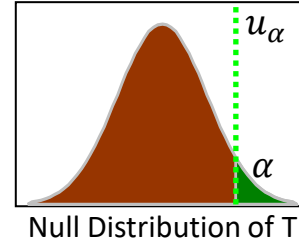
level-one (within-subject)

level-two
(between-subject)

Statistics: hypothesis testing & inference



- ▶ Significance level α :
Acceptable false positive rate α
 \Rightarrow threshold u_α



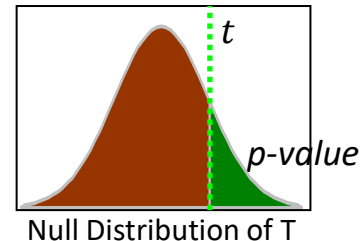
$$t = \frac{c^T \hat{\beta}}{\sqrt{\text{var}(c^T \hat{\beta})}}$$

Threshold u_α controls the false positive rate $\alpha = p(T > u_\alpha | H_0)$

- ▶ Conclusion about the hypothesis:
Reject the null hypothesis H_0 if $t > u_\alpha \rightarrow$ favour the alternative hypothesis H_A

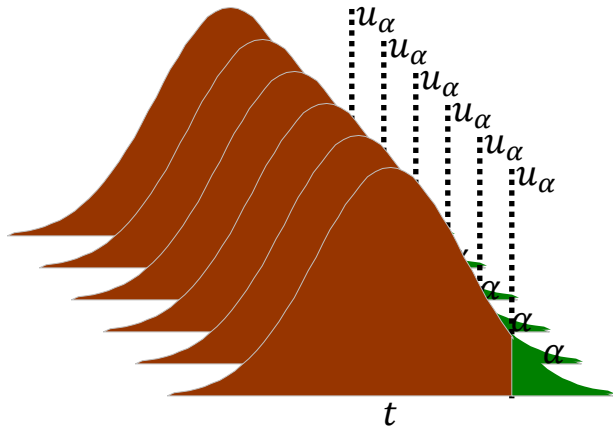
- ▶ p-value: $p(T > t | H_0)$

- *evidence against H_0 .*
- “chance of observing value more extreme than t under H_0 .”



$$y = X\beta + e$$
$$e \sim \mathcal{N}(0, C)$$

Statistics: multiple comparison problem



With 100000 voxels & $\alpha = .05$
 \Rightarrow **5000 false positive voxels.**

Need to

- define a H_0 for a collection of tests
- use corrected p-values.

Existing solutions

- ▶ “Family-wise error rate” (**FWER**) & “False discovery rate” (**FDR**)
- ▶ Should account for image smoothness, i.e. Bonferroni too conservative!
- ▶ Parametric vs non-parametric approaches



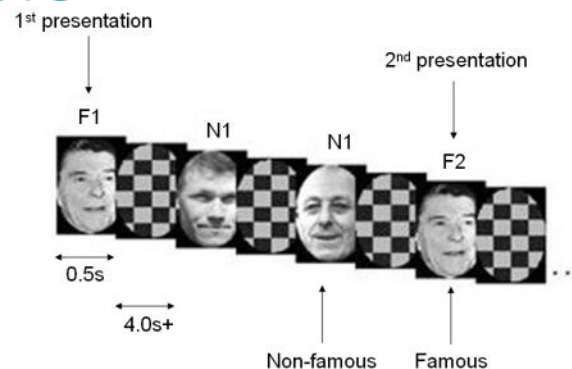
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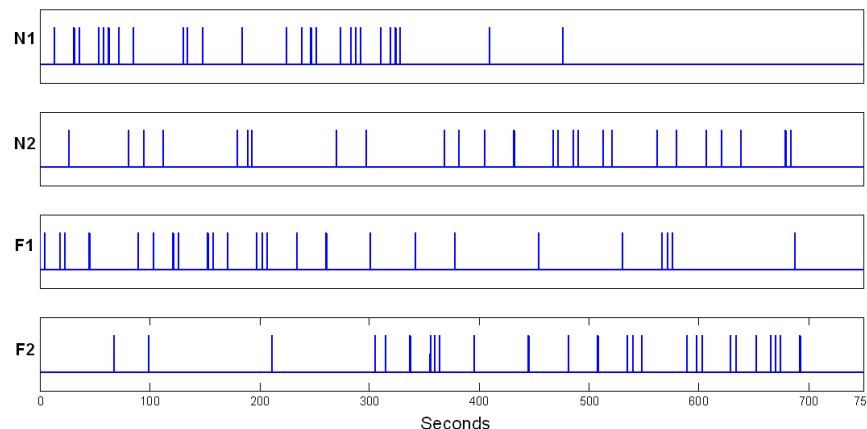
“Vanilla fMRI protocol” example



- ▶ 2x2 factorial design:
 - “famous” (F) vs “non-famous” (N) faces
 - first (1) vs repeated (2) presentation



- ▶ Timing of the presentations:
 - Same task for all subjects
- ▶ 12 subjects
 - ~350 fMRIs, TR = 2s
 - 1 anatomical MRI



Spatial processing: within-subject

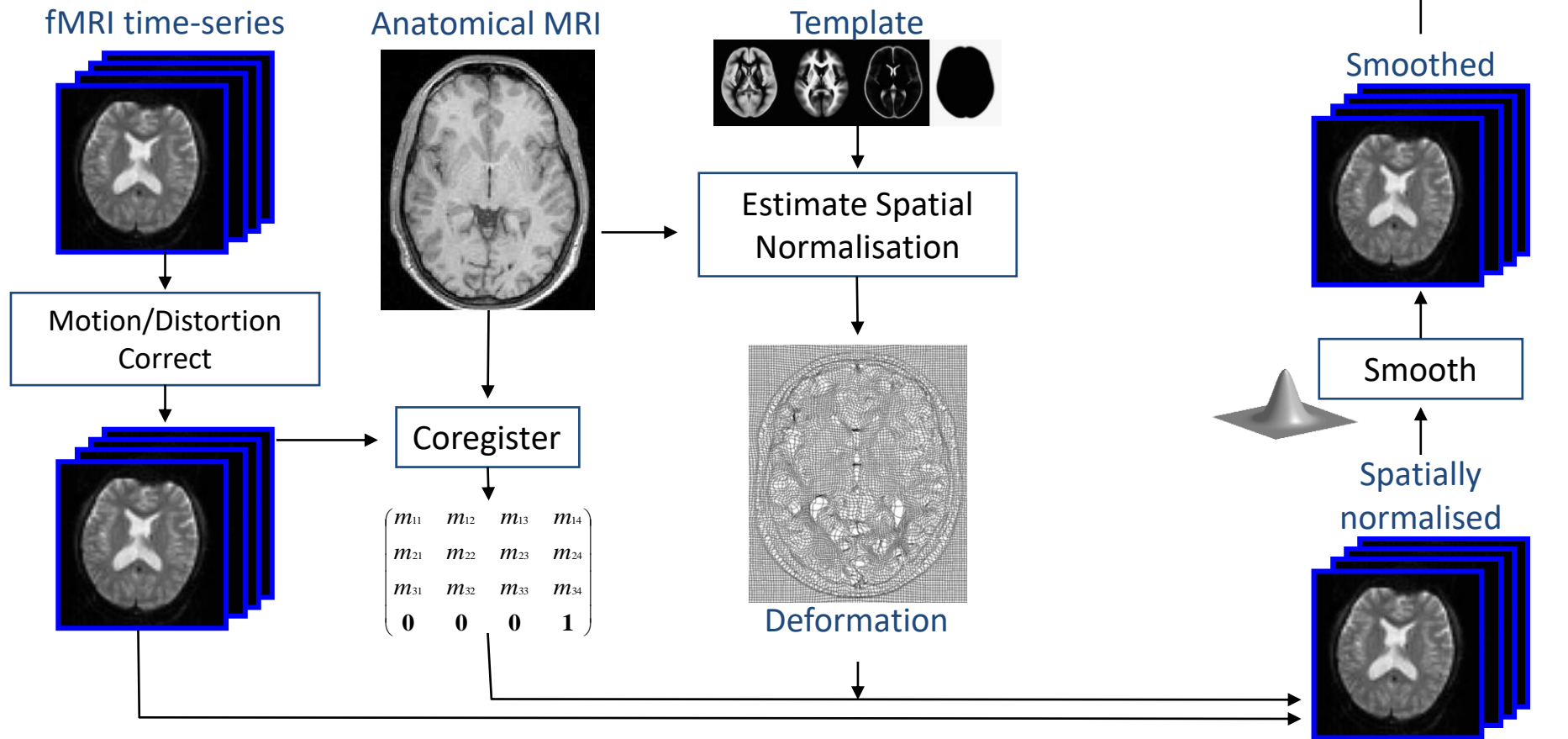


- ▶ Head movement during ~12 minutes of fMRI acquisition
→ “realignment”
- ▶ Match anatomical and (mean) functional MRI
→ “coregistration”
- ▶ Bring all subjects brain image into same reference space
→ “spatial normalization”, aka. “warping”
- ▶ Variance reduction
→ “smoothing”

Other possible steps:

slice time correction, fMRI artefact correction, diffeomorphic warping,...

fMRI + aMRI spatial pre-processing



Statistical analysis: within-subject, i.e. FFX



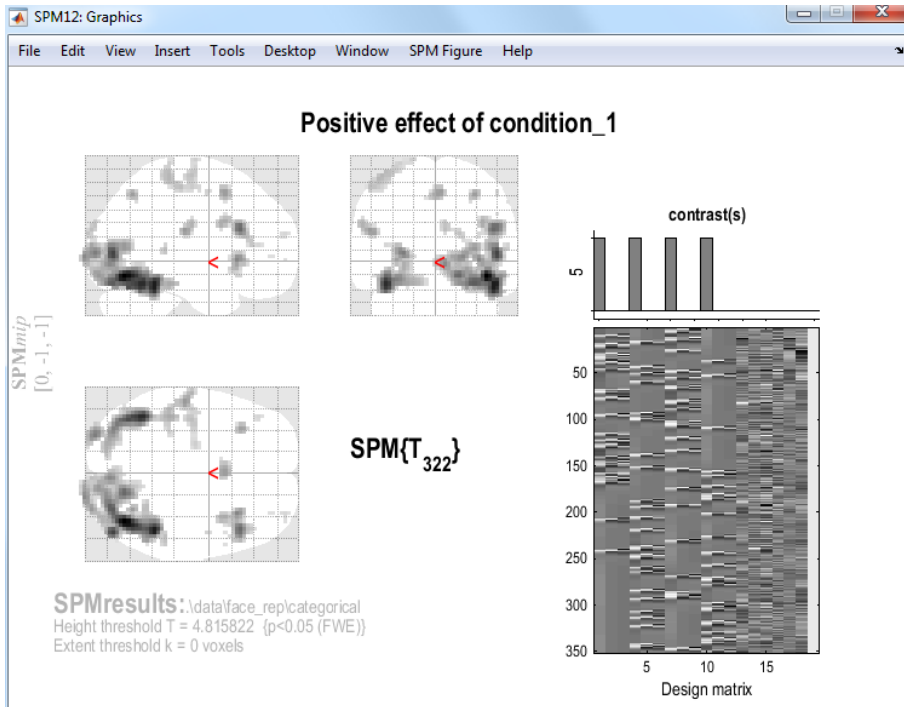
- ▶ Experimental design through “General Linear Model”, i.e. model the 4 “conditions” (N1, N2, F1, F2) + movement parameters
- ▶ Contrast definition to test effect of interest at subject level

Single subject's activation



Contrast: *Faces > Baseline*

i.e. “which part of the brain lights up when I see a face?”



Statistics: p-values adjusted for search volume

set-level		cluster-level				peak-level					mm mm mm		
p	c	$P_{FWE-corr}$	$q_{FDR-corr}$	k_E	P_{uncorr}	$P_{FWE-corr}$	$q_{FDR-corr}$	T	$(Z_{=})$	P_{uncorr}			
0.000	18	0.000	0.000	1171	0.000	0.000	0.000	14.76	Inf	0.000	39	-70	-13
						0.000	0.000	13.35	Inf	0.000	45	-46	-19
						0.000	0.000	11.60	Inf	0.000	48	-79	5
		0.000	0.000	380	0.000	0.000	0.000	12.65	Inf	0.000	-42	-55	-19
						0.000	0.000	11.17	Inf	0.000	-39	-67	-22
						0.000	0.000	7.14	6.88	0.000	-42	-34	-19
		0.000	0.000	144	0.000	0.000	0.000	9.97	Inf	0.000	45	23	23
						0.000	0.000	7.08	6.82	0.000	36	11	29
		0.000	0.000	79	0.000	0.000	0.000	9.00	Inf	0.000	-27	-94	5
						0.000	0.000	8.72	Inf	0.000	33	20	-1
						0.001	0.028	5.68	5.54	0.000	54	17	2
						0.003	0.069	5.47	5.34	0.000	51	20	-13
		0.000	0.000	51	0.000	0.000	0.000	7.86	7.51	0.000	-54	-22	23
						0.000	0.000	6.72	6.50	0.000	-60	-16	26
		0.000	0.000	44	0.000	0.000	0.000	7.71	7.38	0.000	0	11	50
		0.000	0.001	21	0.001	0.000	0.000	7.60	7.28	0.000	30	-64	50
		0.000	0.000	27	0.000	0.000	0.000	7.45	7.15	0.000	-33	23	-1
		0.000	0.000	148	0.000	0.000	0.000	6.59	6.38	0.000	-45	-34	65
						0.000	0.002	6.26	6.07	0.000	-39	-16	65
						0.000	0.002	6.21	6.03	0.000	-54	-25	56
		0.000	0.004	15	0.002	0.000	0.002	6.27	6.08	0.000	51	-37	8
		0.006	0.162	3	0.126	0.003	0.079	5.44	5.31	0.000	48	-4	53
		0.002	0.056	6	0.037	0.006	0.139	5.30	5.19	0.000	33	59	20

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 4.82, p = 0.000 (0.050)
Extent threshold: k = 0 voxels
Expected voxels per cluster, <k> = 1.337
Expected number of clusters, <c> = 0.05
FWE: 4.816, FDR: 5.581, FWEc: 1, FDRc: 15

Degrees of freedom = [1.0, 322.0]
FWHM = 10.7 10.7 10.3 mm mm mm; 3.6 3.6 3.4 (voxels)
Volume: 1612683 = 59729 voxels = 1229.6 resels
Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 43.44 voxels)

Page 1



Statistical analysis: between-subject, i.e. RFX

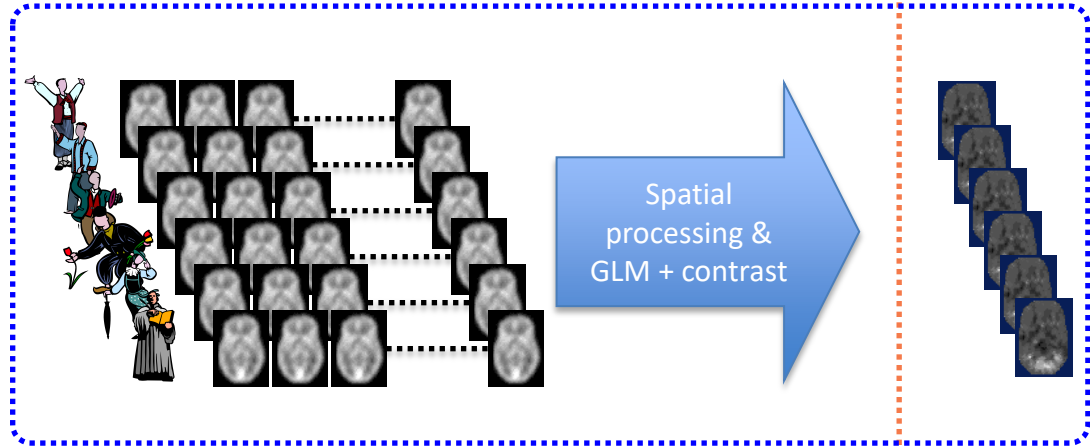


- ▶ Experimental design through “General Linear Model”, i.e. model the 4 “conditions” (N1, N2, F1, F2) + movement parameters
- ▶ Contrast definition to test effect of interest at subject level
- ▶ Group-level analysis, i.e. “Random Effect” analysis
 - Summarize effect of interest at subject level, i.e. contrast of interest
 - Group-level 1-sample t-test
- ▶ Classical inference with t-/F-test
- ▶ Correction for “multiple comparison problem”

Group-level analysis, i.e. RFX



12
subjects



level-one (within-subject)



Two
one-sample t-test,
regression, ...

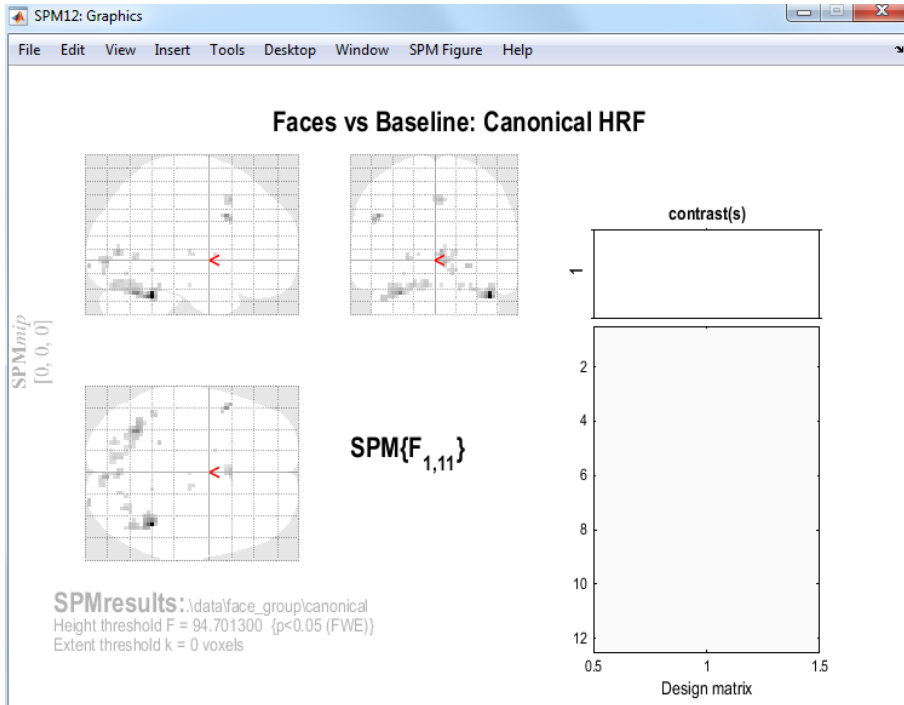
*“effect of interest”
i.e. contrast images*

level-two
(between-subject)

Group-level activation



- ▶ 12 subjects, with “*Faces > Baseline*” contrast
- ▶ 1-sample t-test model, no regressor



Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level				mm mm mm			
<i>p</i>	<i>c</i>	<i>P</i> _{FWE-corr}	<i>q</i> _{FDR-corr}	<i>k</i> _E	<i>P</i> _{uncorr}	<i>P</i> _{FWE-corr}	<i>q</i> _{FDR-corr}	<i>F</i>	(<i>Z</i> _{max})	<i>P</i> _{uncorr}			
0.000	17	0.000	0.000	45	0.000	0.000	0.036	547.52	6.36	0.000	42	-48	-30
		0.000	0.000	72	0.000	0.003	0.497	160.81	5.28	0.000	45	-63	-24
		0.000	0.000	31	0.000	0.000	0.246	277.52	5.78	0.000	-30	-60	-27
						0.006	0.535	144.80	5.18	0.000	-9	-78	-21
						0.011	0.575	127.99	5.06	0.000	-18	-66	-21
		0.000	0.000	8	0.000	0.000	0.246	251.67	5.69	0.000	-48	12	33
		0.000	0.000	14	0.000	0.001	0.381	192.97	5.45	0.000	6	-84	-3
						0.002	0.381	187.35	5.42	0.000	3	-75	6
						0.014	0.610	122.01	5.01	0.000	12	-87	-12
		0.000	0.000	2	0.021	0.003	0.497	166.76	5.31	0.000	3	15	45
		0.003	0.028	2	0.021	0.004	0.535	152.29	5.22	0.000	24	-99	-6
		0.003	0.028	2	0.021	0.007	0.535	140.56	5.15	0.000	-21	-42	-21
		0.000	0.000	7	0.000	0.007	0.535	139.89	5.14	0.000	-45	-48	-33
		0.000	0.001	5	0.001	0.008	0.535	137.04	5.12	0.000	-24	-63	0
		0.000	0.000	7	0.000	0.008	0.535	135.44	5.11	0.000	30	-69	-24
		0.000	0.001	5	0.001	0.014	0.610	121.89	5.01	0.000	-21	-78	-24
		0.012	0.088	1	0.088	0.021	0.766	112.16	4.93	0.000	15	-48	-9
		0.000	0.001	5	0.001	0.022	0.766	111.11	4.92	0.000	18	-75	-21
		0.012	0.088	1	0.088	0.027	0.777	106.85	4.88	0.000	-15	3	3
		0.000	0.001	5	0.001	0.029	0.777	105.26	4.87	0.000	15	-18	6
		0.012	0.088	1	0.088	0.044	0.950	97.35	4.79	0.000	-27	-69	-12
		0.012	0.088	1	0.088	0.047	0.955	95.96	4.77	0.000	3	-18	-21

table shows 3 local maxima more than 8.0mm apart

Height threshold: F = 94.70, p = 0.000 (0.050) Degrees of freedom = [1.0, 11.0]
 Extent threshold: k = 0 voxels FWHM = 13.1 13.2 13.8 mm mm mm; 4.4 4.4 4.6 (voxels)
 Expected voxels per cluster, <k> = 0.352 Volume: 1392120 = 51560 voxels = 5212 resels
 Expected number of clusters, <c> = 0.14 Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 88.07 voxels)
 FWEp: 94.701, FDRp: 547.516, FWEc: 1, FDRc: 2



Program

- ▶ MRI “flavours”
- ▶ MRI data processing
 - Within-/between-subject processing
 - Subject-/reference-space
 - Statistical inference
- ▶ “Vanilla fMRI protocol” example
- ▶ Take home message

“MRI data processing” take home message



- ▶ MRI = very flexible technique
- ▶ Multiple “flavours” of MRIs can be acquired in 1 session
- ▶ ...but not all, as scanning time is limited (subject’s comfort!)
- ▶ ...so must chose what is relevant for the project!
- ▶ Data curation (safe storage, clear filenaming & organization) required
- ▶ **Complicated data to process :**
 - multiple steps/tools
 - different steps/tools for different MRI flavours
- ▶ Computer intensive data processing, i.e. need scripting!

“MRI data processing” take home message



Use existing tools to process and analyse your data!

- ▶ SPM & many extensions, <https://www.fil.ion.ucl.ac.uk/spm/>
- ▶ FSL, <https://fsl.fmrib.ox.ac.uk/fsl/>
- ▶ AFNI, <https://afni.nimh.nih.gov/>
- ▶ fMRIPrep, <https://fmriprep.org/en/stable/>
- ▶ MRtrix3, <https://www.mrtrix.org/>
- ▶ ANTs, <https://stnava.github.io/ANTs/>
- ▶ ...

Favour open-source and well-established tools !

Thank you for your attention!

