fMRI Preprocessing

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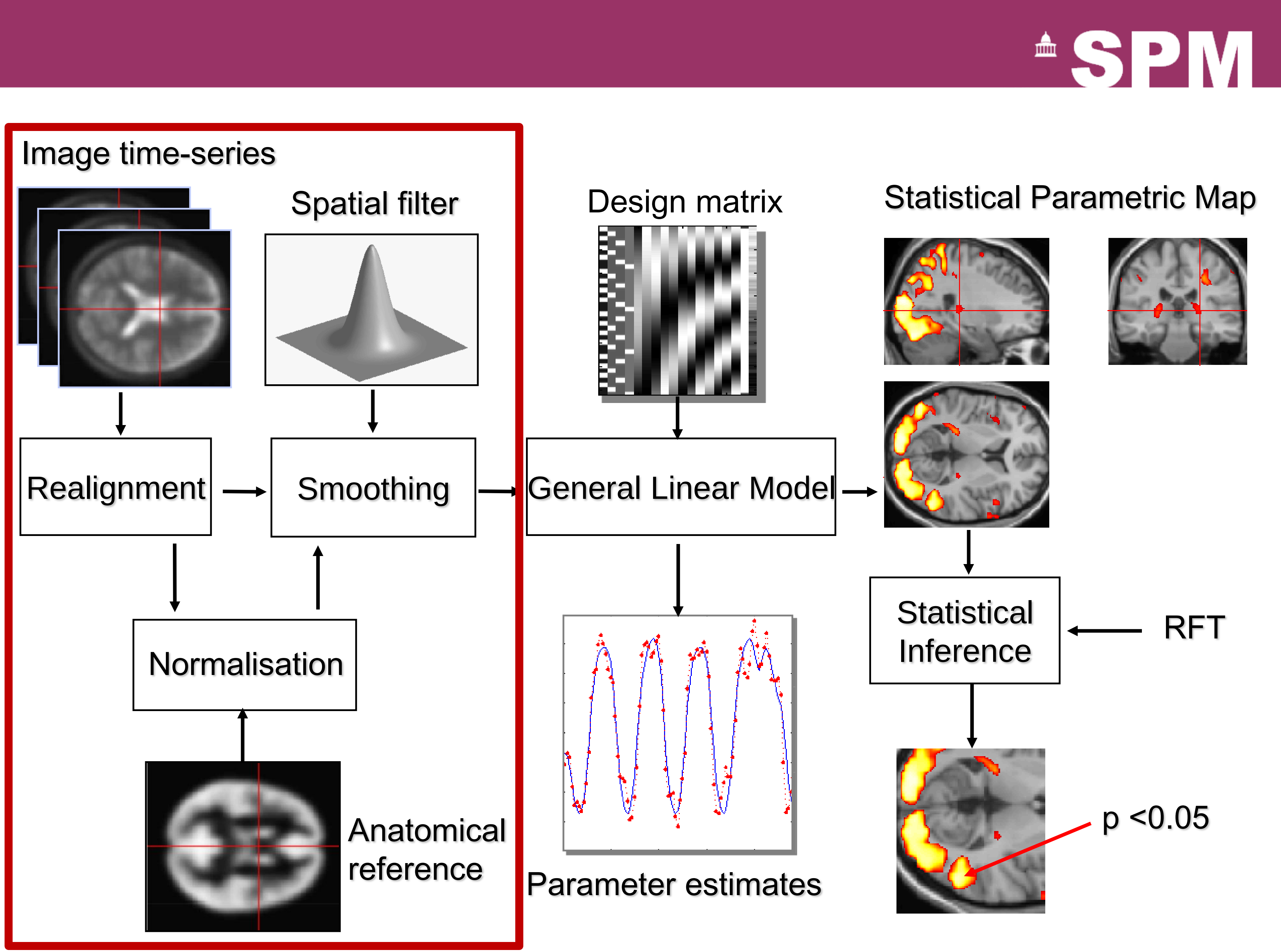
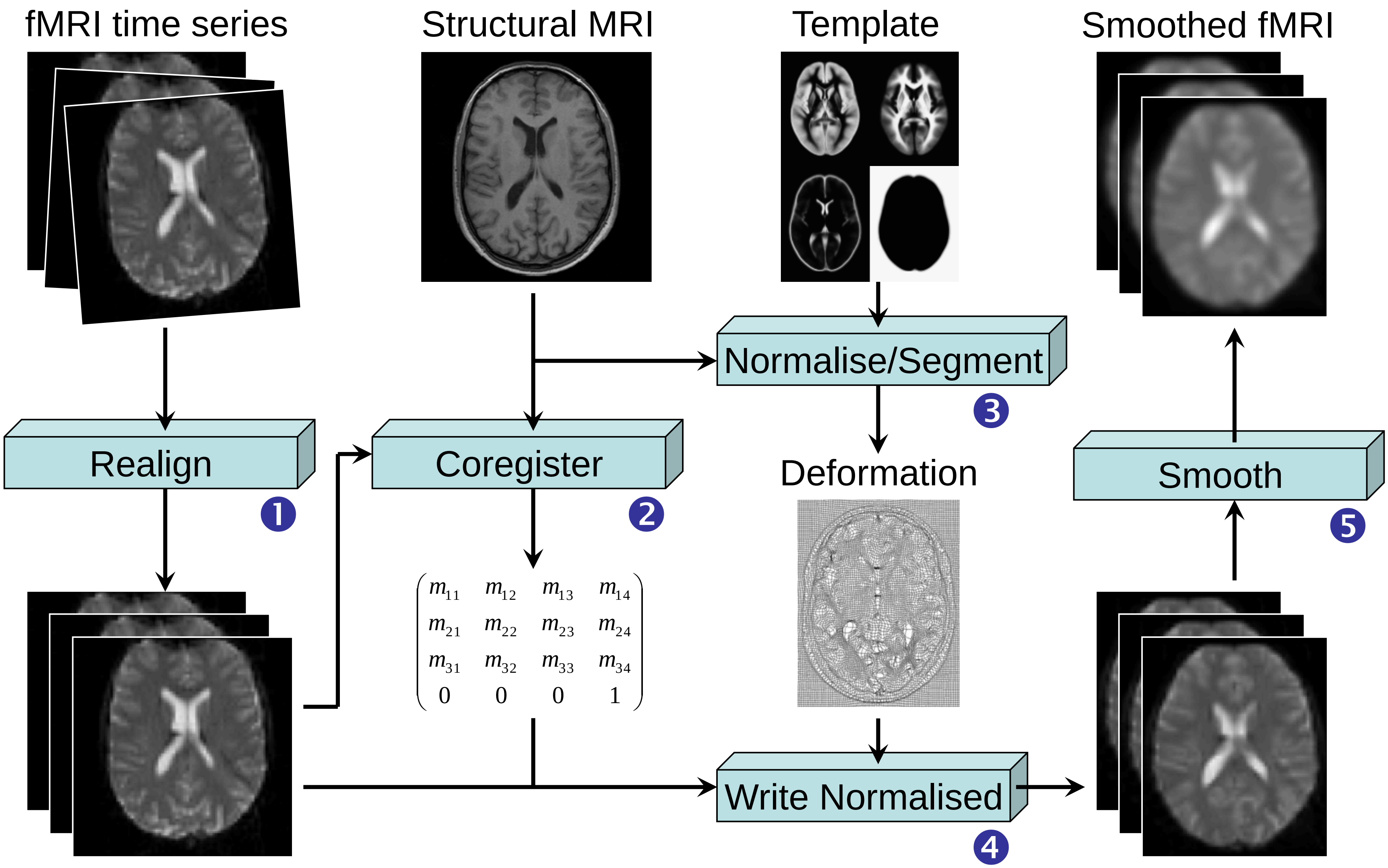
SPM Course
Chicago, 22-23 Oct 2015


SPM
Image time-series
Spatial filter
Design matrix
Statistical Parametric Map
Realignment
Smoothing
General Linear Model
Normalisation
Statistical Inference
RFT
Anatomical reference
Parameter estimates
p <0.05



fMRI time series
Structural MRI
Template
Smoothed fMRI
Normalise/Segment
3
Realign
1
Coregister
2
Deformation
Smooth
5
$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$
Write Normalised
4

Contents

- Registration basics
- Motion and realignment
- Inter-modal coregistration
- Spatial normalisation
- Gaussian smoothing

Contents

- **Registration basics**
  - Voxel-to-world mapping
  - Transformation
  - Similarity measure
  - Optimisation
  - Interpolation
- Motion and realignment
- Inter-modal coregistration
- Spatial normalisation
- Gaussian smoothing

Representation of imaging data

- Three dimensional images are made up of **voxels**.
- Voxel intensities are stored on disk as lists of numbers.
- Meta-information about the data:
  - The image dimensions
    - Allowing conversion from list to 3D array
  - The "voxel-to-world mapping"
    - Spatial transformation that maps from data coordinates (voxel column *i*, row *j*, slice *k*) into a real-world position (*x*,*y*,*z* mm) in a coordinate system e.g.:
      - Scanner coordinates
      - T&T/MNI coordinates

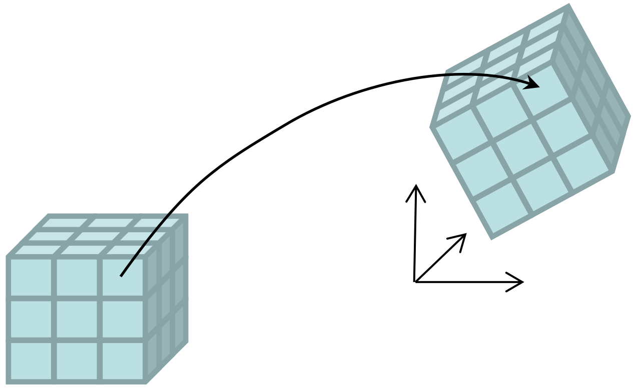
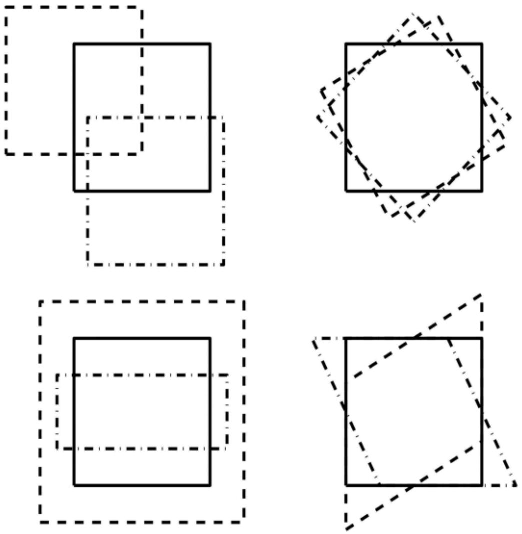


Image registration

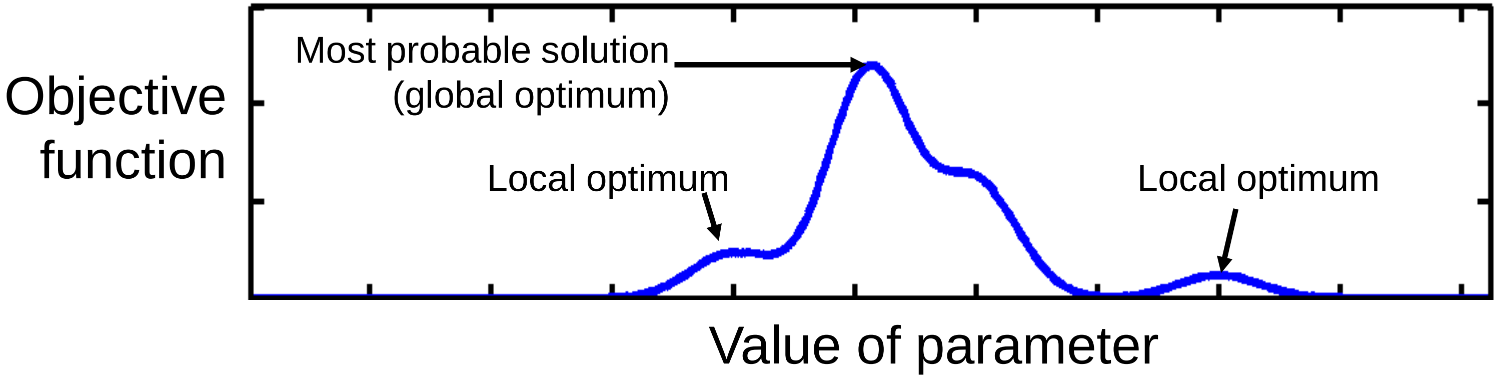
- Process of transforming different set of images into one coordinate system.



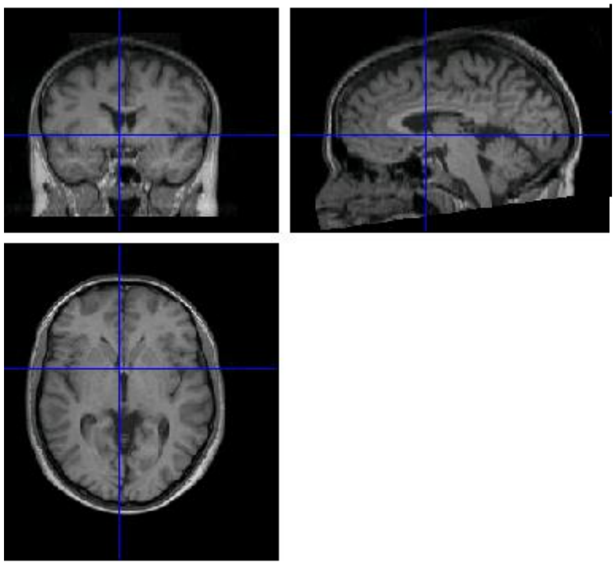
- Two key ingredients:
  - **Transformation type**:
    - Rigid — Within-subject
    - Affine
    - Non-linear — Between-subject (Affine, Non-linear)
  - **Similarity measure**:
    - Mean-squared difference — Within-modality
    - Correlation coefficient
    - Mutual information — Between-modality (Correlation coefficient, Mutual information)

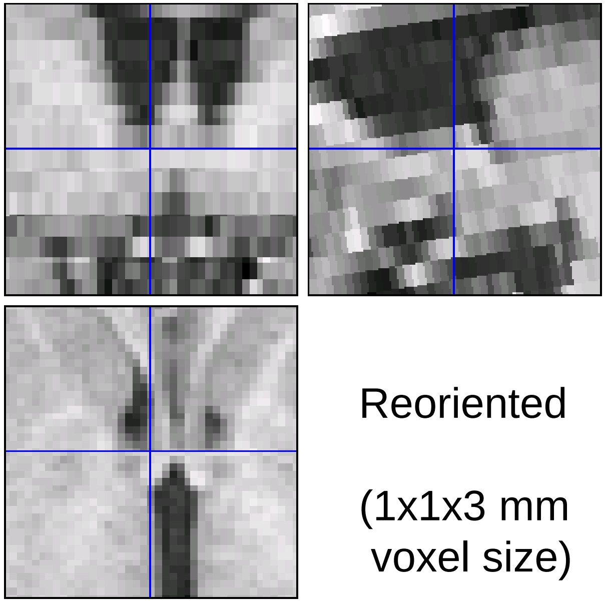
Optimisation

- Automatic image registration is done by using an optimisation algorithm.
- Optimisation involves finding some “best” parameters according to an “objective function”, which is either minimised or maximised.



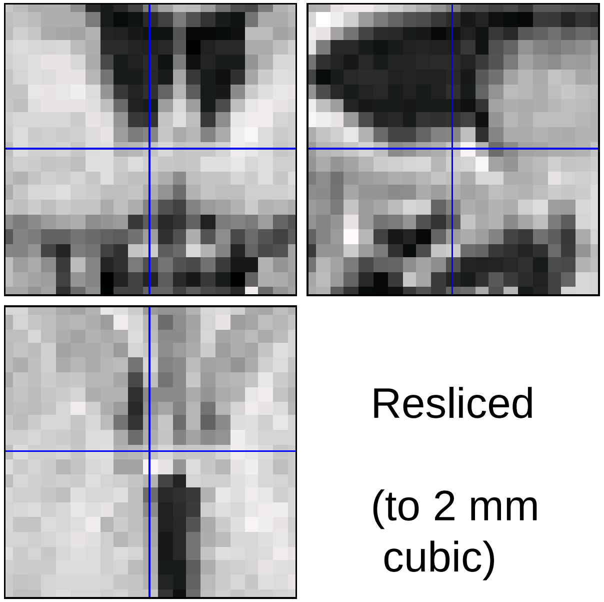
Reslicing / Interpolation





Reoriented

(1x1x3 mm voxel size)



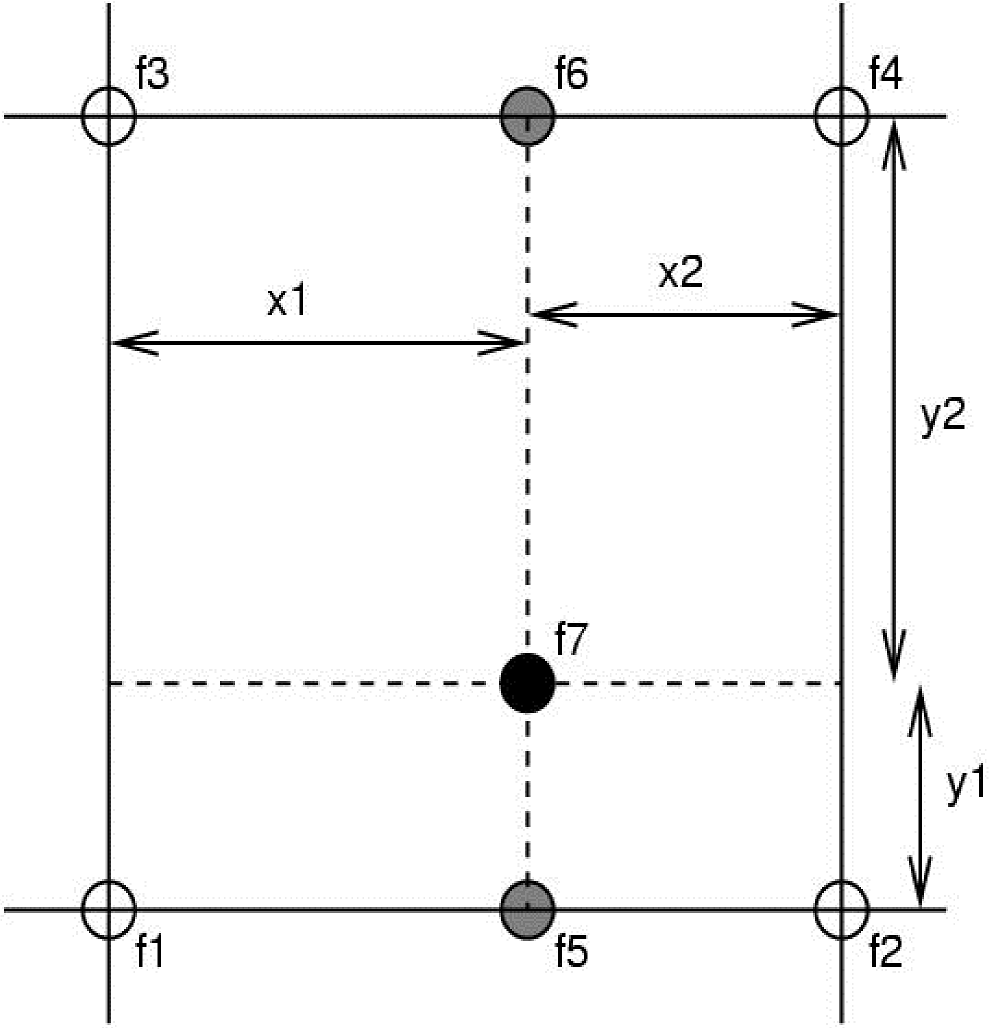
Resliced

(to 2 mm cubic)

- ❑ Applying the transformation parameters, and re-sampling the data onto the same grid of voxels as the target image
  - reslicing, interpolation, regridding, transformation, and writing

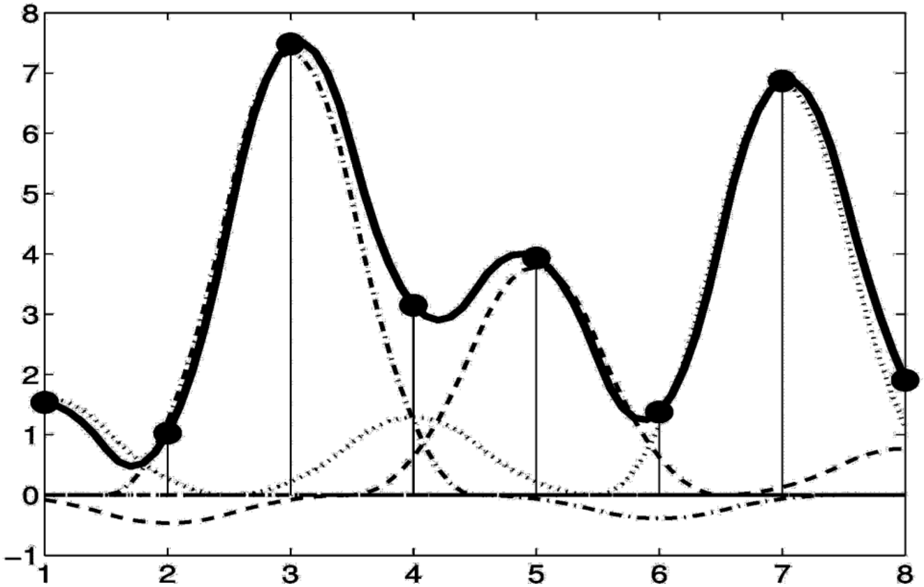
Simple Interpolation

- Nearest neighbour
  - Take the value of the closest voxel
- Tri-linear
  - Just a weighted average of the neighbouring voxels
  - $f_5 = f_1\, x_2 + f_2\, x_1$
  - $f_6 = f_3\, x_2 + f_4\, x_1$
  - $f_7 = f_5\, y_2 + f_6\, y_1$

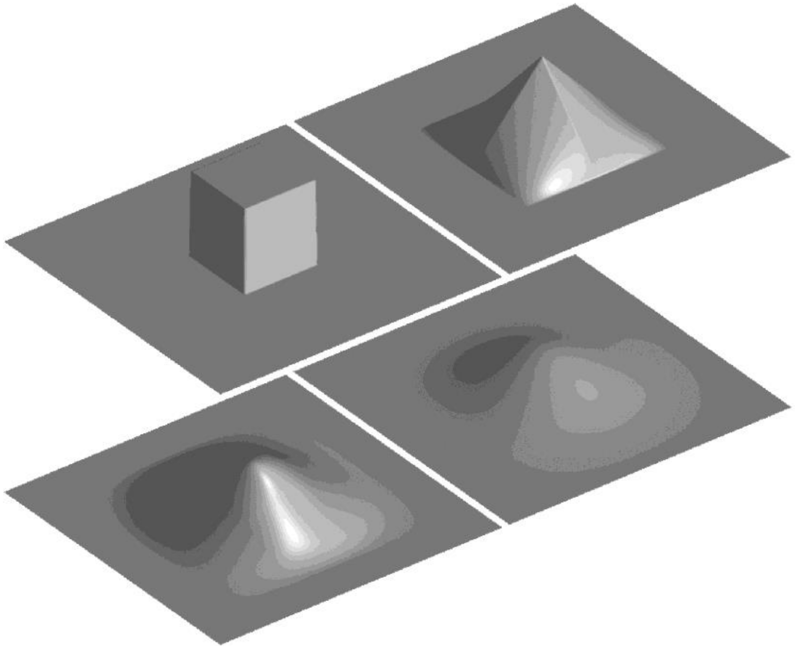


B-spline Interpolation

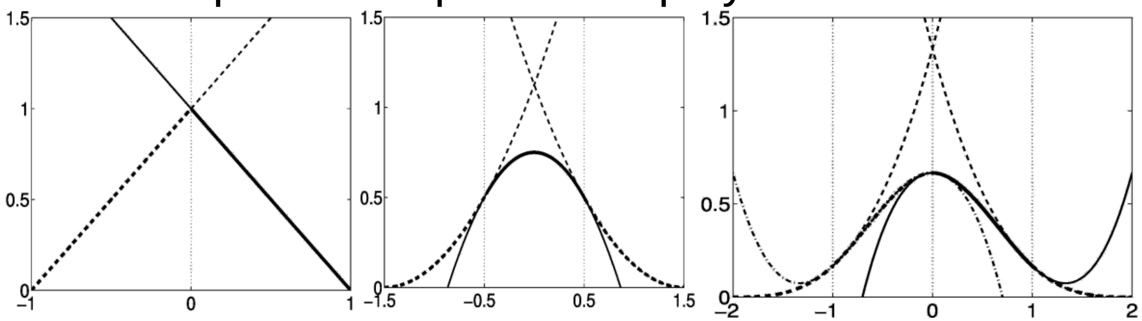
A continuous function is represented by a linear combination of basis functions



2D B-spline basis functions of degrees 0, 1, 2 and 3



B-splines are piecewise polynomials



Nearest neighbour and trilinear interpolation are the same as B-spline interpolation with degrees 0 and 1.

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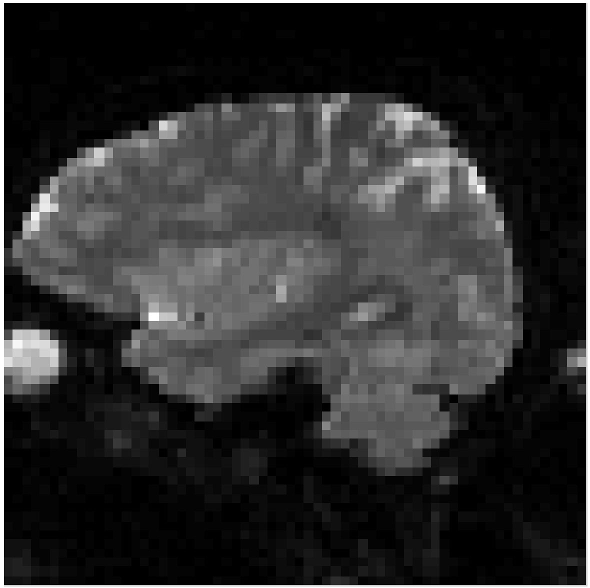
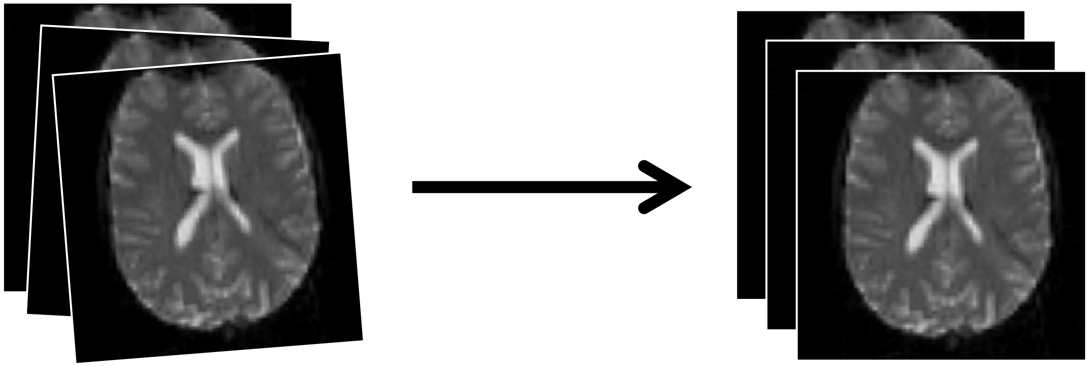
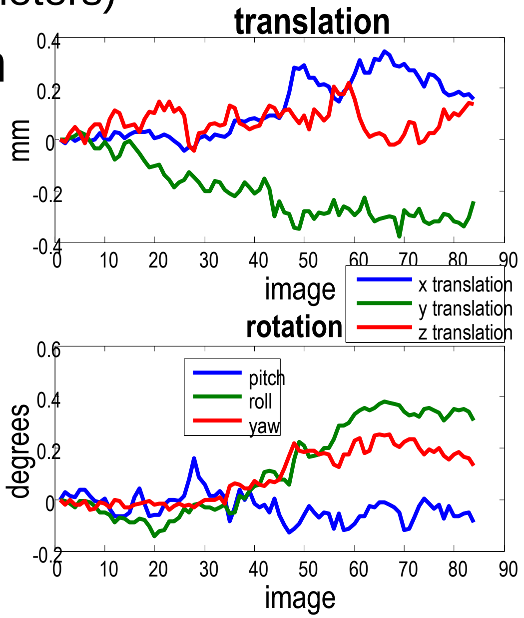
Motion correction

- Head movement is a very large source of variance in fMRI data.
- Motion correction: realign a time-series of images acquired from the same subject.
  - Within-subject transformation: rigid-body (6 parameters)
  - Within-modality: least squares objective function







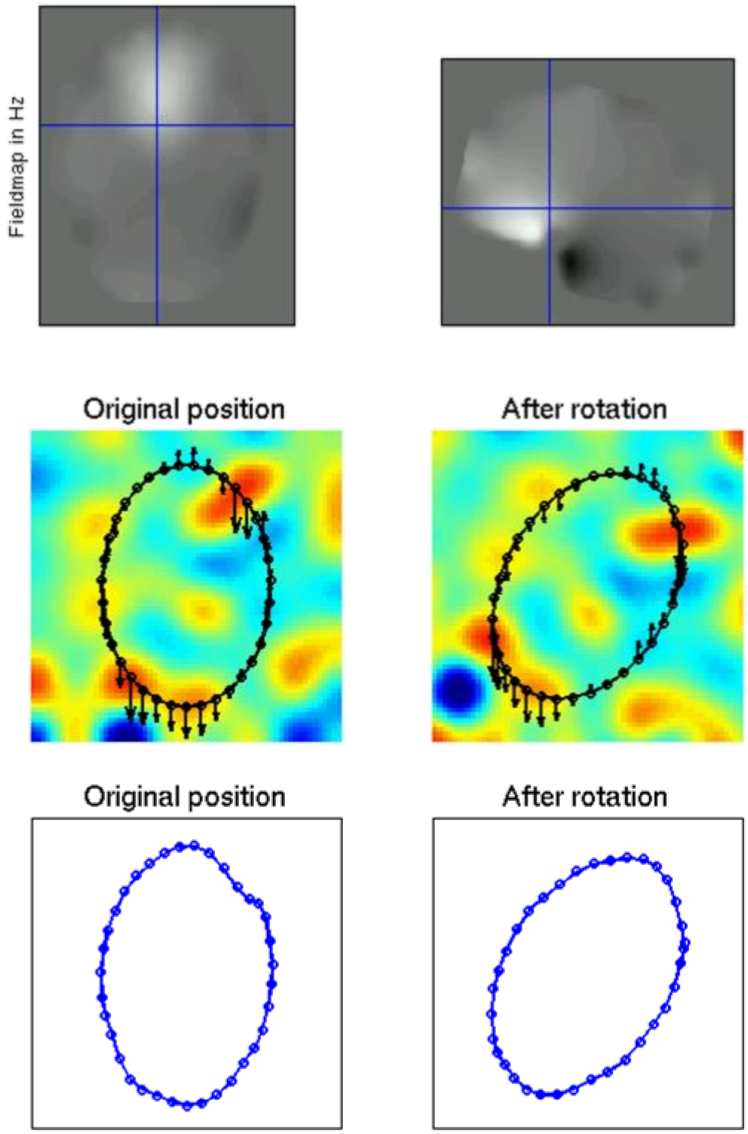
Residual Errors from aligned fMRI

- Slices are not acquired simultaneously
  - rapid movements not accounted for by rigid body model
- Resampling can introduce interpolation errors
  - especially tri-linear interpolation
- Image artefacts may not move according to a rigid body model
  - image distortion
  - image dropout

- Functions of the estimated motion parameters can be modelled as confounds in subsequent analyses

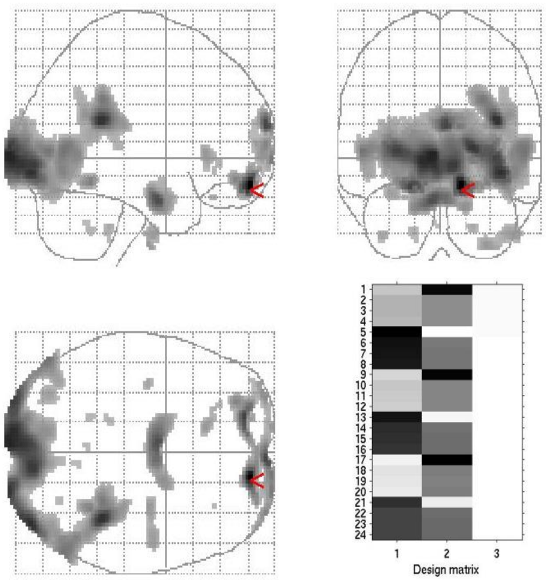
Movement by Distortion Interaction of fMRI

- Subject disrupts B_0 field, rendering it inhomogeneous
  - Distortions in phase-encode direction
- Subject moves during EPI time series
  - Distortions vary with subject orientation
  - Shape varies (non-rigidly)
- **“Realign & Unwarp”**: generative model that combines a model of geometric distortions and a model of subject motion to correct images.

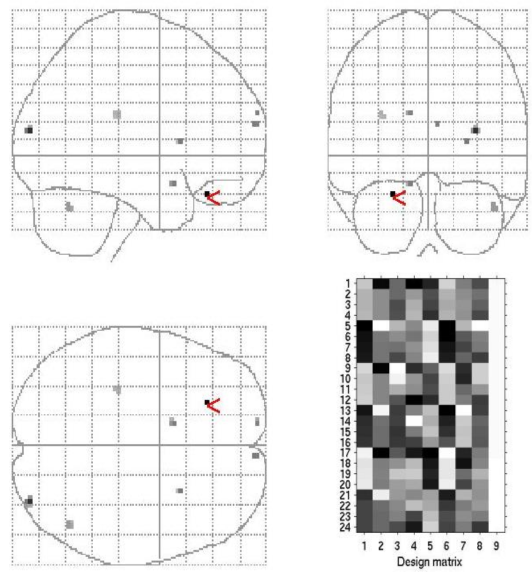


Movement correction strategies

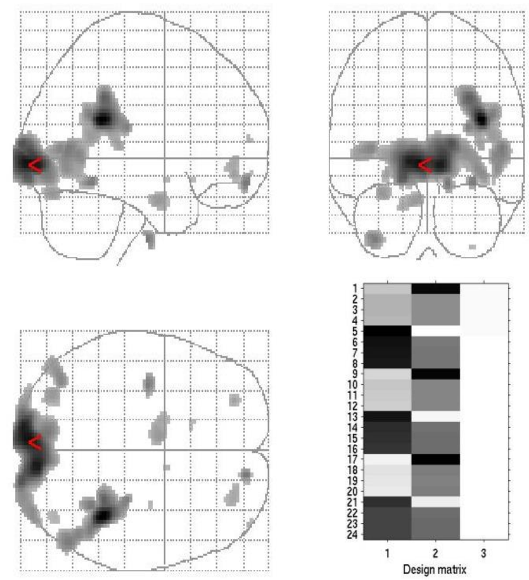
No correction



Correction by covariation



Correction by Unwarp



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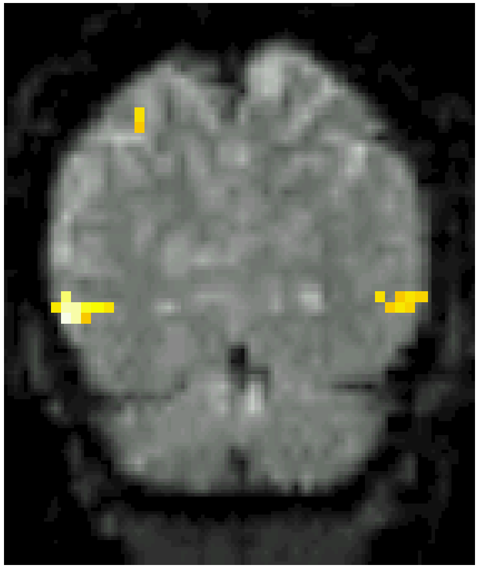
Coregistration
(intra-subject, inter-modal)

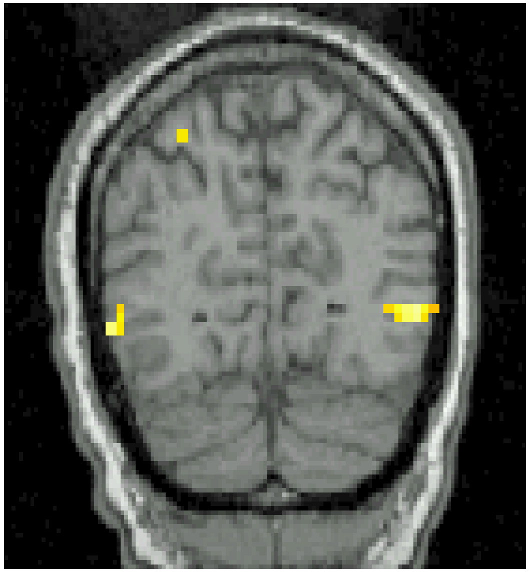
- Inter-modal registration.

- Match images from same subject but different modalities:

  - anatomical localisation of single subject activations

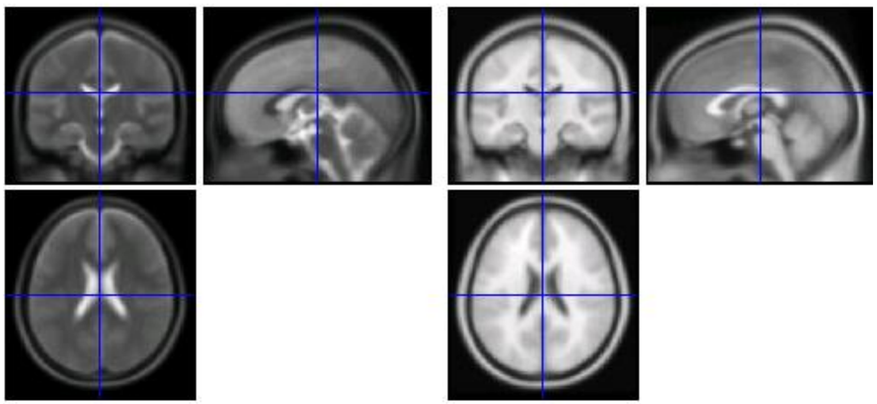
  - achieve more precise spatial normalisation of functional image using anatomical image.

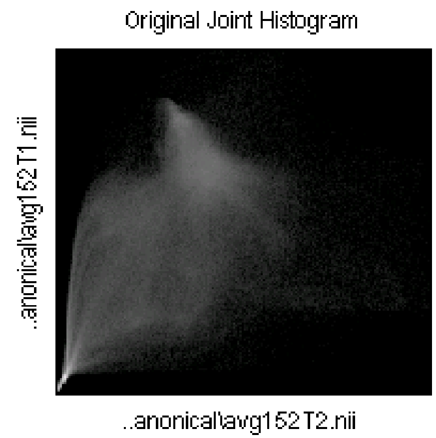


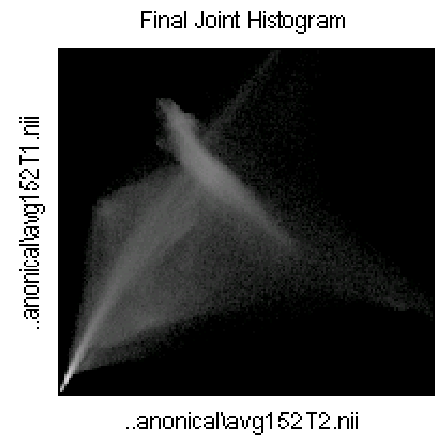


Coregistration maximises Mutual Information

Between-modality registration:
Seek to measure shared information in some sense.

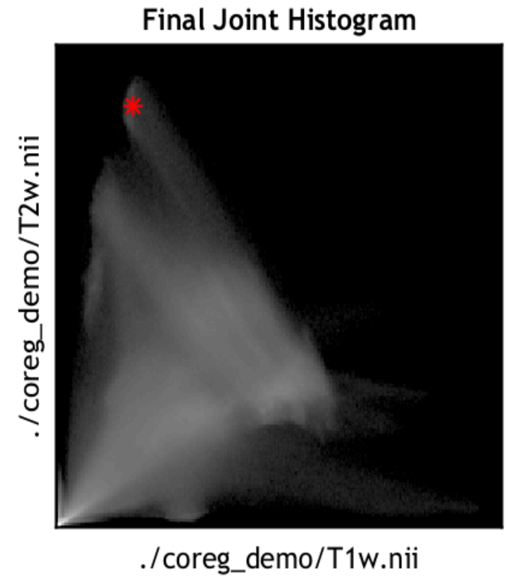


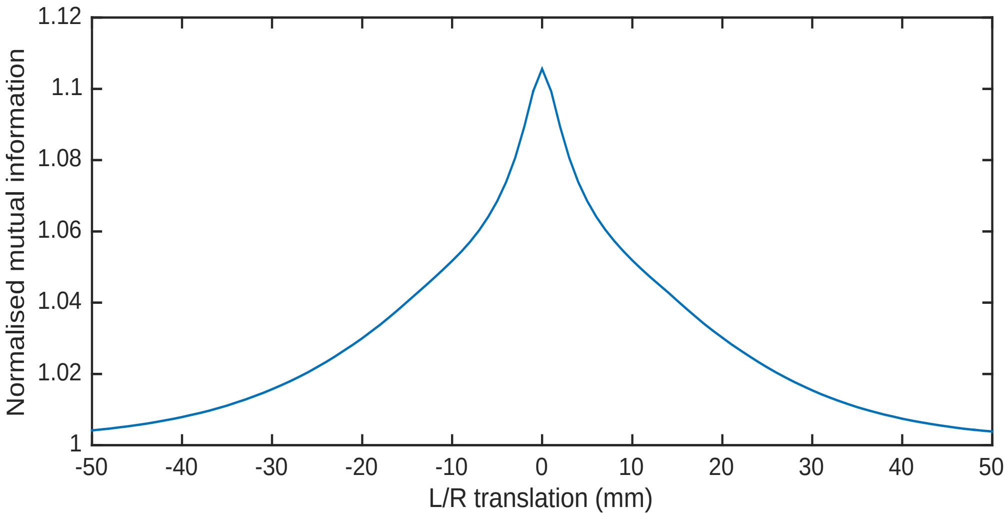




Joint histogram sharpness correlates with image alignment.
Mutual information and related measures attempt to quantify how well one image predicts the other.

Coregistration





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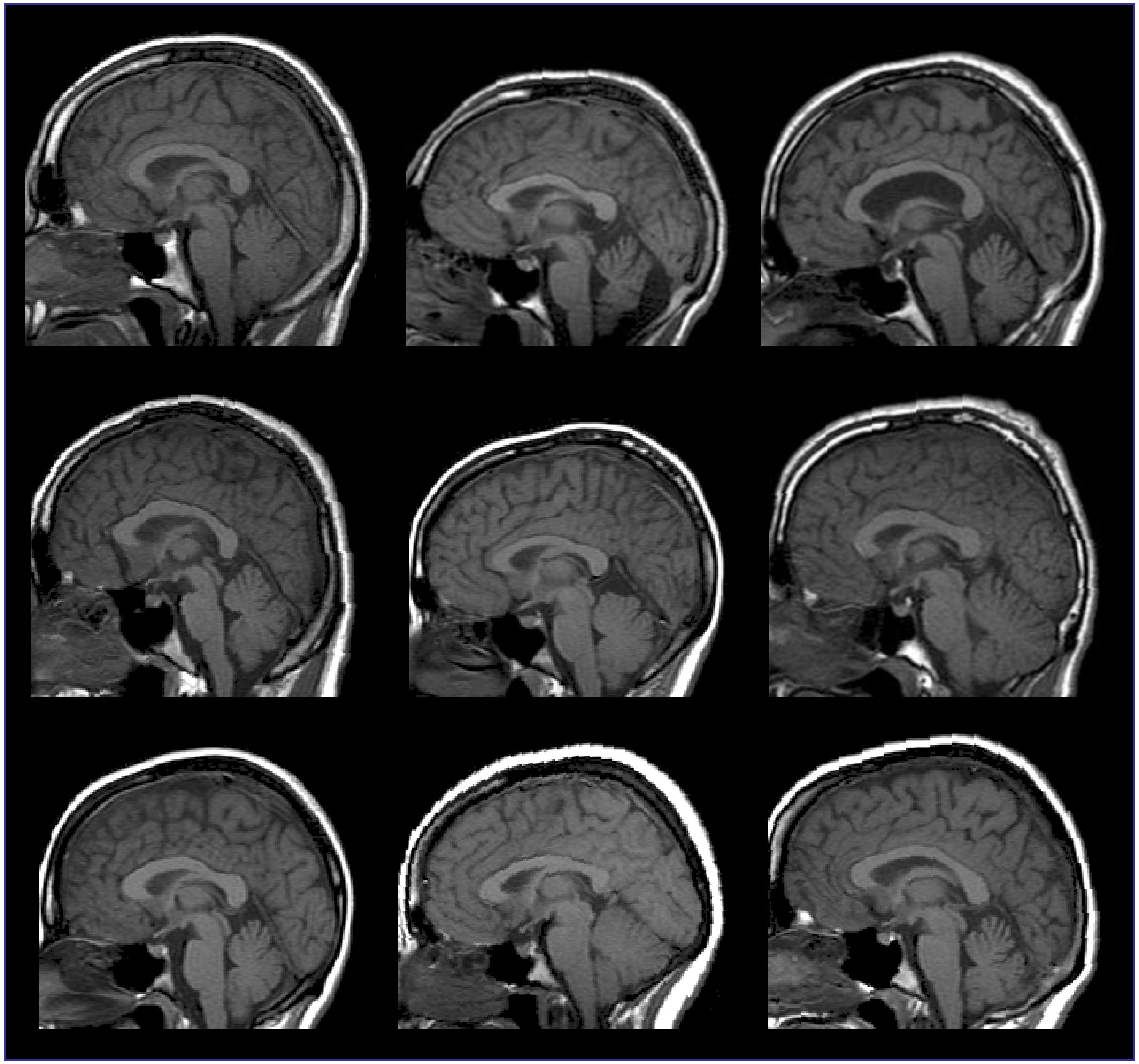
- **Spatial normalisation**
  - **Unified segmentation**
- Gaussian smoothing

Spatial Normalisation

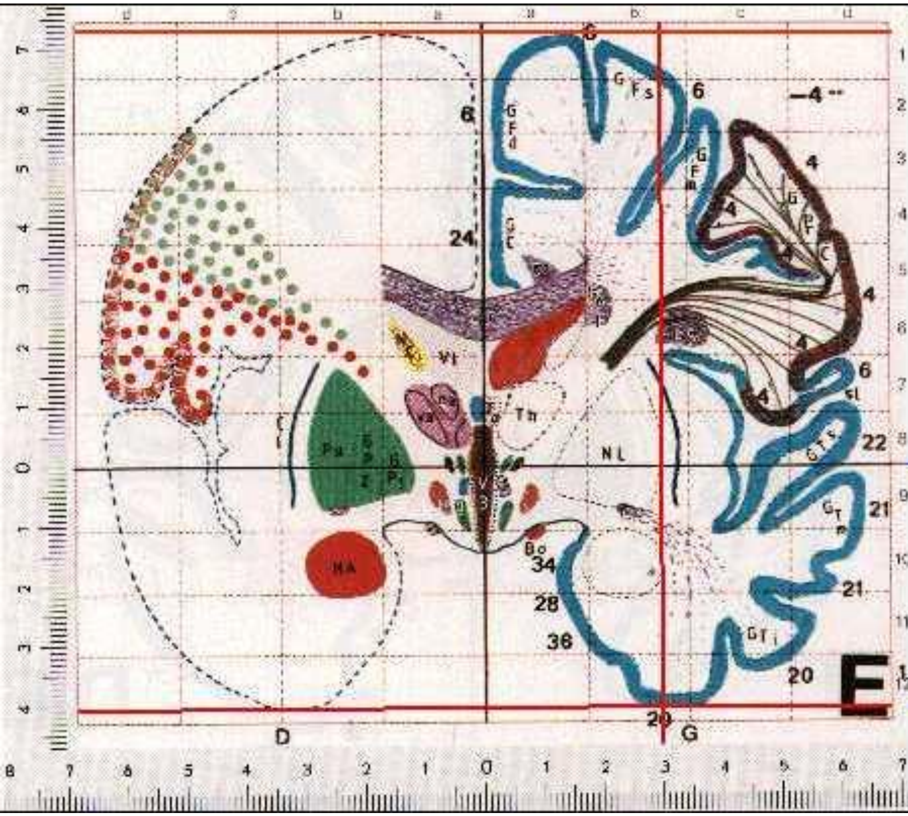


Spatial Normalisation - Reasons

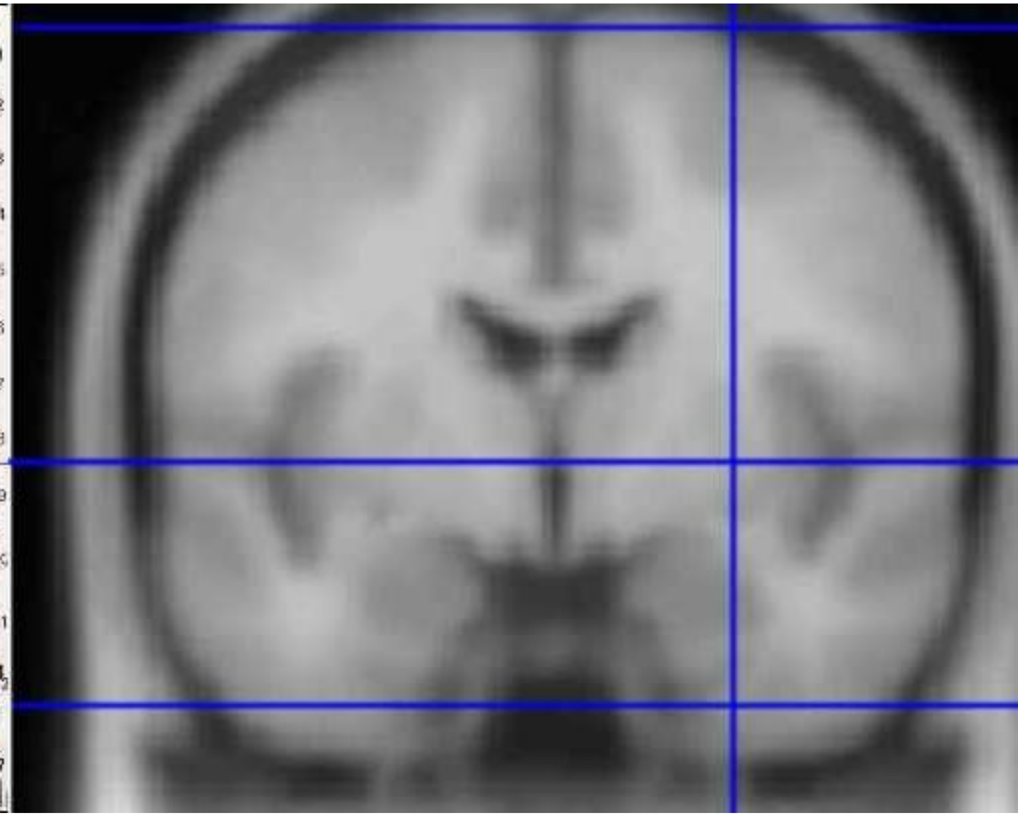
- Inter-subject averaging
  - Increase sensitivity with more subjects
    - Fixed-effects analysis
  - Extrapolate findings to the population as a whole
    - Random-effects analysis
- Make results from different studies comparable by aligning them to standard space.

Standard spaces

Talairach Atlas



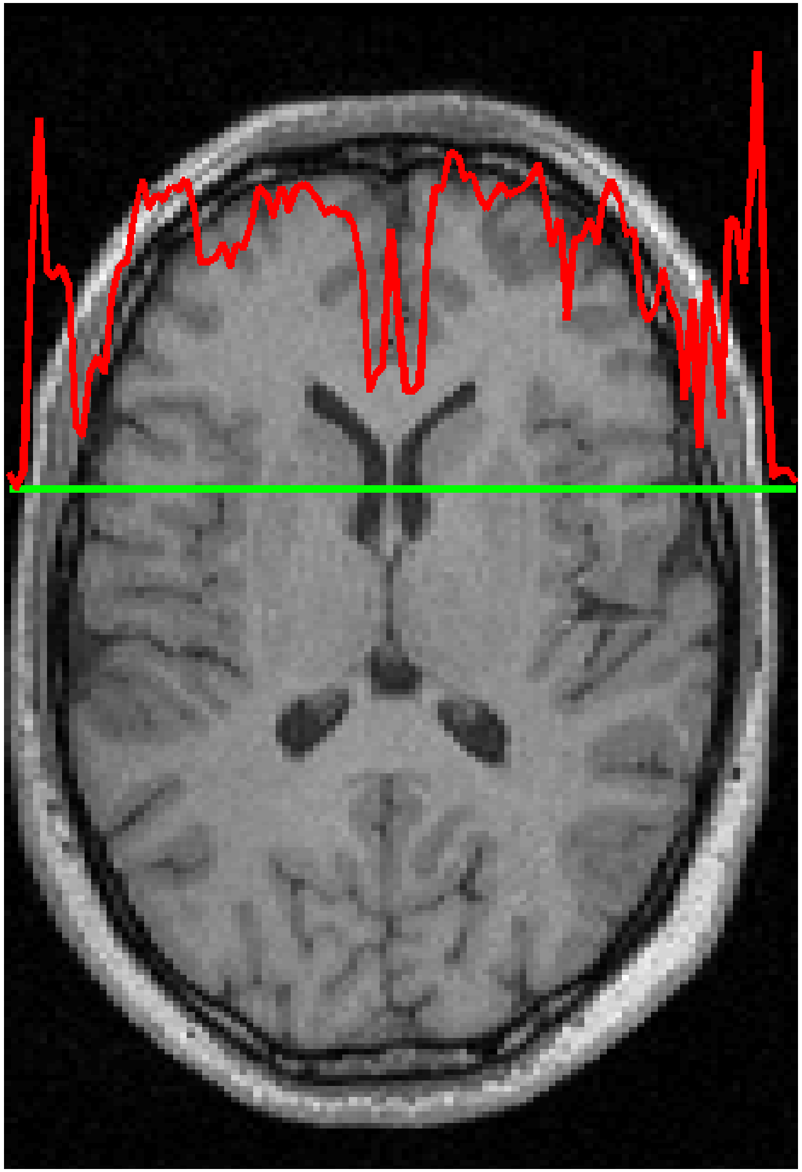
MNI/ICBM AVG152 Template



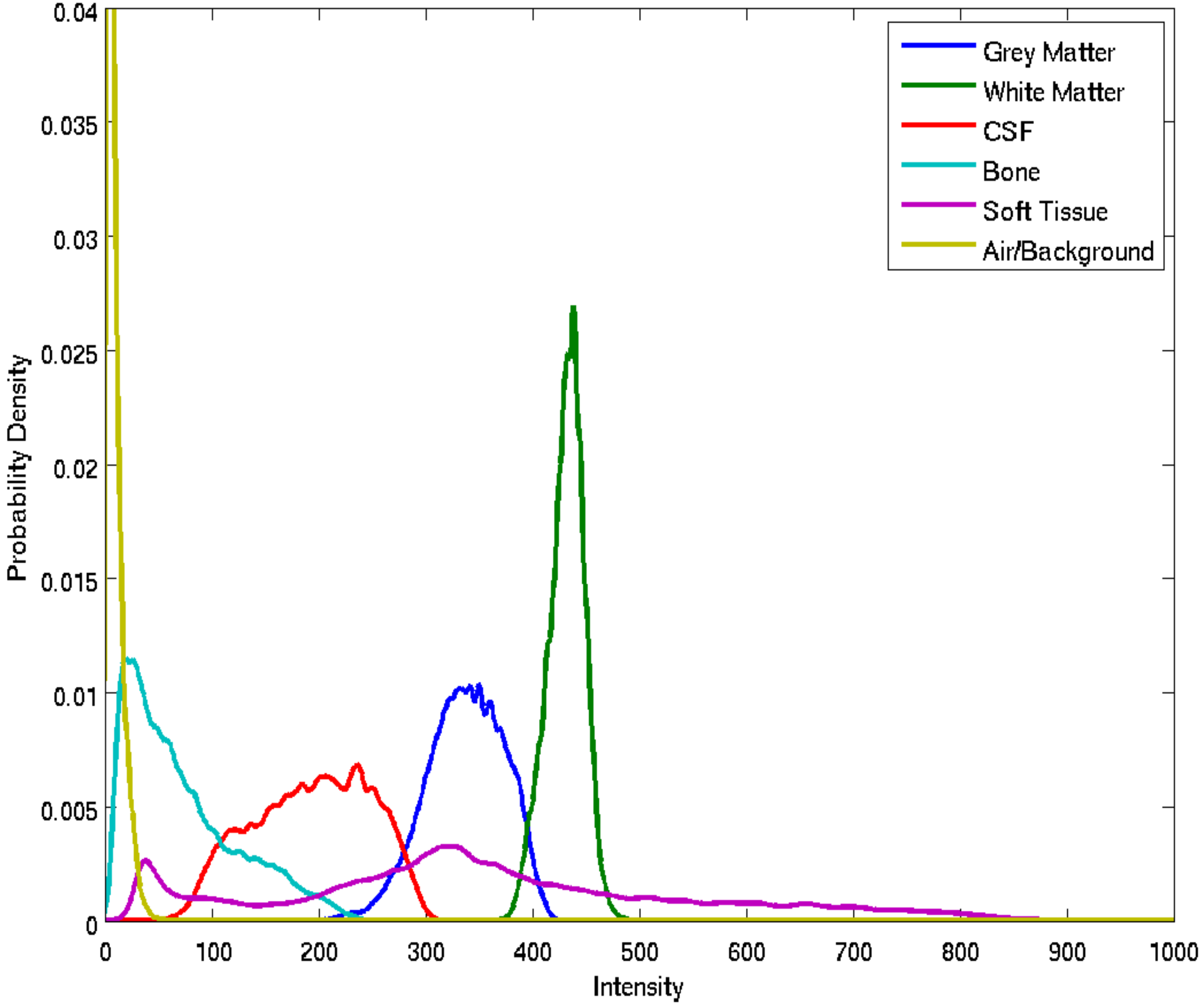
The MNI template follows the *convention* of T&T, but doesn't match the *particular brain* (http://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach)

Unified Segmentation

- ❑ Normalising segmented tissue maps should be more robust and precise than using the original images.
- ❑ Tissue segmentation benefits from spatially-aligned prior tissue probability maps.
- ➢ Combining normalisation and segmentation in a unified model:
  - Gaussian mixture model segmentation
  - Intensity inhomogeneity (bias field) correction
  - Warping (non-linear registration)

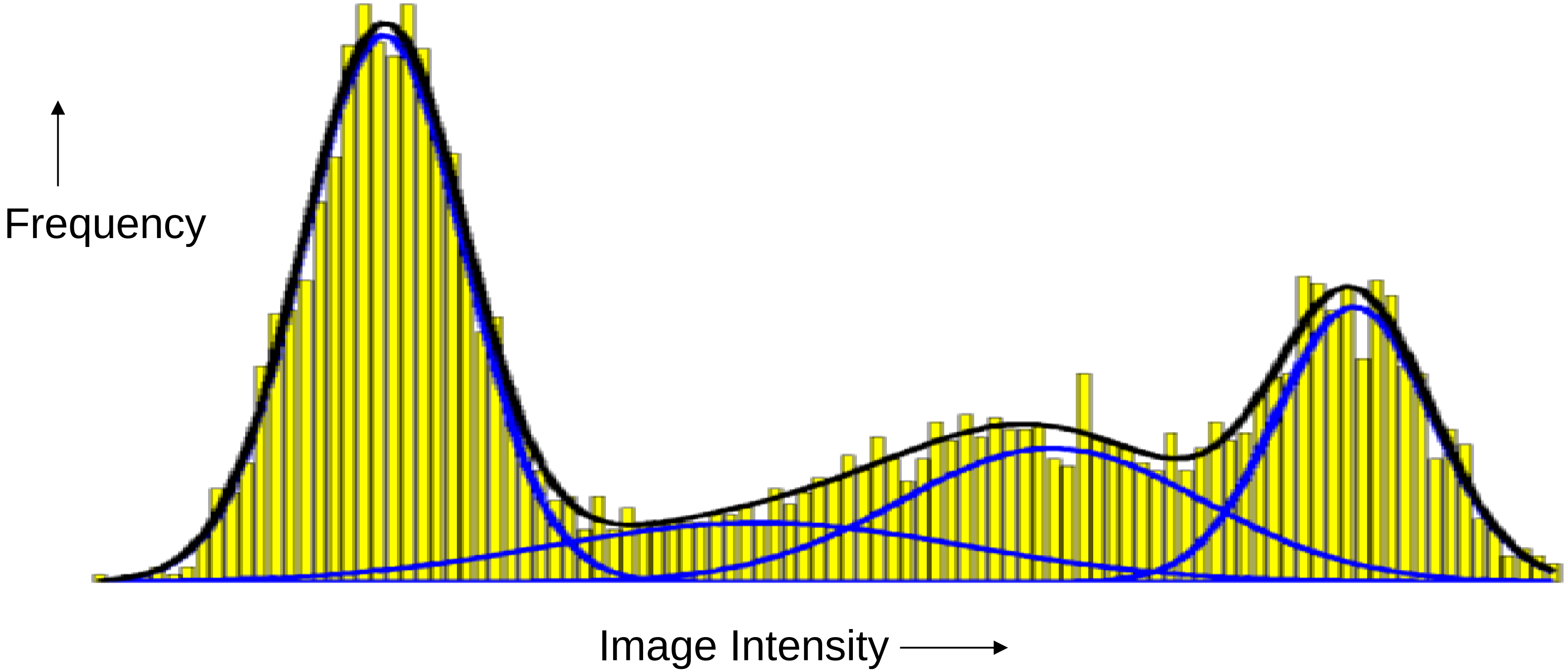


Tissue intensity distributions (T1-weighted MRI)



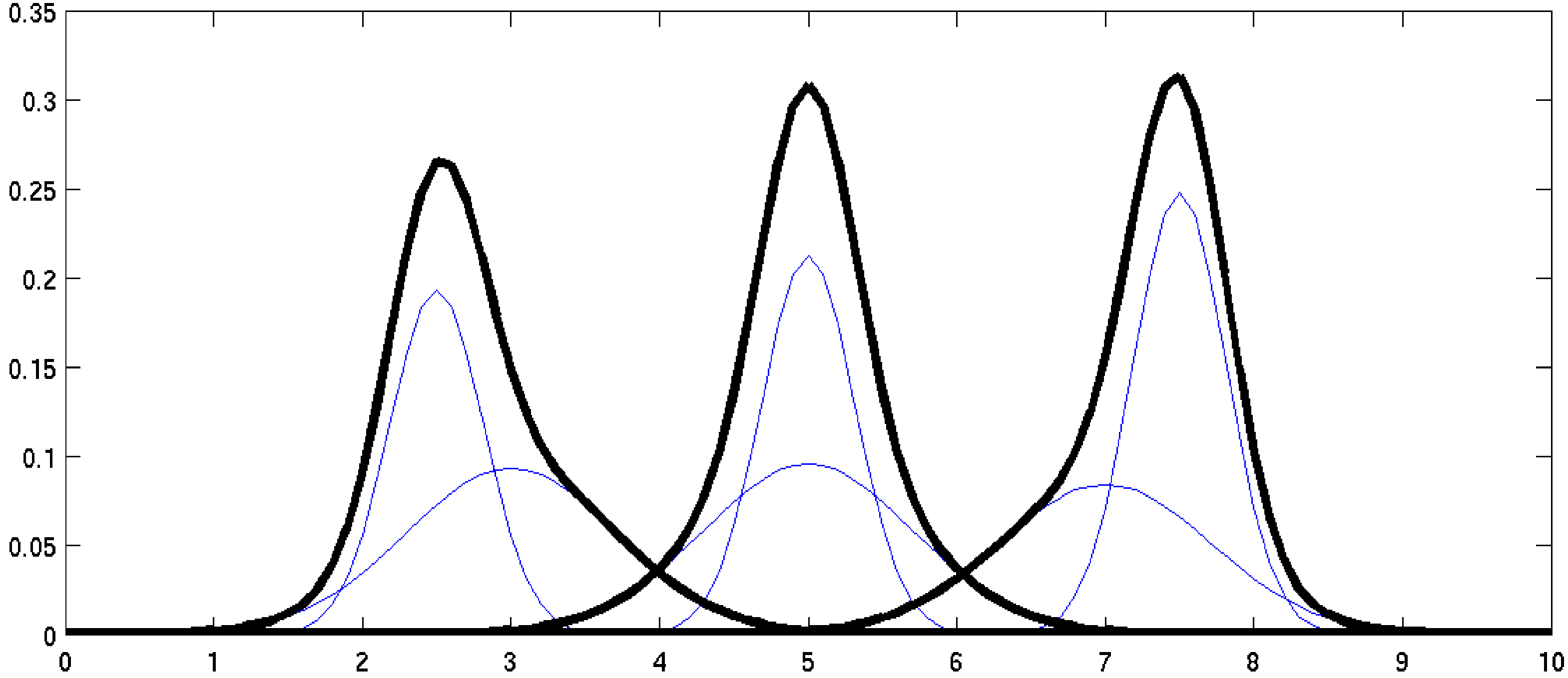
Mixture of Gaussians

- Classification is based on a Mixture of Gaussians model, which represents the intensity probability density by a number of Gaussian distributions.



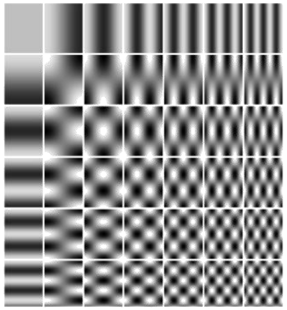
Non-Gaussian Intensity Distributions

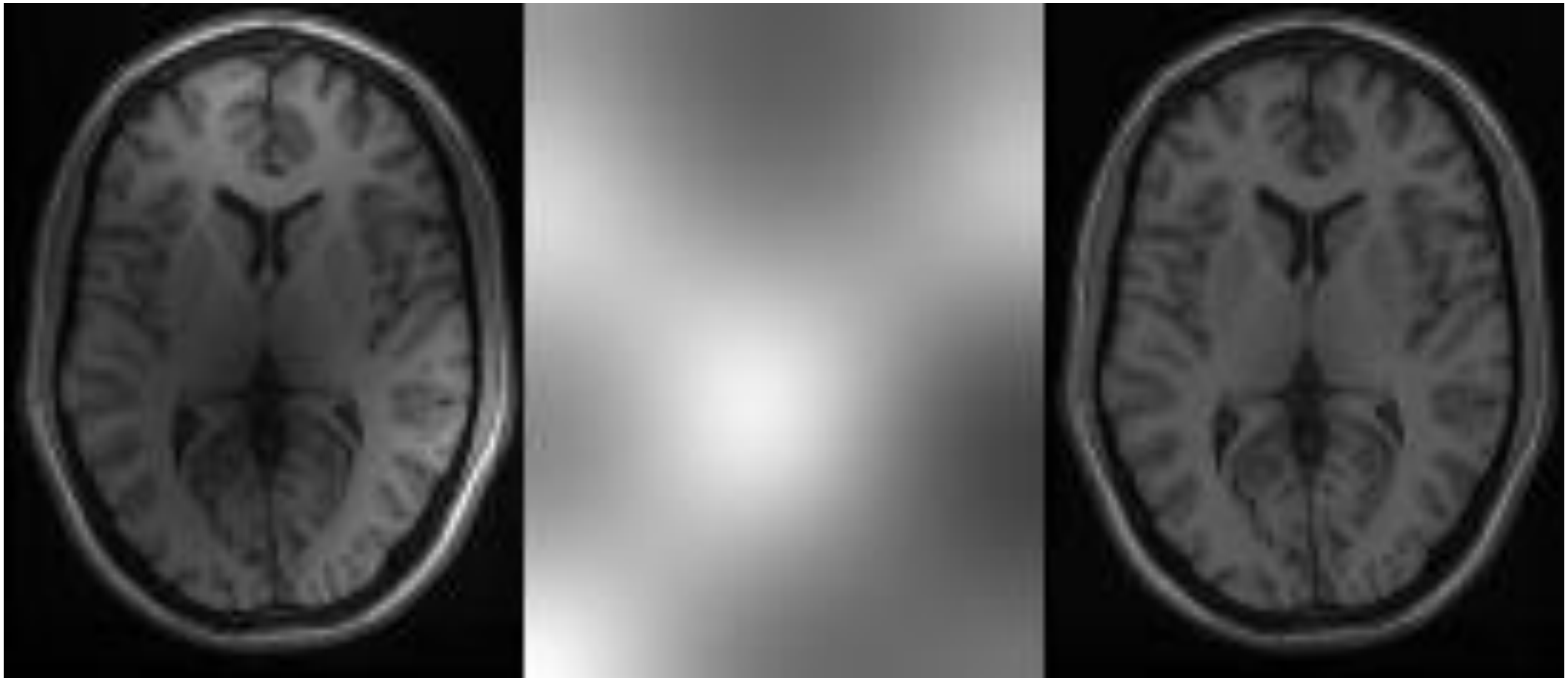
- Multiple Gaussians per tissue class allow non-Gaussian intensity distributions to be modelled.
  - E.g. accounting for partial volume effects



Modelling inhomogeneity

- A multiplicative bias field is modelled as a spatially smooth image (a linear combination of basis functions).

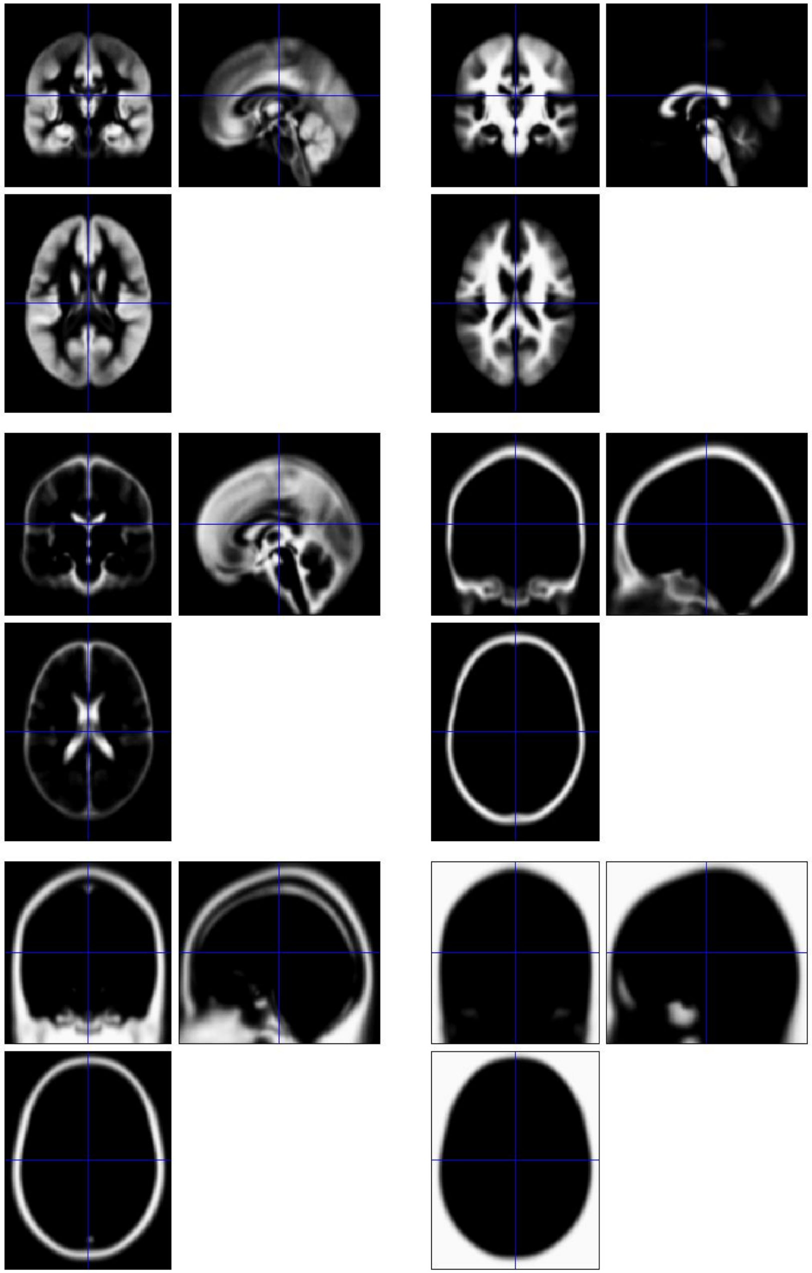




Corrupted image **Bias Field** **Corrected image**

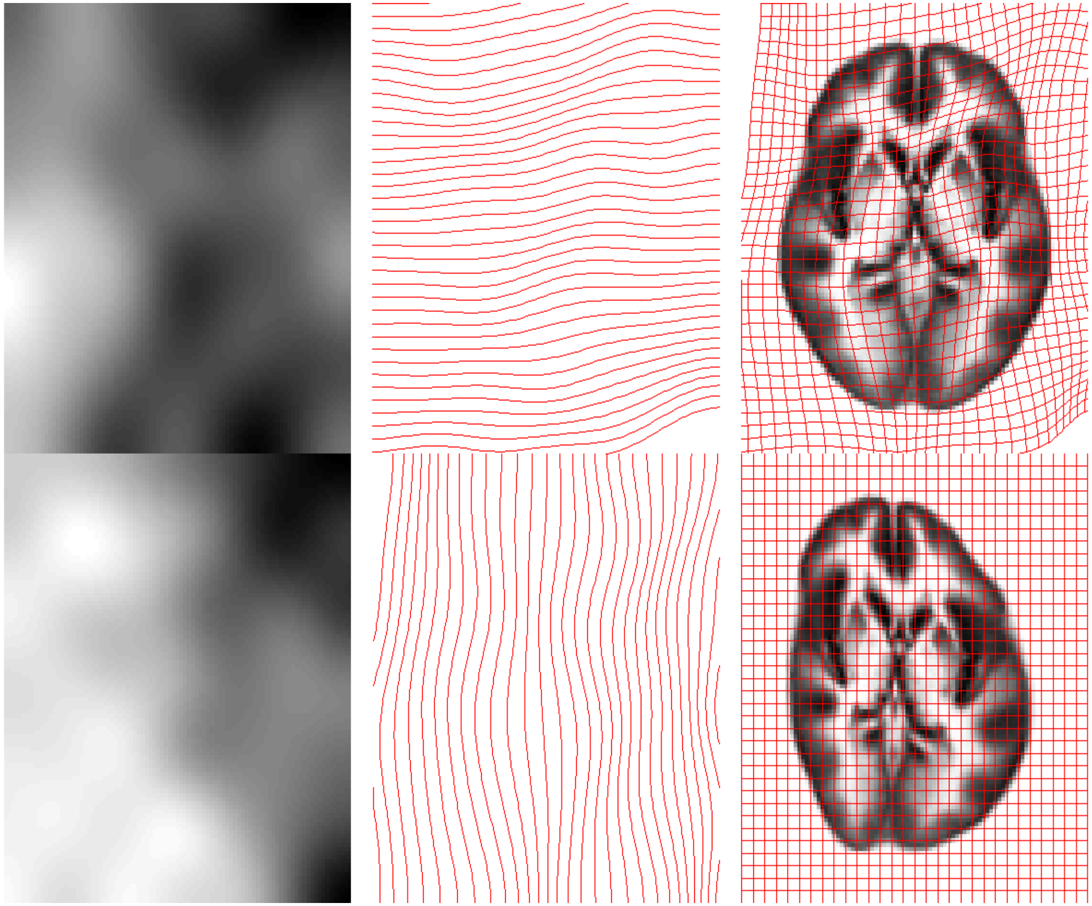
Tissue Probability Maps

- Each TPM indicates the prior probability for a particular tissue at each point in MNI space.
- SPM12's TPMs are derived from the IXI dataset initialised with the ICBM 452 atlas and other data.



Deforming the Tissue Probability Maps

- Tissue probability images are warped to match the subject.
- The inverse transform warps to the TPMs.
- Warps are constrained to be reasonable by penalising various distortions (regularisation).

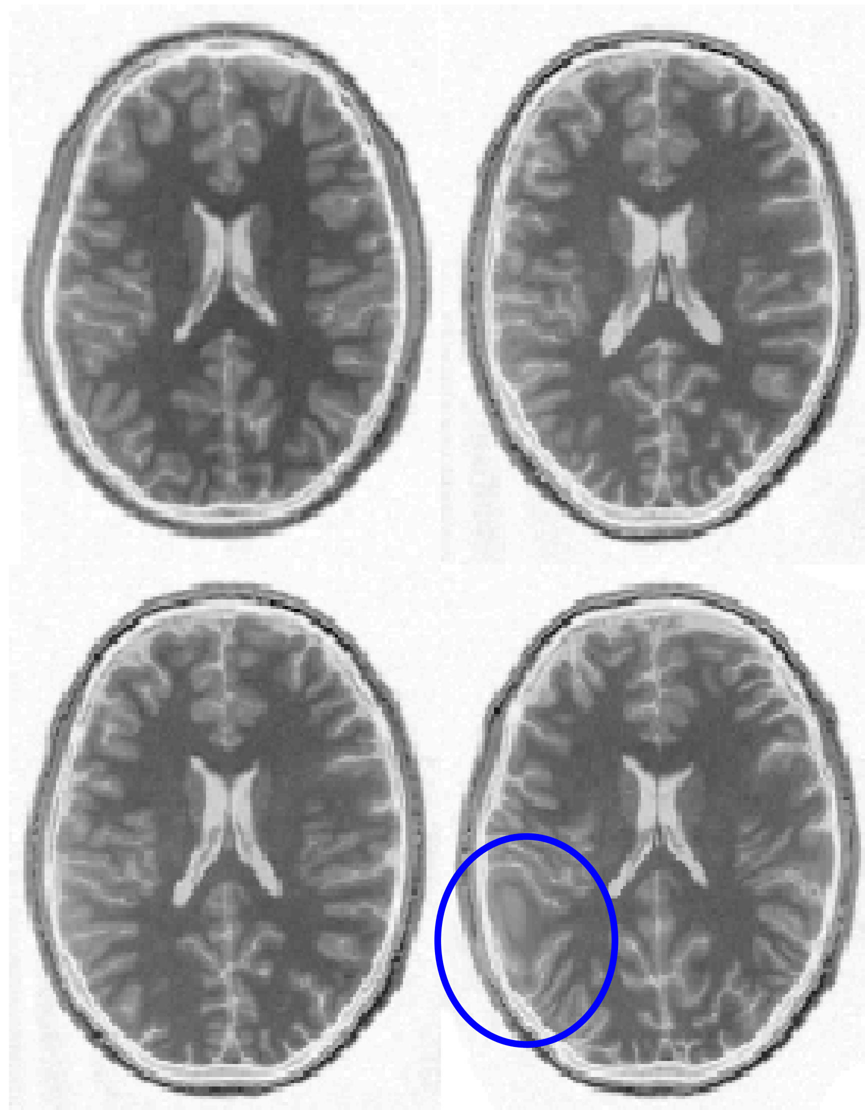


Spatial Normalisation – Overfitting

Without regularisation, the non-linear normalisation can introduce unnecessary deformation

Template image

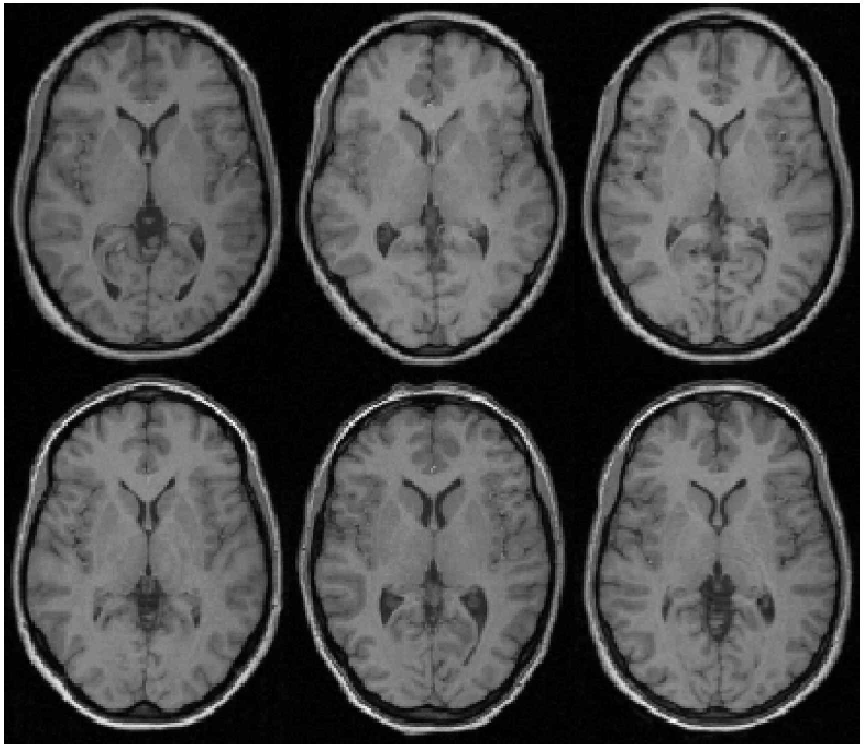
Affine registration. (SSE = 472.1)

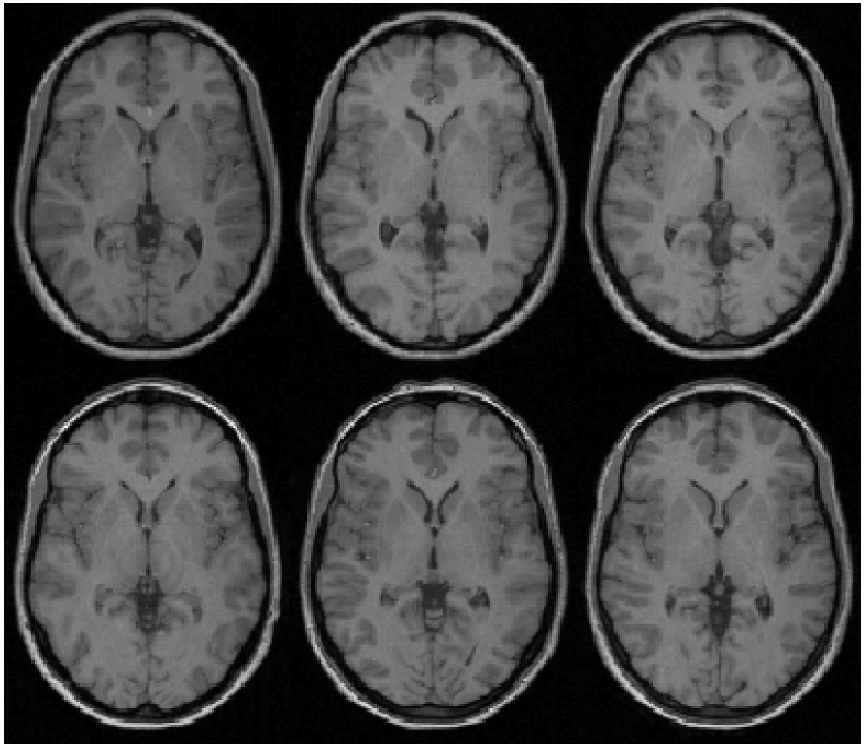


Non-linear registration using regularisation. (SSE = 302.7)

Non-linear registration without regularisation. (SSE = 287.3)

Spatial Normalisation – Results





Affine registration

Non-linear registration

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

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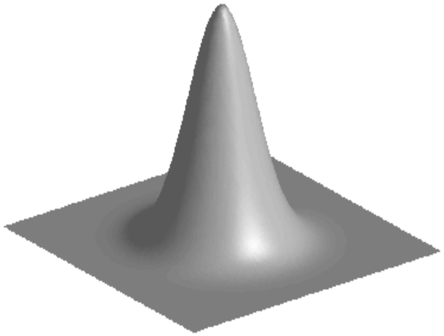
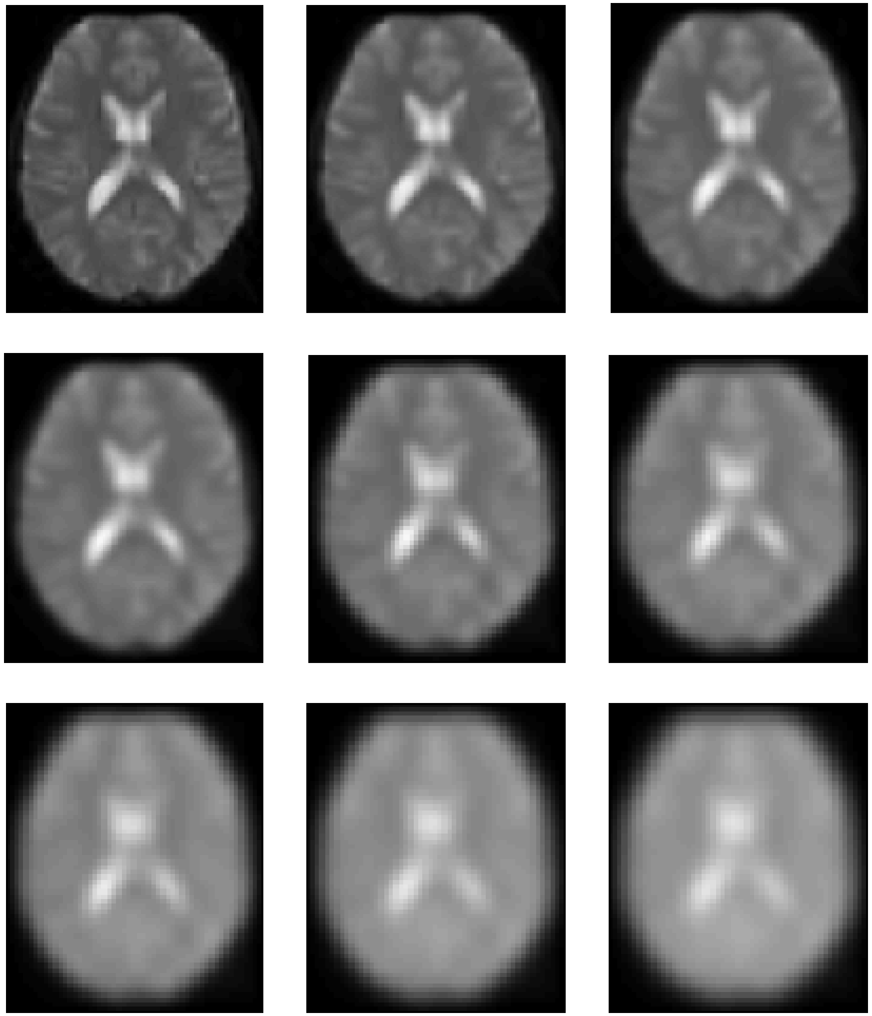
Smoothing



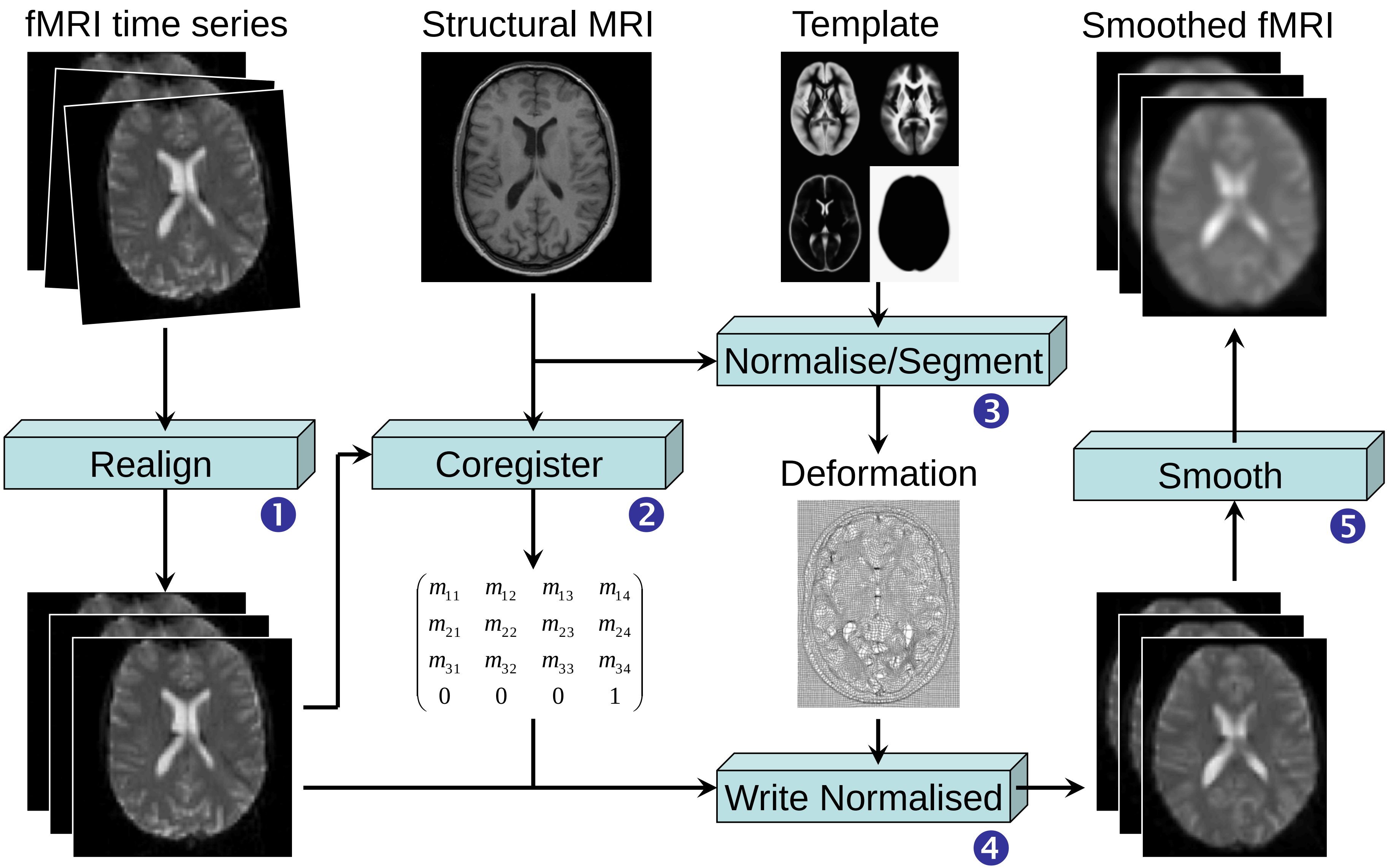
- Why would we deliberately blur the data?
  - Improves spatial overlap by blurring over minor anatomical differences and registration errors
  - Averaging neighbouring voxels suppresses noise
  - Increases sensitivity to effects of similar scale to kernel (matched filter theorem)
  - Makes data more 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

Effect of smoothing



3D Gaussian smoothing with FWHM: 0, 2, 4, 6, 8, 10, 12, 14, 16 mm isotropic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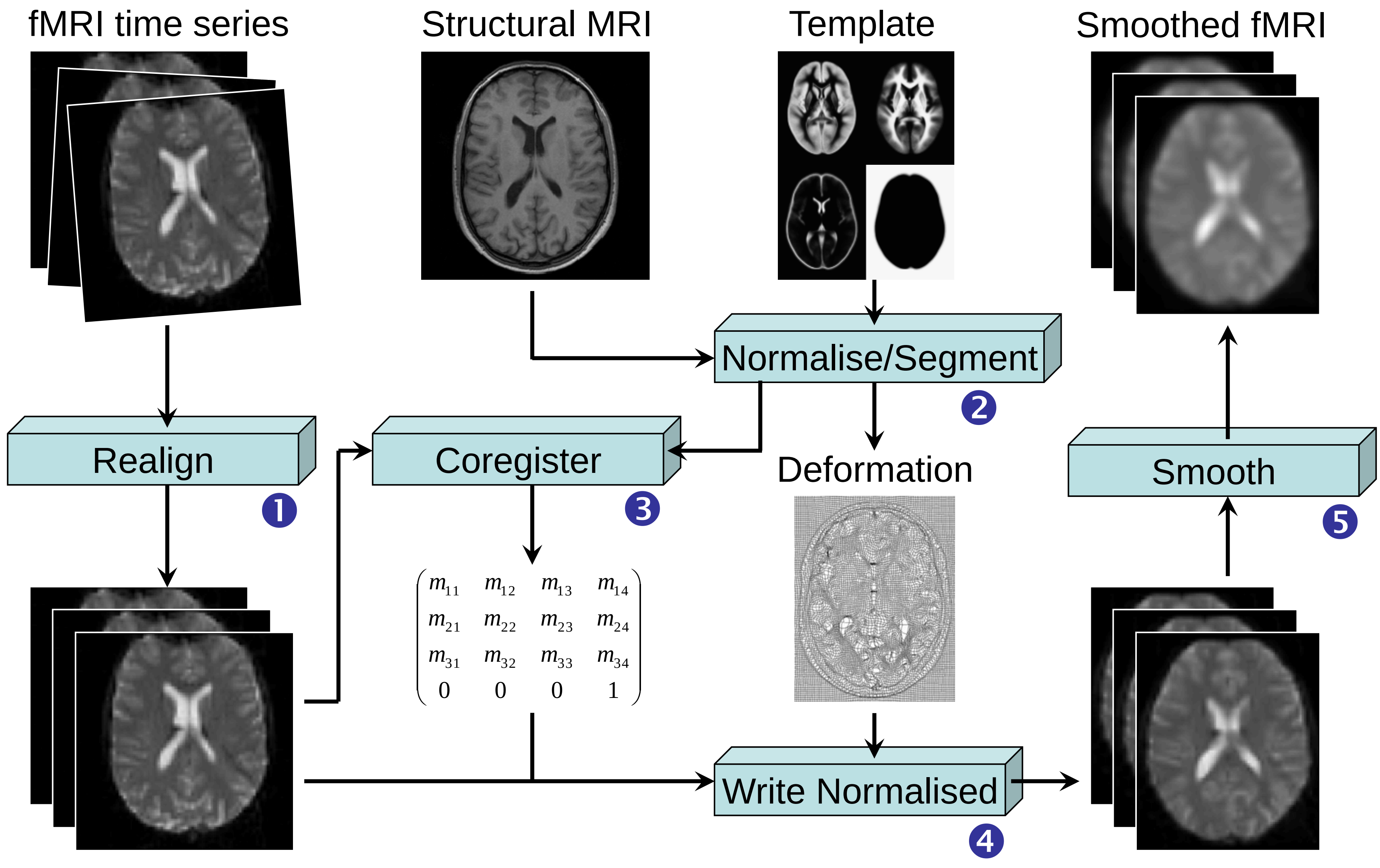

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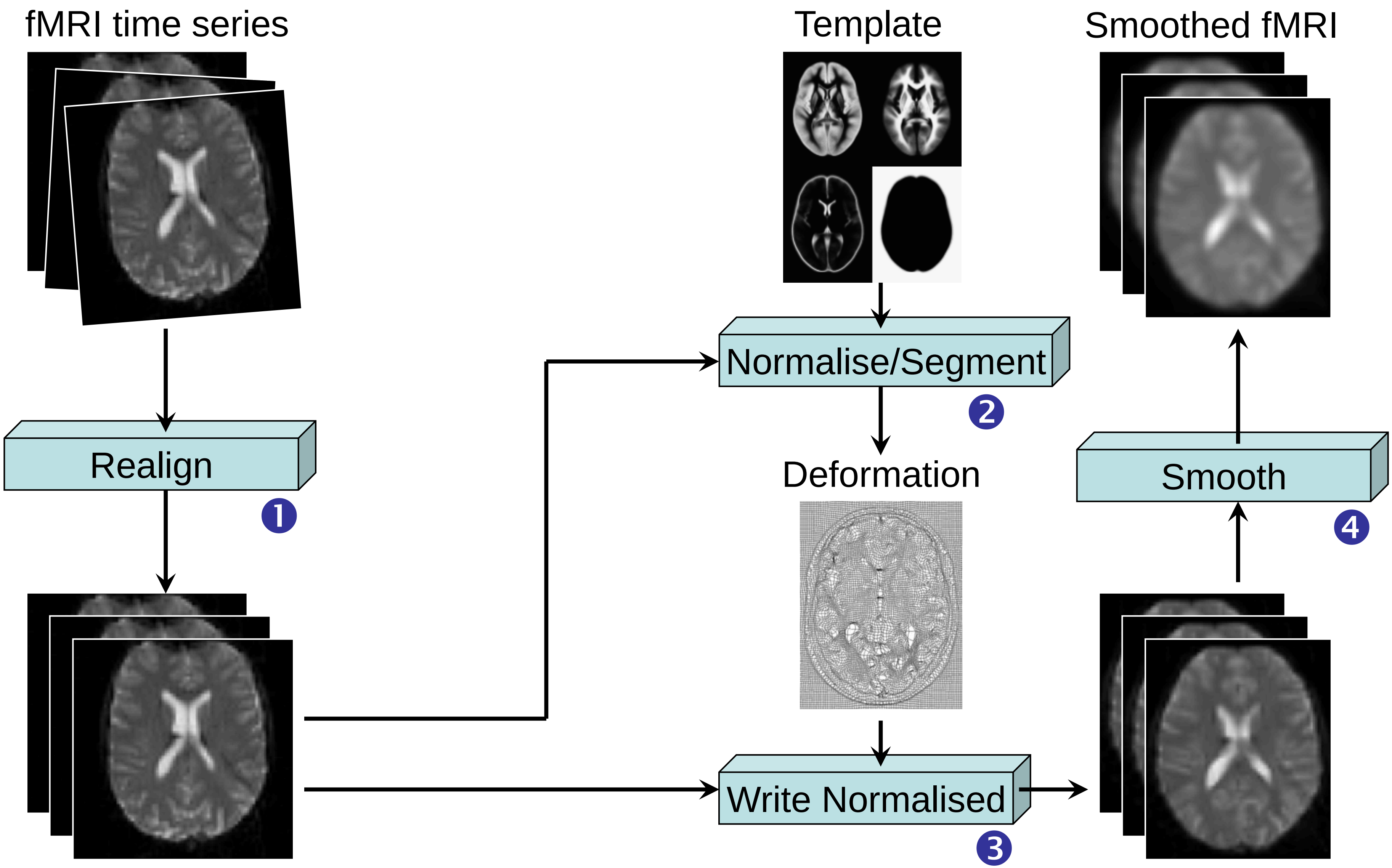
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References

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