fMRI data analysis

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Data analysis proceeds in three steps

1) Preprocessing of invidividual data

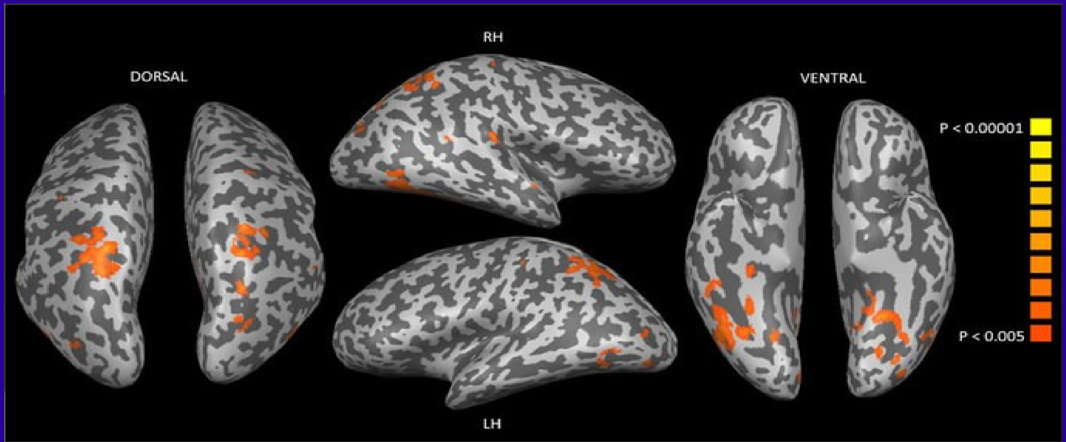
=> cleaned (preprocessed) fMRI data

2) Statistical analysis of single participants

=> individual maps of effect sizes (conditions vs. baseline) and/or activations in Regions of Interest

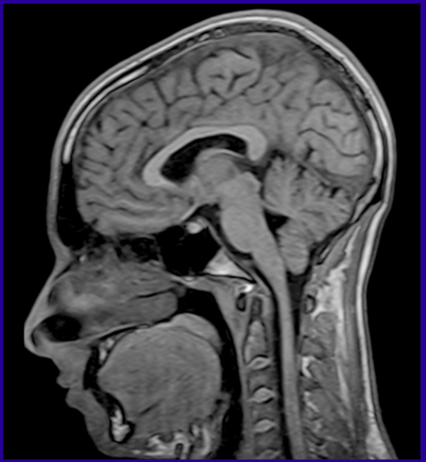
3) Statistical group analysis

=> testing hypotheses at the population level

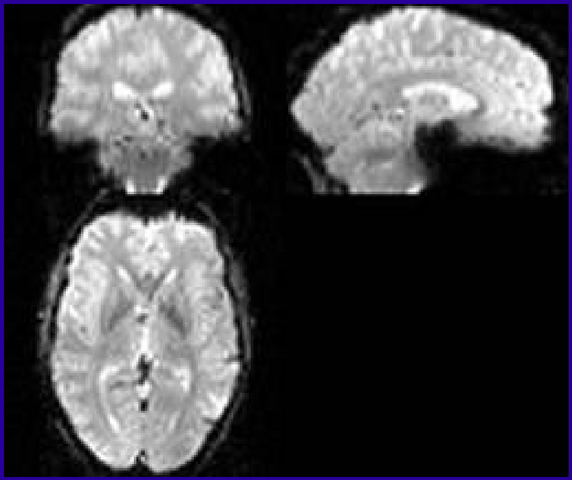


Preprocessing of individual data

Each participant's raw data constist of:



- One 3D anatomical scan (T1 weighted image to constrast grey and white matter)
- One or several functional 4D functional images (T2* weighted)



- Optionaly, additional scans (DTI, fieldmap to correct for geometric distortions, signal loss...)
- In case of stimulation/task, the precise timing of stimulation and of subject's responses during the functional runs.
- Optionaly :
  - eye tracking recordings.
  - physiological recordings (heart beats, respiration...)

The typical pre-processing pipeline

1) Detection & correction of movements between functional scans

2) Correction for slice-timing acquisition differences

3) Correction for spatial variations in intensity

4) Segmentation into grey/white matter and CSF

5) Spatial normalisaation of the the Anatomy to a common template

6) Coregistration of anatomical scan and functional scans

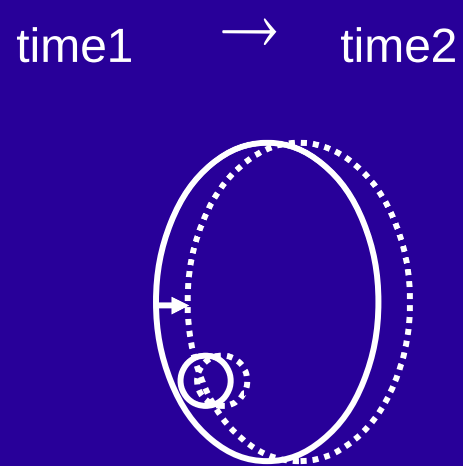
7) Spatial normalisation of functional images

8) Spatial smoothing

Realignment of functional scans (movement correction)

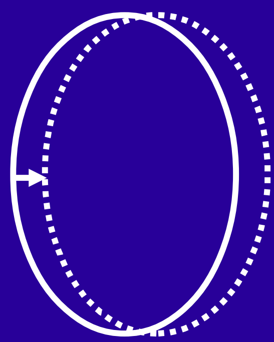
The issue:

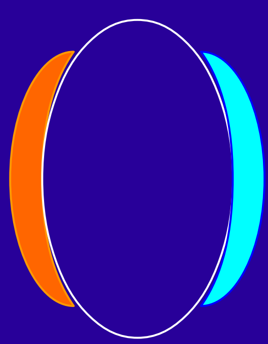
if the head shifts, the signal in a selected region of the image will sample a different part of the brain over time



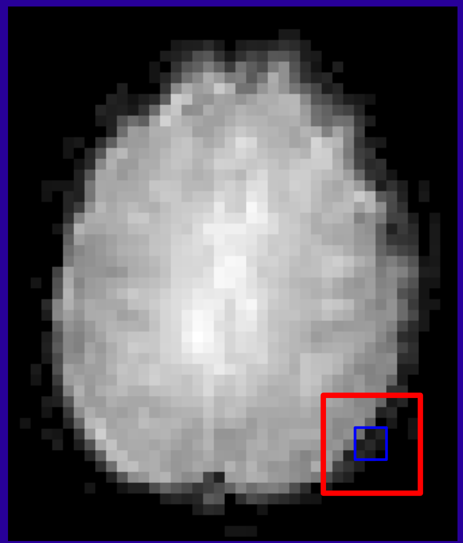
Issue: Spurious Activation at Edges

time1 → time2

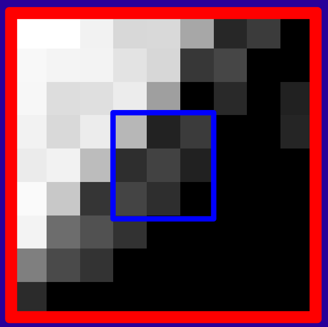




A

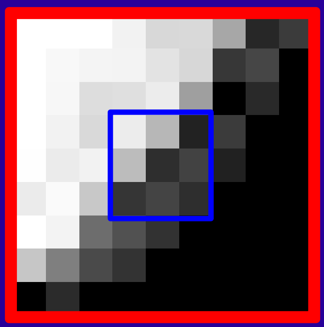


B



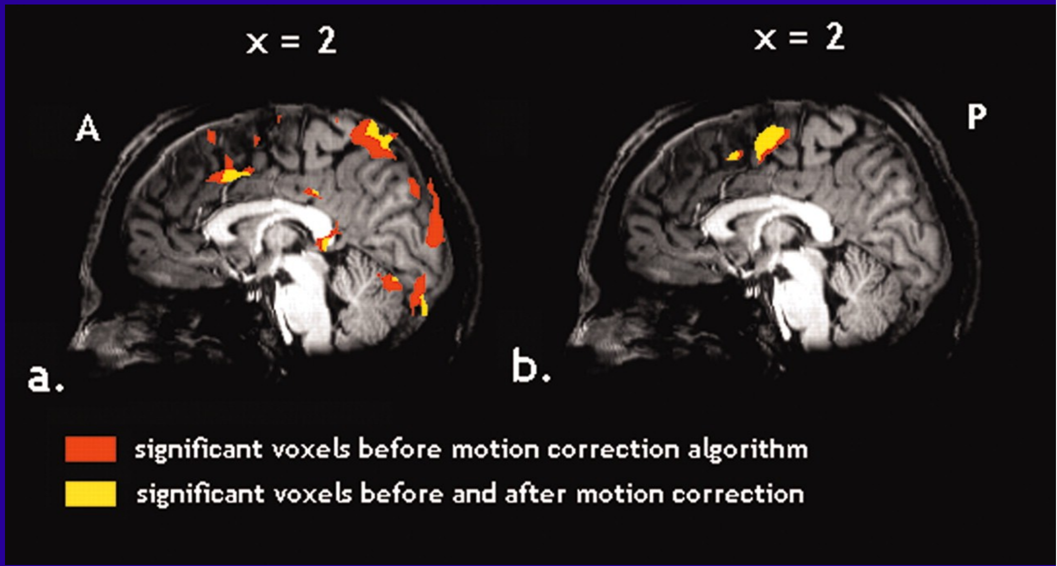
507	89	154
119	171	83
179	117	53

C

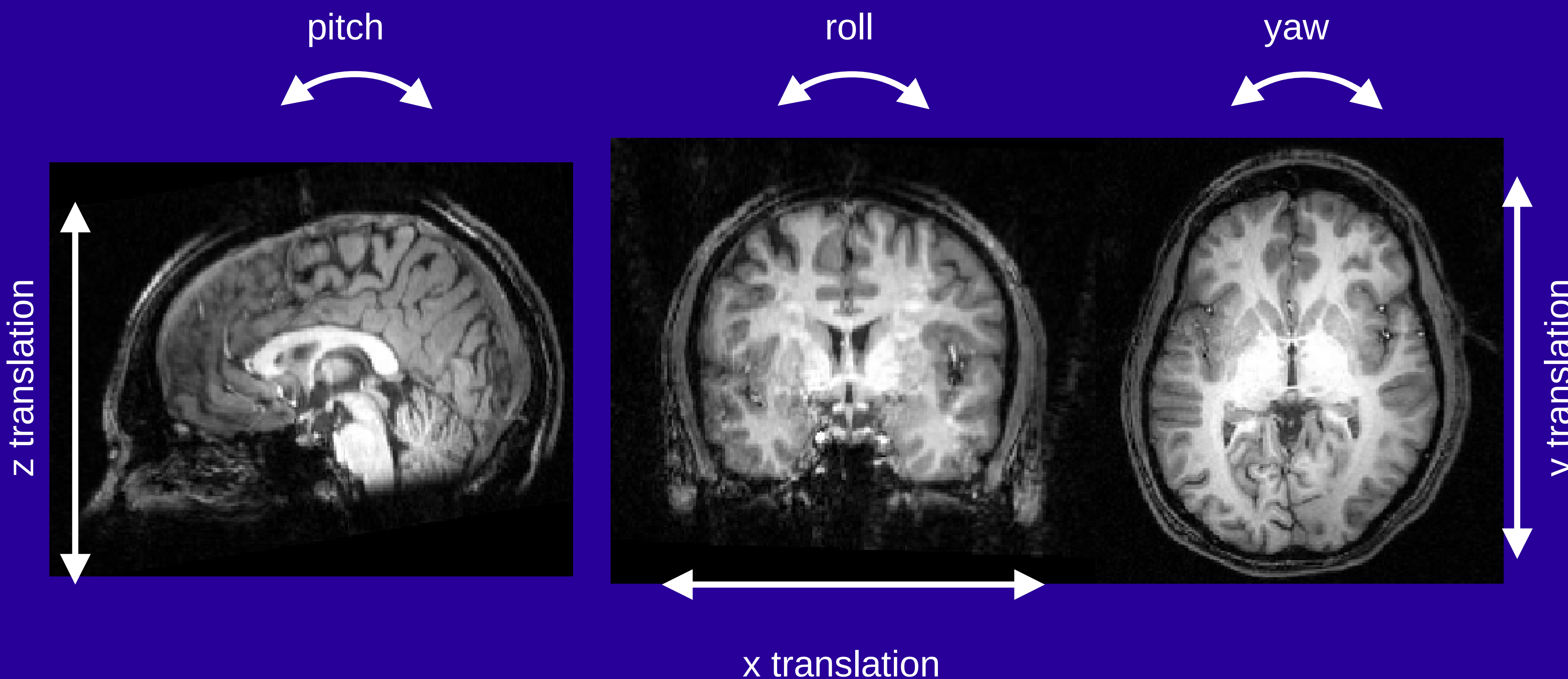


663	507	89
520	119	171
137	179	117

Example of analysis without and with mvt correction

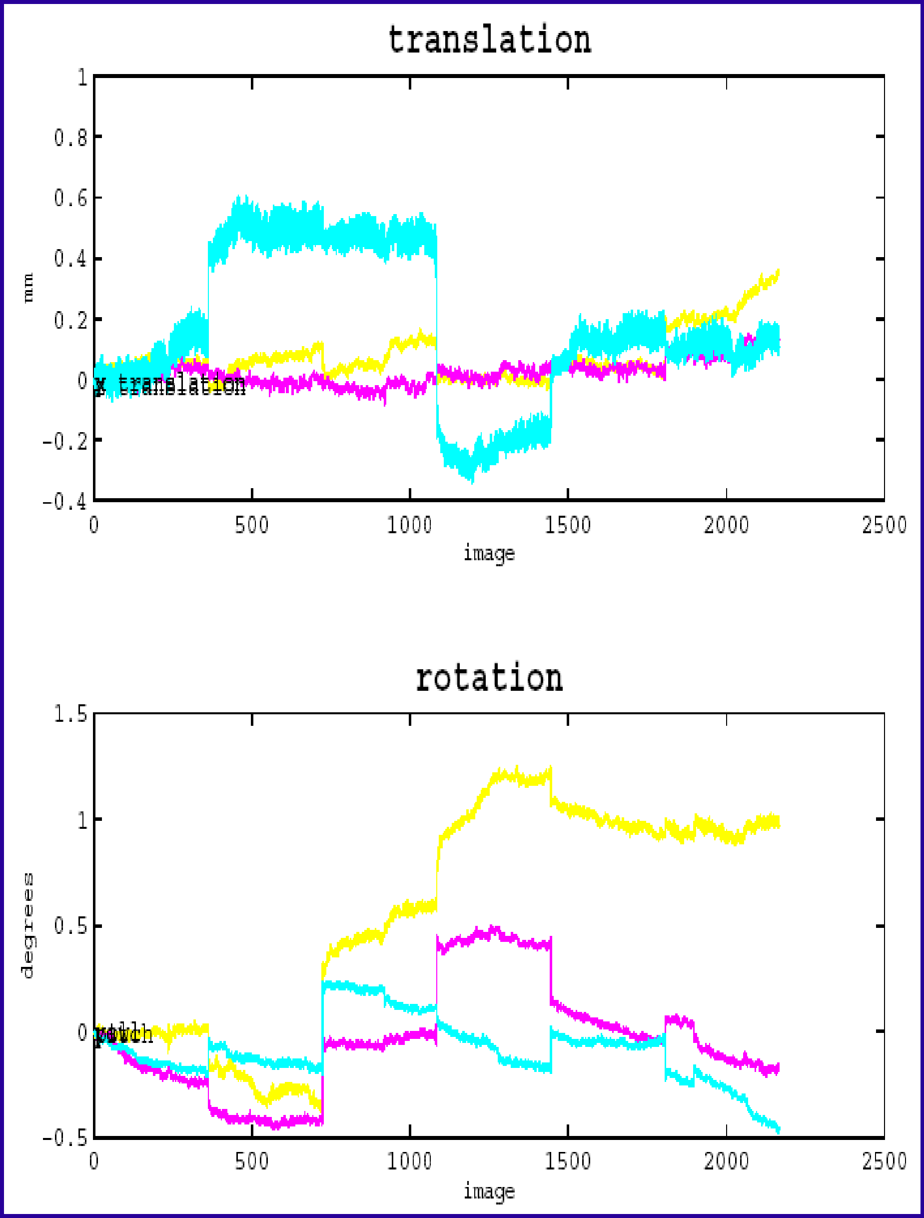


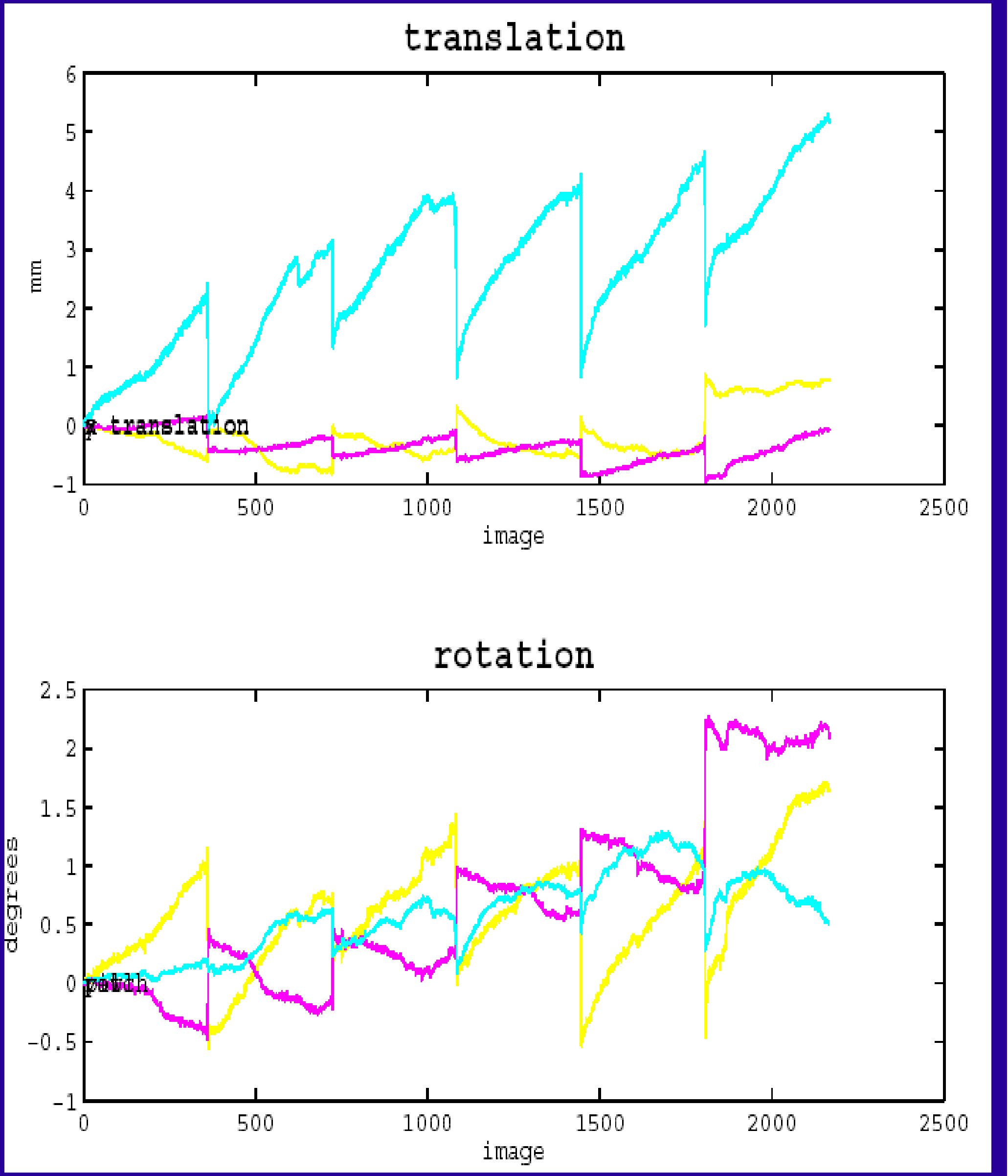
Motion Correction Algorithms



Align each volume of the brain to a target volume (e.g. the first of the session) using six parameters: three translations and three rotations

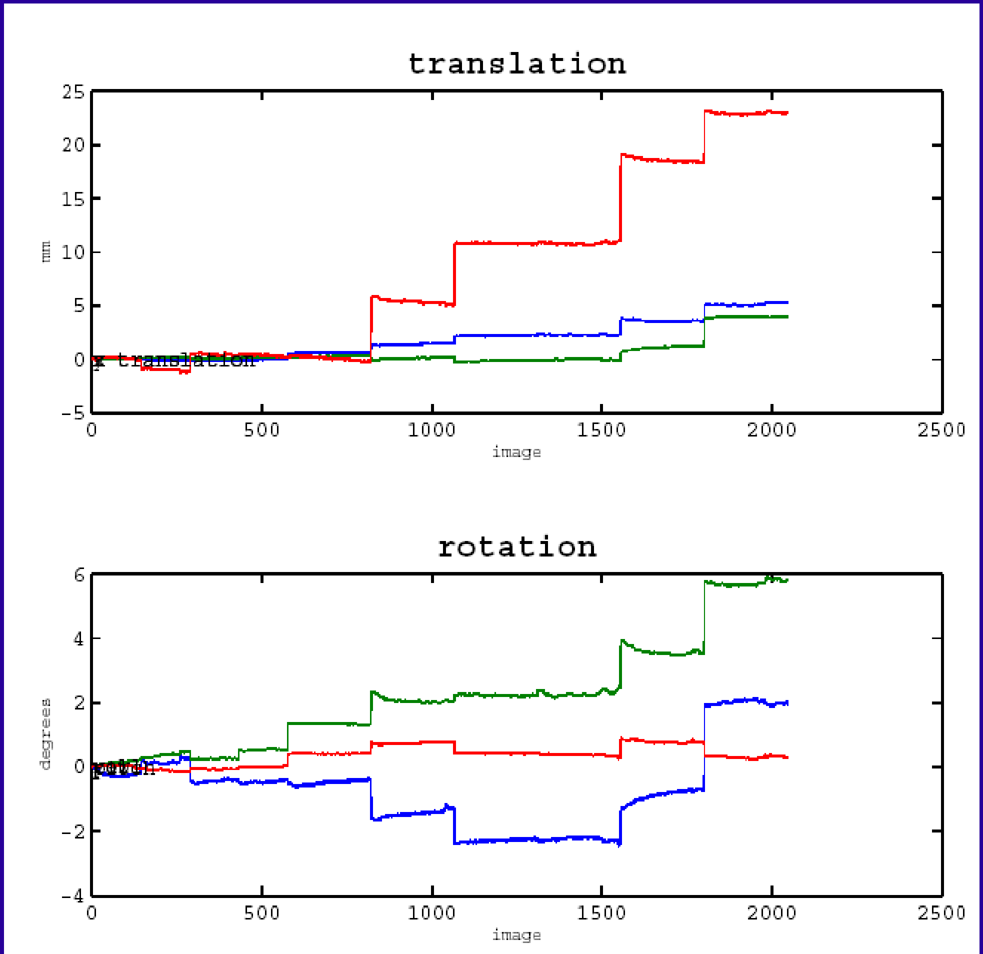
Head Motion: Good, Bad,…

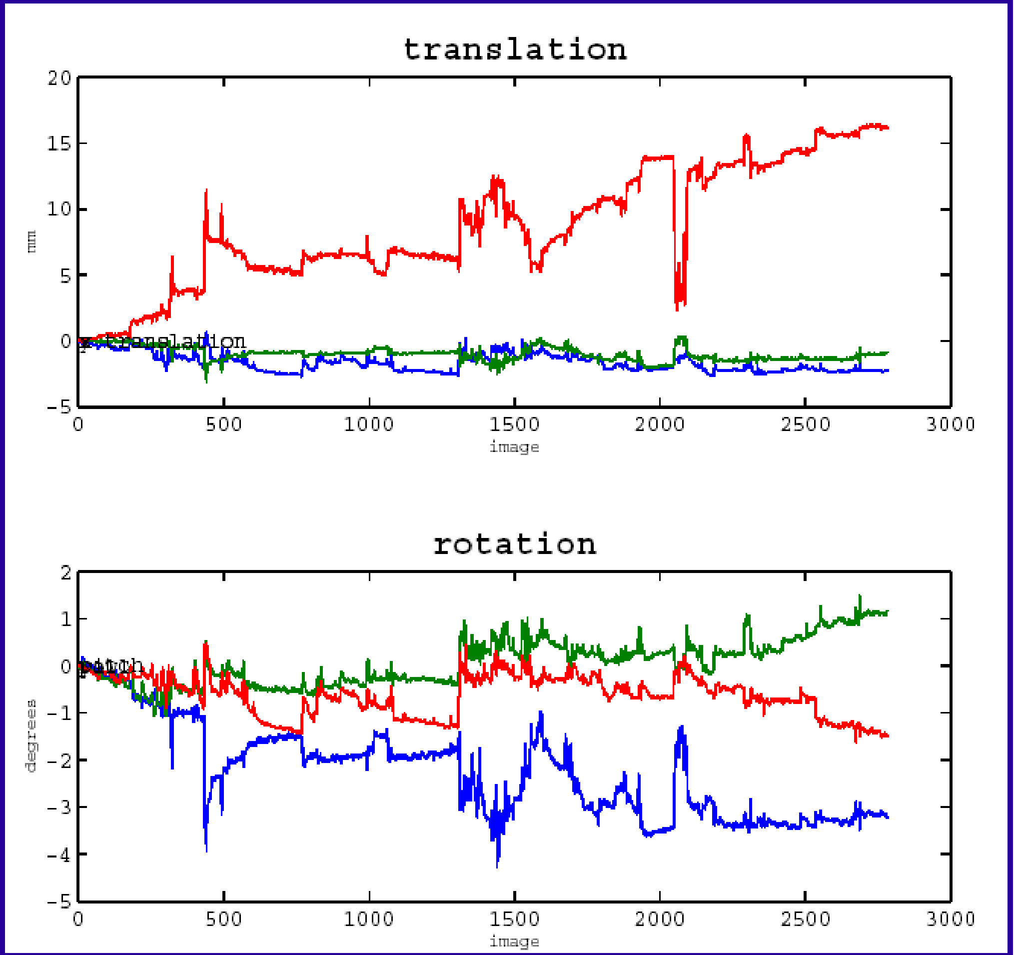




Slide from Duke course

... and catastrophically bad





Limits

Motion correction algorithms are not perfect. They only partially manages to correct the issue of spurious activations.

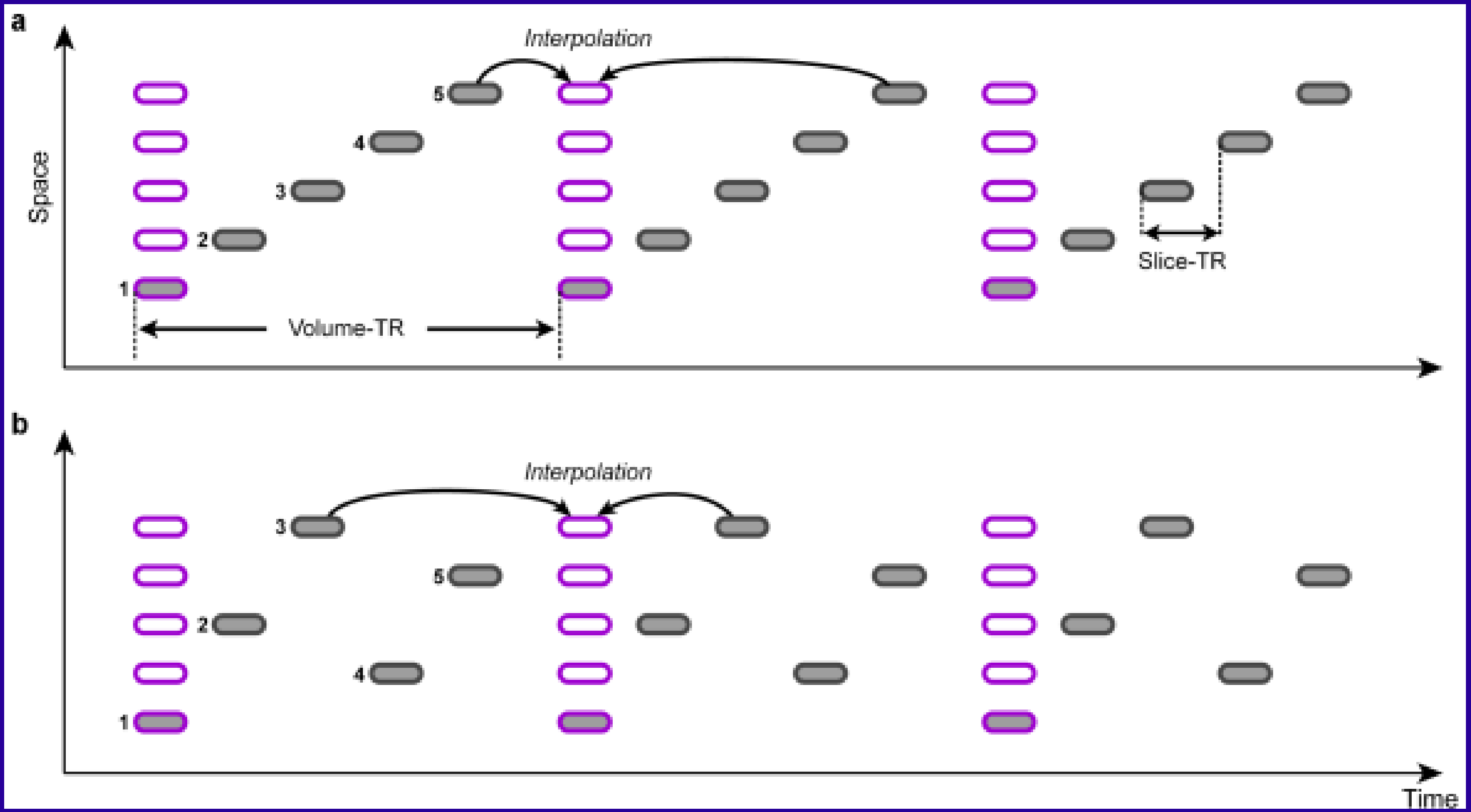
Moreover, they can introduce artifacts, confounding movement and real activations (and removing the latest!) (Friere & Mangin, 2001, *NeuroImage*)

Therefore, it is better to **prevent head movements during acquisition** as much as possible !

Correction for slice timing differences

Corrects for differences in acquisition time within a TR

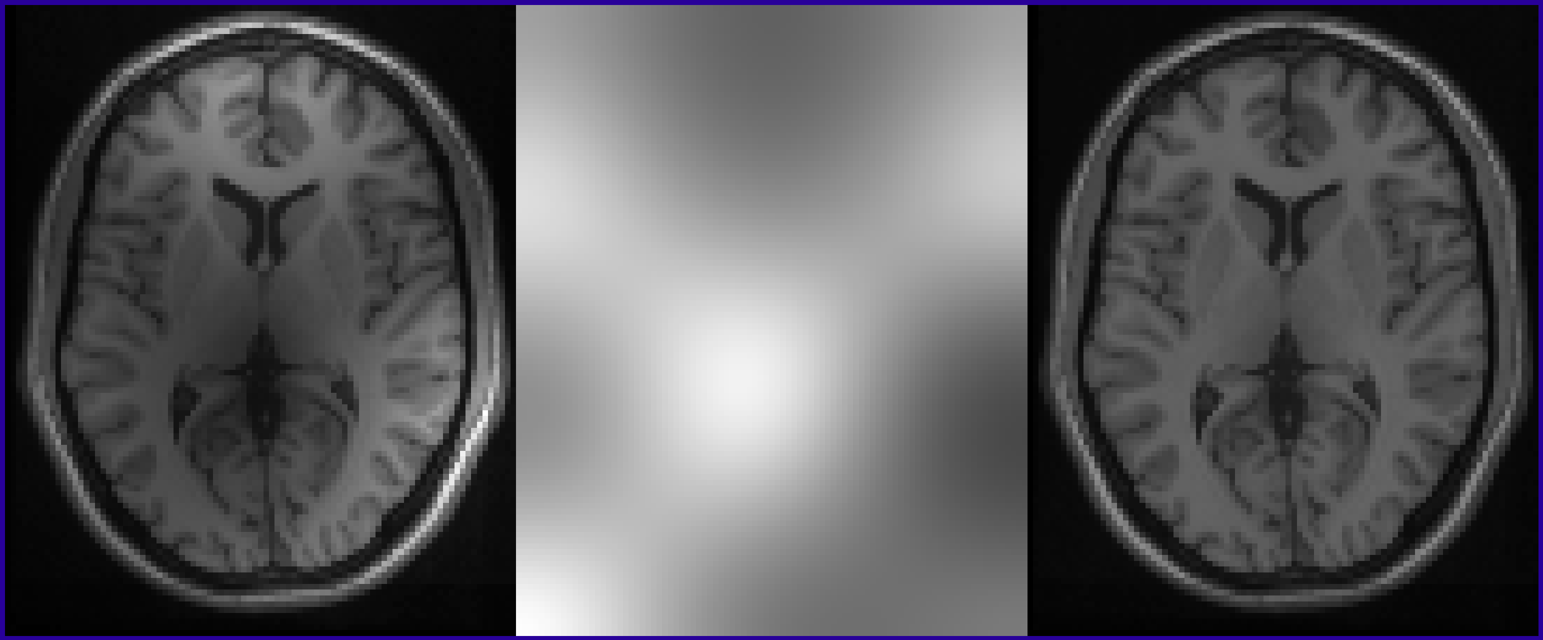
Especially important for long TRs



Spatial normalisation of th Anatomy

Bias correction

Correction of the intra-scan intensity inhomogeneities (due to RF inhomogeneities/antenna)



Note: this step is especially important if one wants to segment grey/white matter (e.g. to perform voxel-based morphometry (VBM) analyses).

Segmentation

- Classifies voxels within an image into different anatomical divisions
  - Gray Matter
  - White Matter
  - Cerebro-spinal Fluid (CSF)

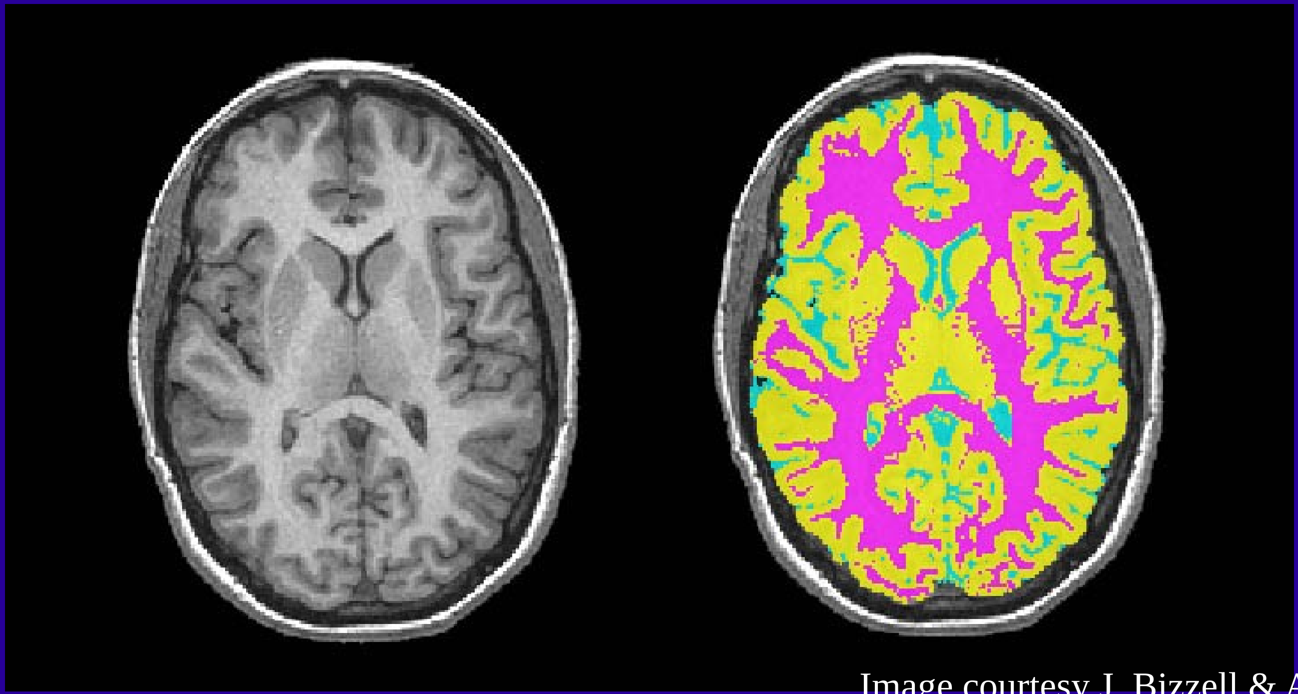
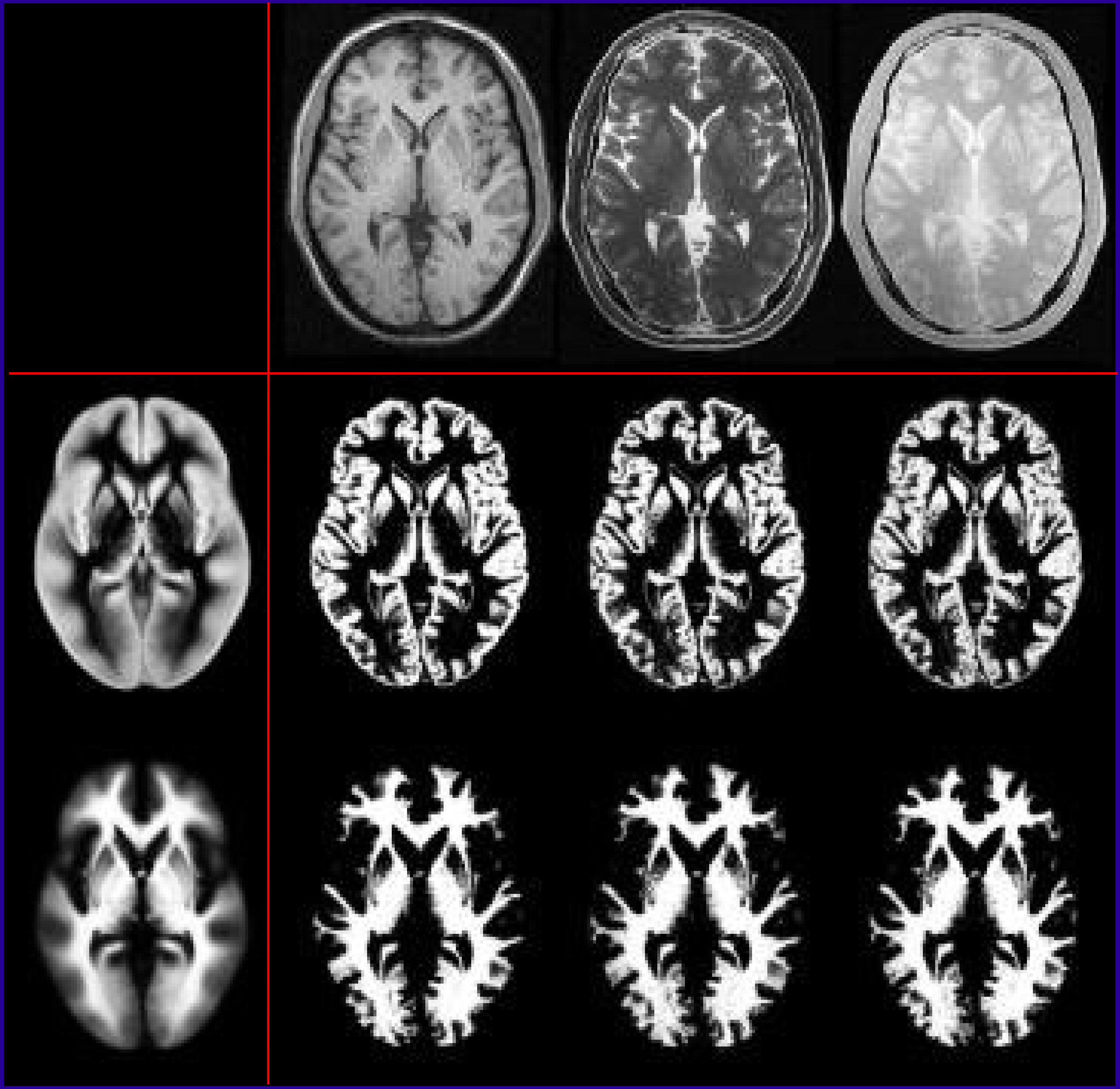


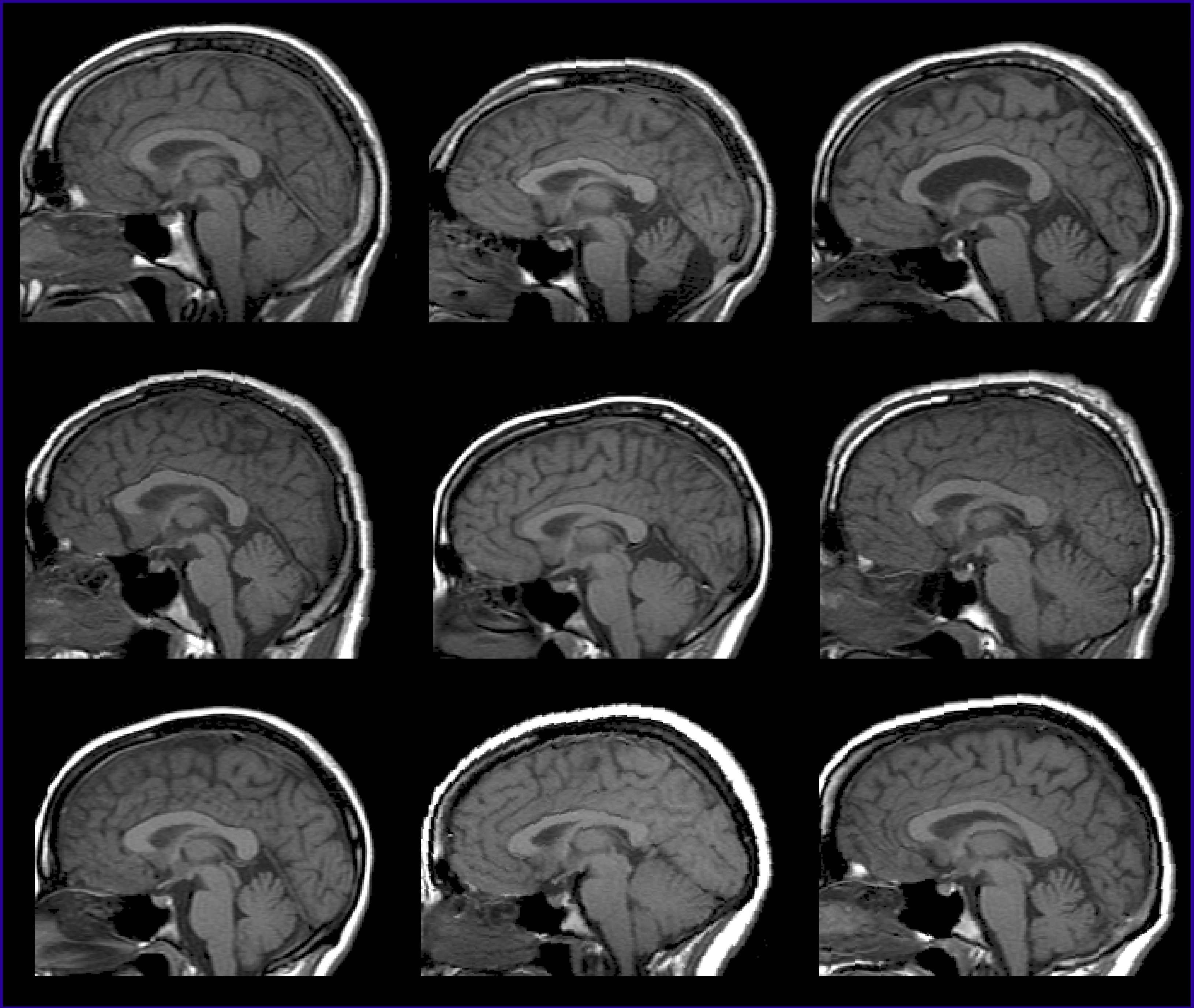
Image courtesy J. Bizzell & A. Belger

Segmentation of anatomical scans



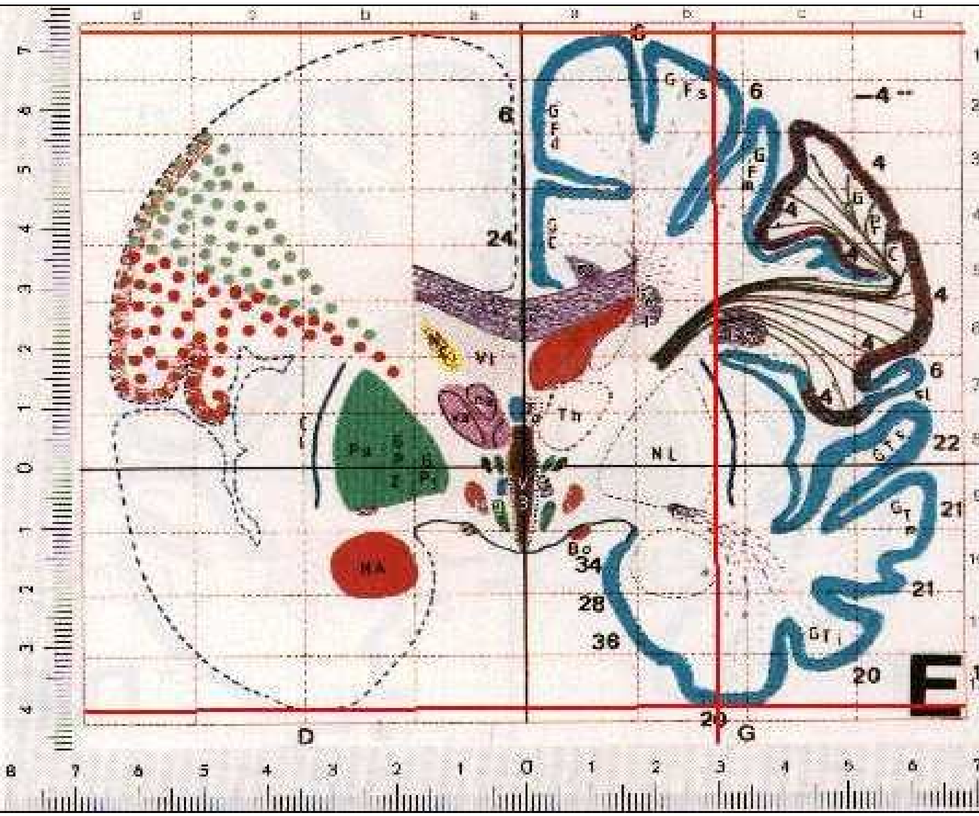
Spatially normalised BrainWeb phantoms (T1, T2 and PD)

Tissue probability maps of GM and WM



Standard spaces

The Talairach Atlas



The MNI/ICBM AVG152 Template

The MNI template follows the *convention* of T&T, but doesn't match the *particular brain*

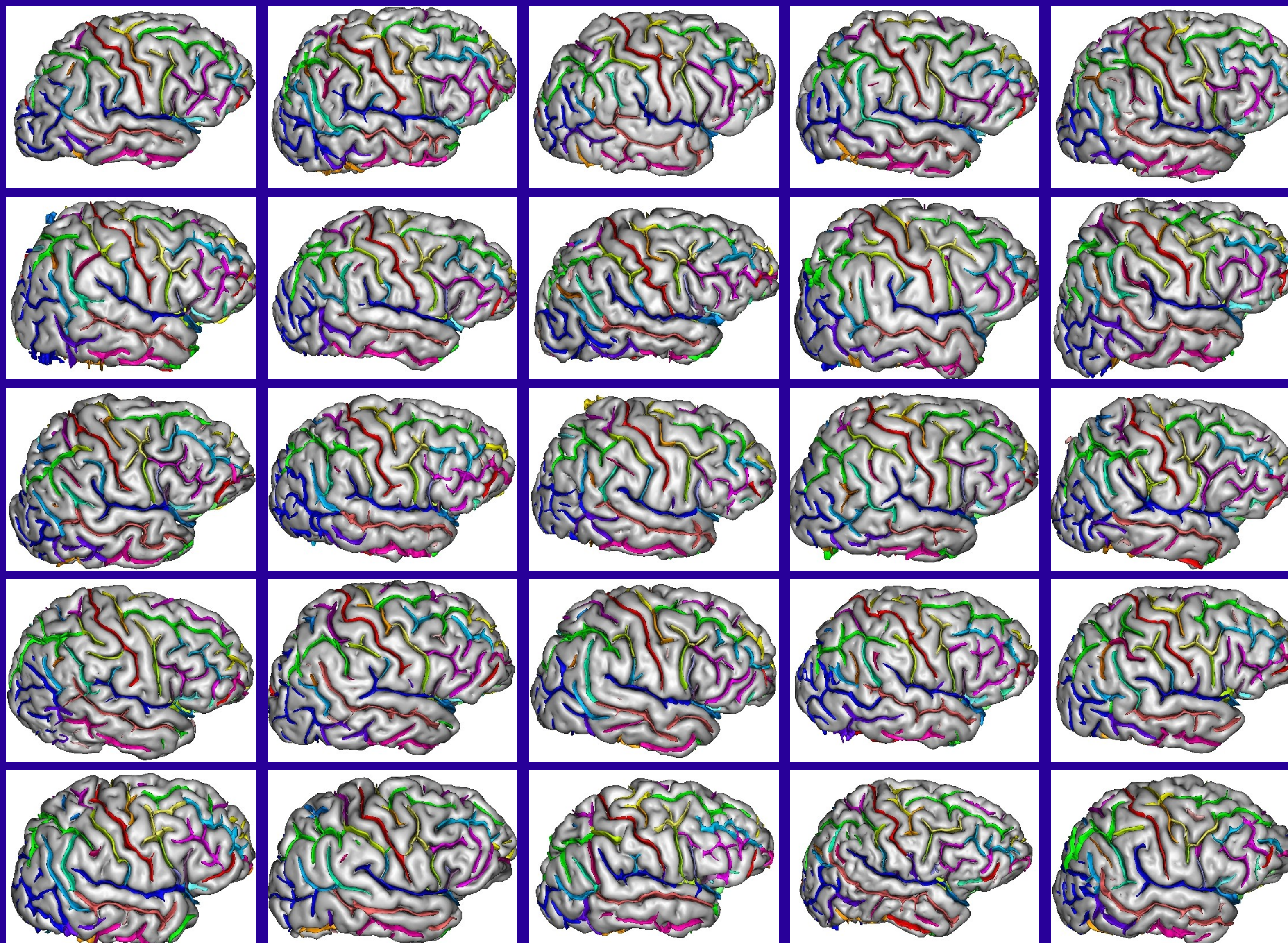
Recommended reading:Brett et al. (2002). The problem of functional localization. *Nat. Neurosci.*

Reporting a voxel-based fMRI analysis using standardized coordinates

Anatomical area	Cluster size	Hemisphere	*x*	*y*	*z*	*Z* value
POS CUE > NON-CUE						
Putamen	27	L	−23	3	12	3.47
Precentral G. (BA 6)	182	L	−24	−12	49	4.24
Precuneus (BA 7)	164	R	18	−66	50	4.49
Superior parietal L. (BA 7)	255	L	−19	−63	52	4.34
Middle occipital G. (BA 19)	1620	R	26	−84	8	5.36
Lingual G. (BA 18)		L	−12	−85	−12	5.32
Cerebellum (declive)		L	−23	−76	−17	5.06
NON-CUE > POS CUE						
No suprathreshold clusters						

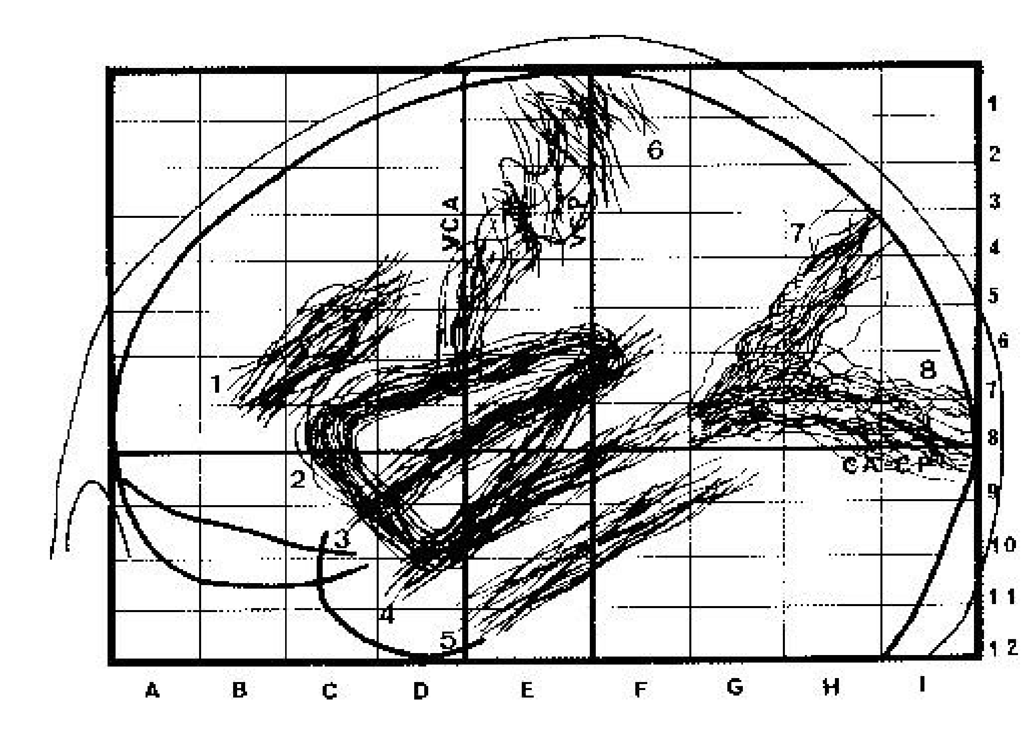
Results are reported in Talairach coordinates for peak voxel activations after a False Discovery Rate (FDR) correction ($p < 0.05$; minimum size of each cluster was 25 contingent voxels). Indented rows indicate subordinate clusters. Hemispheres: R (Right) or L (Left); Abbreviations: BA, Brodmann Area; G, Gyrus; L, Lobule.

A database of manually labelled sulci

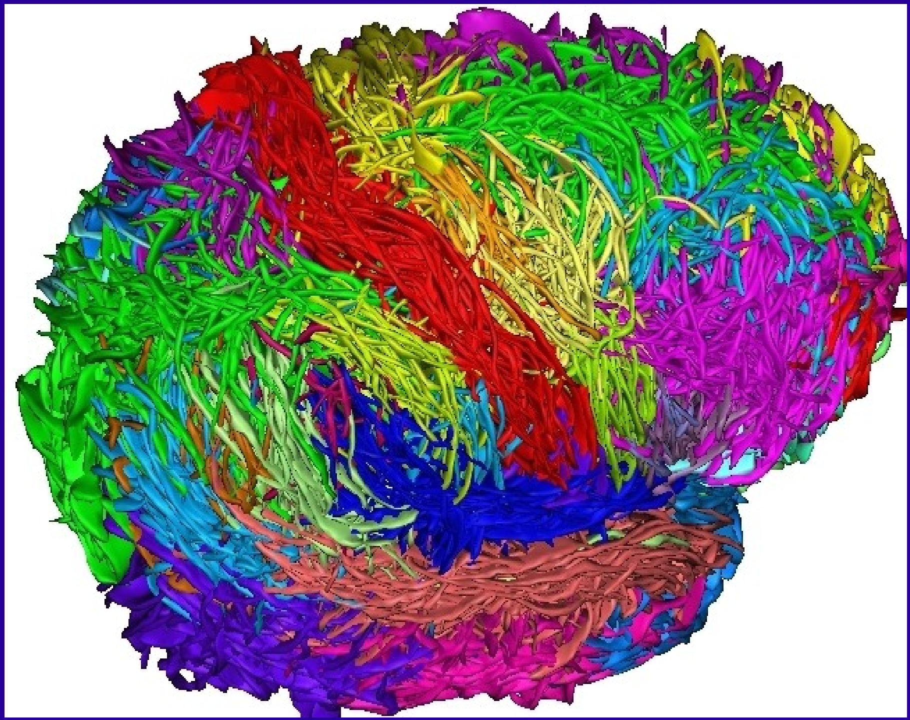


Jean-Francois Mangin & Denis Riviere, SHFJ, Orsay

Variability of Sulci after affine normalization

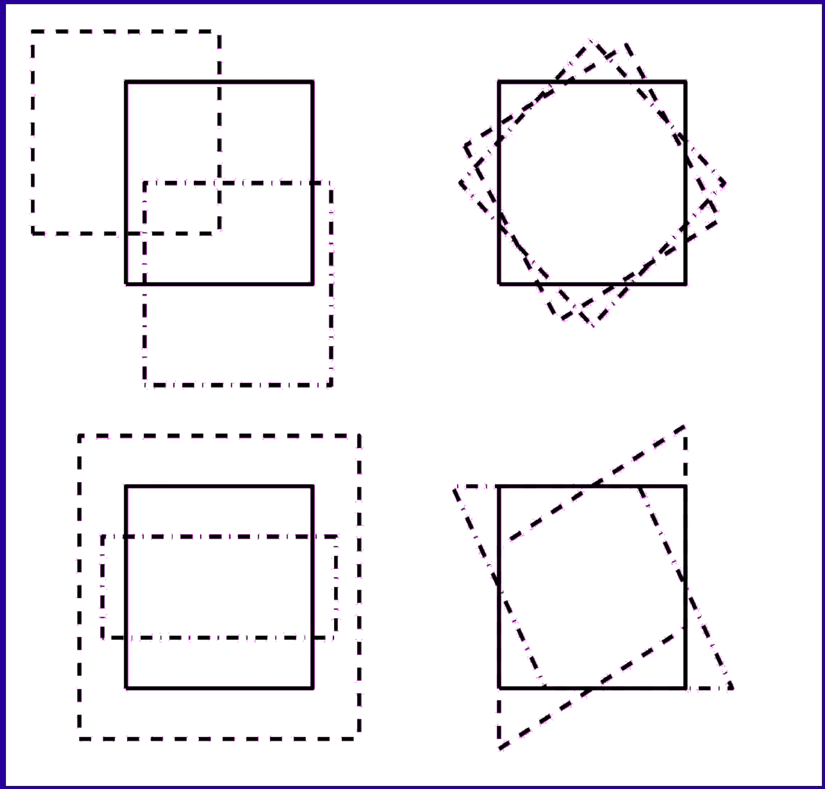


Source: Szikla et al., 1977 in Tamraz & Comair, 2000



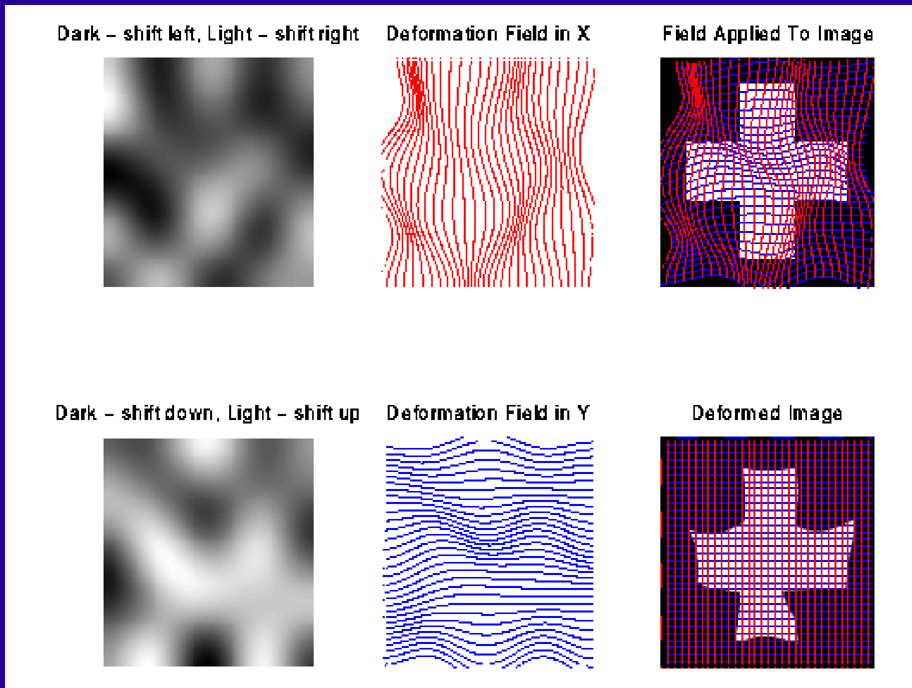
Spatial Normalisation - Affine

- The first part is a 12 parameter affine transform
  - 3 translations
  - 3 rotations
  - 3 zooms
  - 3 shears
- Fits overall shape and size



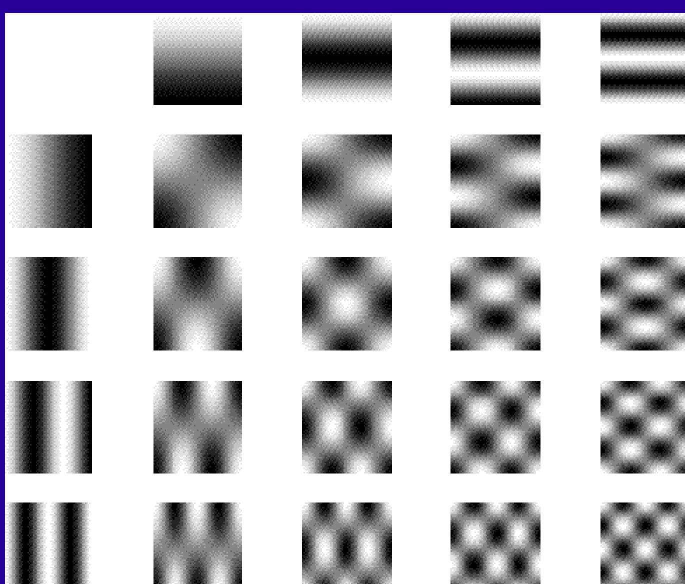
- Algorithm minimises the mean-squared difference between template and source image

Spatial Normalisation - Non-linear



Deformations consist of a linear combination of smooth basis functions

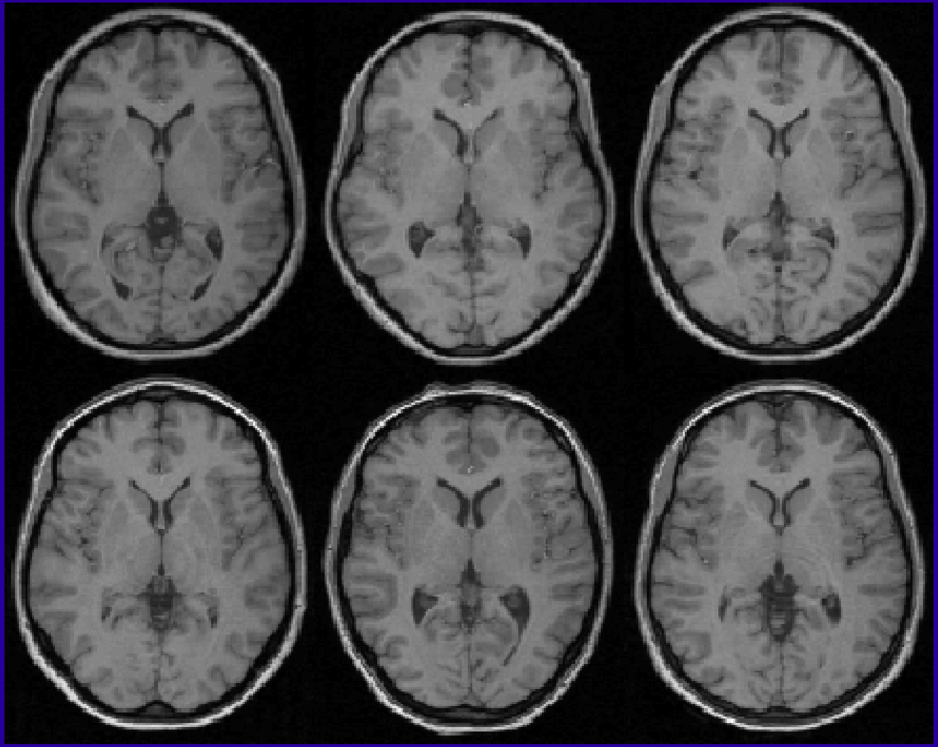
These are the lowest frequencies of a 3D discrete cosine transform (DCT)



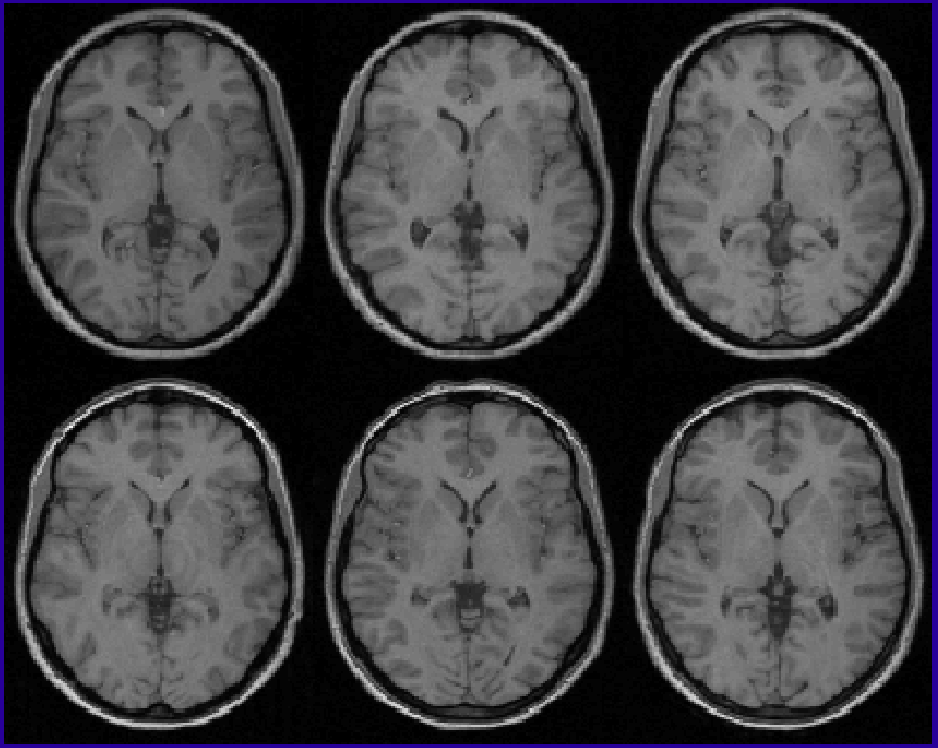
Algorithm simultaneously minimises

- Mean squared difference between template and source image
- Squared distance between parameters and their known expectation

Spatial normalisation
(affine vs. Non-linear registration)



Affine registration



Non-linear registration

Should you normalize?

Advantages

- Allows generalization of results to larger population
- Improves comparison with other studies
- Provides **coordinate space** for reporting results
- Enables averaging across subjects

Disadvantages

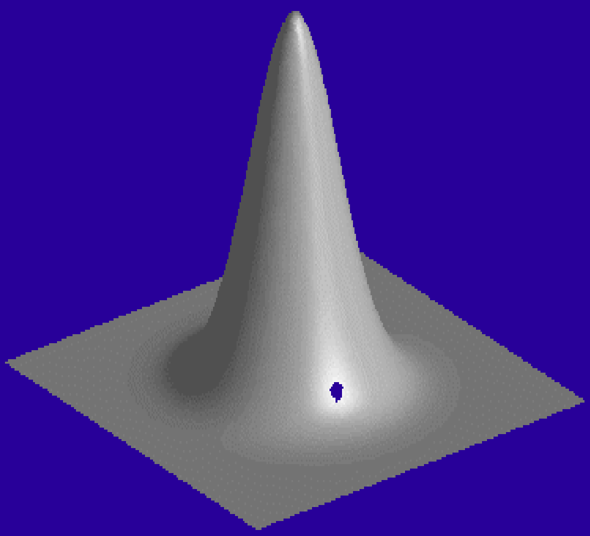
- Reduces spatial resolution
- May <u>reduce</u> activation strength by subject averaging
- Potentially problematic if the algorithm fails

Smoothing

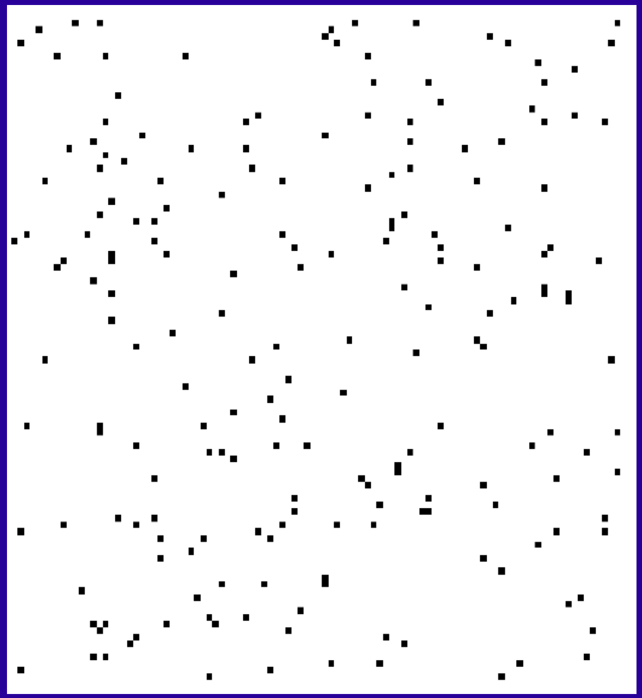
Smoothing

Smoothing is done by convolution.

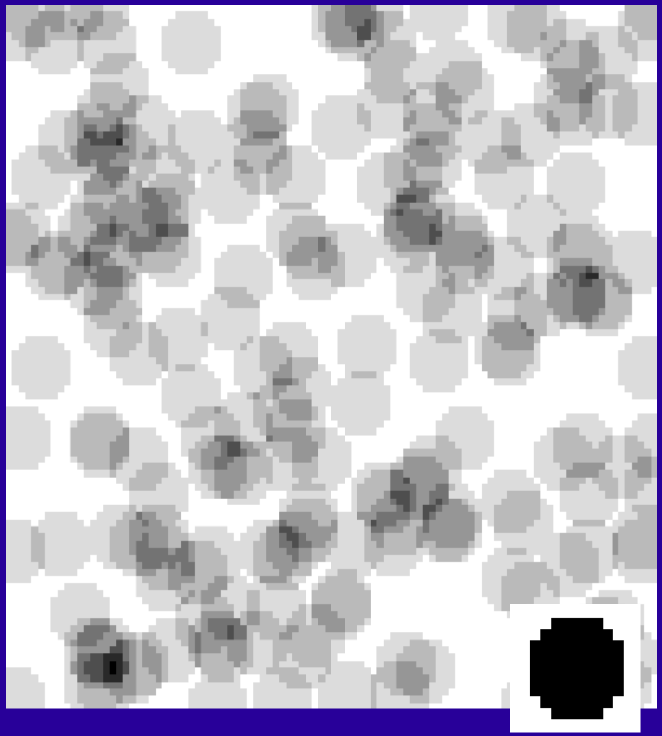
Each voxel after smoothing effectively becomes the result of applying a weighted region of interest (ROI).



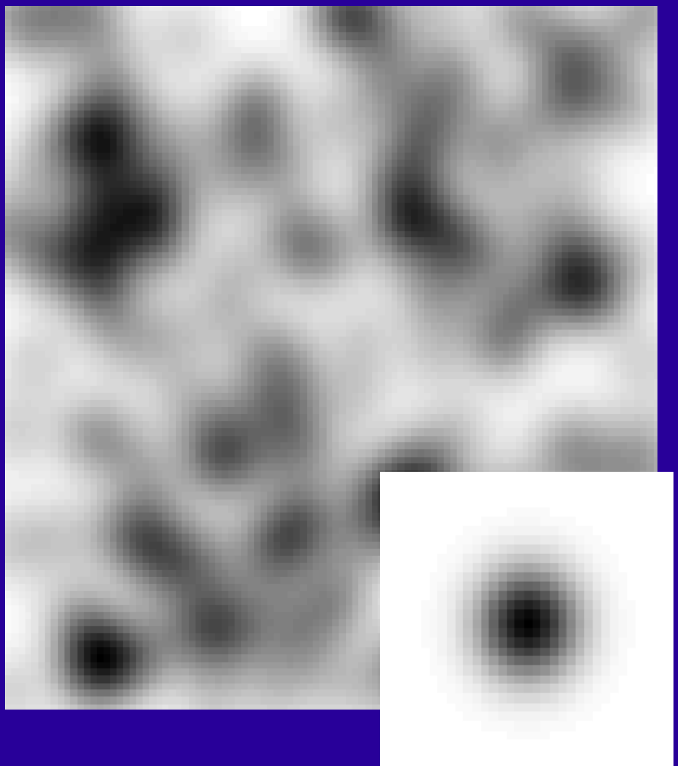
Before convolution



Convolved with a circle



Convolved with a Gaussian



Should you spatially smooth?

Advantages

- Increases Signal to Noise Ratio (SNR)
  - Matched Filter Theorem: Maximum increase in SNR by filter with same shape/size as signal
- Reduces number of comparisons
  - Allows application of Gaussian Field Theory
- May improve comparisons across subjects
  - Signal may be spread widely across cortex, due to intersubject variability

Disadvantages

- Reduces spatial resolution
- Challenging to smooth accurately if size/shape of signal is not known

Slide from Duke course