

# Data pre-processing framework in SPM

Bogdan Draganski

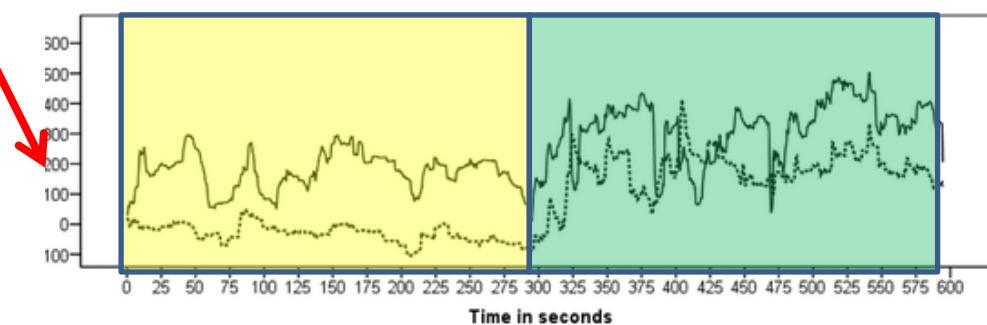
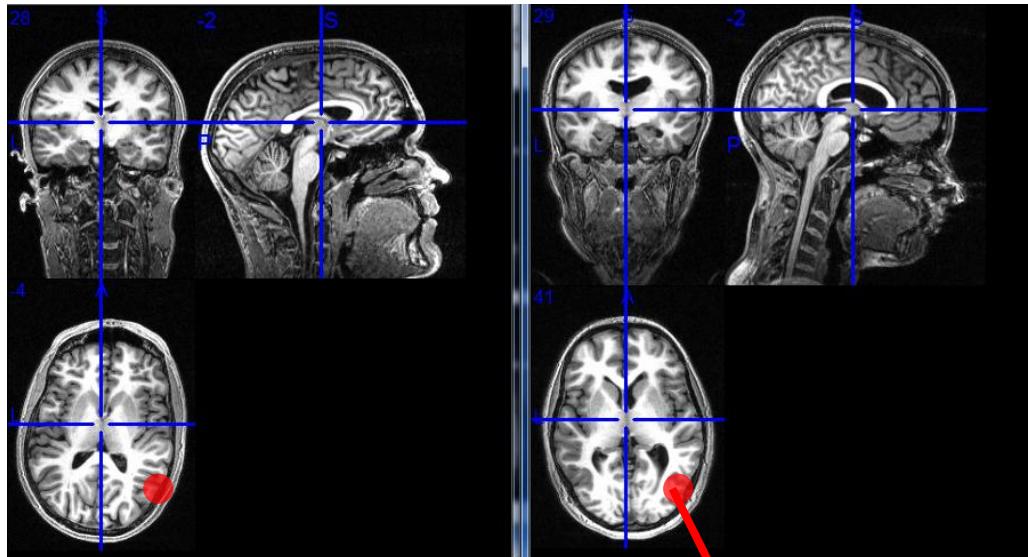
With special thanks to Ged Ridgway, Guillaume Flandin, John Ashburner and FIL's Methods group

# Outline

- Why do we need pre-processing?
- Overview
- Structural MRI pre-processing
- fMRI pre-processing

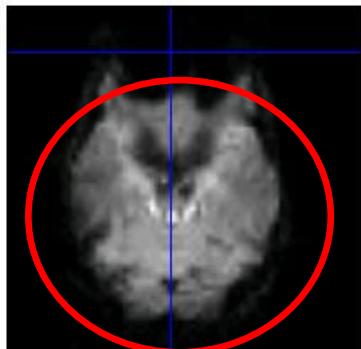
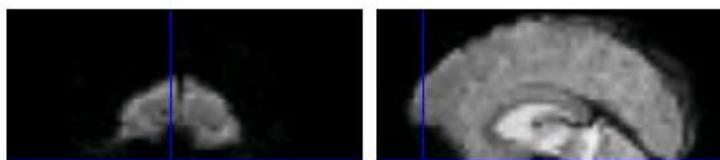
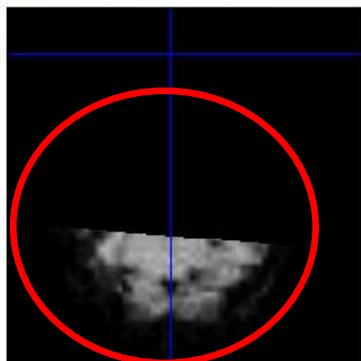
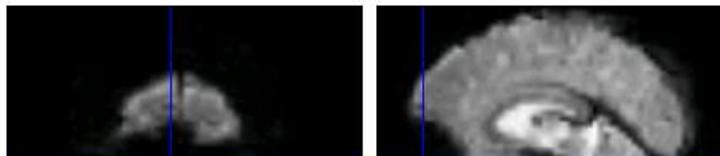
# Why do we need pre-processing?

# What do we want?

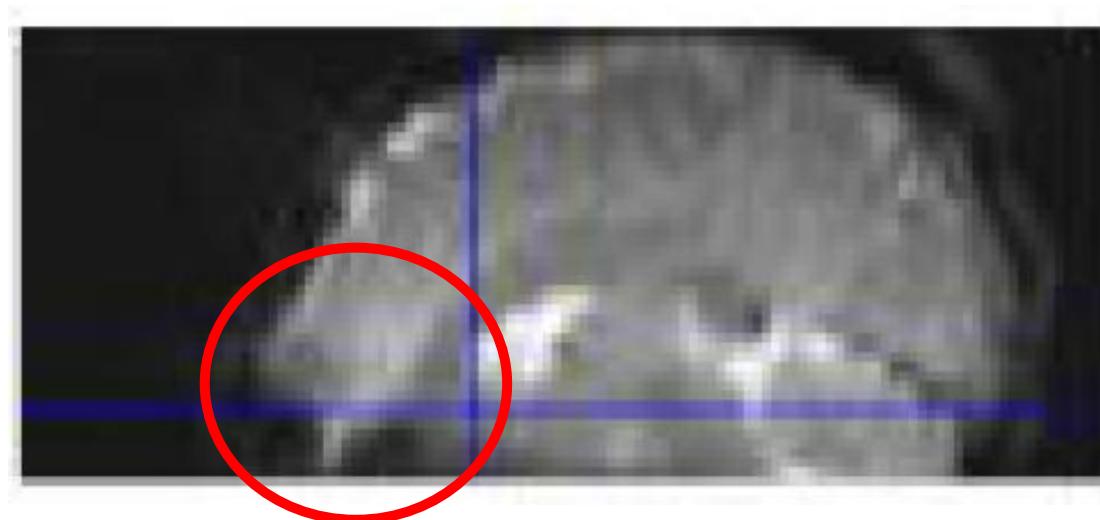


- Inter-subject averaging
  - Increase sensitivity with more subjects
    - Fixed-effects analysis
  - Extrapolate findings to the population as a whole
    - Mixed-effects analysis
- Make results from different studies comparable by aligning them to standard space
  - e.g. The T&T convention, using the MNI template

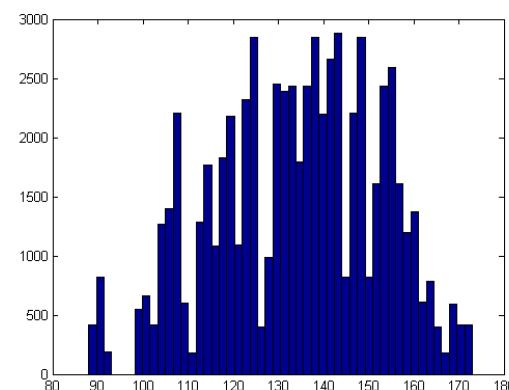
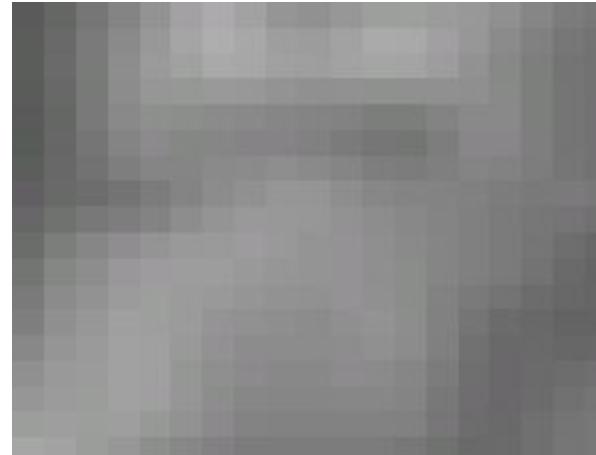
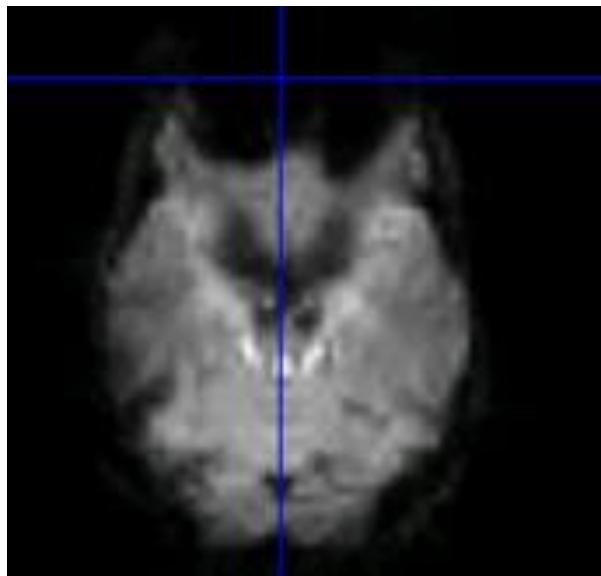
# Movement

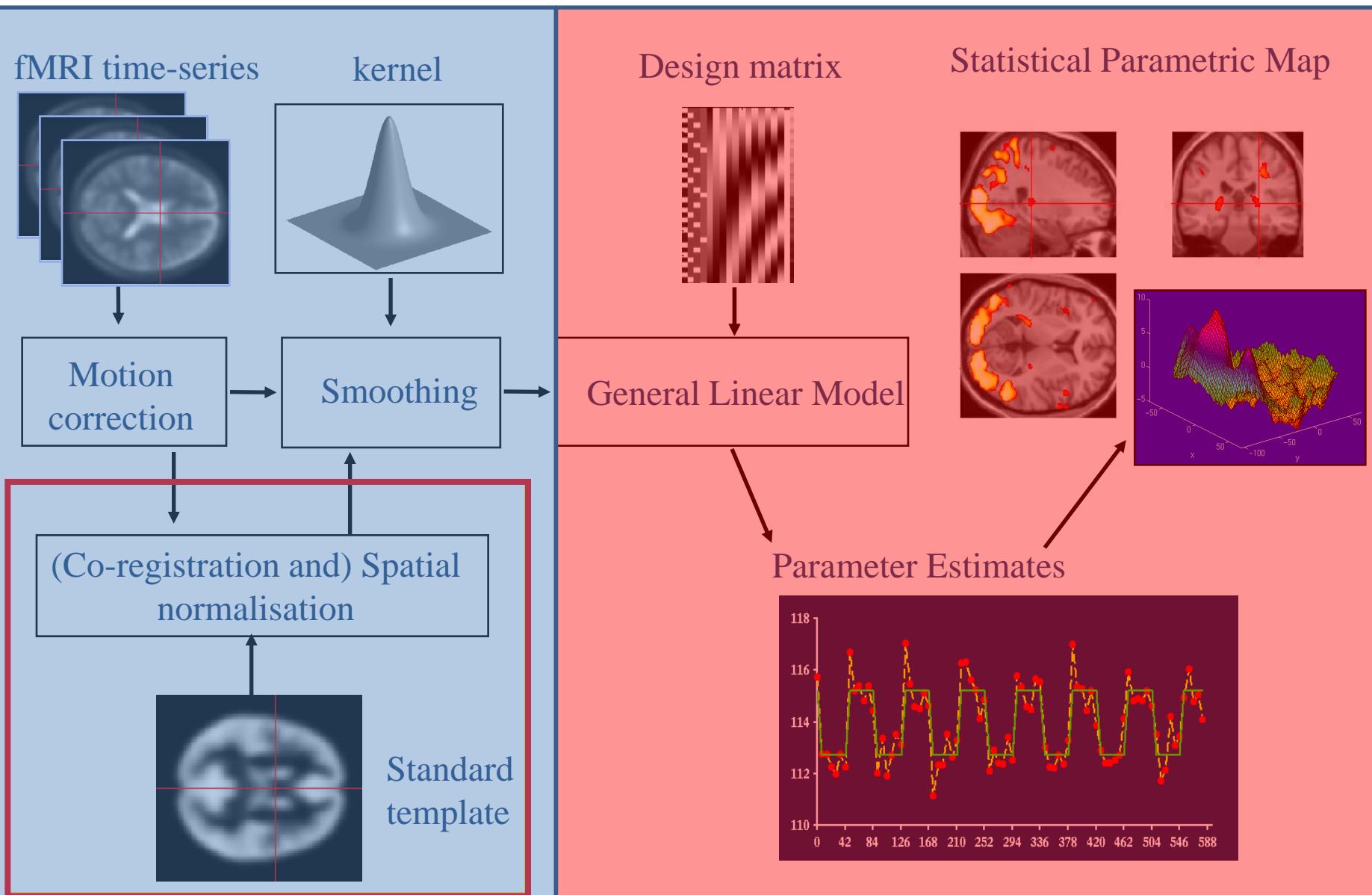


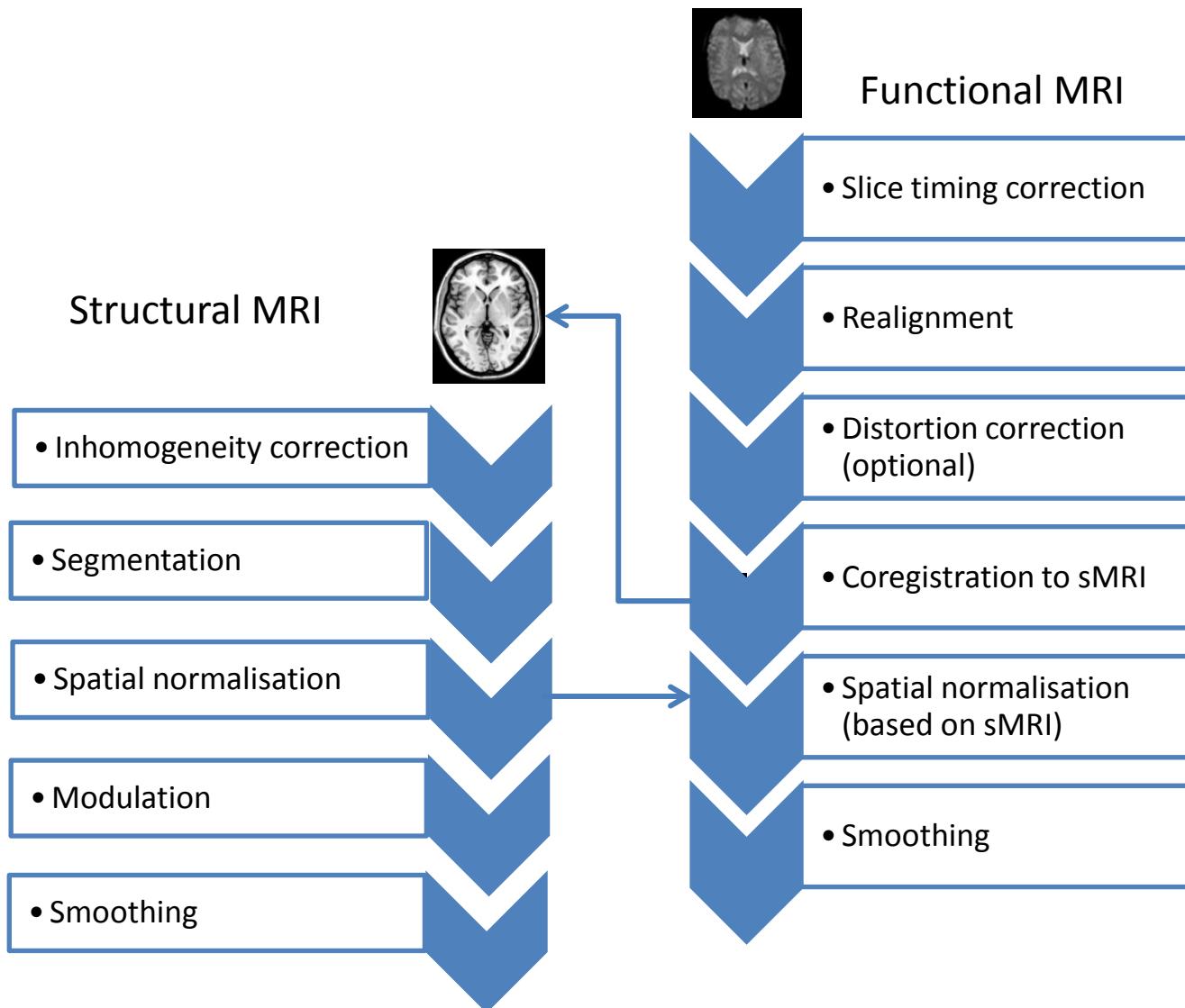
# Distortions



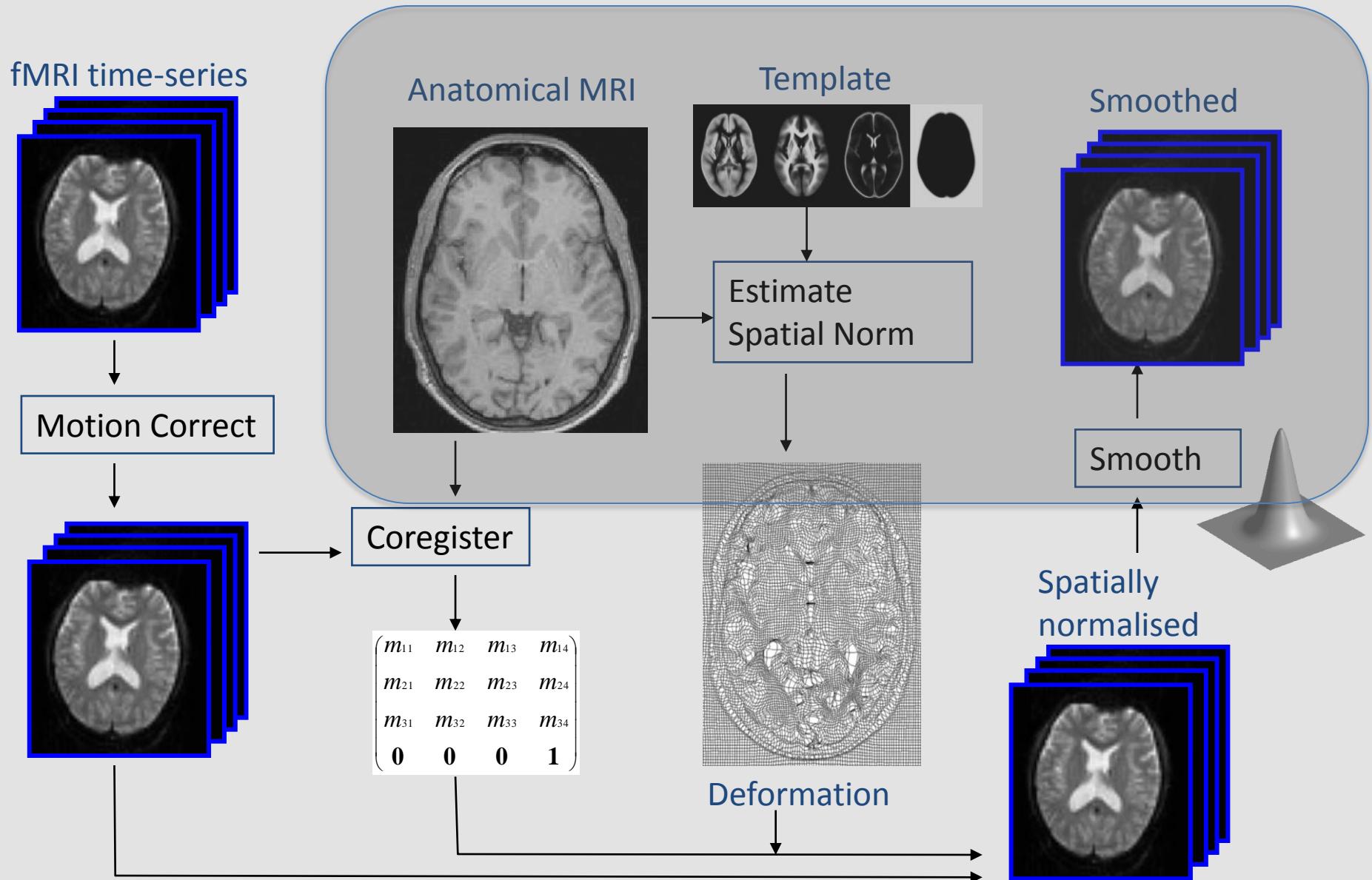
# Non-gaussian distribution



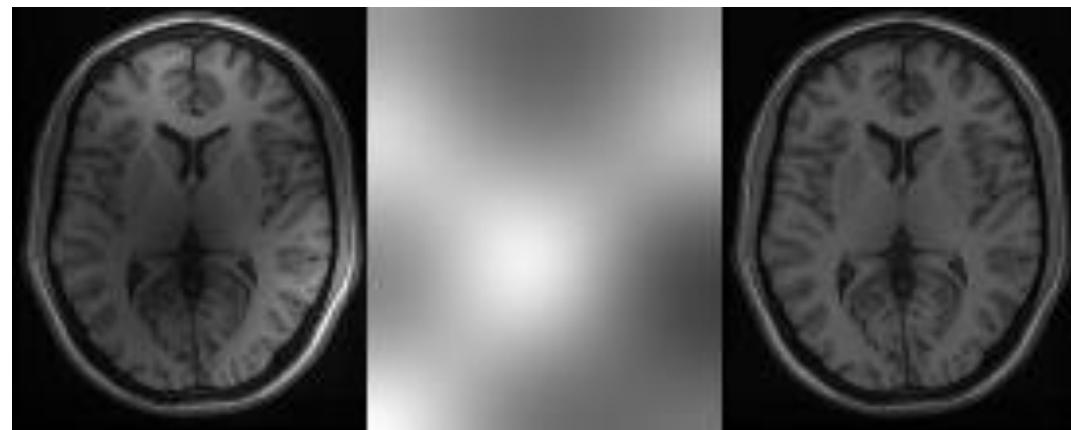
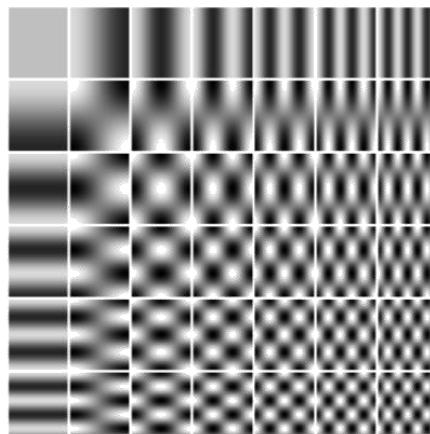




# Pre-processing Overview



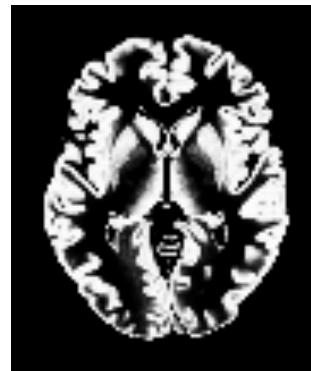
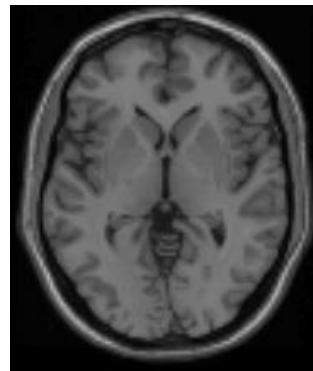
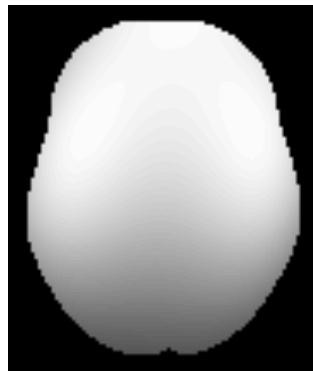
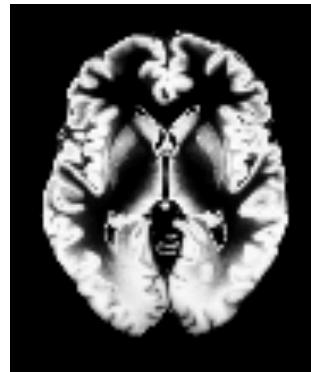
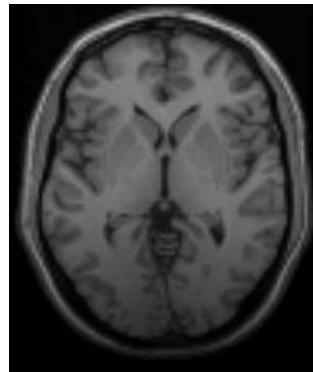
- MR Images are corrupted by smoothly varying intensity **inhomogeneity** caused by magnetic field imperfections and subject-field interactions
  - Would make intensity distribution spatially variable
- A smooth intensity **correction** can be modelled by a linear combination of DCT (discrete cosine transform) basis functions



# Inhomogeneity correction

- Field inhomogeneity will disrupt intensity based segmentation
- Bias correction required

no correction



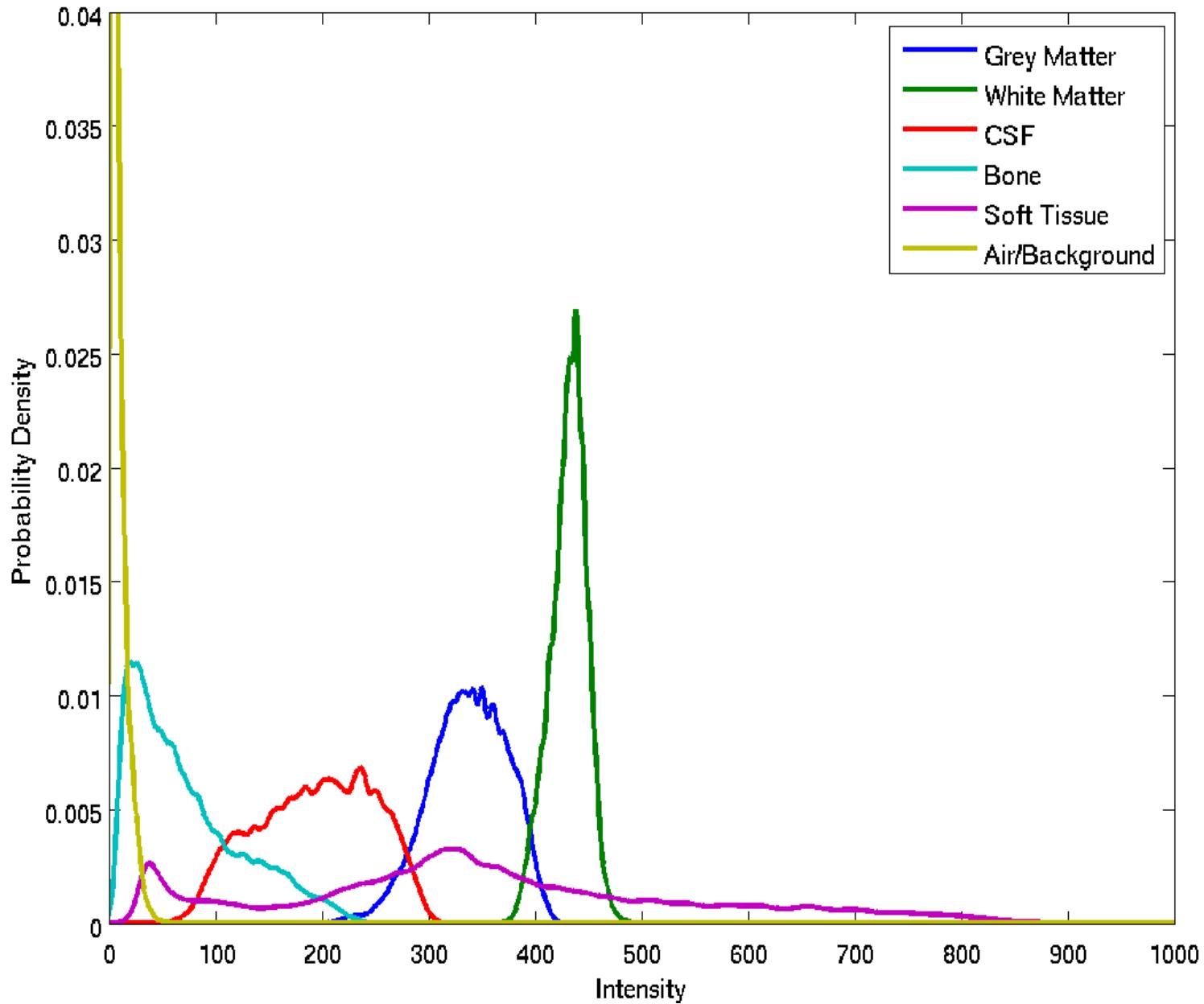
Estimate

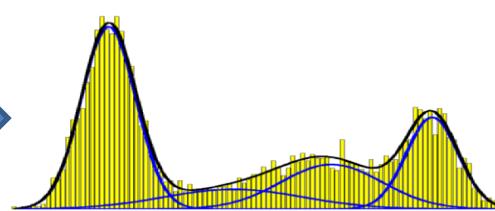
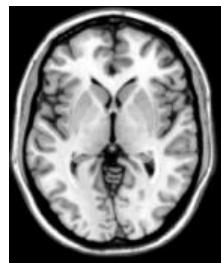
$T_1$

GM

WM

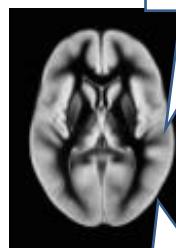
# Tissue intensity distributions – T1w MRI





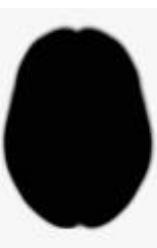
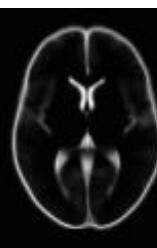
**P=0.95**

**P=0.95**



**P=0.95**

**P=0.05**

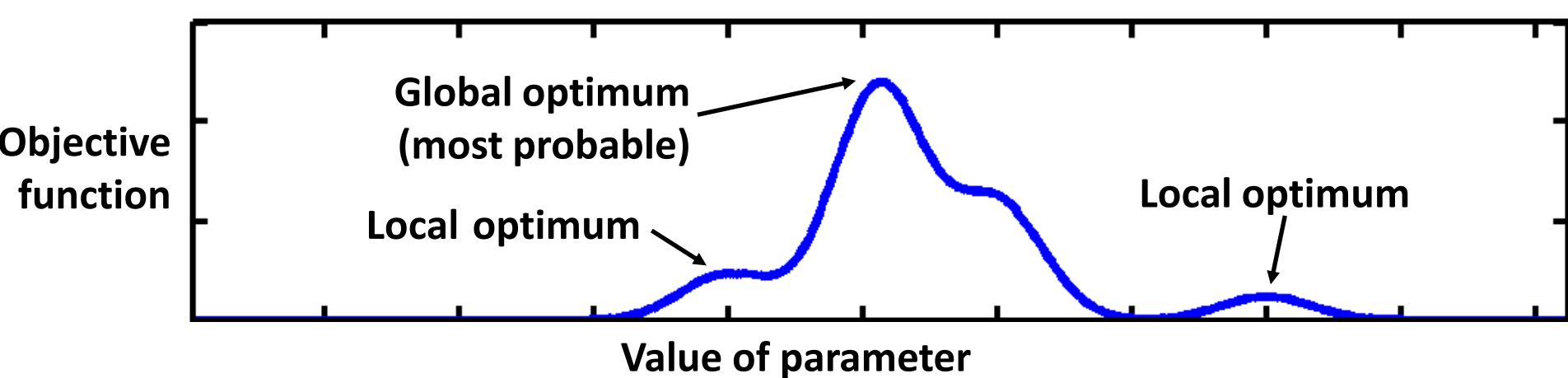


**P=0.95\*0.95=0.90**

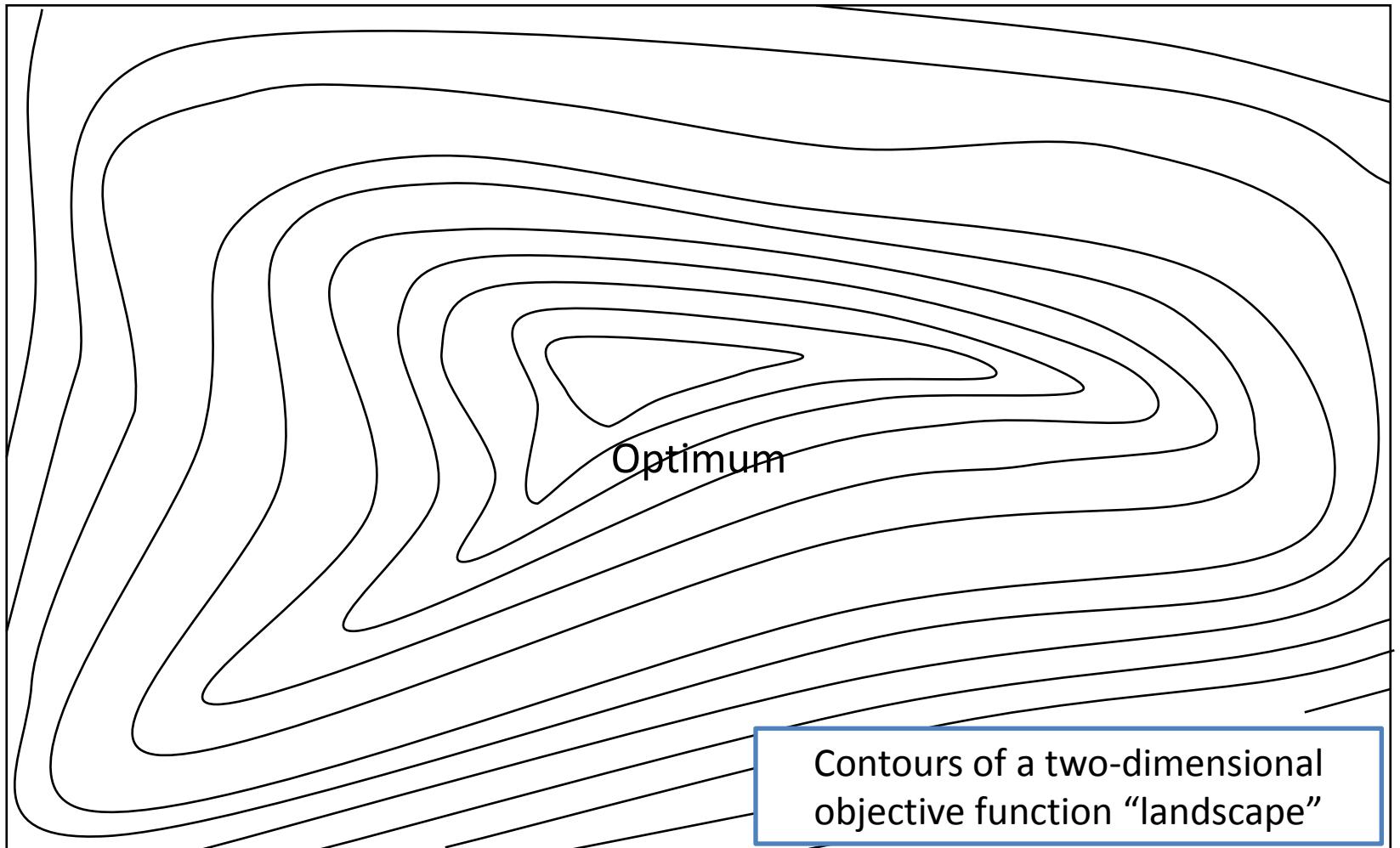
**P=0.95\*0.05=0.05**

# Optimisation

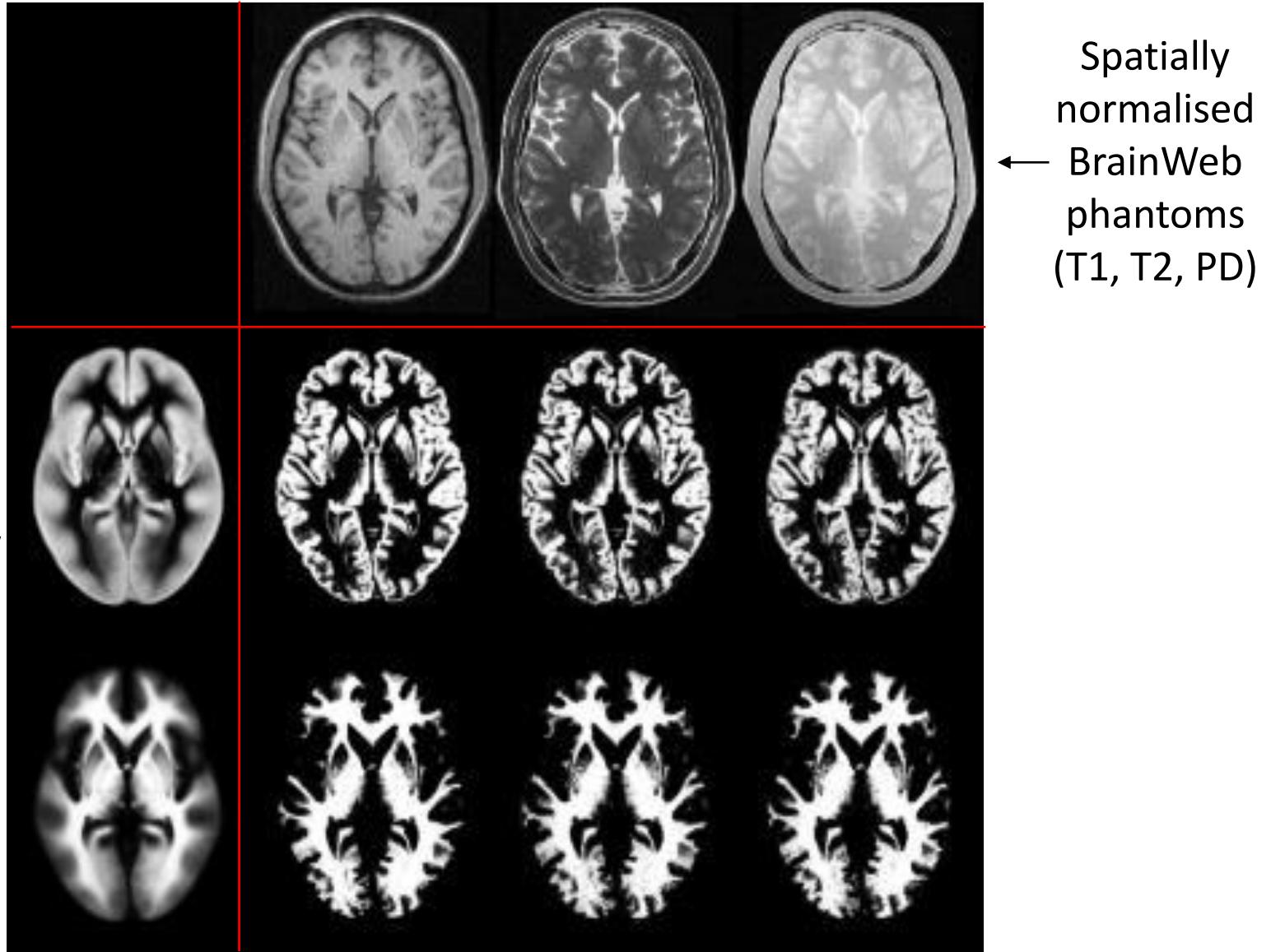
- Find the “best” parameters according to an “objective function” (minimised or maximised)
- Objective functions can often be related to a probabilistic model (Bayes -> MAP -> ML -> LSQ)



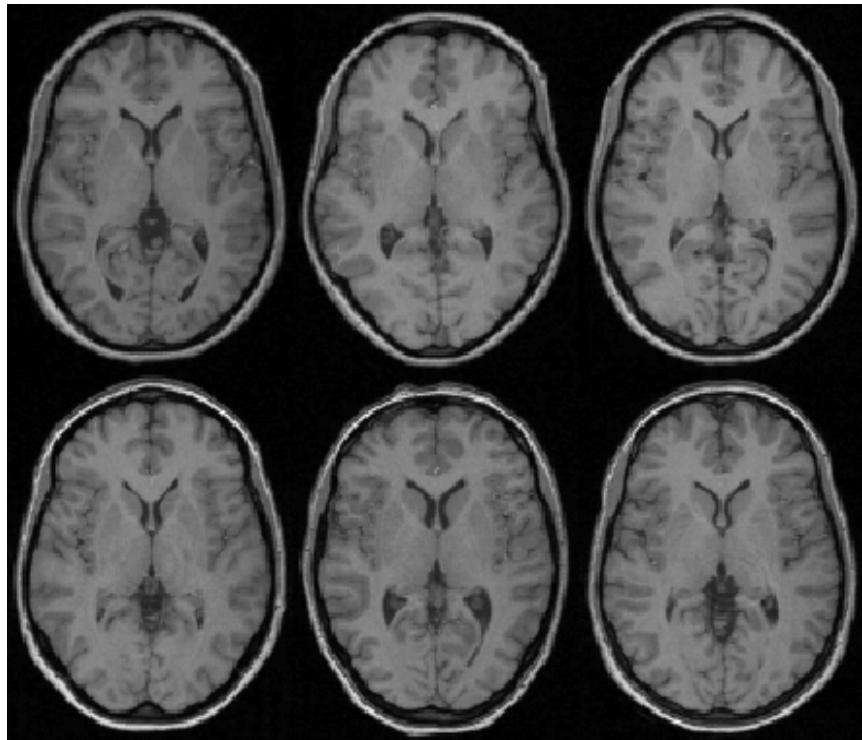
# Optimisation of multiple parameters



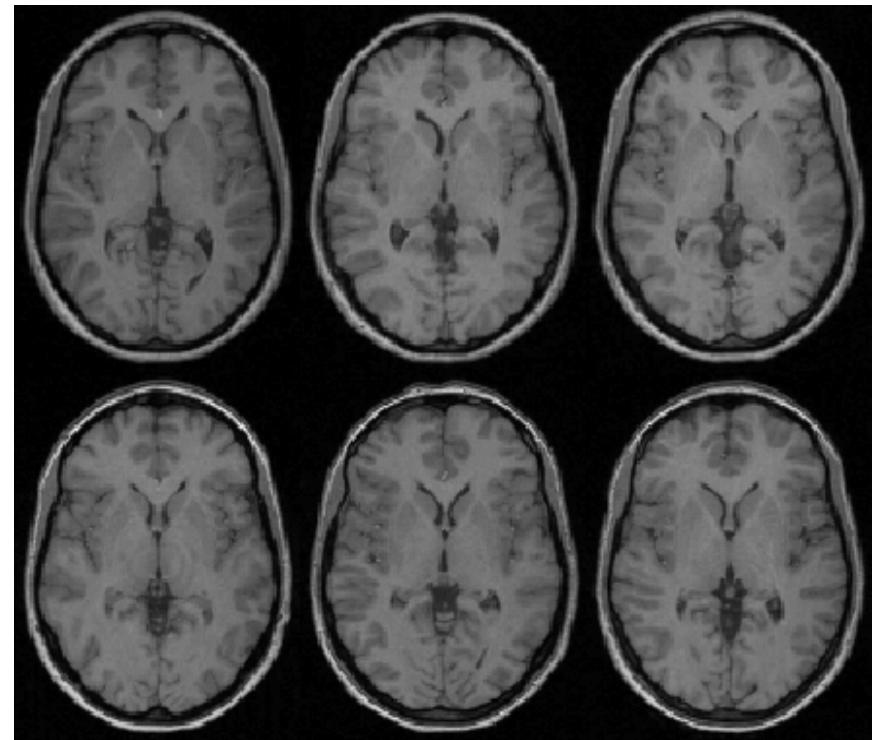
# Segmentation results



# Spatial normalisation



Affine registration



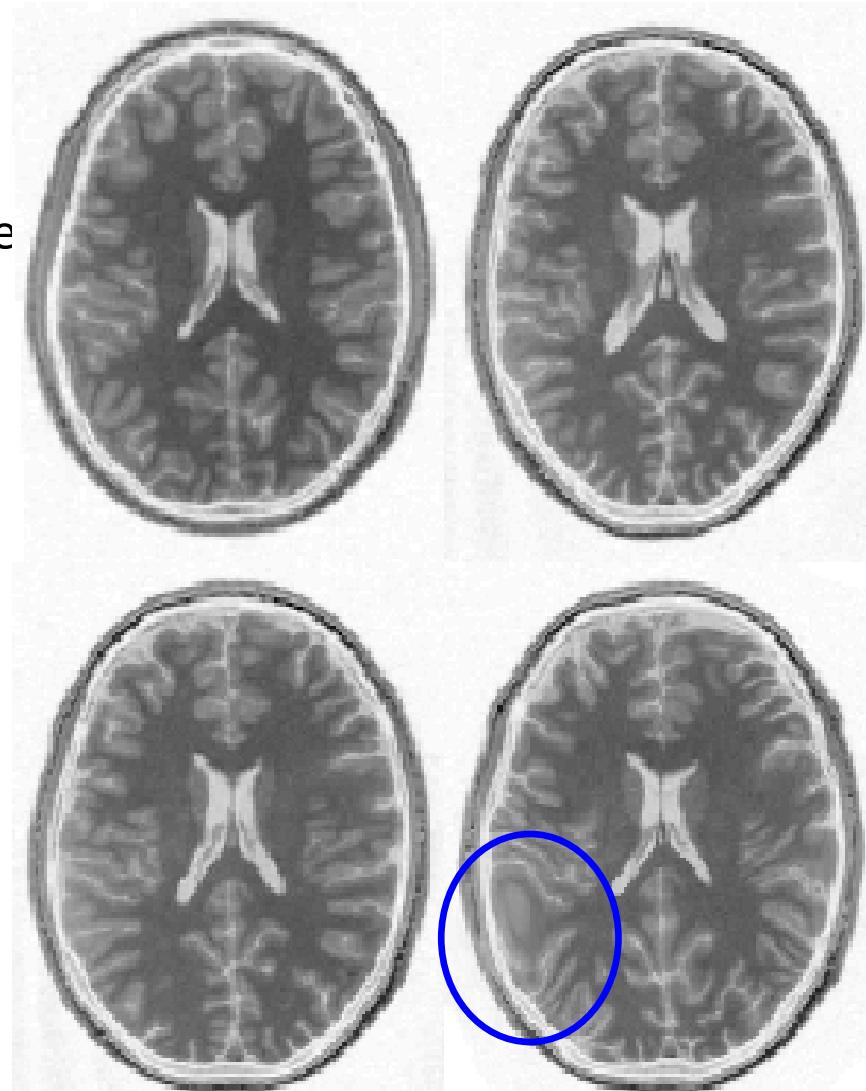
Non-linear registration

# Spatial normalisation - Overfitting

Without regularisation,  
the non-linear spatial  
normalisation can  
introduce unwanted  
deformation

Non-linear  
registration  
using  
regularisation  
(error = 302.7)

Template  
image



Affine  
registration  
(error = 472.1)

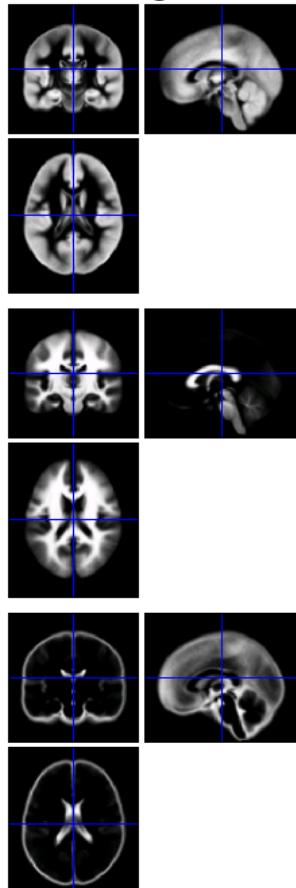
Non-linear  
registration  
without  
regularisation  
(error = 287.3)

# Spatial normalisation - Limitations

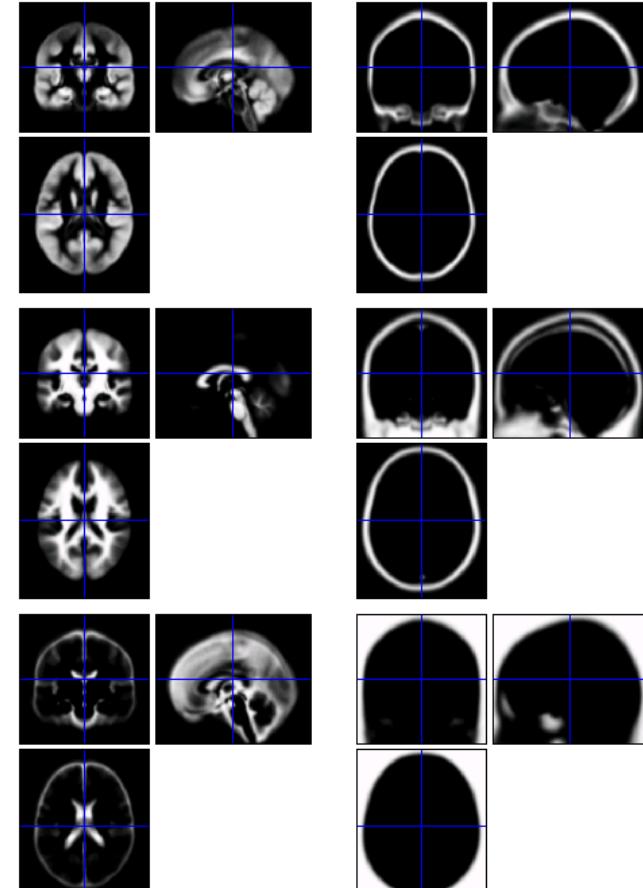
- Seek to match **functionally** homologous regions, but...
  - No exact match between structure and function
  - Different cortices can have different folding patterns
  - Challenging high-dimensional optimisation
    - Many local optima
- Compromise
  - Correct relatively large-scale variability (sizes of structures)
  - Smooth over finer-scale residual differences

- Uses information from tissue probability maps (TPMs) and the intensities of voxels in the image to work out the probability of a voxel being GM, WM or CSF

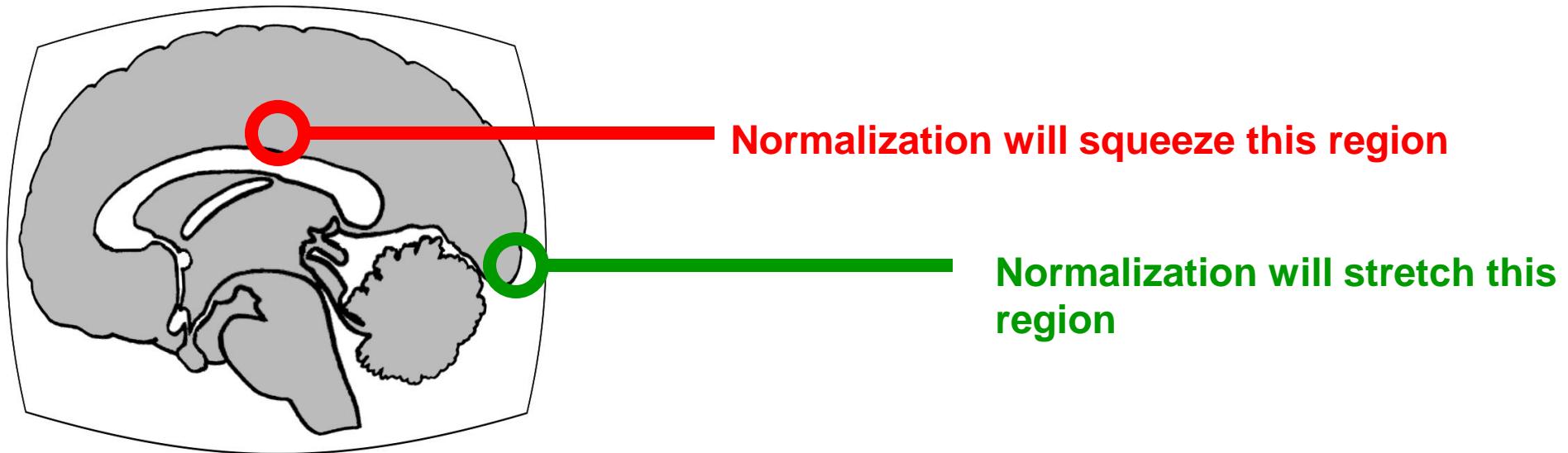
Old Segmentation



New Segmentation



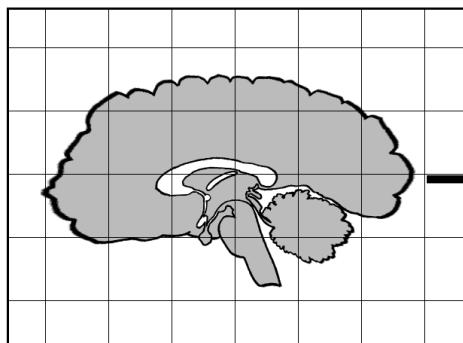
- If someone has atrophy, normalisation will stretch grey matter to make brain match healthy template
- This will reduce ability to detect differences



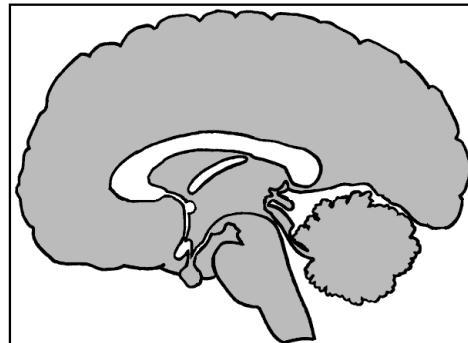
# Modulation

Analogy: as we blow up a balloon, the surface becomes thinner.

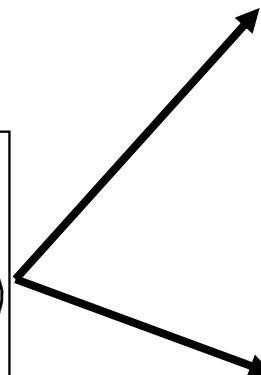
Likewise, as we expand a brain area it's volume is reduced.



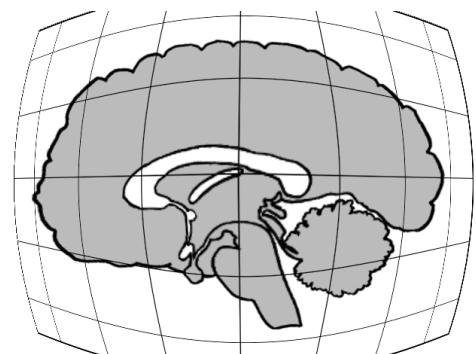
**Source**



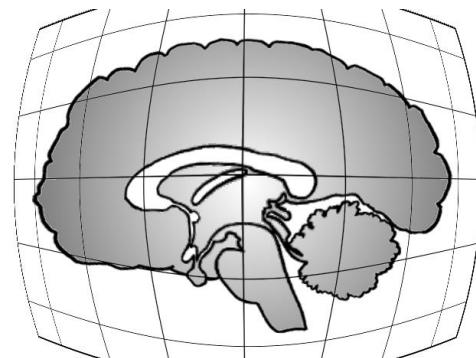
**Template**



**Without  
modulation**

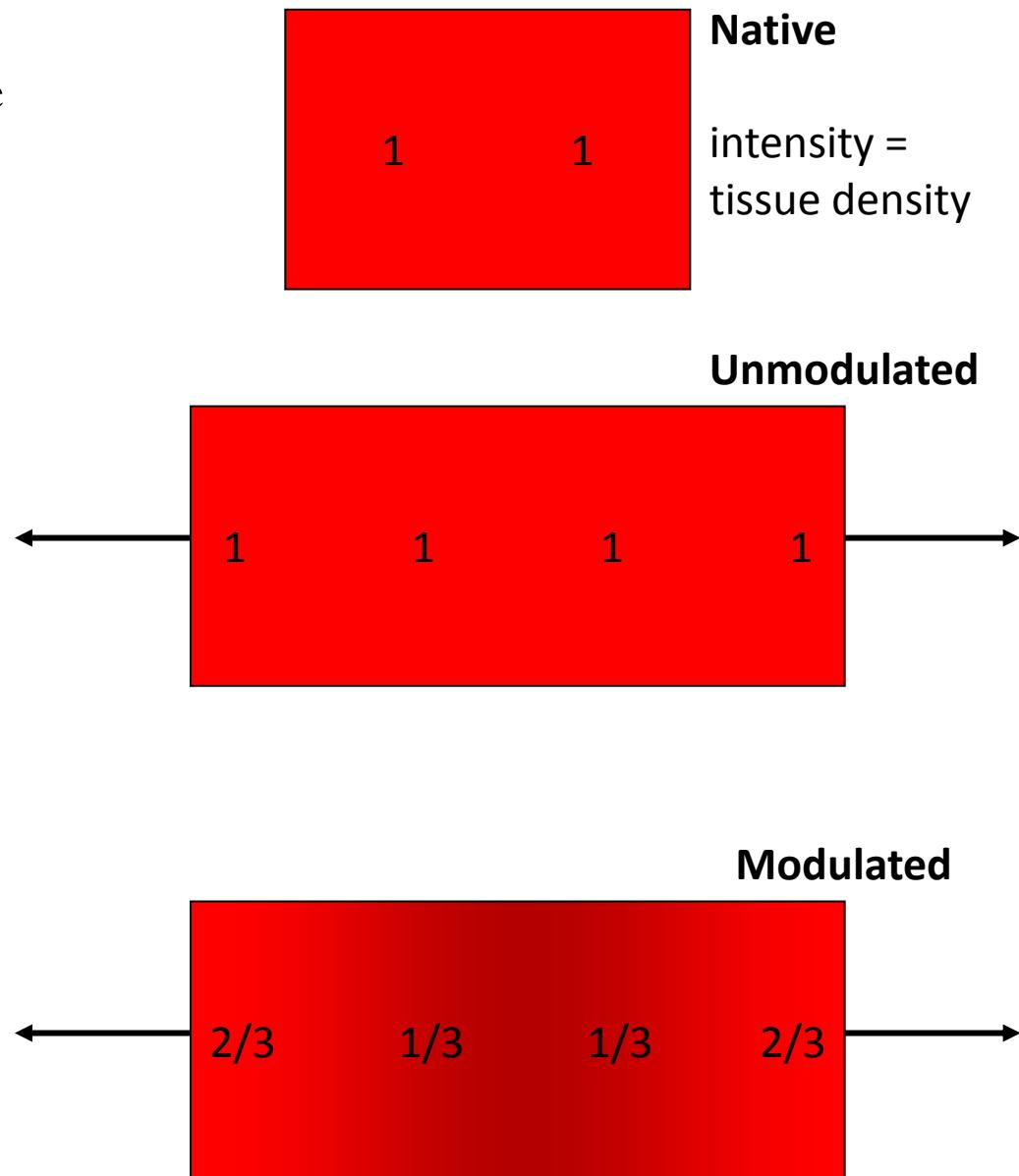


**Modulated**

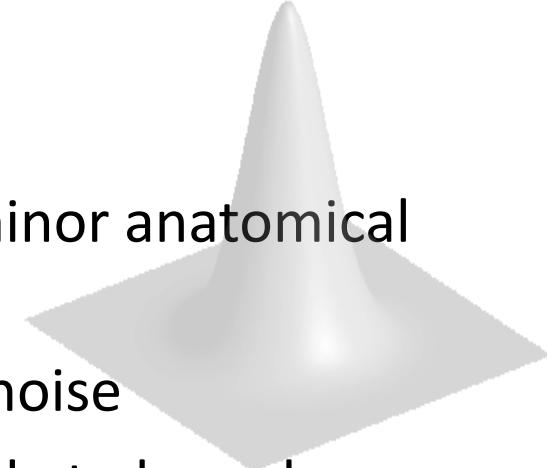


# Modulation

- Multiplication of the warped (normalised) tissue intensities so that their regional or global volume is preserved
  - Can detect differences in completely registered areas
- Otherwise, we *preserve concentrations*, and are detecting *mesoscopic* effects that remain after approximate registration has removed the macroscopic effects
  - Flexible (not necessarily “perfect”) registration may not leave any such differences

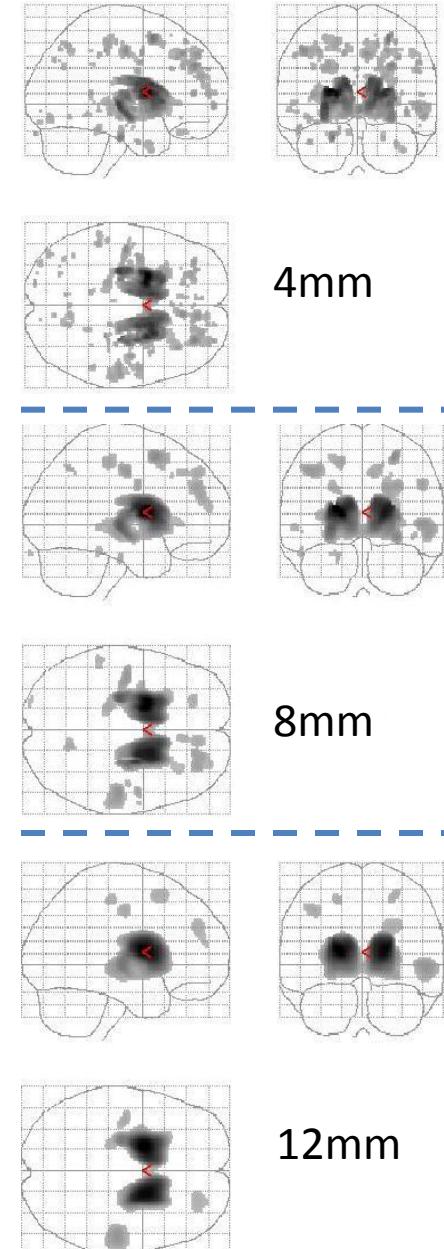


- Why would we deliberately blur the data?
  - Improves spatial overlap by blurring over minor anatomical differences and registration errors
  - Averaging neighbouring voxels suppresses noise
  - Increases sensitivity to effects of similar scale to kernel (matched filter theorem)
  - Makes data more normally distributed (central limit theorem)
  - Reduces the effective number of multiple comparisons
- How is it implemented?
  - Convolution with a 3D Gaussian kernel, of specified full-width at half-maximum (FWHM) in mm



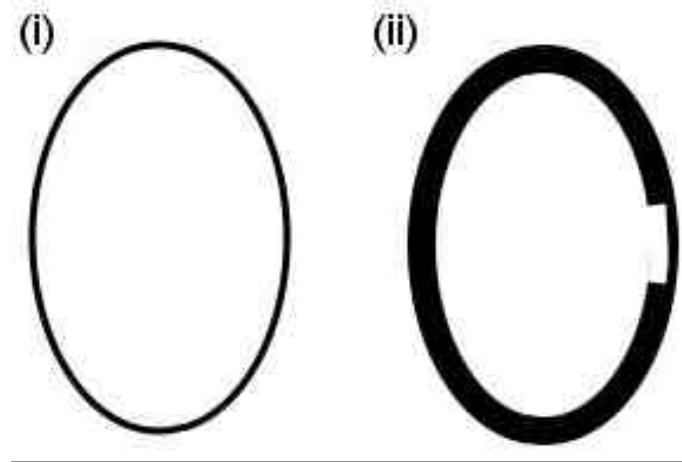
# Smoothing

- Smoothing kernel - should match the shape and size of the expected effect
- Benefits
  - more “Gaussian distribution” of the data
  - Smooth out incorrect registration
- RFT requires FWHM > 3 voxels



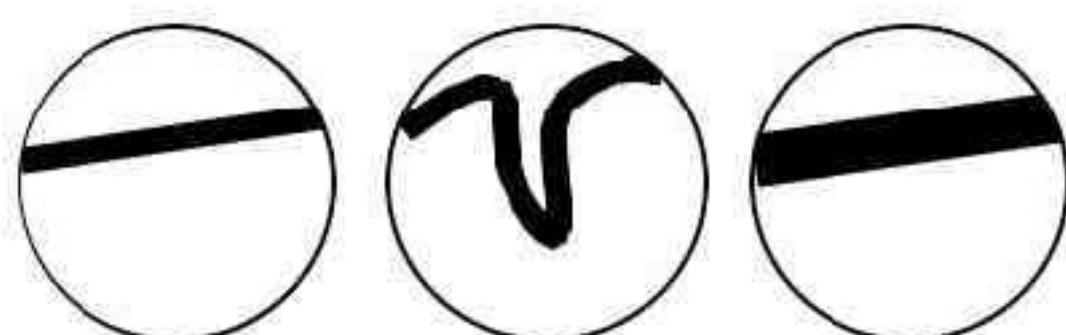
# Global normalisation

- Shape is really a multivariate concept
  - Dependencies among volumes in different regions
- SPM is mass univariate
  - Combining voxel-wise information with “global” integrated tissue volume provides a compromise



Above: (ii) is globally thicker, but locally thinner than (i) – either of these effects may be of interest to us.

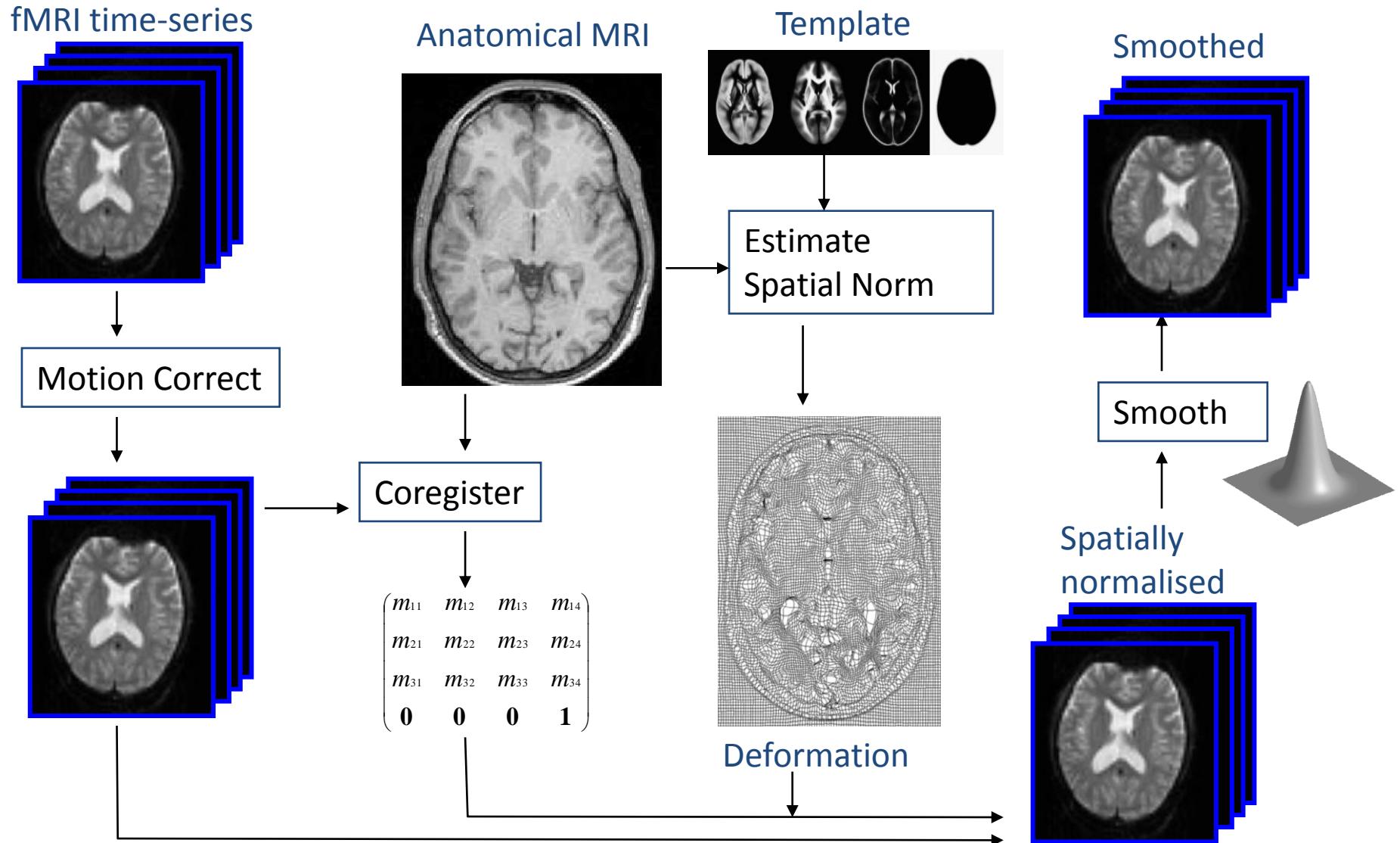
Below: The two “cortices” on the right both have equal volume...



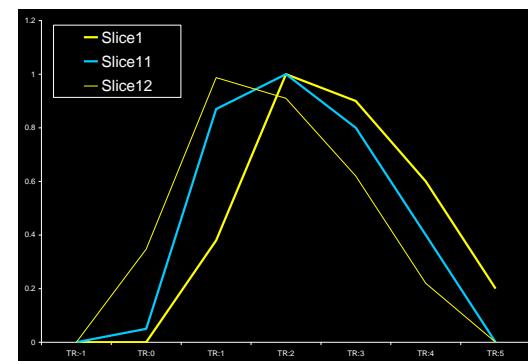
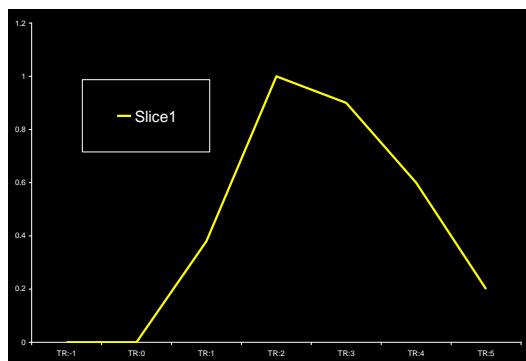
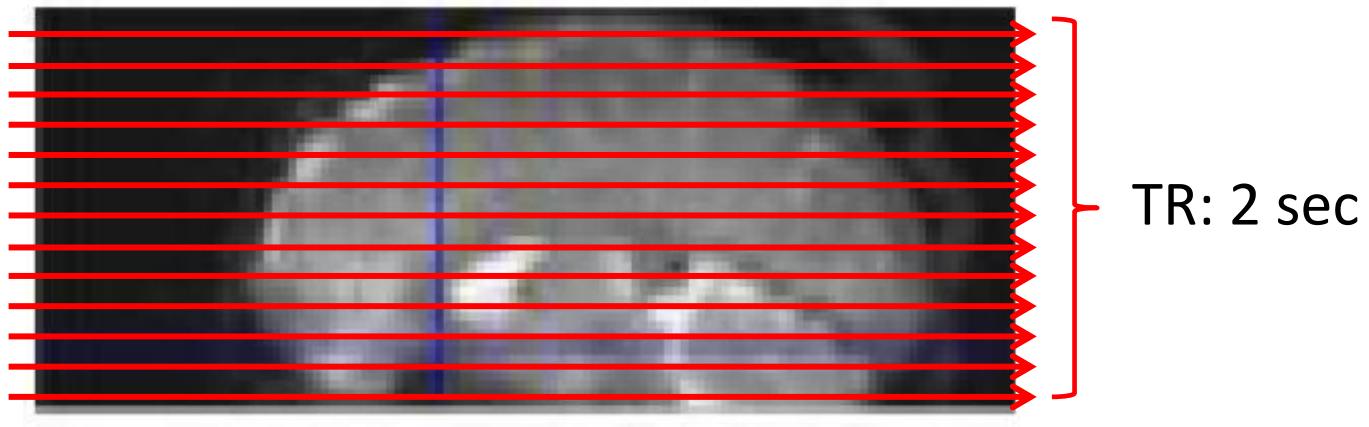
# fMRI pre-processing

- Slice timing correction (optional)
- Realignment (Motion correction)
- Unwarping (Motion correction x B0 correction)
- Co-registration
  - Link functional scans to anatomical scan
- Spatial normalisation (unified segmentation)
  - Fitting images to a standard brain
- Smoothing
  - Increases signal-to-noise ratio and approximates a Gaussian distribution

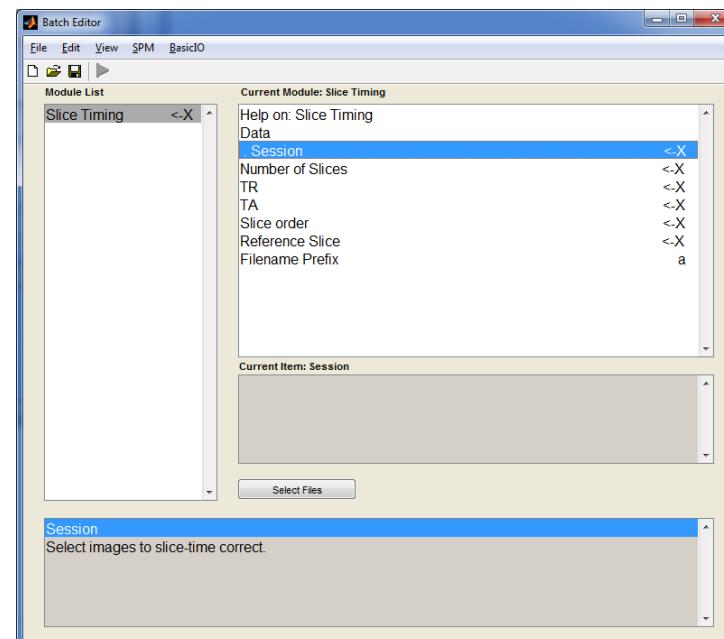
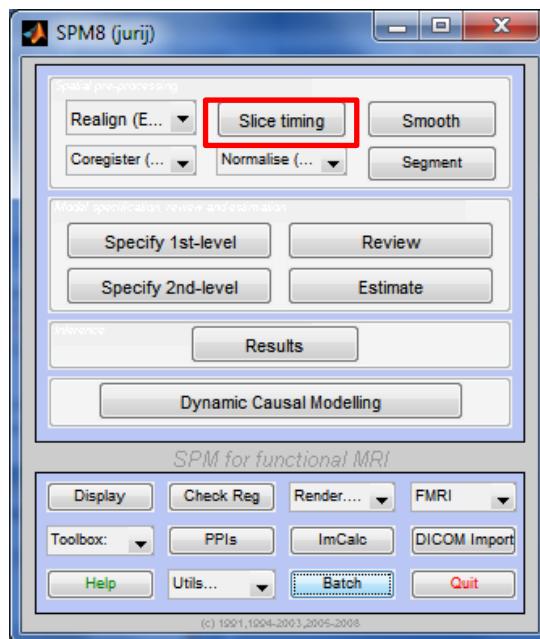
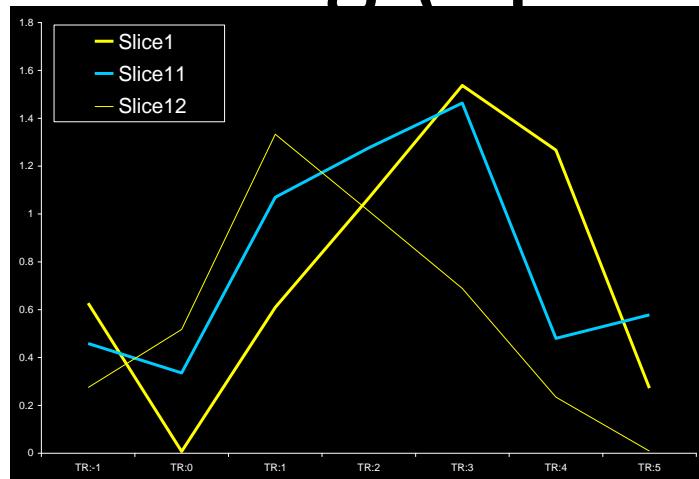
# Pre-processing Overview



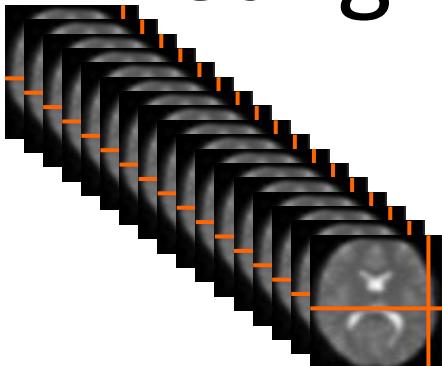
# Slice timing (optional)



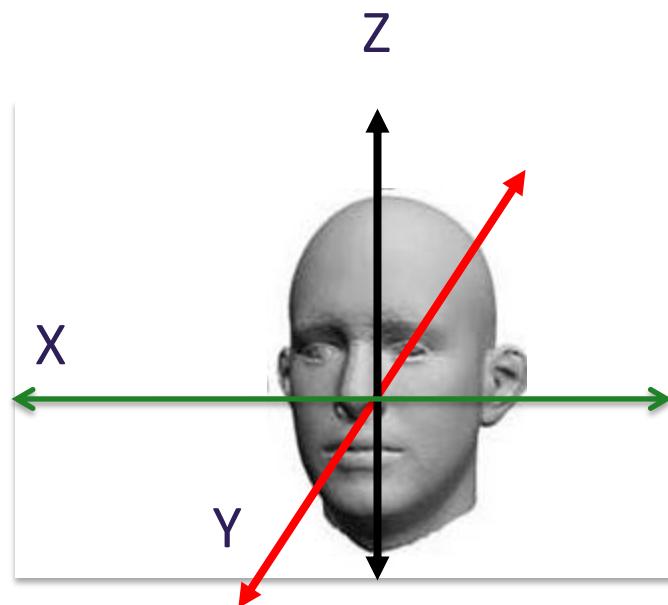
# Slice timing (optional)



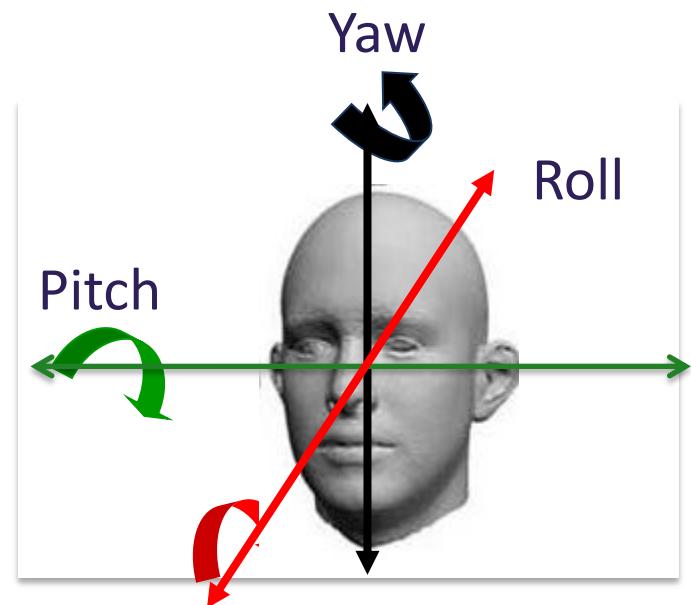
# Realignment - motion correction



Translation



Rotation



# Realignment - motion correction

Rigid body transformations parameterised by:

Translations

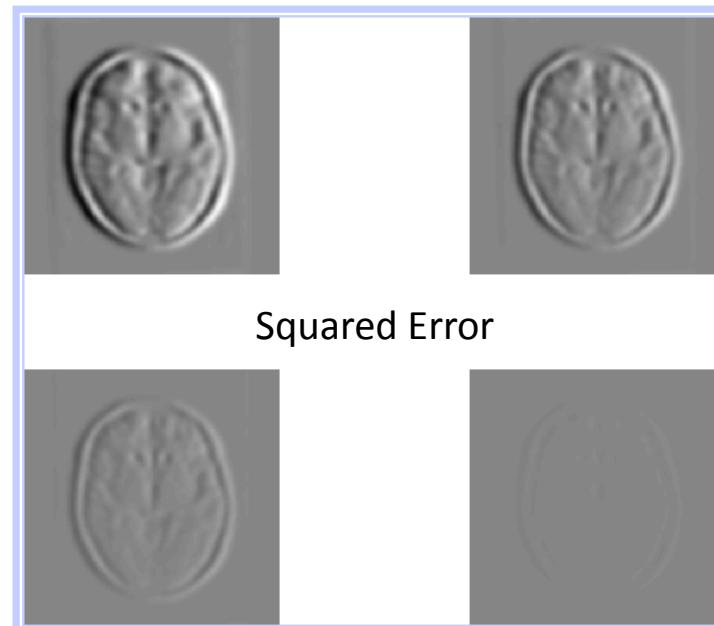
Pitch  
about X axis

Roll  
about Y axis

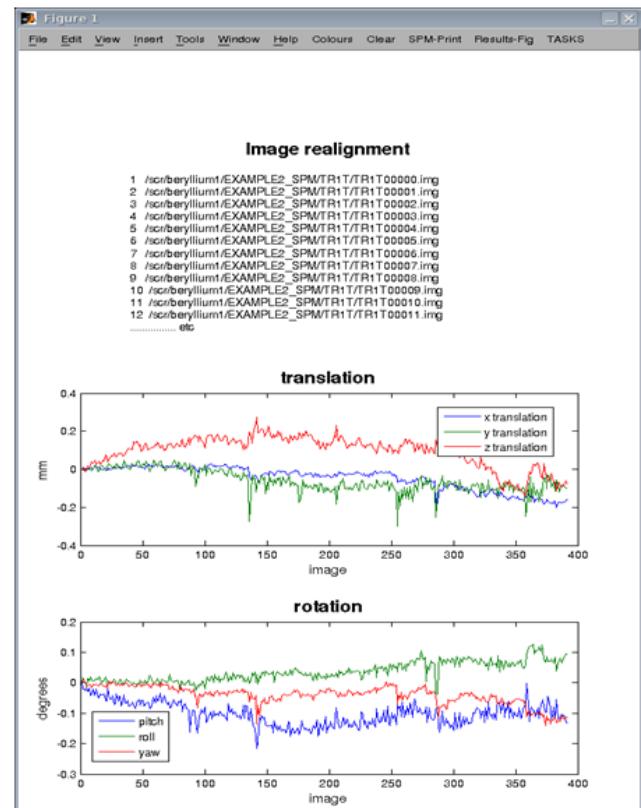
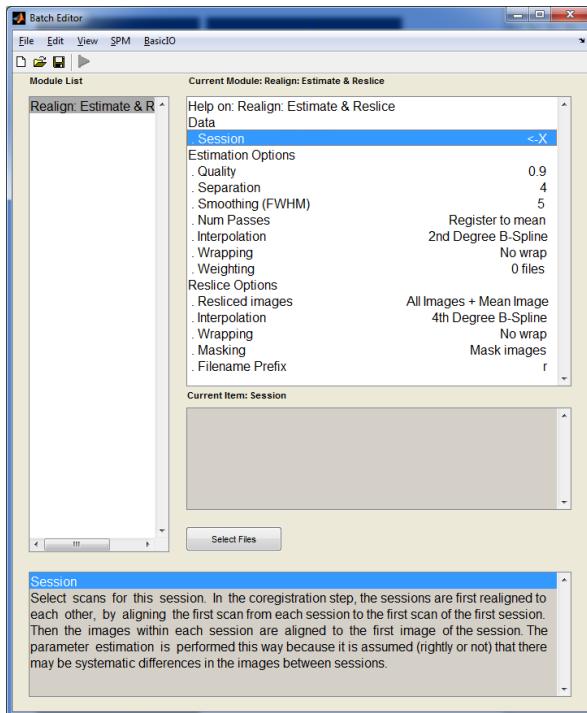
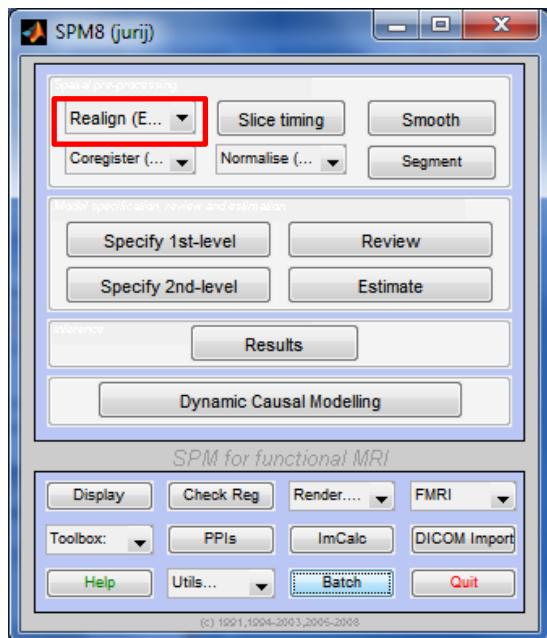
Yaw  
about Z axis

$$\begin{pmatrix} 1 & 0 & 0 & \text{Xtrans} \\ 0 & 1 & 0 & \text{Ytrans} \\ 0 & 0 & 1 & \text{Ztrans} \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & \cos(\Phi) & \sin(\Phi) & 0 \\ 0 & -\sin(\Phi) & \cos(\Phi) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} \cos(\Theta) & 0 & \sin(\Theta) & 0 \\ 0 & 1 & 0 & 0 \\ -\sin(\Theta) & 0 & \cos(\Theta) & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} \cos(\Omega) & \sin(\Omega) & 0 & 0 \\ -\sin(\Omega) & \cos(\Omega) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Minimizing the squared difference (error) between the images

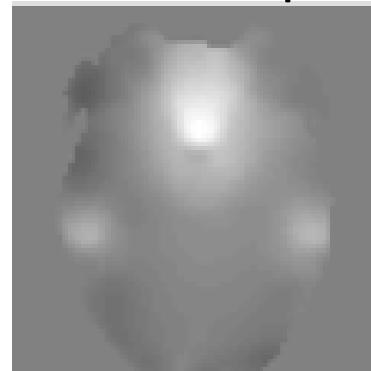


# Realignment motion correction

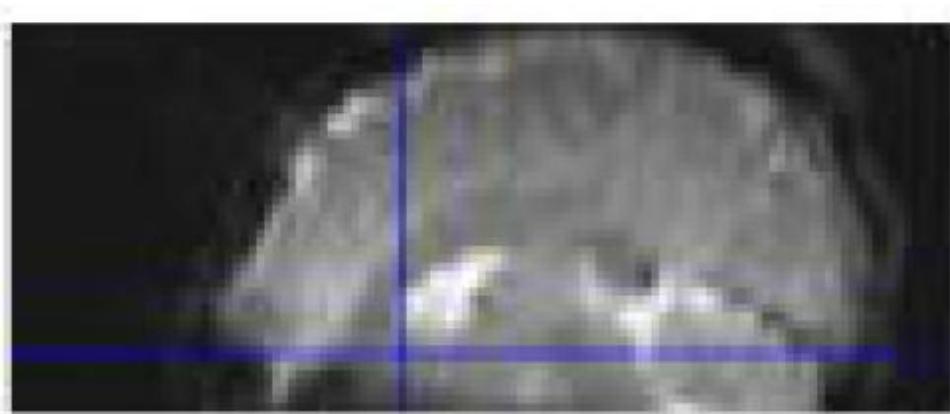


# Unwarp

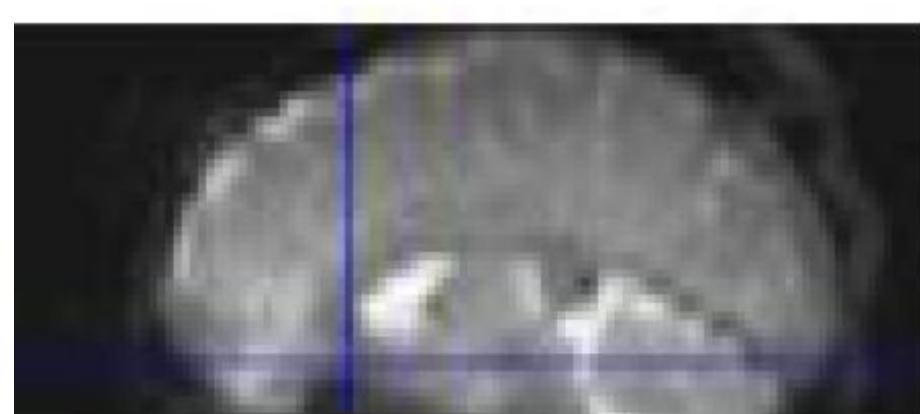
Fieldmap



Raw EPI

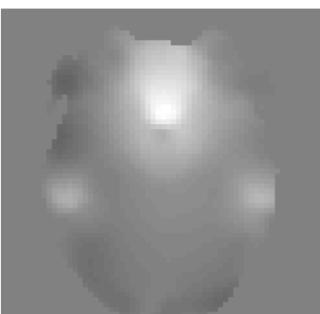


Undistorted EPI

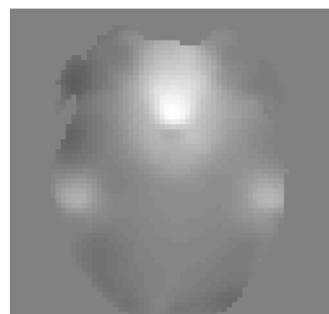


# Unwarp can estimate changes in distortion from movement

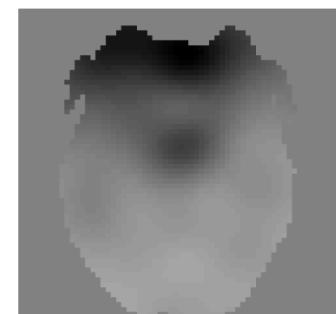
Resulting field map at each time point



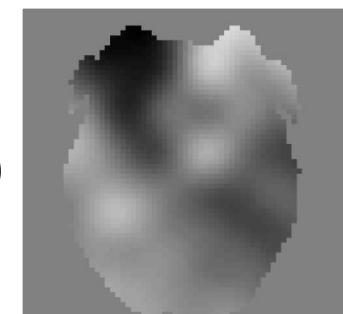
Measured field map



Estimated change in field wrt change in pitch (x-axis)



Estimated change in field wrt change in roll (y-axis)



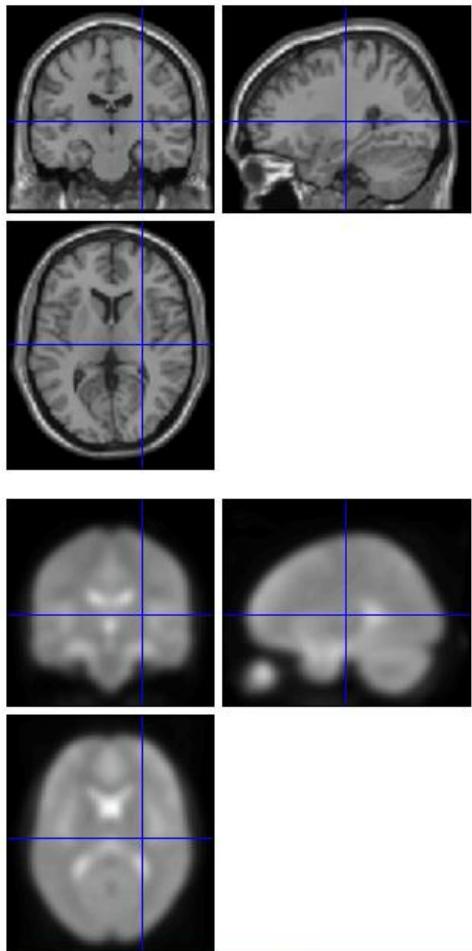
=

$$+ \Delta\varphi$$

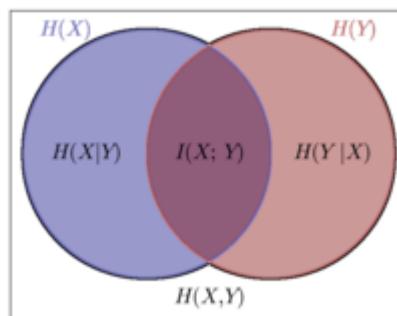
$$+ \Delta\theta$$

- distortions in a reference image (FieldMap)
- subject motion parameters (that we obtain in realignment)
- change in deformation field with subject movement (estimated via iteration)

# Co-registration



Normalized mutual information



Visual Image



Thermal Image



Chess Image after Registration

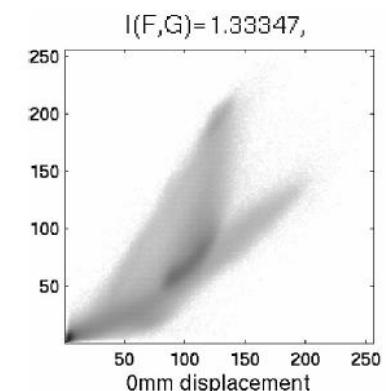
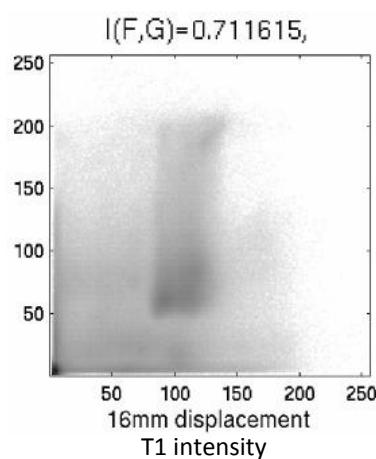
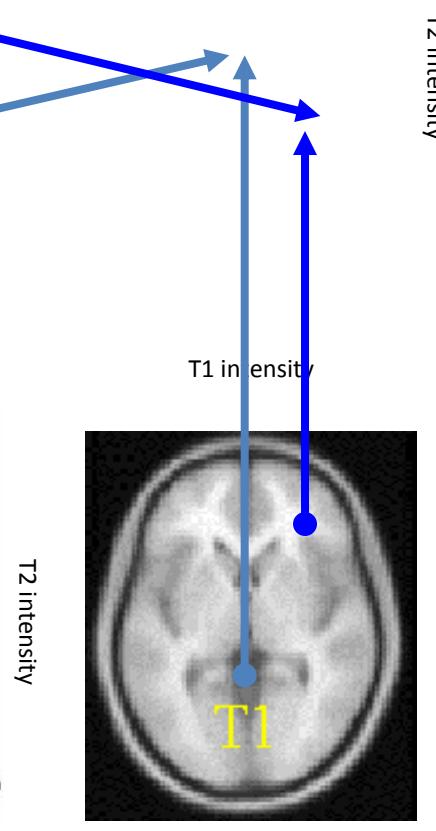
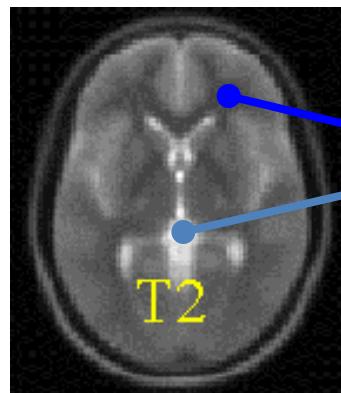


Image after Fusion



functional and  
structural images in  
the same space

# Co-registration

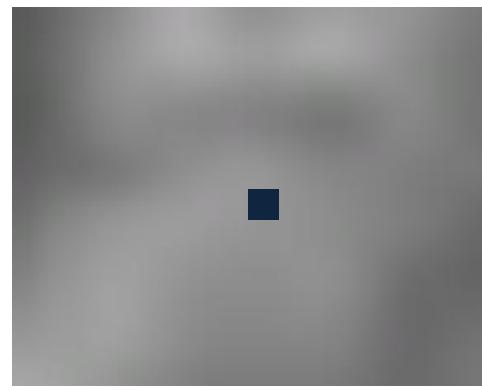
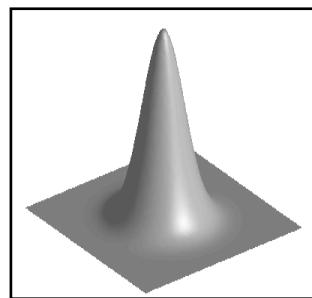
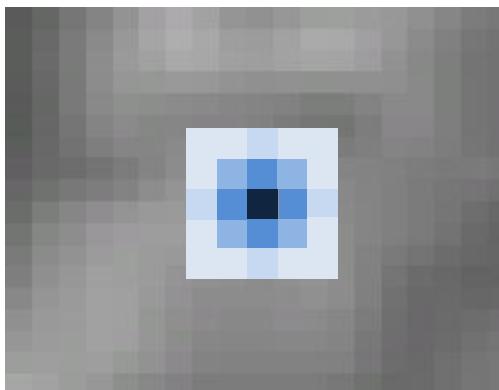


# Spatial registration

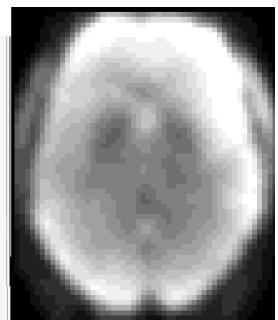
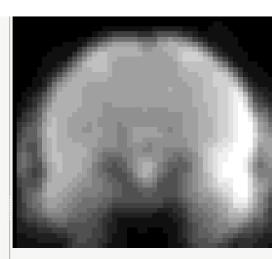
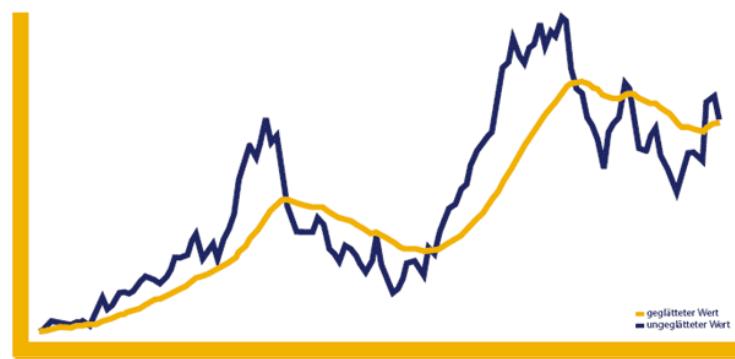
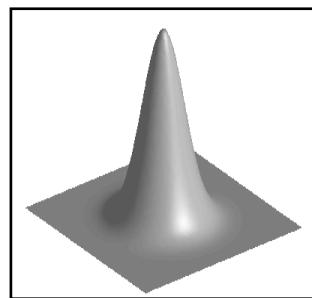
Registration of structural images to a standard brain template (standard space)

- The obtained transformation (warping) parameters can be applied on co-registered fMRI data
- Improved spatial normalization based on high resolution structural information

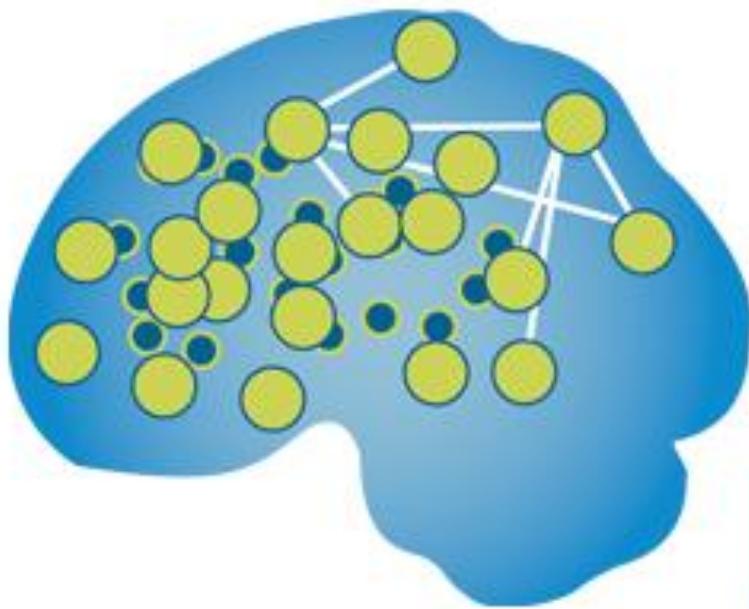
# Smoothing



# Smoothing



Thank you



**LREN**

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