

# **UBC SPM Course 2010**

## **Spatial Preprocessing**

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Wellcome Trust Centre  
for Neuroimaging

# Preprocessing overview

REALIGN

COREG

SEGMENT

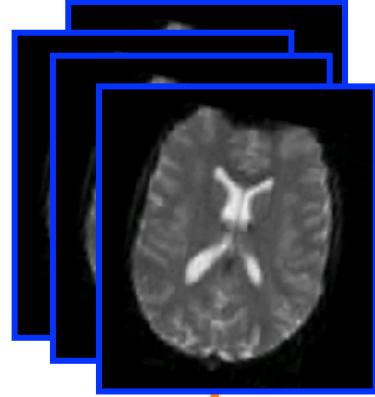
NORM  
WRITE

SMOOTH

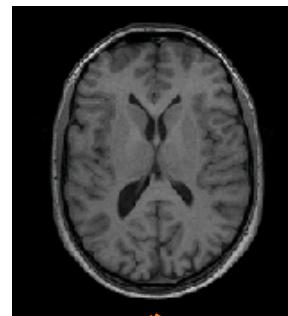
ANALYSIS

# Preprocessing overview

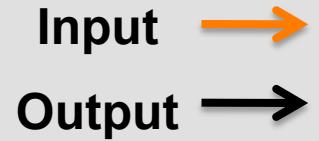
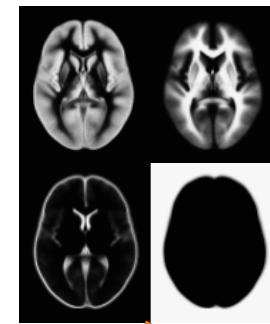
Func. time-series



Anatomical MRI

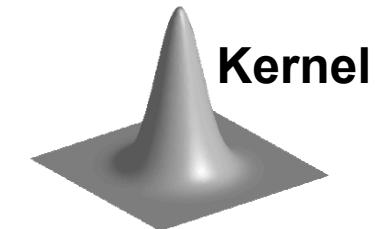


TPMs

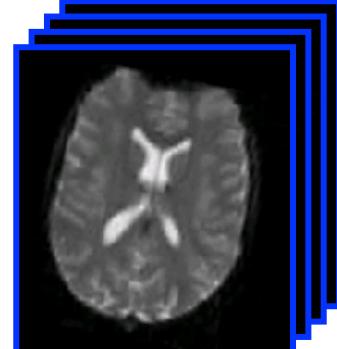


Segmentation

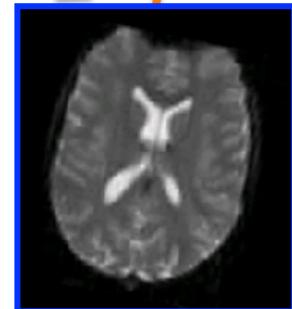
Transformation  
(seg\_sn.mat)



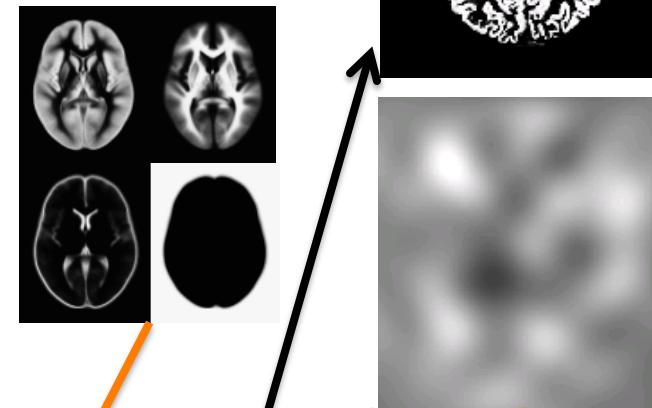
REALIGN



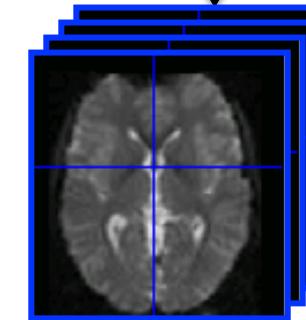
COREG



SEGMENT



NORM  
WRITE



Motion corrected

Mean  
functional

(Headers  
changed)

ANALYSIS

$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

MNI Space

# Contents

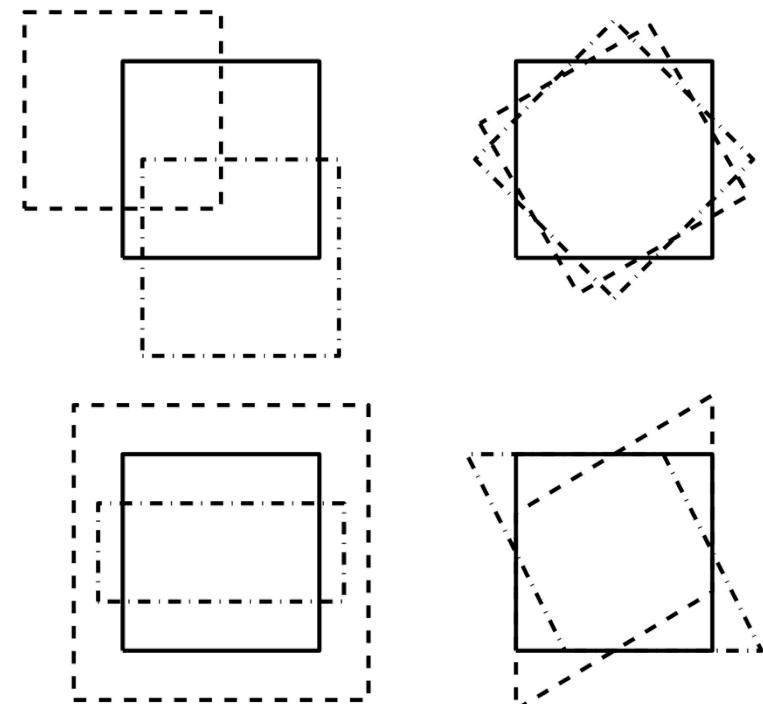
- 1. Registration basics**
2. Motion and realignment
3. Inter-modal coregistration
4. Spatial normalisation
5. Unified segmentation
6. Gaussian smoothing

# Special cases of affine registration

- \* Manual reorientation
- \* Rigid intra-modal realignment
  - \* **Motion correction of functional time-series**
  - \* Within-subject longitudinal registration of serial sMRI
- \* Rigid inter-modal coregistration
  - \* **Aligning structural and (mean) functional images**
  - \* Multimodal structural registration, e.g. T1-T2
- \* Affine inter-subject registration
  - \* First stage of non-linear spatial normalisation
  - \* Approximate alignment of tissue probability maps

# Affine transformations

- \* Rigid rotations have six degrees of freedom (DF)
  - \* Three translations and a 3D rotation (e.g. 3 axis rots.)
- \* Voxel-world mappings usually include three scaling DF (for a possible total of 9 DF)
- \* General 3D affine transformations add three shears (12 DF total)
- \* Affine transform properties
  - \* Parallel lines remain parallel
  - \* Transformations form a group



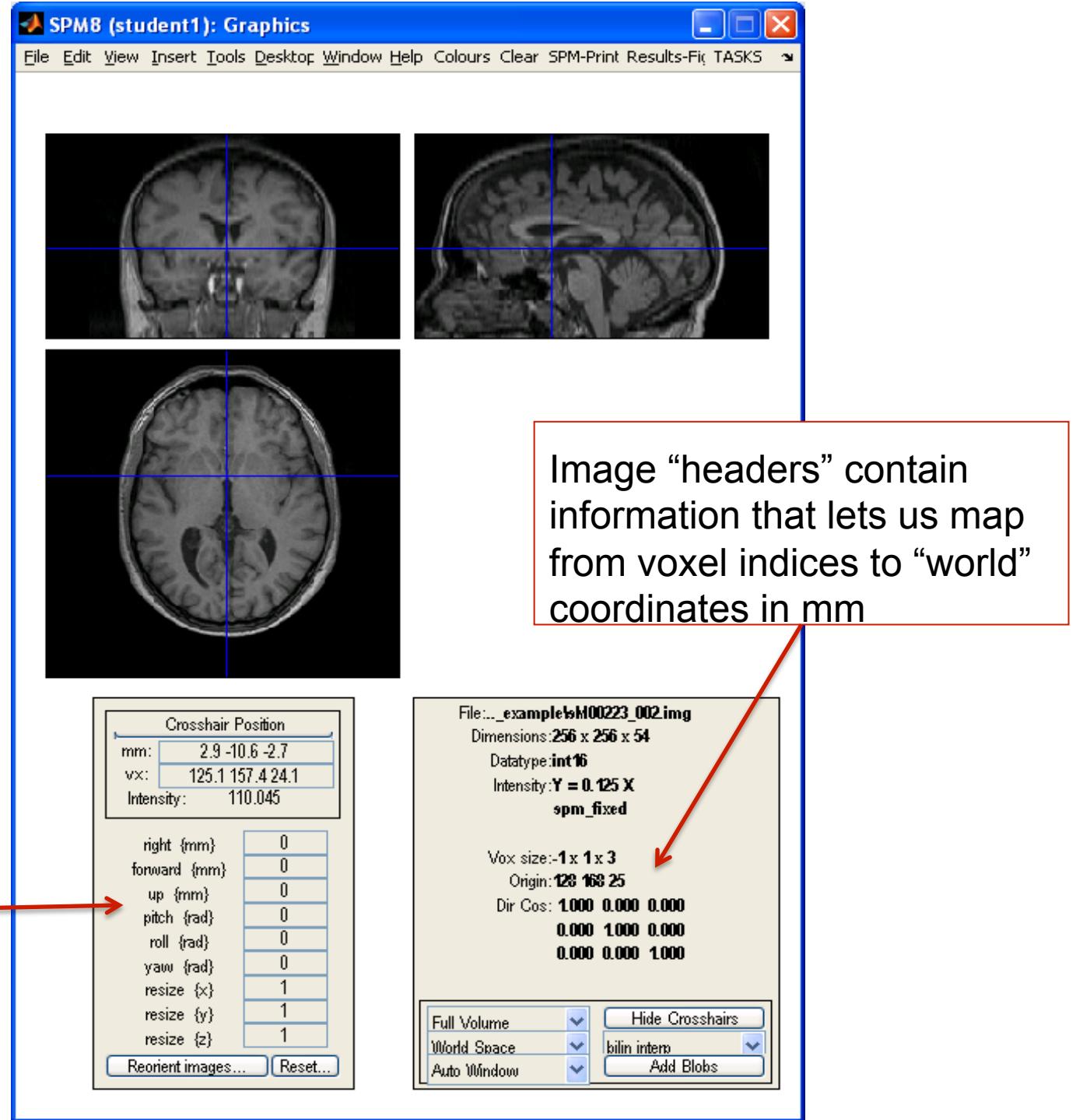
# Other types of registration in SPM

- \* Non-linear spatial normalisation
  - \* Registering different subjects to a standard template
- \* Unified segmentation and normalisation
  - \* Warping standard-space tissue probability maps to a particular subject (can normalise using the inverse)
- \* High-dimensional warping
  - \* Modelling small longitudinal deformations (e.g. AD)
- \* DARTEL
  - \* Smooth large-deformation warps using flows
  - \* Normalisation to group's average *shape* template

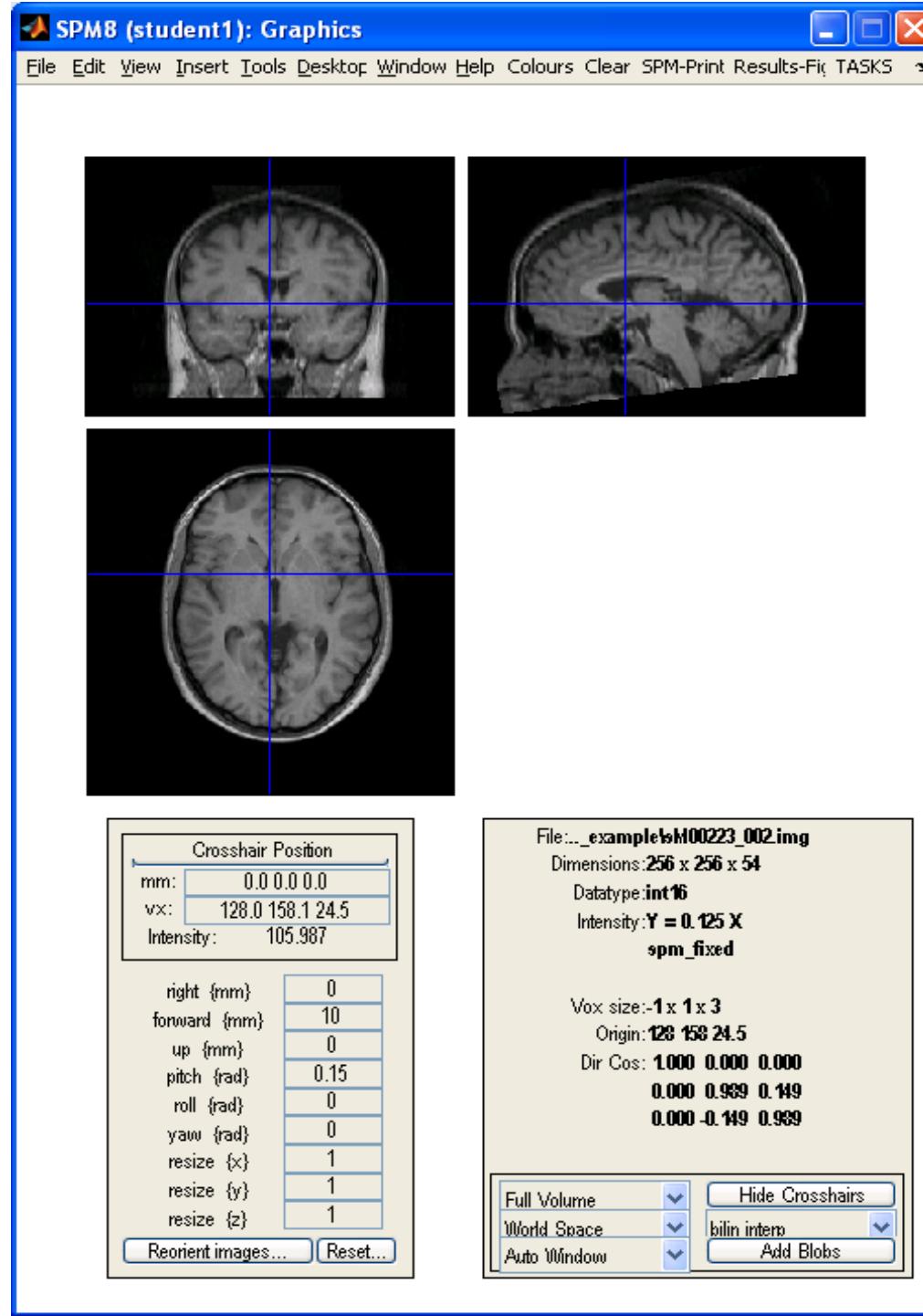
# Voxel-to-world mapping

- \* Affine transform associated with each image
  - \* Maps from voxels ( $x=1..n_x$ ,  $y=1..n_y$ ,  $z=1..n_z$ ) to some world co-ordinate system. e.g.,
    - \* Scanner co-ordinates - images from DICOM toolbox
    - \* T&T/MNI coordinates - spatially normalised
- \* Registering image B (source) to image A (target) will update B's voxel-to-world mapping
  - \* Mapping from voxels in A to voxels in B is by
    - \* A-to-world using  $M_A$ , then world-to-B using  $M_B^{-1} : M_B^{-1} M_A$

# Manual reorientation

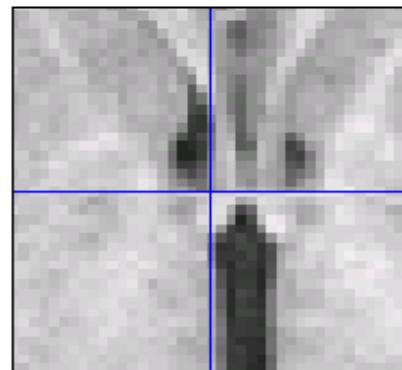
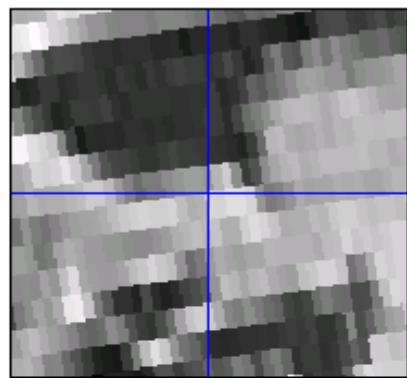
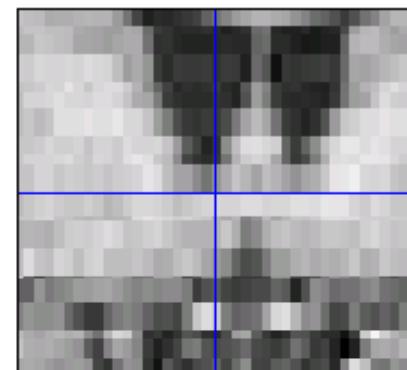


# Manual reorientation

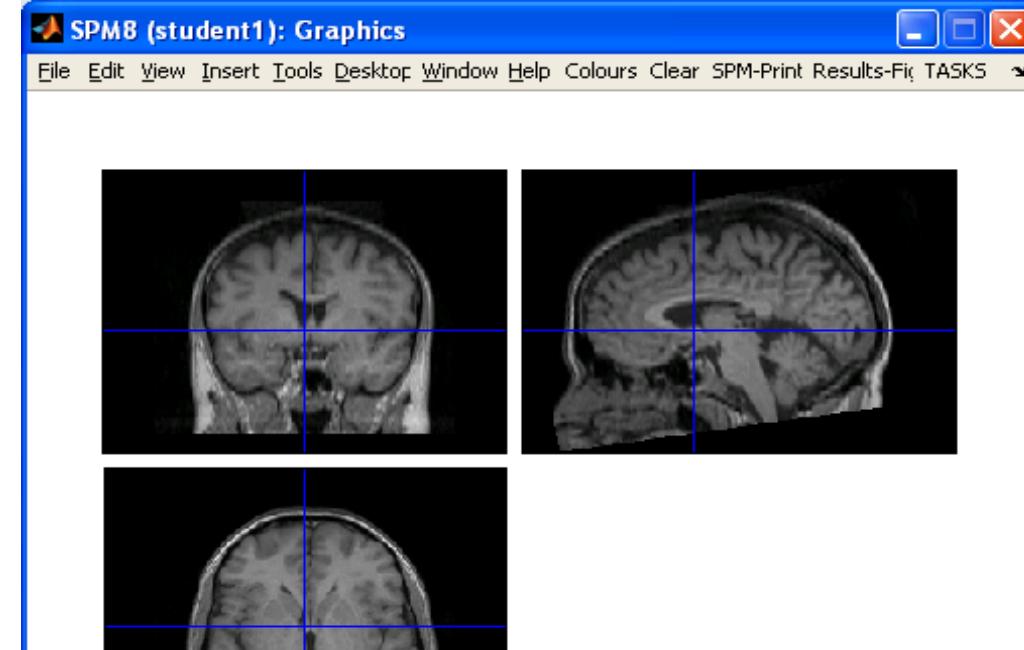


# Manual reorientation

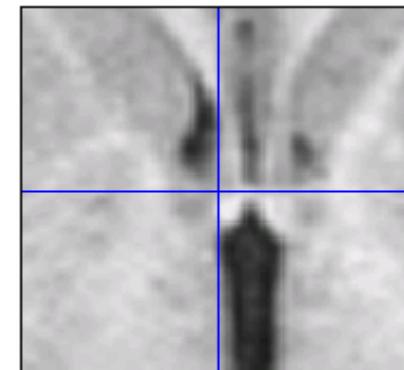
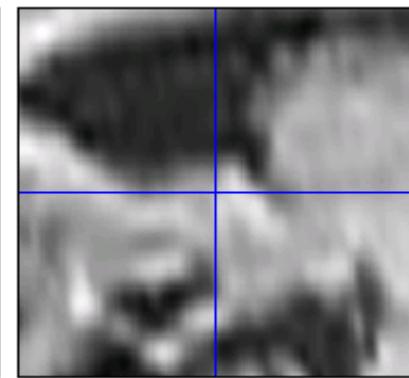
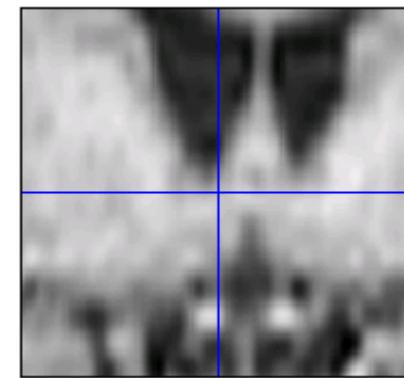
## Interpolation



Nearest  
Neighbour



Crosshair Position	
m:	0.0 0.0 0.0
x:	128.0 158.1 24.5
intensity:	105.987
right {mm}	0
forward {mm}	10
up {mm}	0
pitch {rad}	0.15
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1

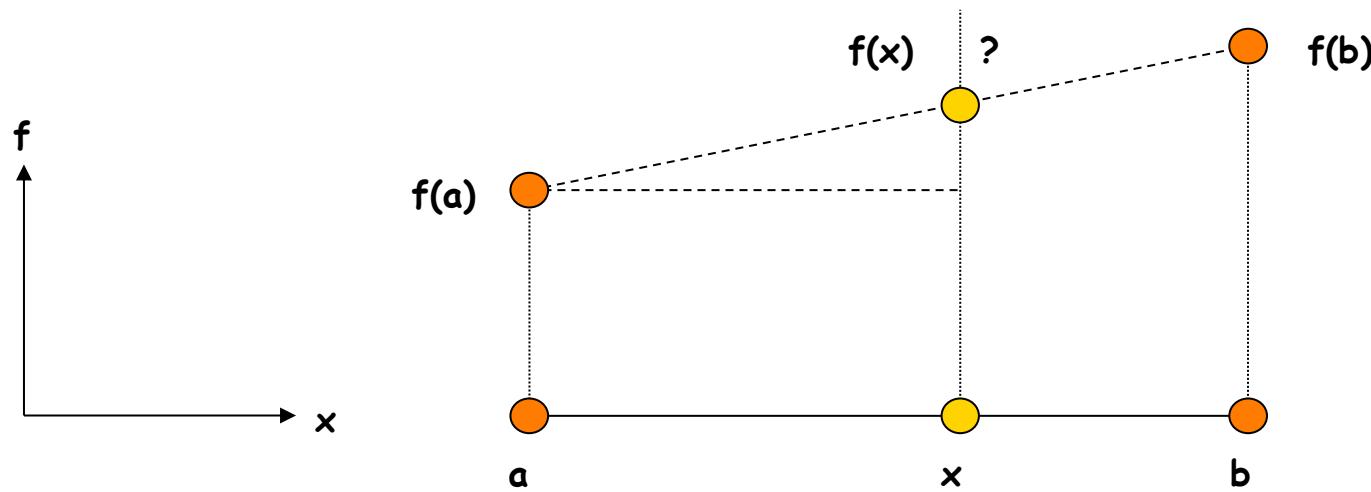


Sinc

# Interpolation

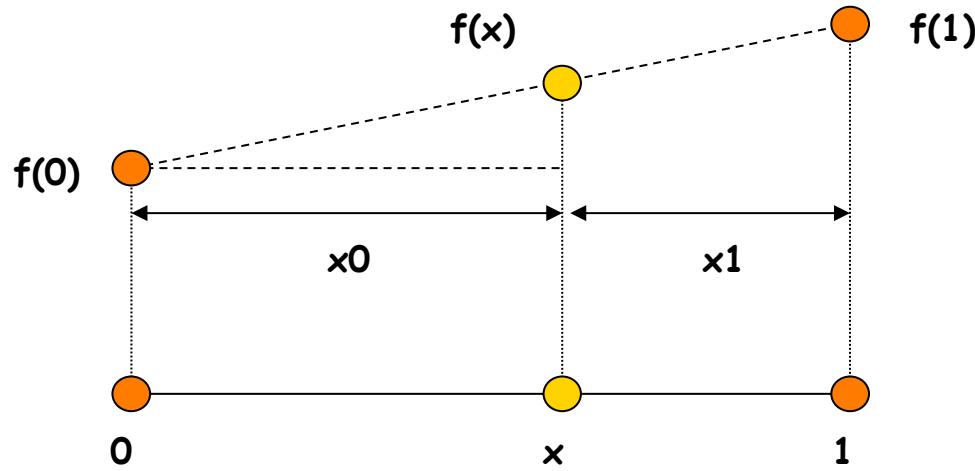
- \* Applying the transformation parameters, and re-sampling the data onto the same grid of voxels as the target image
  - \* AKA reslicing, regridding, transformation, and writing (as in **normalise - write**)
- \* Nearest neighbour gives the new voxel the value of the closest corresponding voxel in the source
- \* Linear interpolation uses information from all immediate neighbours (2 in 1D, 4 in 2D, 8 in 3D)
- \* NN and linear interp. correspond to zeroth and first order B-spline interpolation, higher orders use more information in the hope of improving results
  - \* (Sinc interpolation is an alternative to B-spline)

# Linear interpolation – 1D



$$f(x) = f(a) + \frac{f(b) - f(a)}{b - a} (x - a) = f(a) \frac{b - x}{b - a} + f(b) \frac{x - a}{b - a}$$

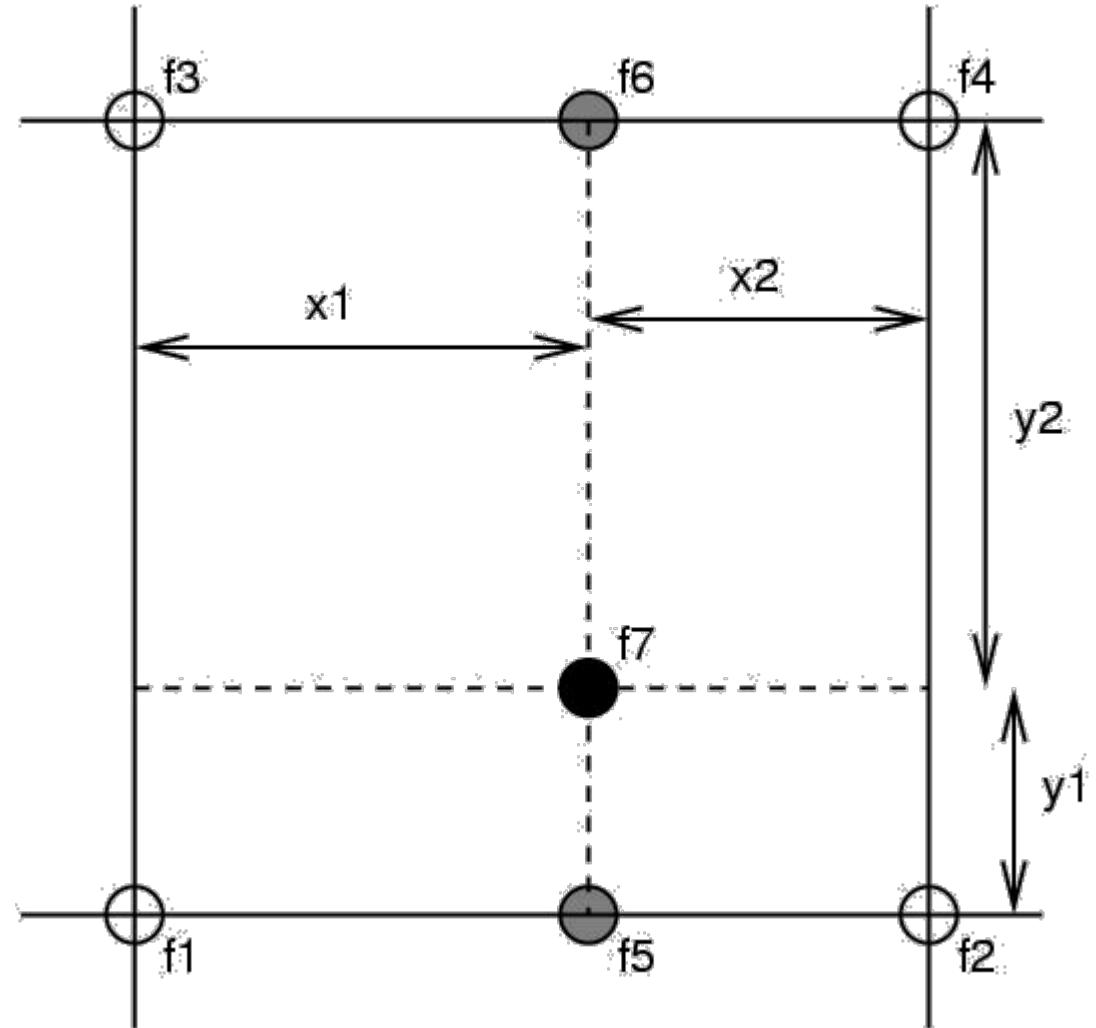
# Linear interpolation – 1D



$$\begin{aligned}f(x) &= f(0) + (f(1) - f(0))x = f(0)(1 - x) + f(1)x \\&= f(0)x_1 + f(1)x_0\end{aligned}$$

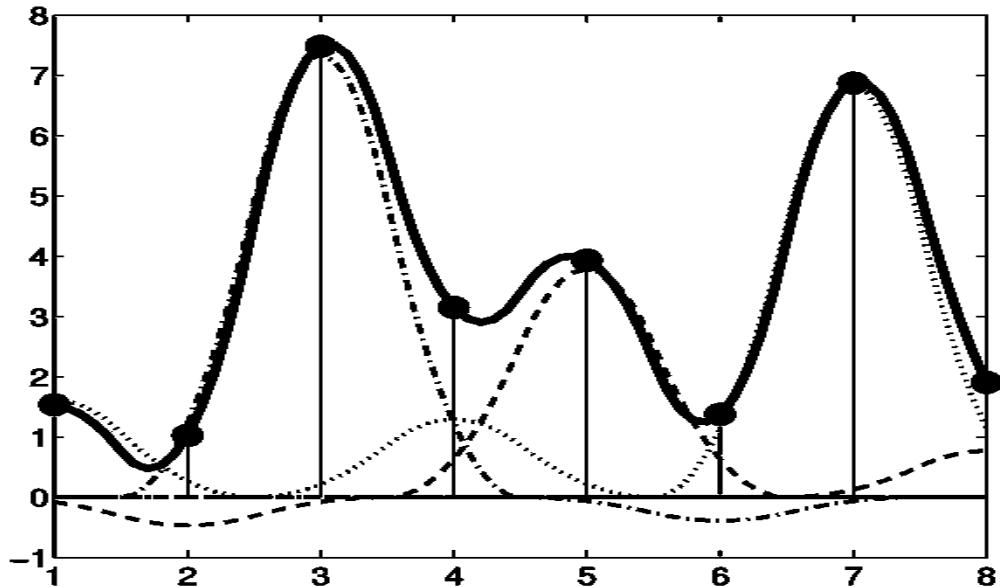
# Linear interpolation – 2D

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

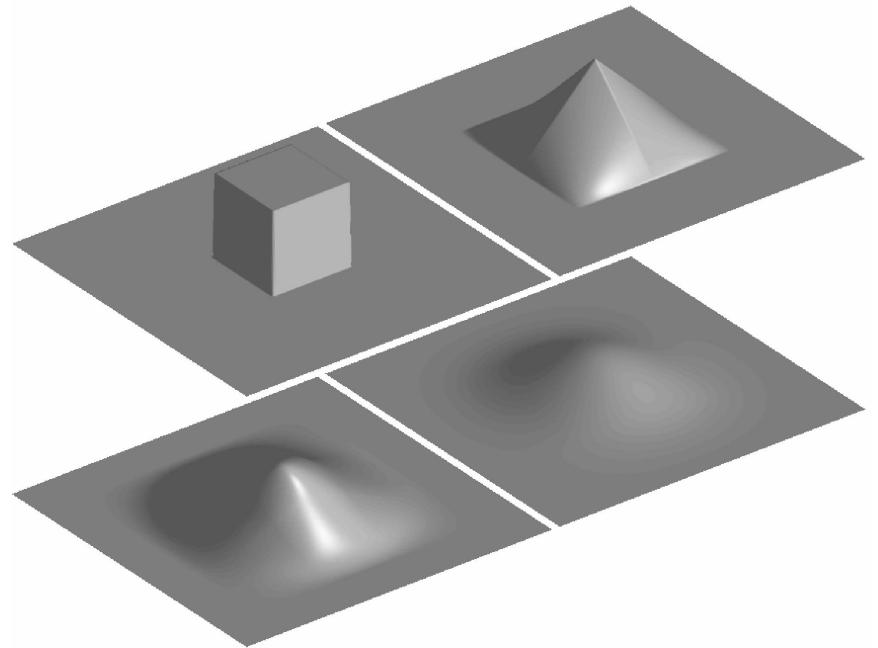


# B-spline Interpolation

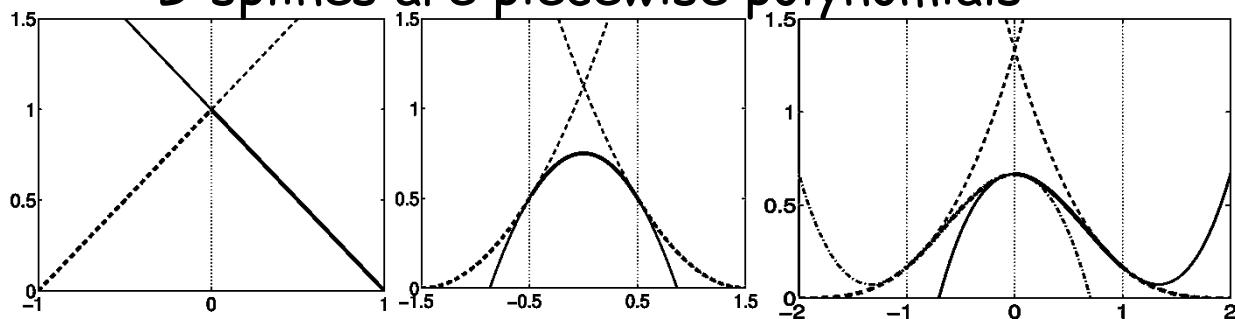
A continuous function is represented by a linear combination of basis functions



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

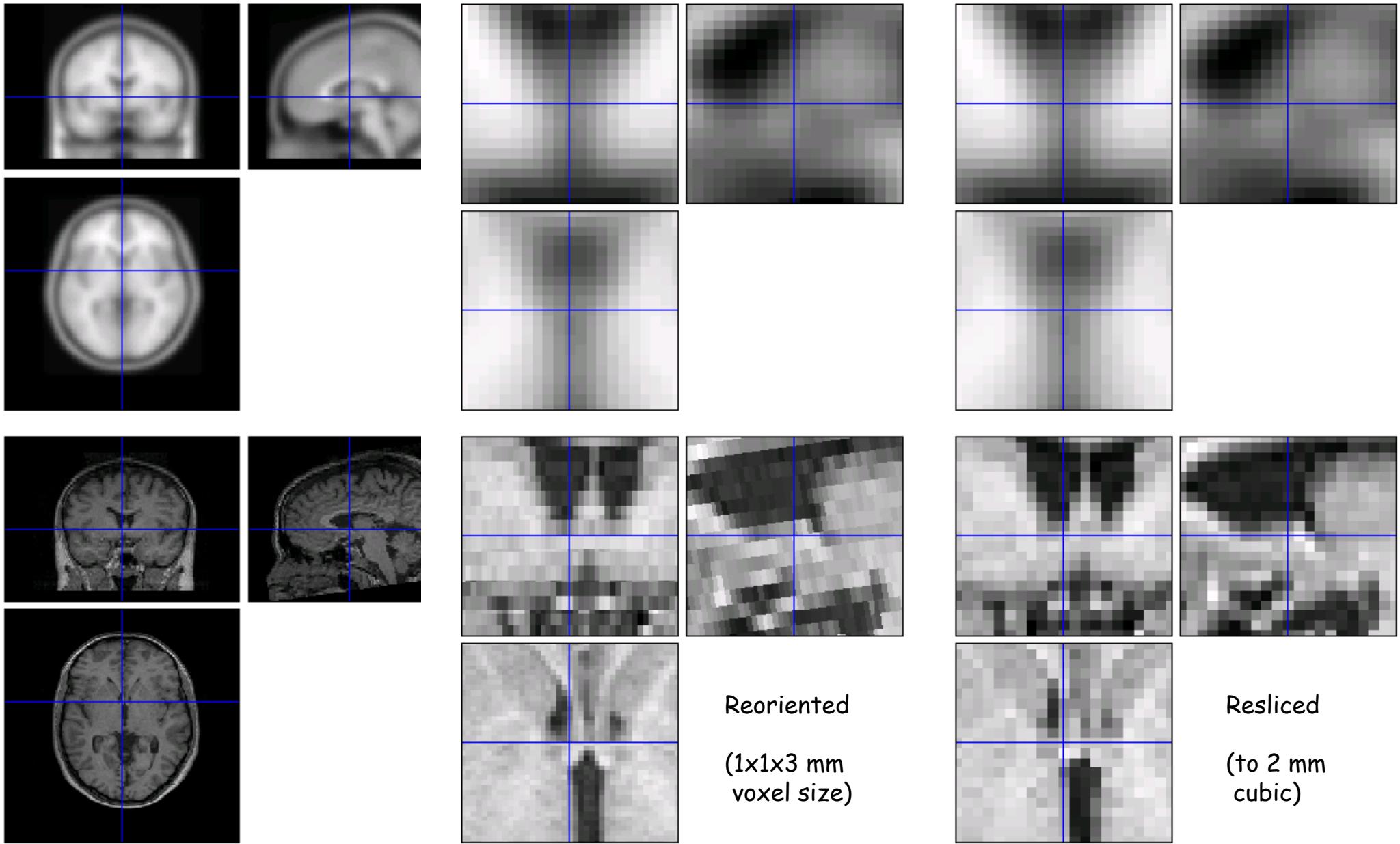


B-splines are piecewise polynomials



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

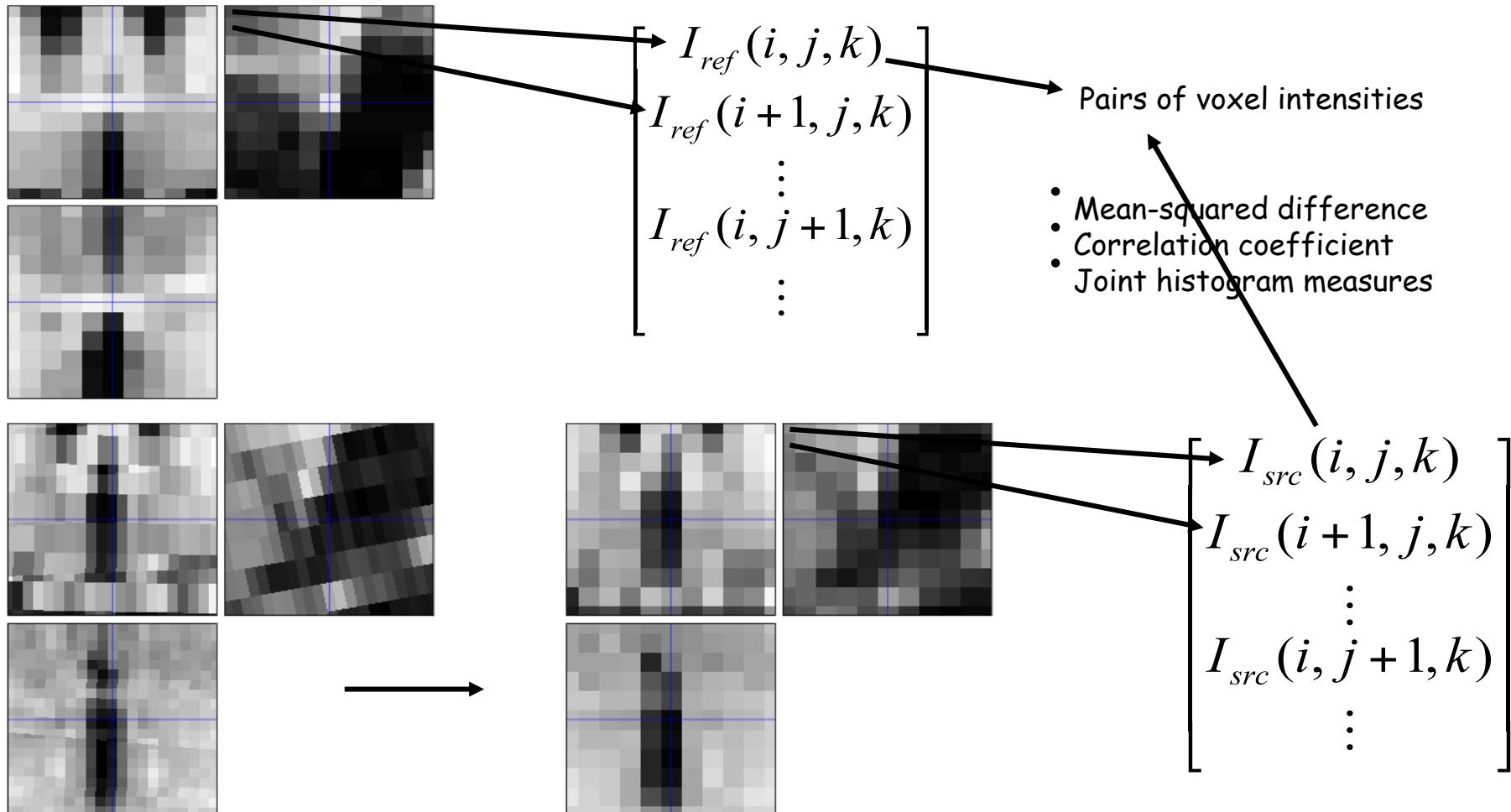
# Manual reorientation – Reslicing



# Quantifying image alignment

- \* Registration intuitively relies on the concept of aligning images to increase their similarity
  - \* This needs to be mathematically formalised
  - \* We need practical way(s) of measuring similarity
- \* Using interpolation we can find the intensity at equivalent voxels
  - \* (equivalent according to the current transformation parameter estimates)

# Voxel similarity measures



# Intra-modal similarity measures

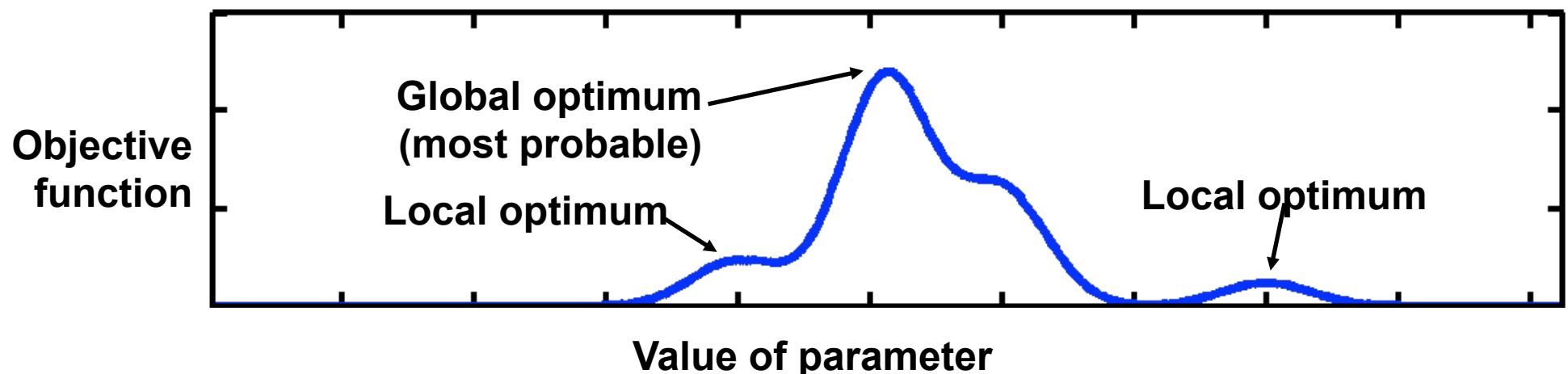
- \* Mean squared error (minimise)
  - \* AKA sum-squared error, RMS error, etc.
  - \* Assumes simple relationship between intensities
  - \* Optimal (only) if differences are i.i.d. Gaussian
  - \* Okay for realignment or sMRI-sMRI coreg
- \* Correlation-coefficient (maximise)
  - \* AKA Normalised Cross-Correlation, Zero-NCC
  - \* Slightly more general, e.g. T1-T1 inter-scanner
  - \* Invariant under affine transformation of intensities

# Automatic image registration

- \* Quantifying the quality of the alignment with a measure of image similarity allows computational estimation of transformation parameters
- \* This is the basis of both realignment and coregistration in SPM
  - \* Allowing more complex geometric transformations or warps leads to more flexible spatial normalisation
- \* Automating registration requires optimisation...

# 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)



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# Motion in fMRI

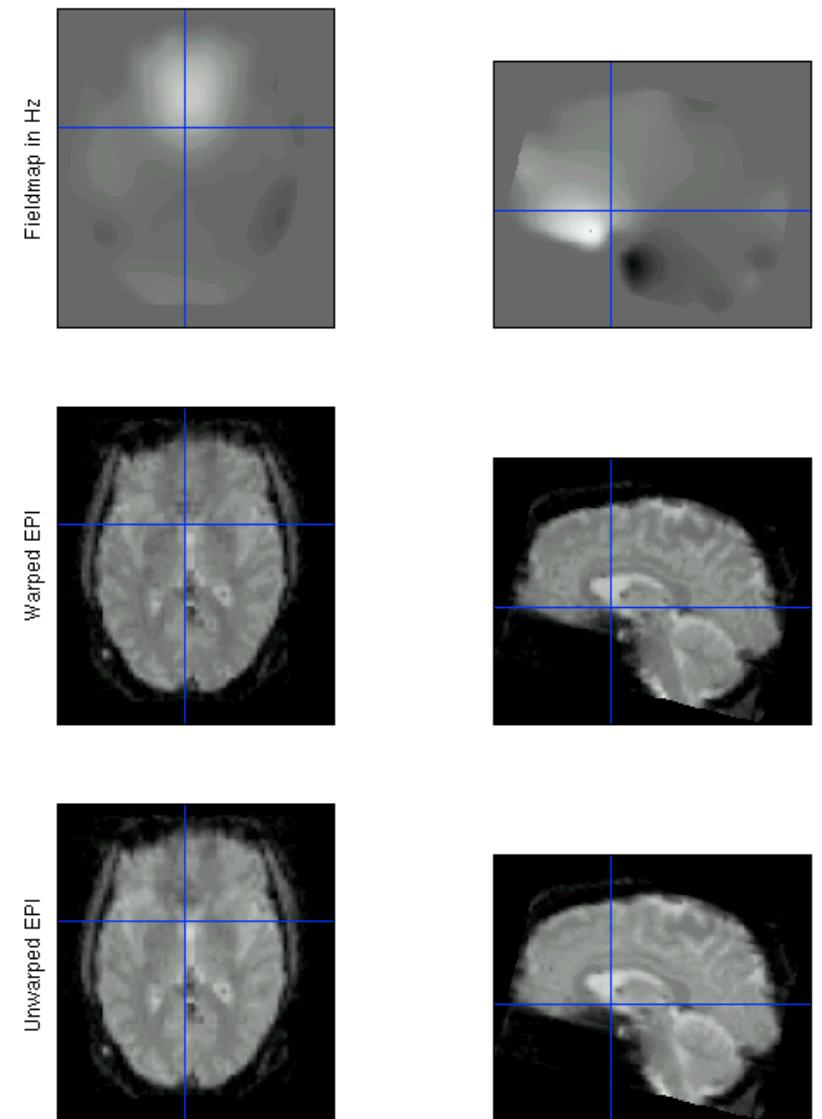
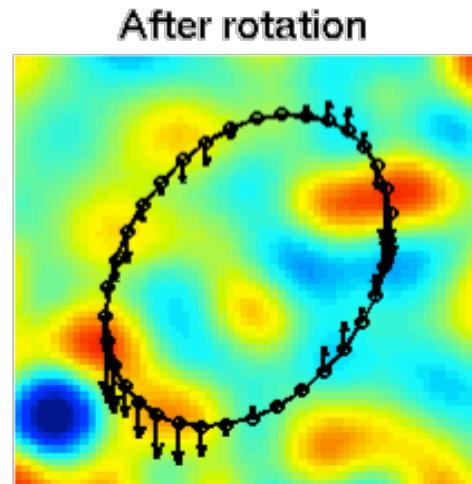
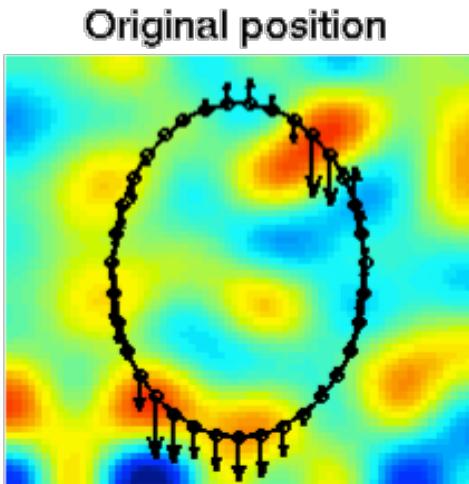
- \* Can be a major problem
  - \* Increase residual variance and reduce sensitivity
  - \* Data may get completely lost with sudden movements
  - \* Movements may be correlated with the task
  - \* Try to minimise movement (don't scan for too long!)
- \* Motion correction using realignment
  - \* Each volume rigidly registered to reference
  - \* Least squares objective function
- \* Realigned images must be resliced for analysis
  - \* Not necessary if they will be normalised anyway

# Residual Errors from aligned fMRI

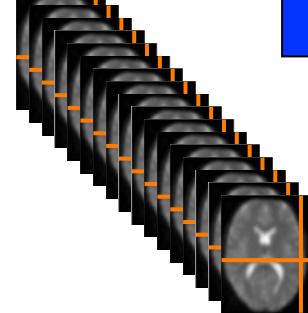
- \* Slices are not acquired simultaneously
  - \* rapid movements not accounted for by rigid body model
- \* Image artefacts may not move according to a rigid body model
  - \* image distortion, image dropout, Nyquist ghost
- \* Gaps between slices can cause aliasing artefacts
- \* Re-sampling can introduce interpolation errors
  - \* especially tri-linear interpolation
- \* Functions of the estimated motion parameters can be modelled as confounds in subsequent analyses

# fMRI movement by distortion interaction

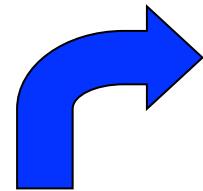
- \* Subject disrupts B0 field, rendering it inhomogeneous
  - \* distortions occur along the phase-encoding direction
- \* Subject moves during EPI time series
  - \* Distortions vary with subject position
  - \* shape varies (non-rigidly)



# Correcting for distortion changes using Unwarp



Estimate movement parameters.



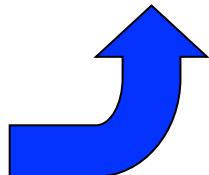
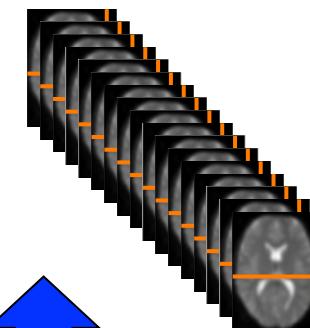
Estimate reference from mean of all scans.



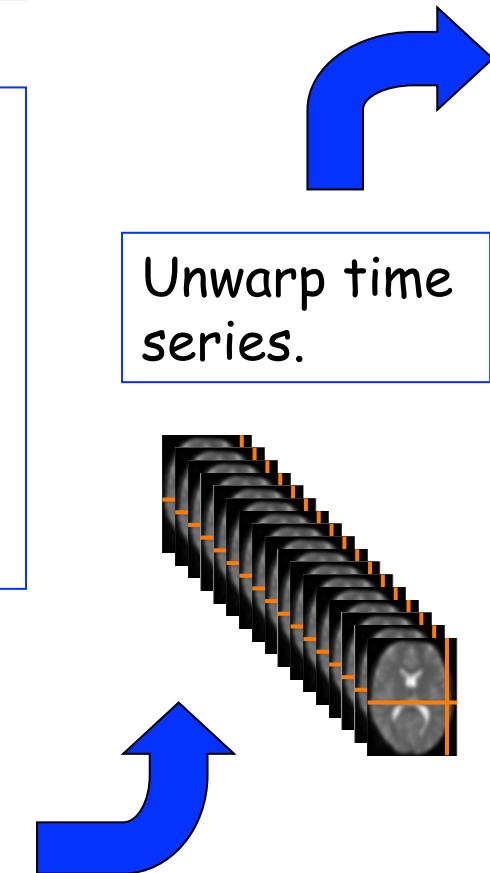
Estimate new distortion fields for each image:

- estimate rate of change of field with respect to the current estimate of movement parameters in pitch and roll.

Unwarp time series.



$$\begin{array}{c} \Delta\varphi \quad +\Delta\theta \\ \partial B_0 / \partial \varphi \quad \partial B_0 / \partial \theta \end{array}$$

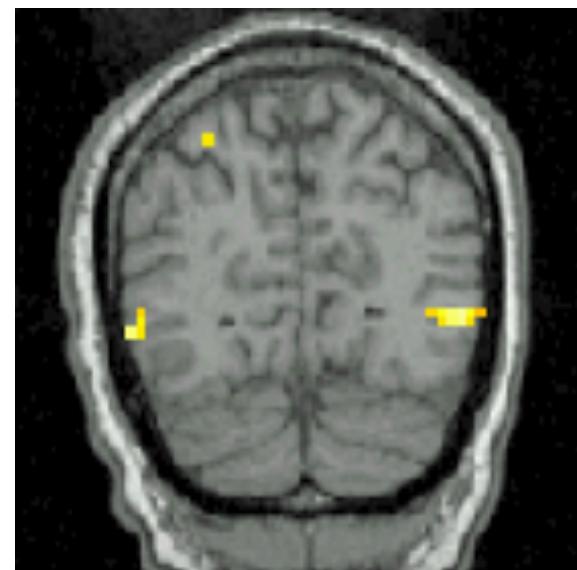
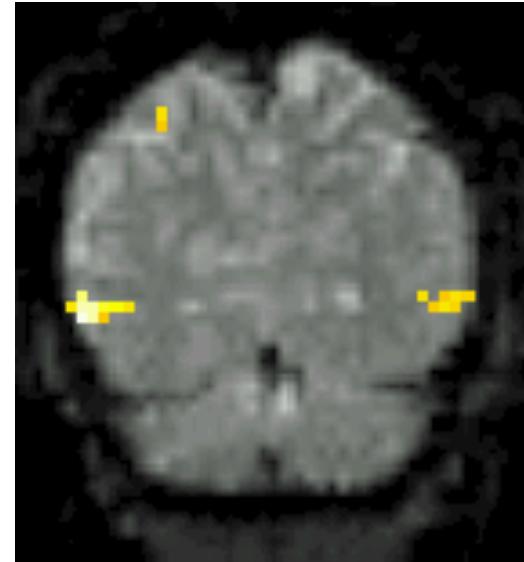


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# Inter-modal coregistration

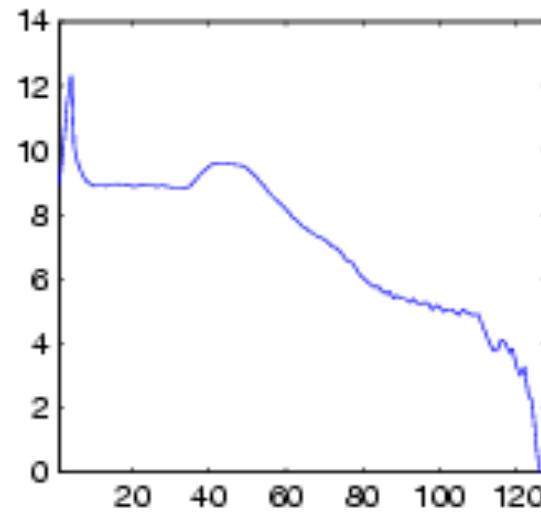
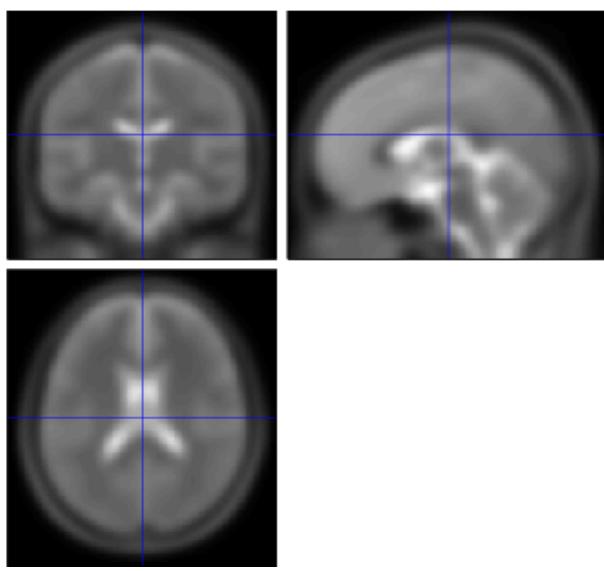
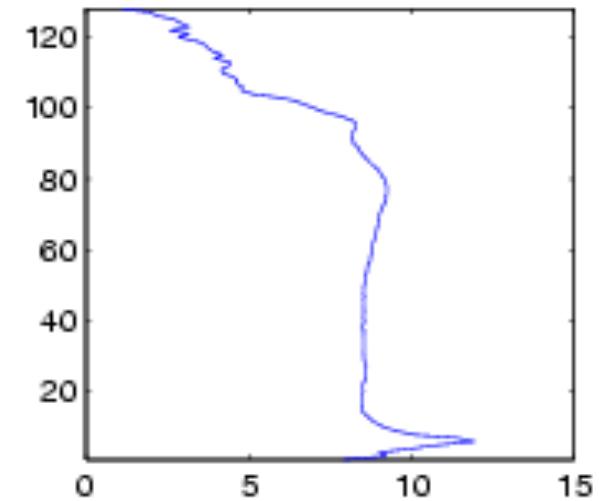
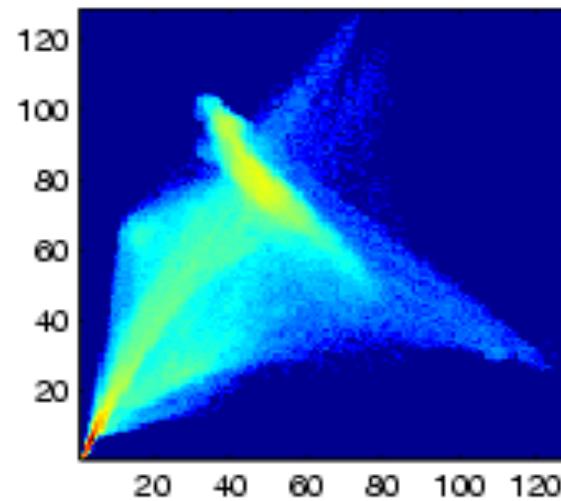
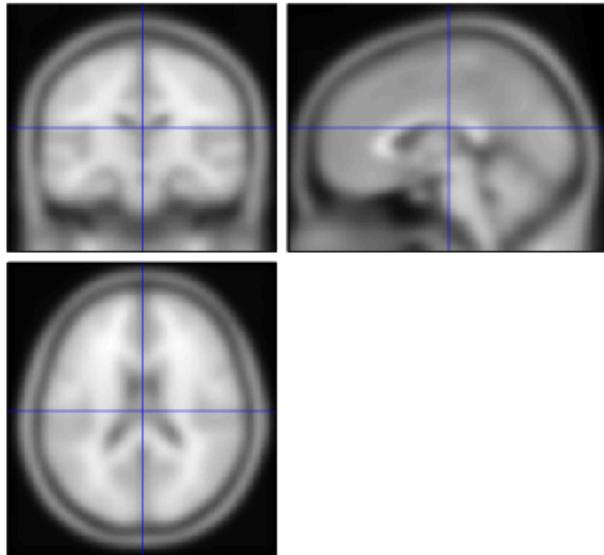
- Match images from same subject but different modalities:
  - anatomical localisation of single subject activations
  - achieve more precise spatial normalisation of functional image using anatomical image.



# Inter-modal similarity measures

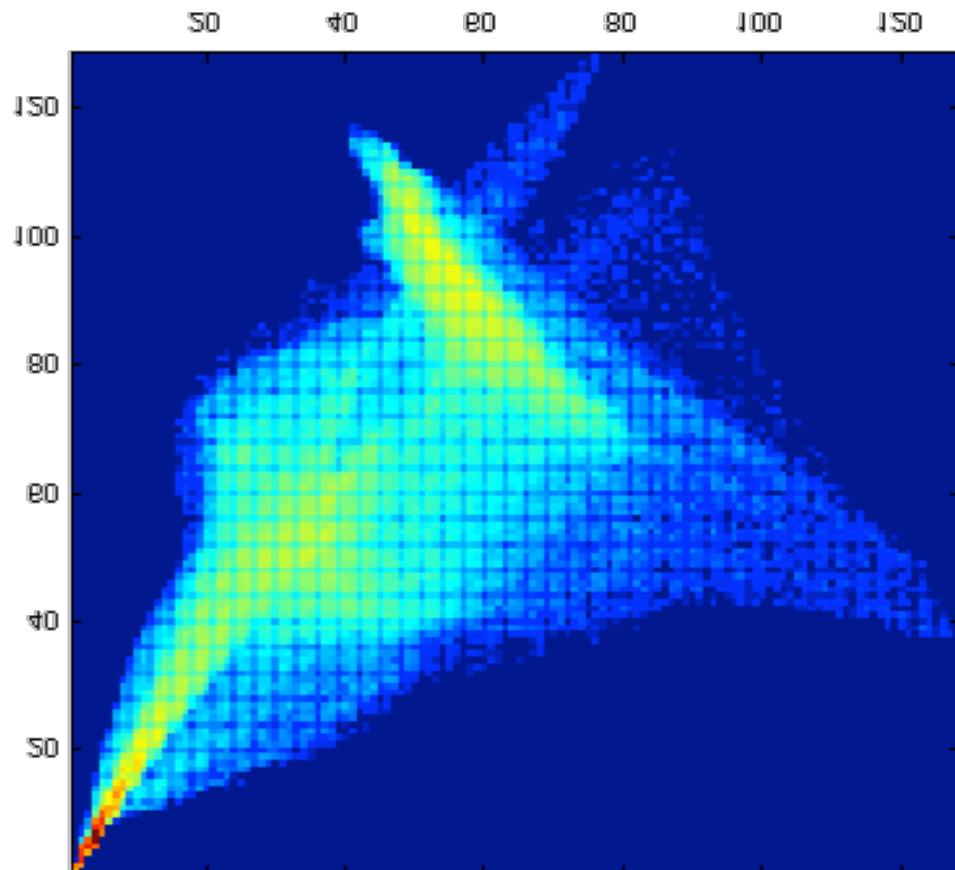
- \* Commonly derived from joint and marginal entropies
  - \* Entropies via probabilities, from histograms
  - \*  $H(a) = -\sum_a P(a) \log_2 P(a)$
  - \*  $H(a,b) = -\sum_{a,b} P(a,b) \log_2 P(a,b)$
- \* Minimise joint entropy  $H(a,b)$
- \* Maximise mutual Information
  - \*  $MI = H(a) + H(b) - H(a,b)$
- \* Maximise normalised MI
  - \*  $NMI = (H(a) + H(b)) / H(a,b)$

# Joint and marginal histograms

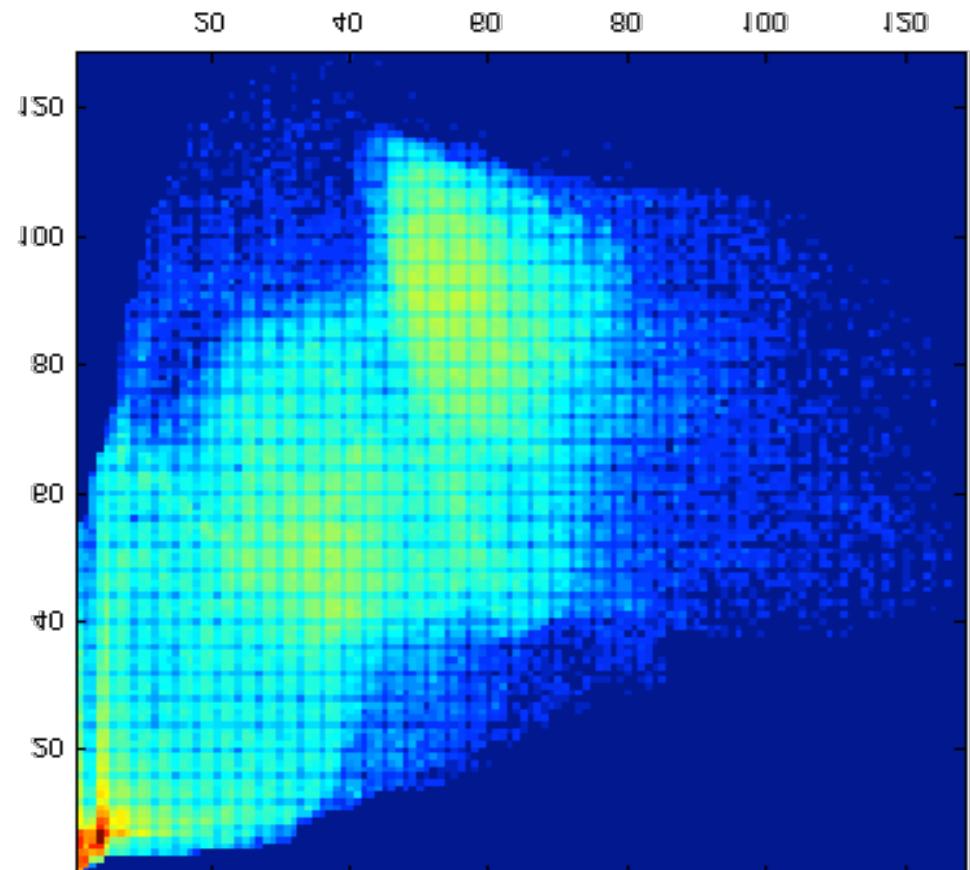


# Joint histogram based registration

Initially registered T1 and T2 templates



After deliberate misregistration  
(10mm relative x-translation)



**Joint histogram sharpness correlates with image alignment**  
Mutual information and related measures attempt to quantify this

**SPM8b (student1)**

**Batch Editor**

**Module List**

**Current Module: Coreg: Estimate**

Help on: Coreg: Estimate  
 Reference Image ...onical\avg152T2.nii,1  
 Source Image ...onical\avg152T1.nii,1  
 Other Images  
 Estimation Options  
**Objective Function** ...ed Mutual Information

Separation [4 2]  
 Tolerances 1x12 double  
 Histogram Smoothing [7 7]

**Current Item: Objective Function**

Mutual Information  
**\*Normalised Mutual Information**  
 Entropy Correlation Coefficient  
 Normalised Cross Correlation

**Object Function**

Registration involves finding parameters that either maximise or minimise some objective function. For inter-modal registration, use Mutual Information, Normalised Mutual Information, or Entropy Correlation Coefficient. For within modality, you could also use Normalised Cross Correlation.

Done 'Coreg: Estimate'  
 Done  
 >>

**SPM8b (student1): Graphics**

File Edit View Insert Tools Desktop Window Help Colours Clear SPM-Print Results-Fit TASKS

### Normalised Mutual Information Coregistration

X1 = 1.000\*X -0.001\*Y -0.004\*Z +0.404  
 Y1 = 0.001\*X +1.000\*Y +0.002\*Z -0.165  
 Z1 = 0.004\*X -0.002\*Y +1.000\*Z -0.201

Original Joint Histogram  
 Final Joint Histogram

.anonical\avg152T1.nii .anonical\avg152T2.nii

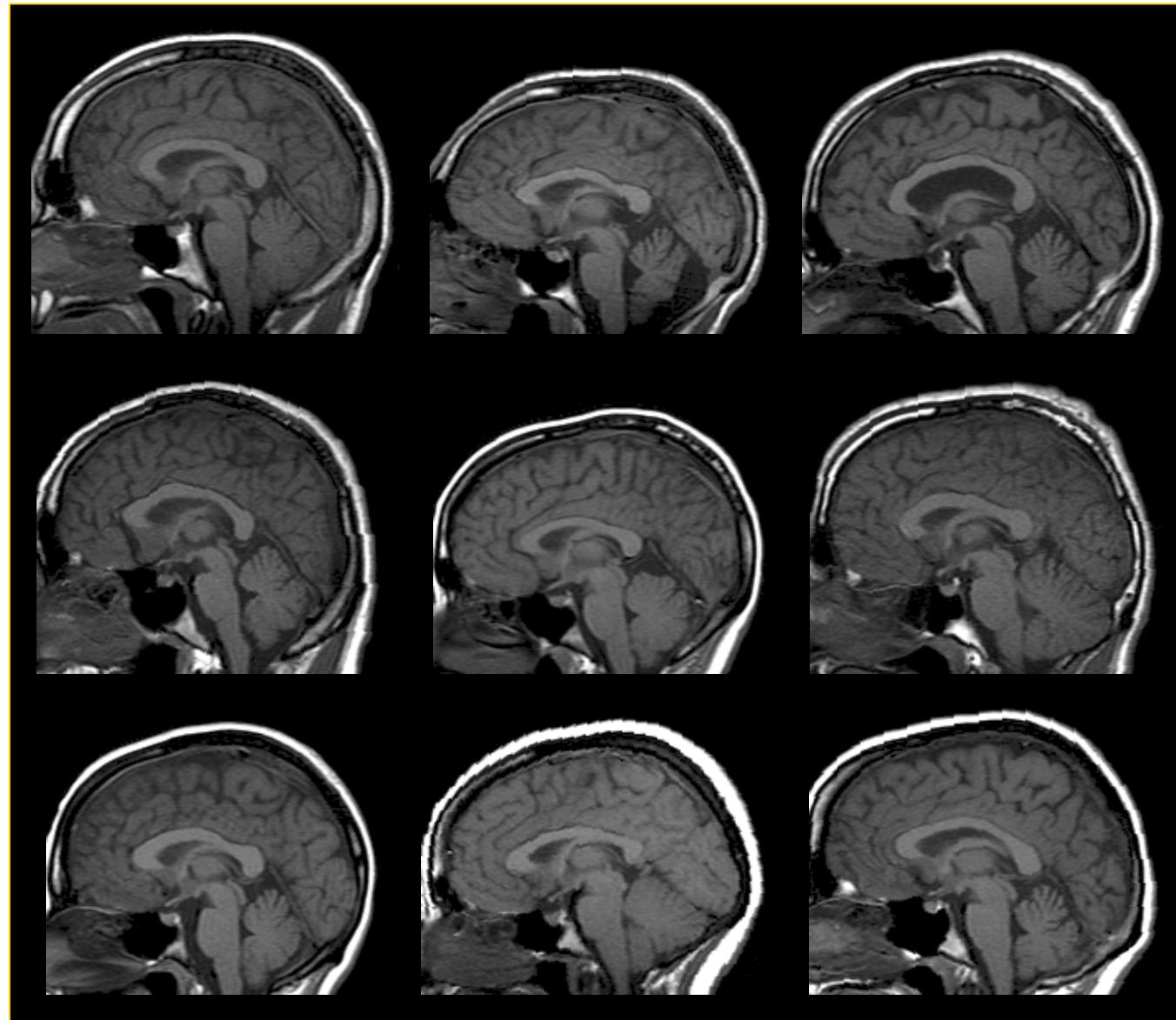
.anonical\avg152T1.nii .anonical\avg152T2.nii

Four brain MRI slices showing axial, coronal, and sagittal planes with registration grids overlaid.

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# Spatial Normalisation

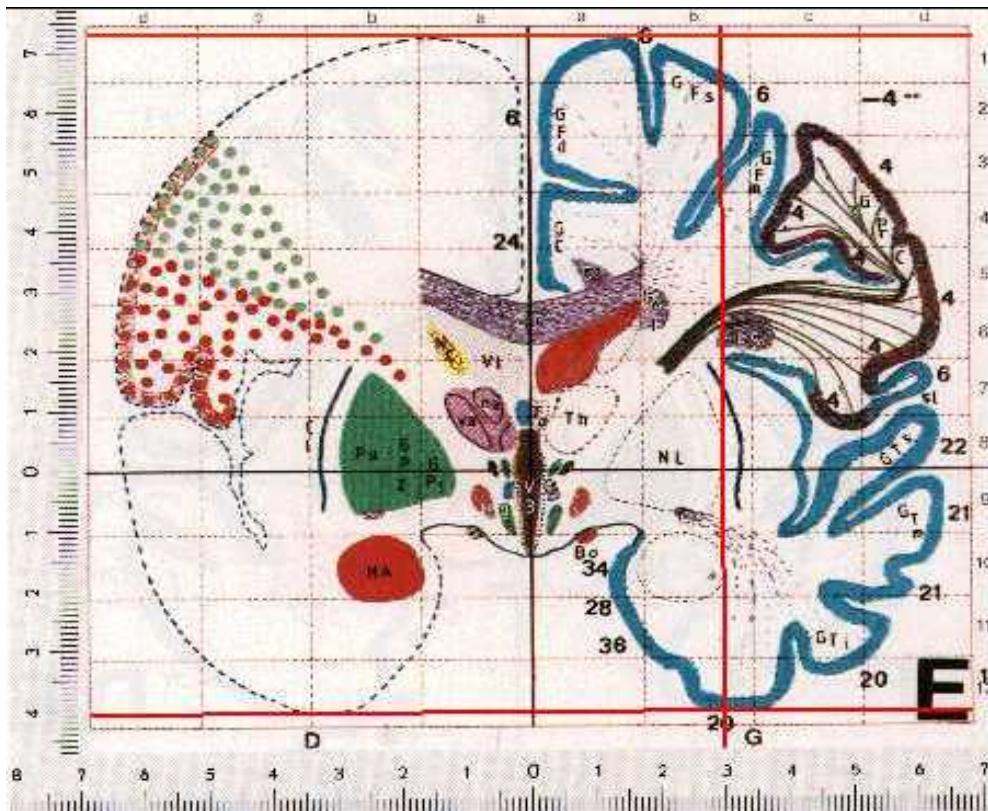


# Spatial Normalisation - Reasons

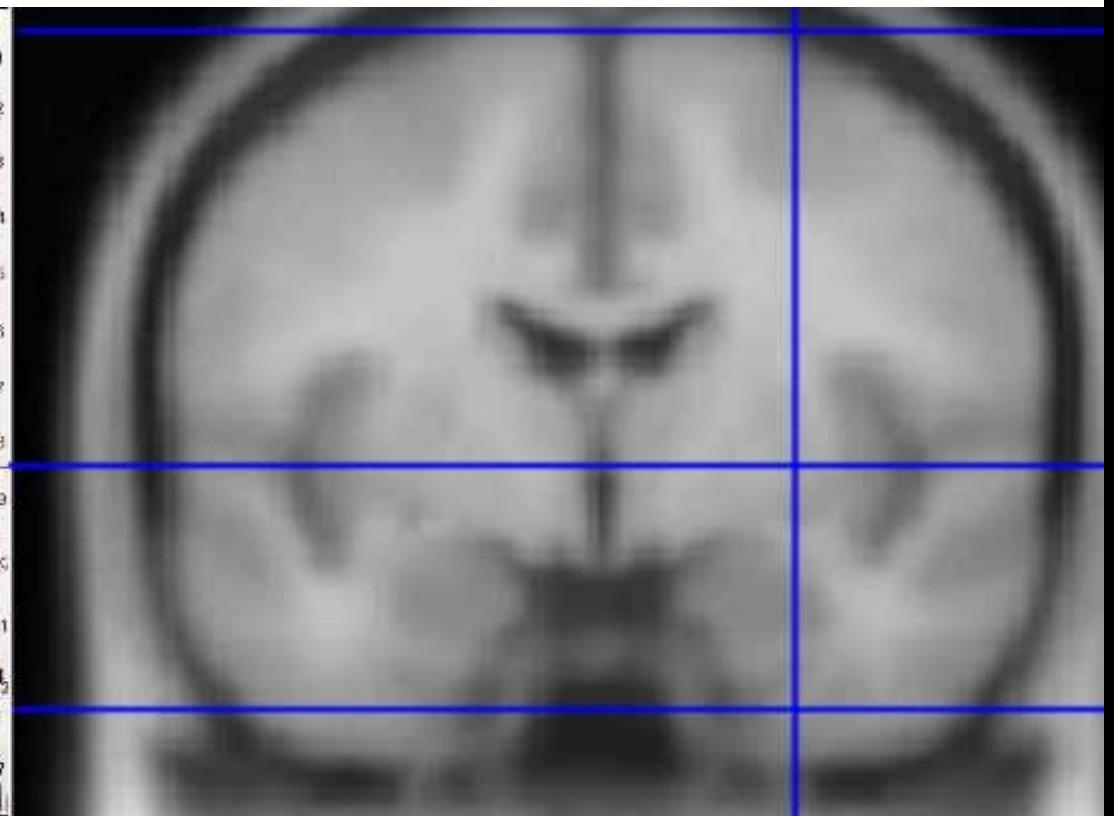
- \* Inter-subject averaging
  - \* Increase sensitivity with more subjects
    - \* Fixed-effects analysis
  - \* Extrapolate findings to the population as a whole
    - \* Mixed-effects analysis
- \* Make results from different studies comparable by aligning them to standard space
  - \* e.g. The T&T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

# Standard spaces

# The Talairach Atlas



## The MNI/ICBM AVG152 Template

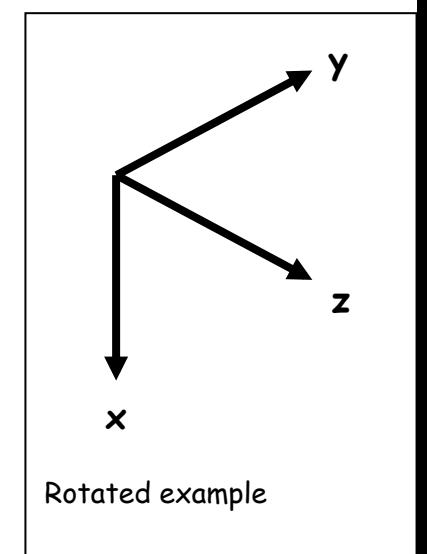
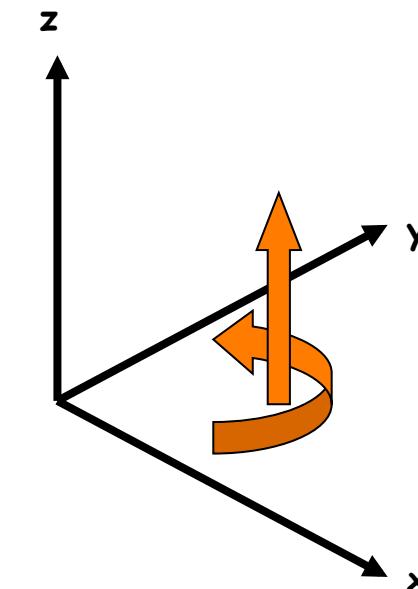
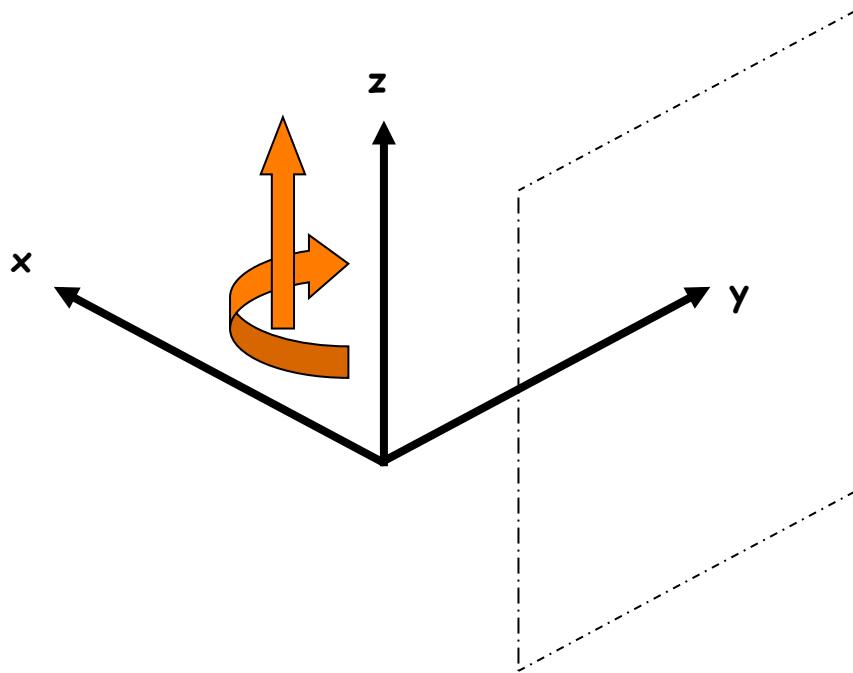


The MNI template follows the convention of T&T, but doesn't match the *particular brain*.

Recommended reading: <http://imaging.mrc-cbu.cam.ac.uk/imaging/MniTalairach>

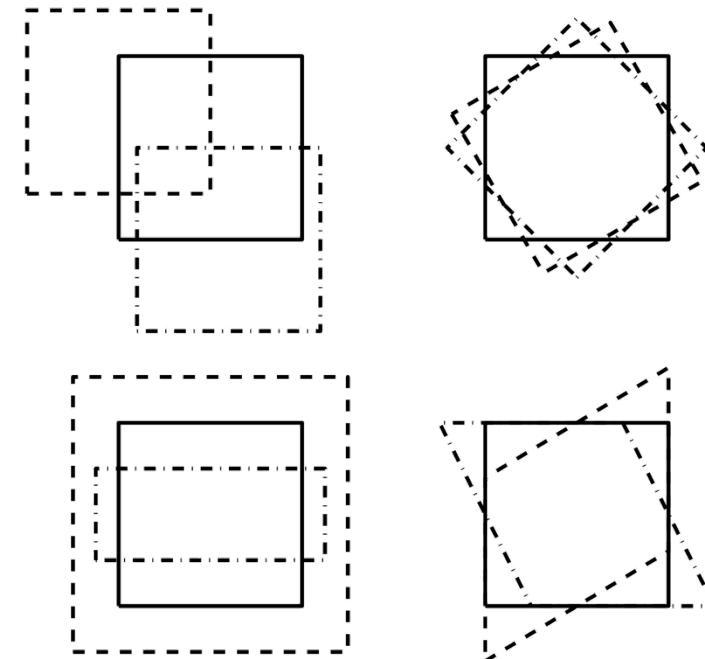
# Coordinate system sense

- \* Analyze™ files are stored in a left-handed system
- \* Talairach space has the opposite (right-handed) sense
- \* Mapping between them requires a reflection or “flip”
  - \* Affine transform with a negative determinant



# Spatial Normalisation – Procedure

- \* Start with a 12 DF affine registration
  - \* 3 translations, 3 rotations
  - 3 zooms, 3 shears
  - \* Fits overall shape and size
- \* Refine the registration with non-linear deformations
- \* Algorithm simultaneously minimises
  - \* Mean-squared difference (Gaussian likelihood)
  - \* Squared distance between parameters and their expected values (regularisation with Gaussian prior)

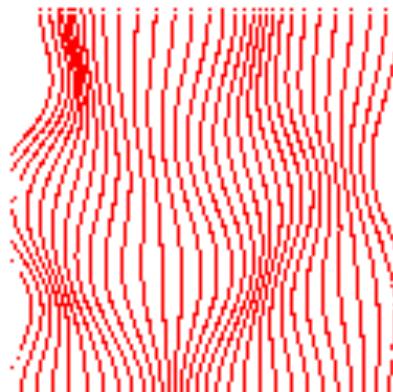


# Spatial Normalisation – Warping

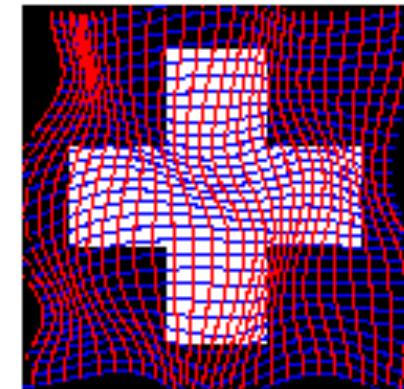
Dark – shift left, Light – shift right



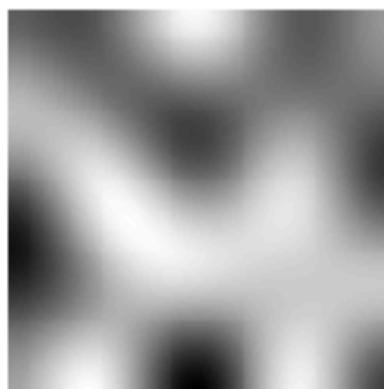
Deformation Field in X



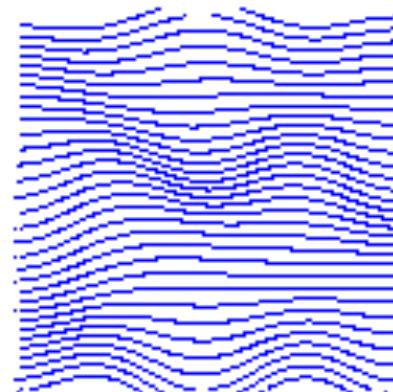
Field Applied To Image



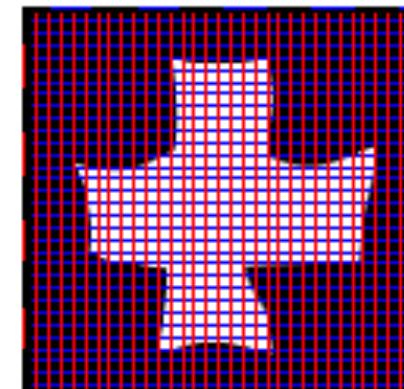
Dark – shift down, Light – shift up



Deformation Field in Y



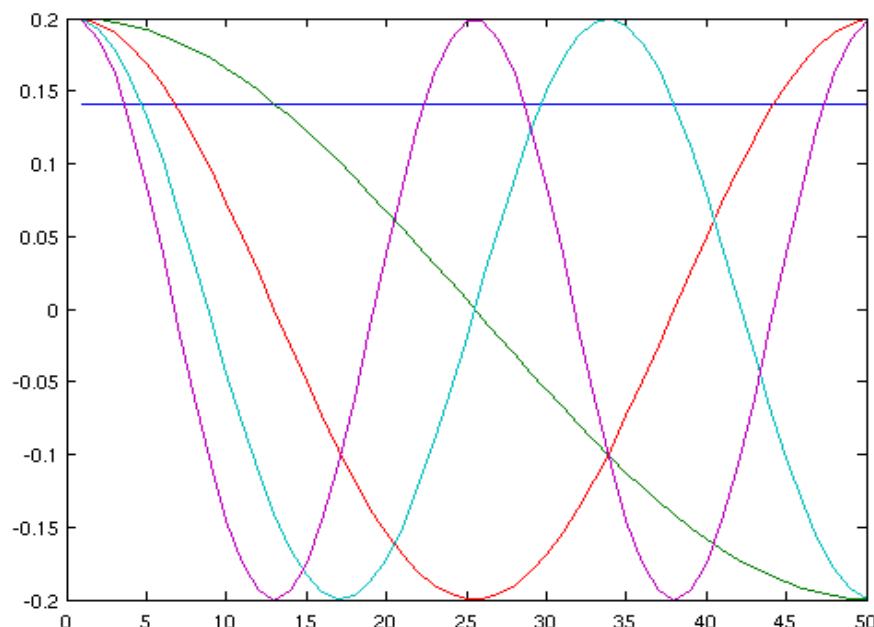
Deformed Image



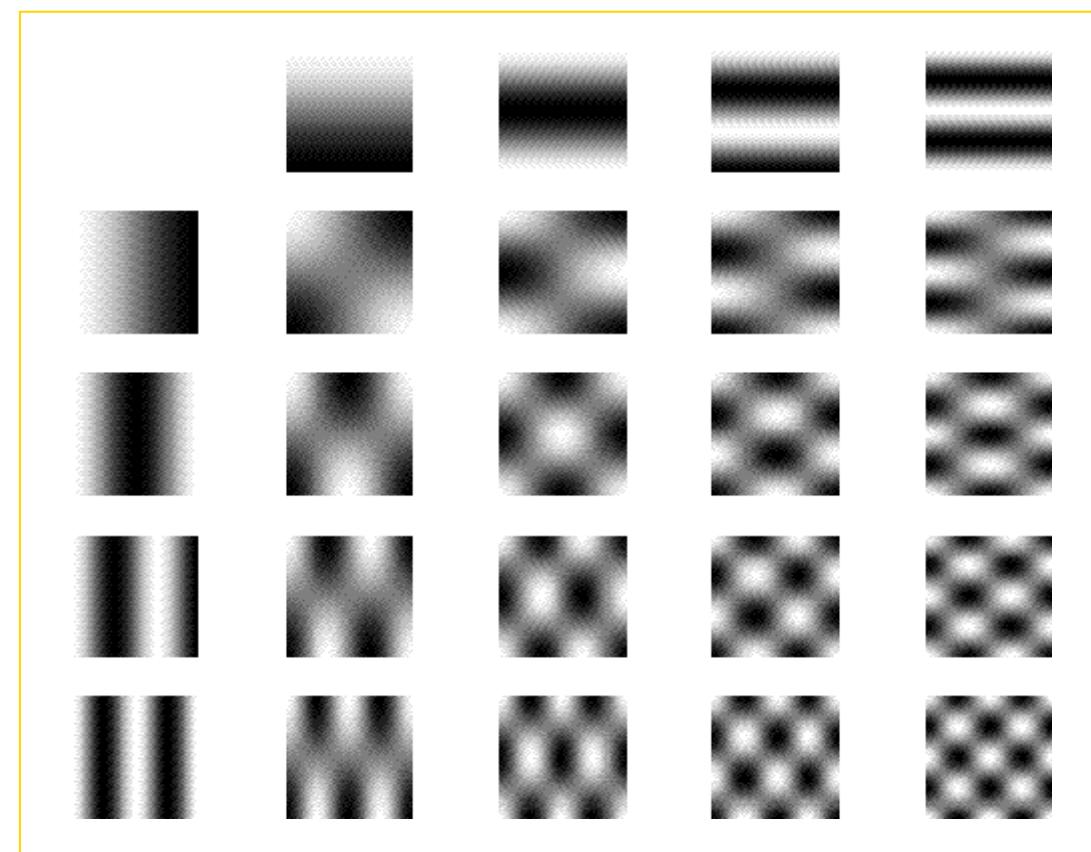
Deformations are modelled with a linear combination of non-linear basis functions

# Spatial Normalisation – DCT basis

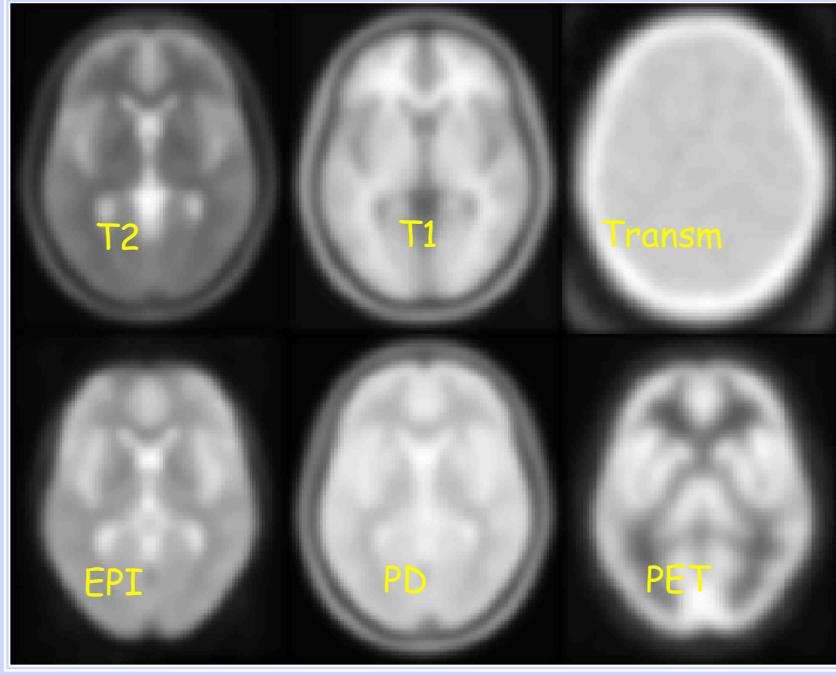
The lowest frequencies of a 3D discrete cosine transform (DCT) provide a smooth basis



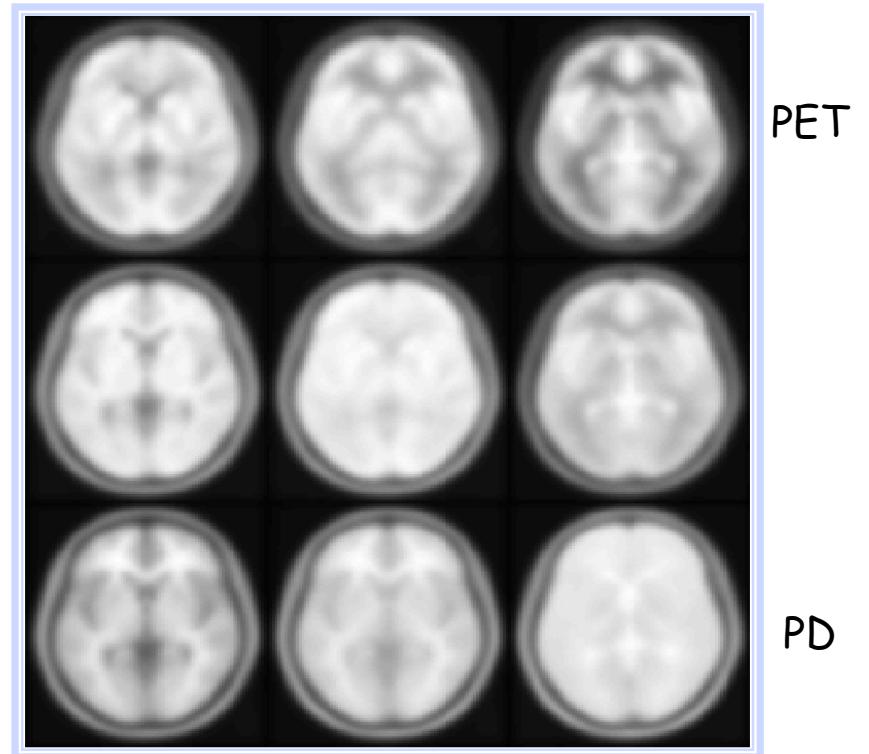
```
plot(spm_dctmtx(50, 5))
```



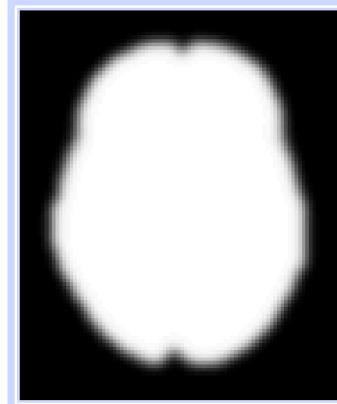
# Spatial Normalisation – Templates and masks



A wider range of contrasts can be registered to a linear combination of template images.

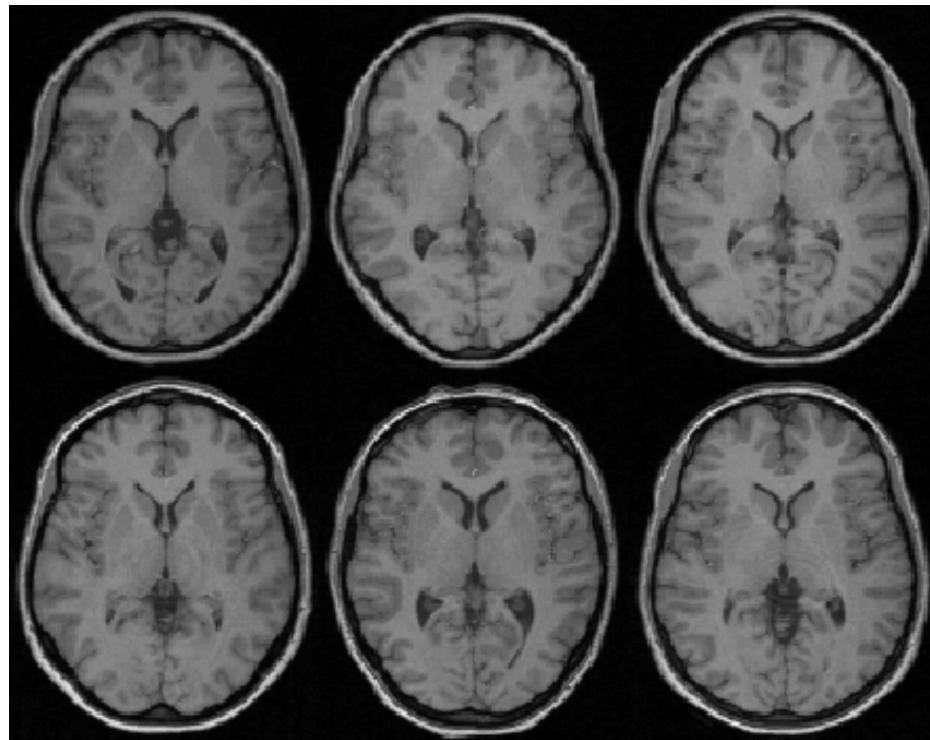


Spatial normalisation can be weighted so that non-brain voxels do not influence the result.

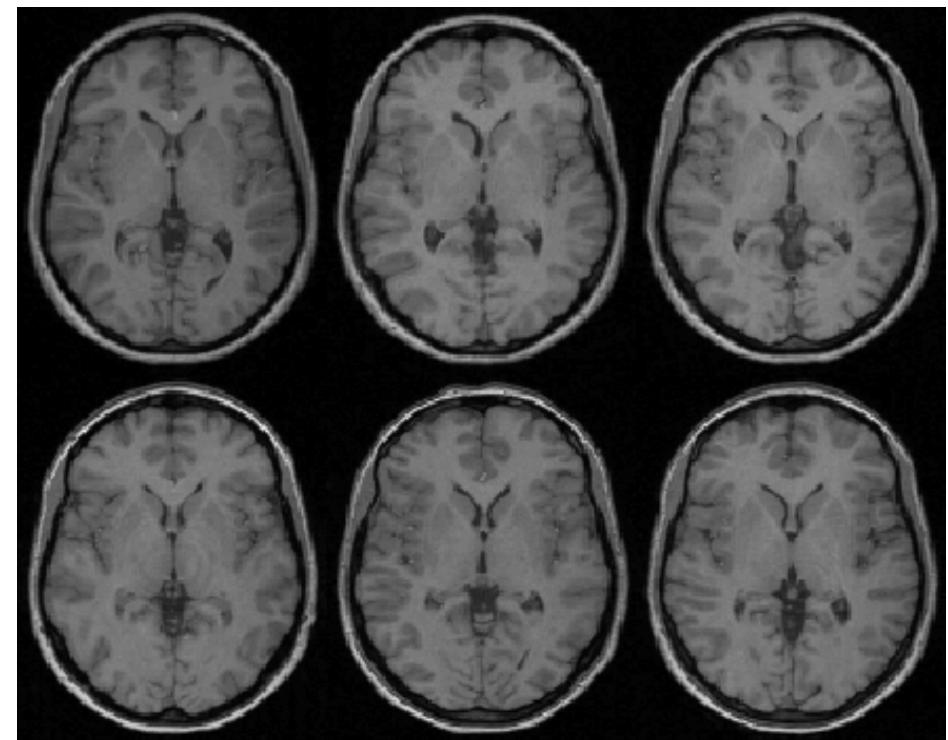


More specific weighting masks can be used to improve normalisation of lesioned brains.

# Spatial Normalisation – Results



Affine registration



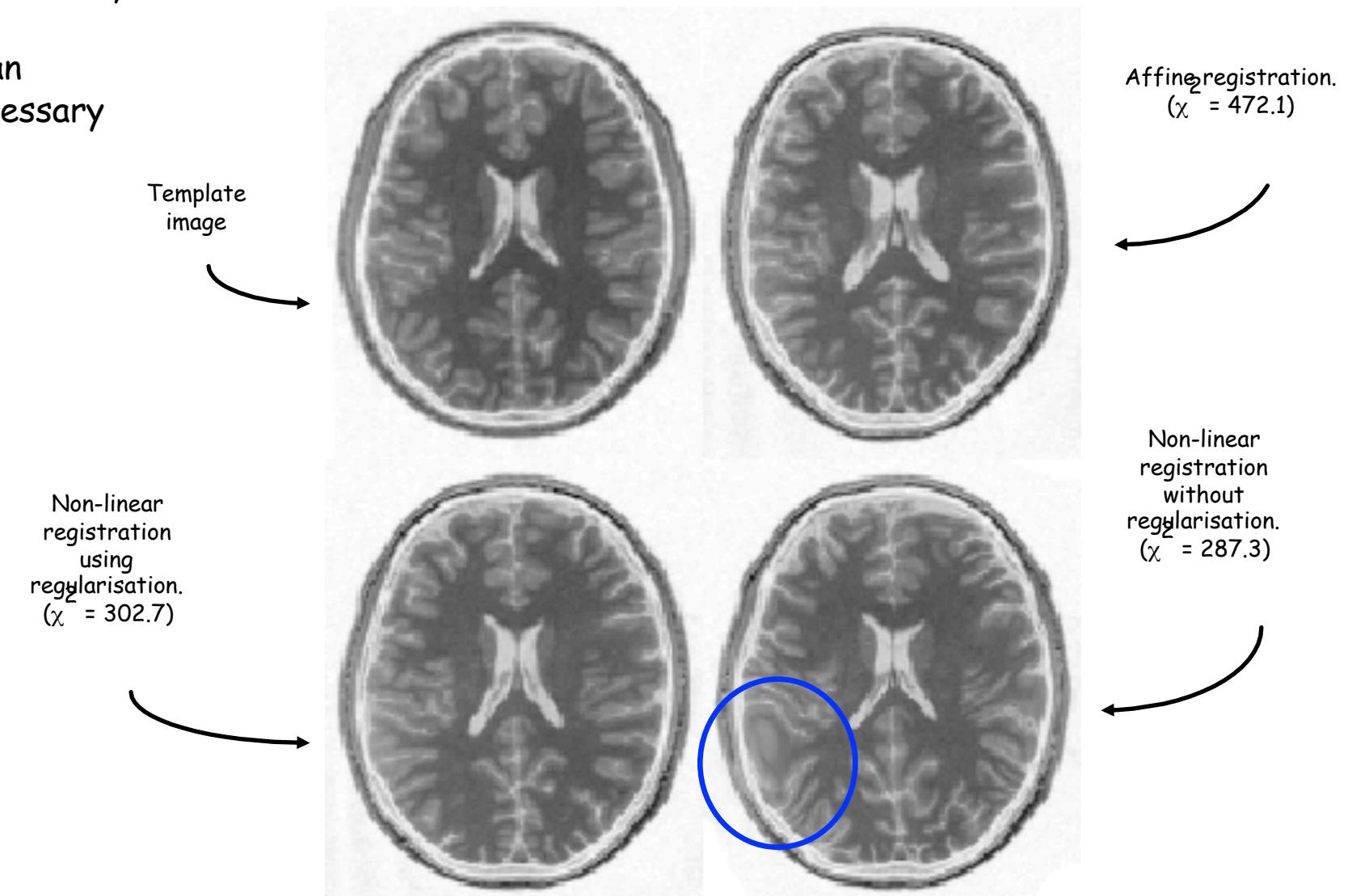
Non-linear registration

# Optimisation – regularisation

- \* The “best” parameters according to the objective function may not be realistic
- \* In addition to similarity, regularisation terms or constraints are often needed to ensure a reasonable solution is found
  - \* Also helps avoid poor local optima
  - \* These can be considered as priors in a Bayesian framework, e.g. converting ML to MAP:
    - \*  $\log(\text{posterior}) = \log(\text{likelihood}) + \log(\text{prior}) + c$

# Spatial Normalisation – Overfitting

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



# Spatial Normalisation – Issues

- \* 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

# Contents

1. Registration basics
2. Motion and realignment
3. Inter-modal coregistration
4. Spatial normalisation
- 5. Unified segmentation**
6. Gaussian smoothing

# Unified segmentation and normalisation

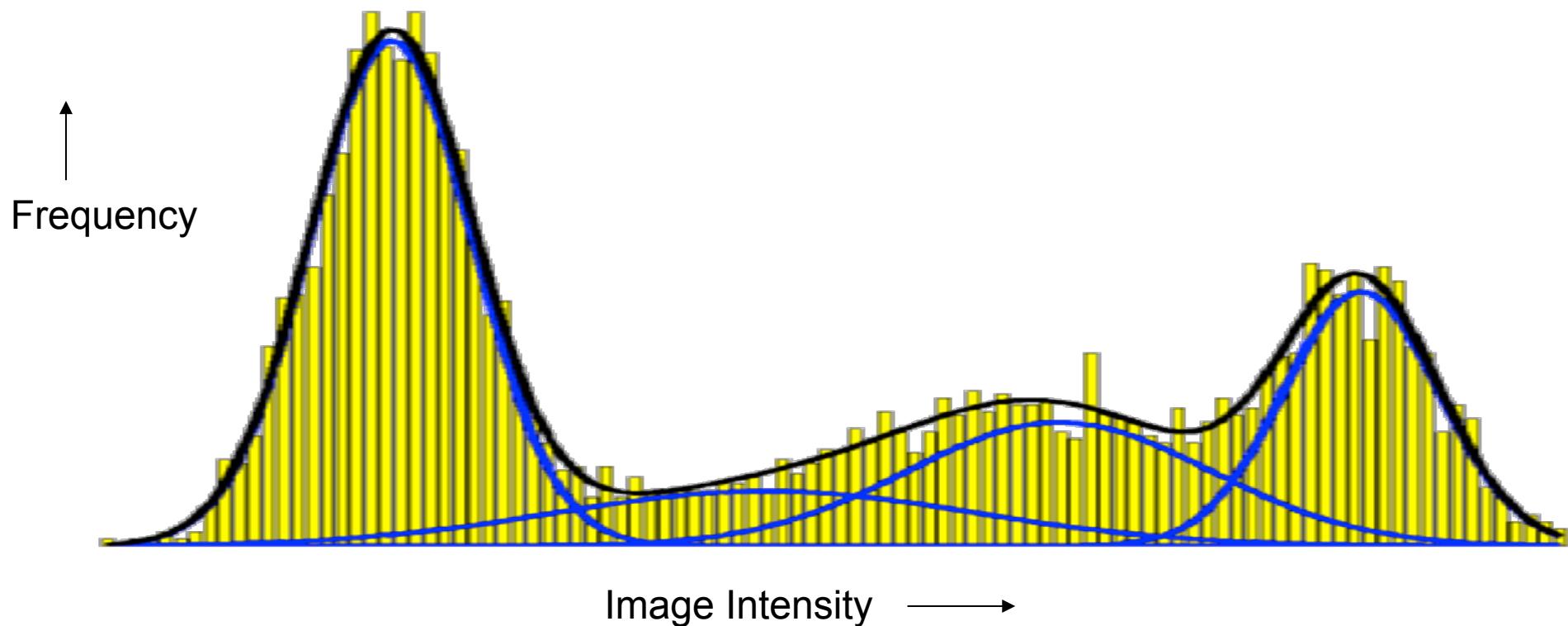
- \* MRI imperfections make normalisation harder
  - \* Noise, artefacts, partial volume effect
  - \* Intensity inhomogeneity or “bias” field
  - \* Differences between sequences
- \* Normalising segmented tissue maps should be more robust and precise than using the original images ...
- \* ... Tissue segmentation benefits from spatially-aligned prior tissue probability maps (from other segmentations)
- \* This circularity motivates simultaneous segmentation and normalisation in a unified model

# Summary of the unified model

- \* SPM8 implements a **generative model**
  - \* Principled Bayesian probabilistic formulation
- \* Gaussian mixture model segmentation with deformable tissue probability maps (priors)
  - \* The inverse of the transformation that aligns the TPMs can be used to normalise the original image
- \* Bias correction is included within the model

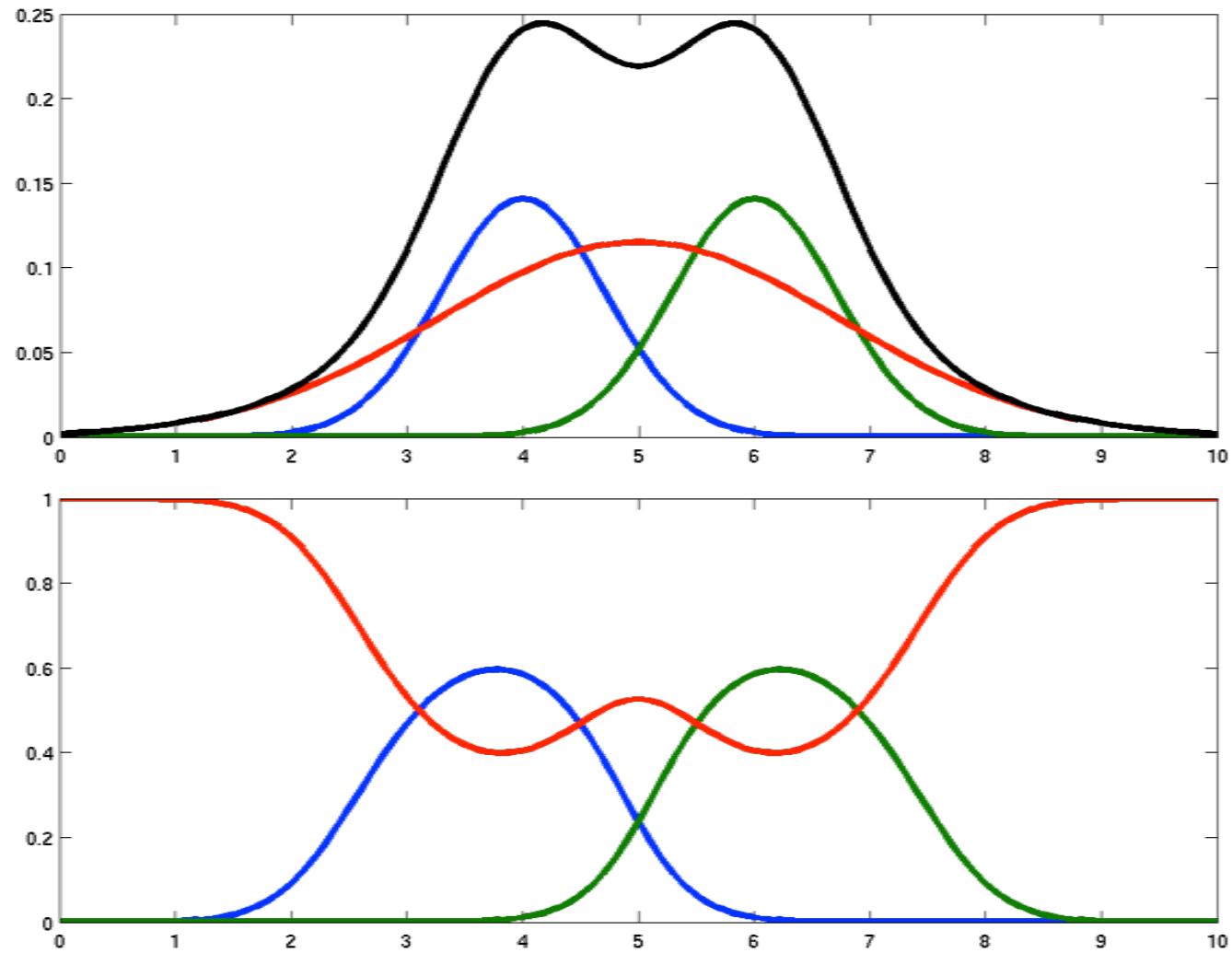
# Mixture of Gaussians (MOG)

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

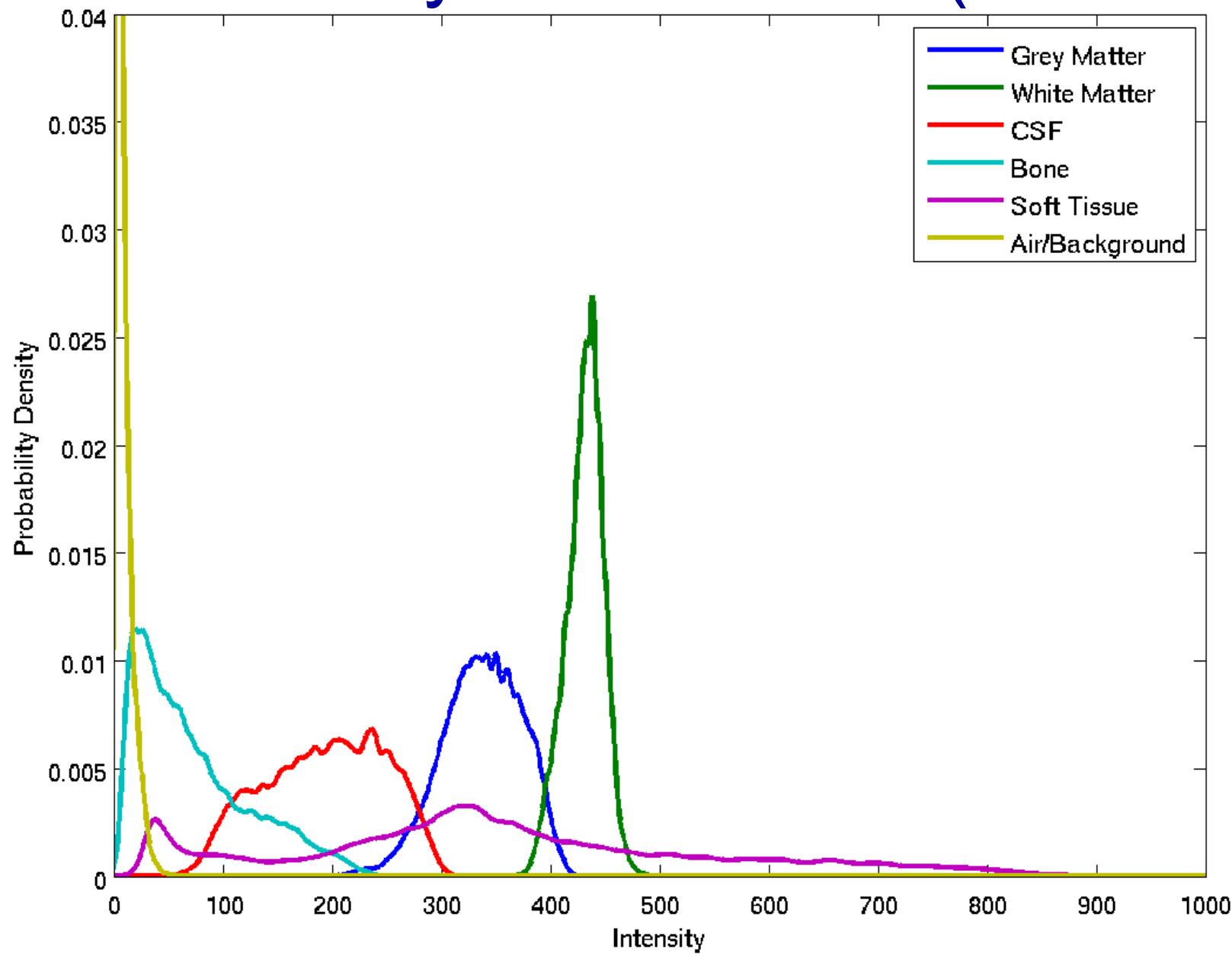


# Belonging Probabilities

Belonging probabilities are assigned by normalising to one.

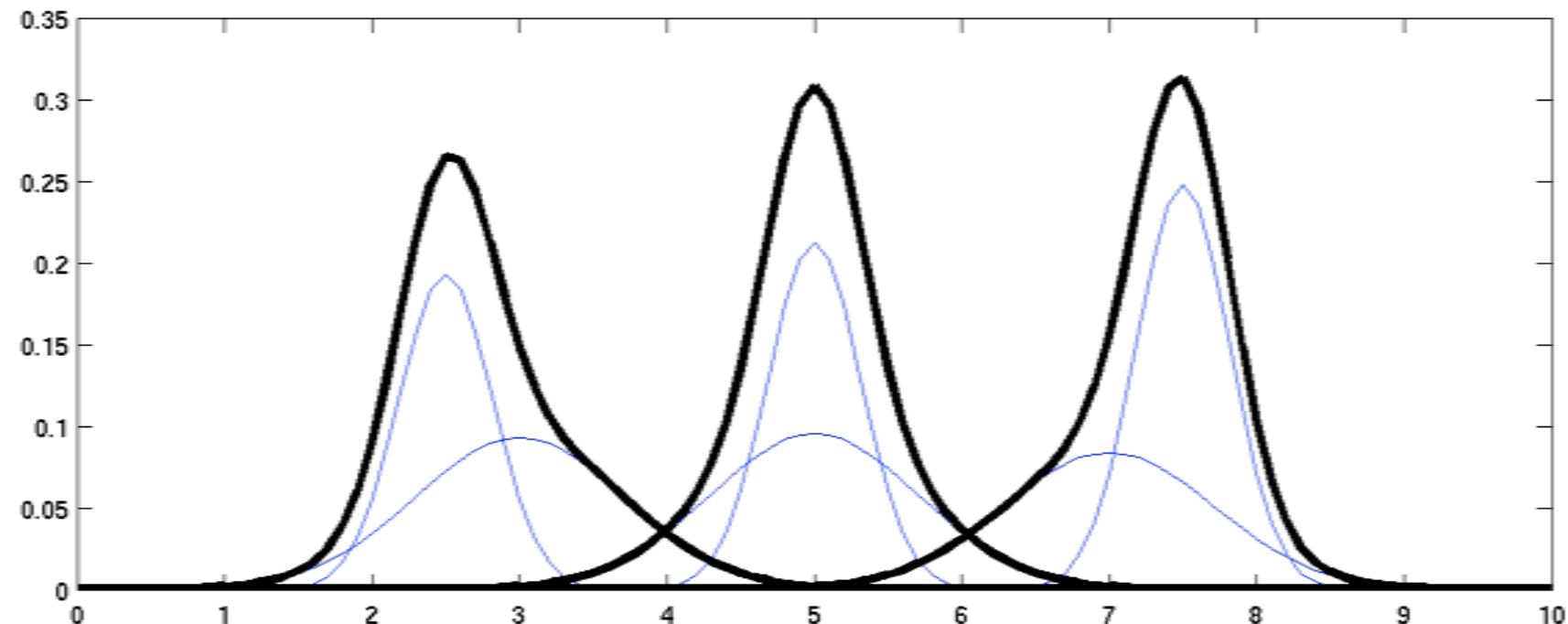


# Tissue intensity distributions (T1-w MRI)



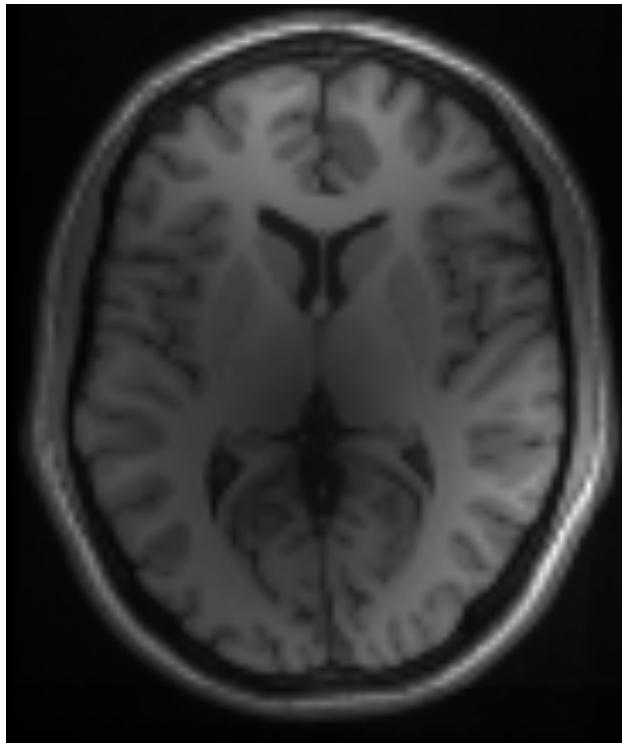
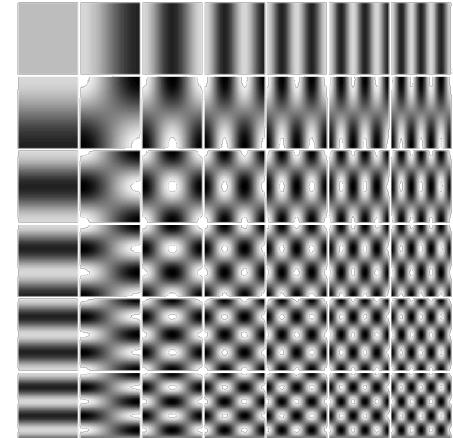
# Non-Gaussian Intensity Distributions

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

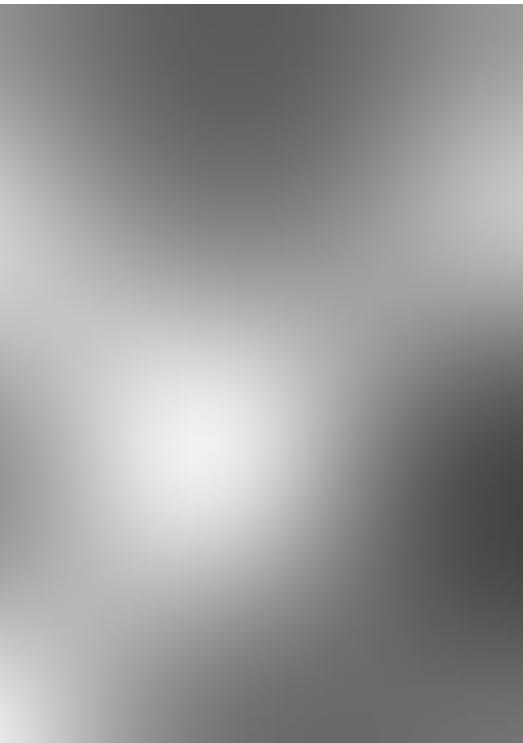


# Modelling inhomogeneity

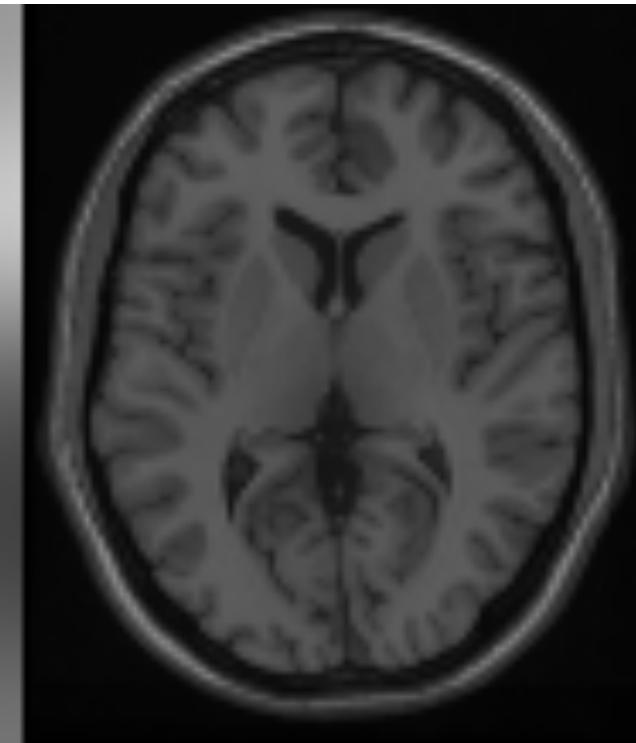
- \* A multiplicative bias field is modelled as a linear combination of basis functions.



Corrupted image



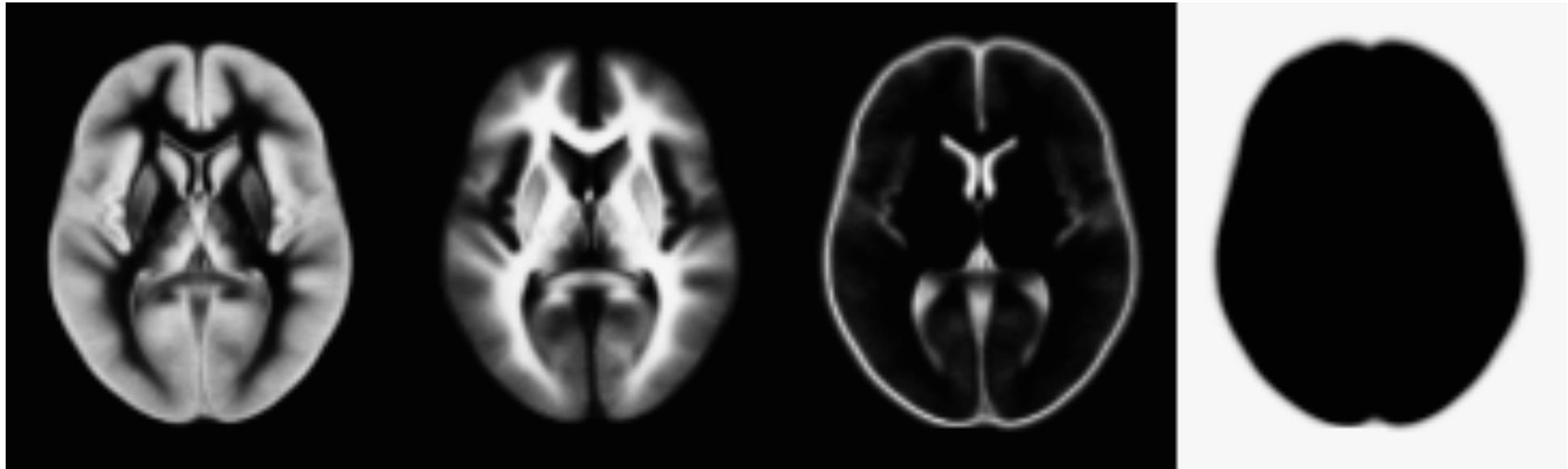
Bias Field



Corrected image

# Tissue Probability Maps

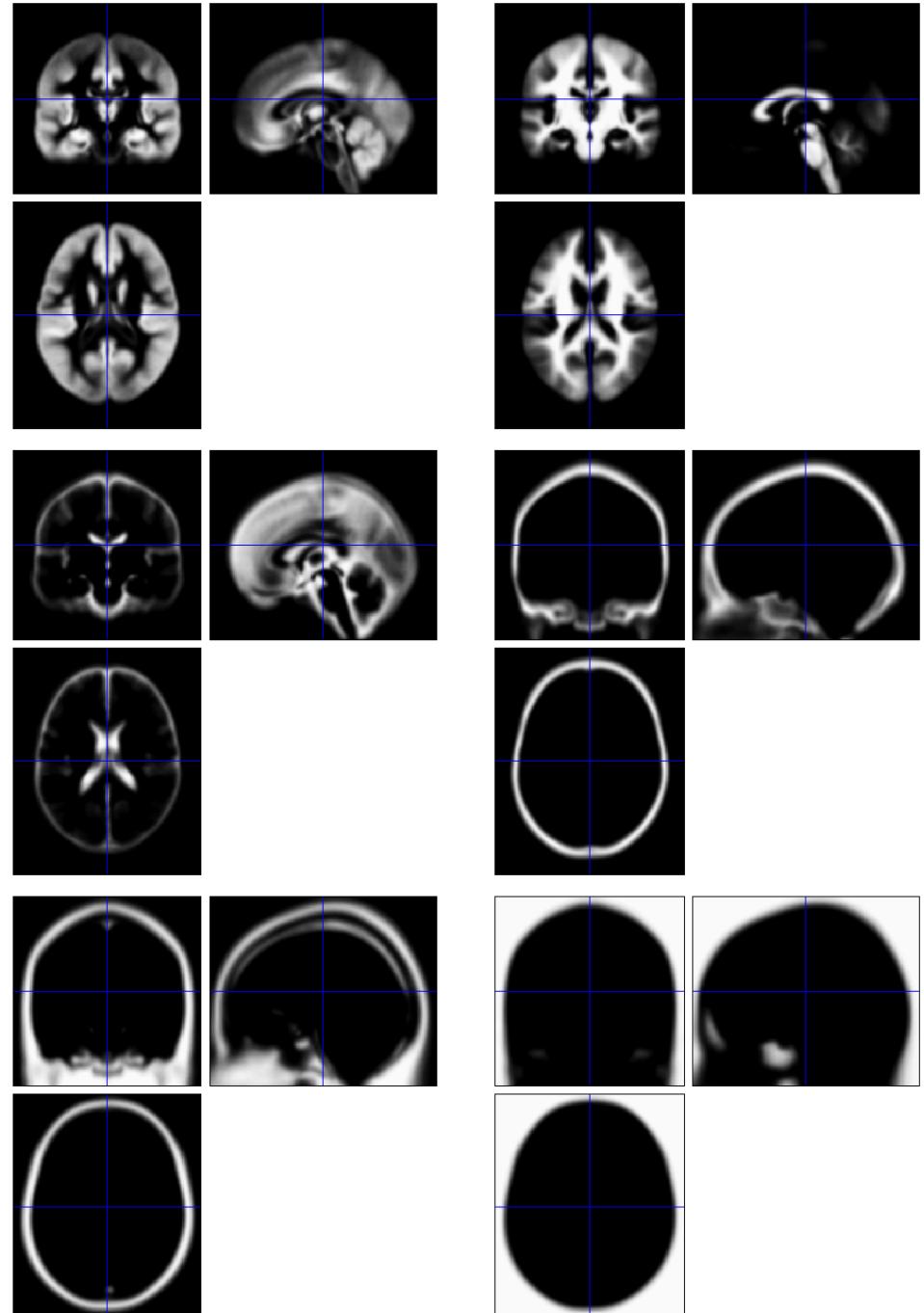
- \* Tissue probability maps (TPMs) are used as the prior, instead of the proportion of voxels in each class

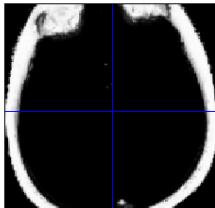
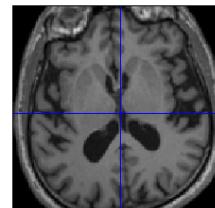
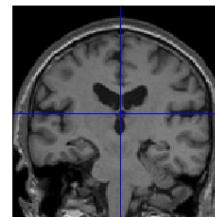
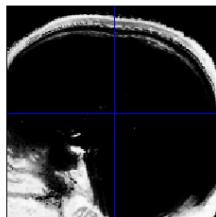
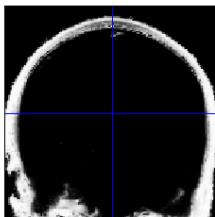
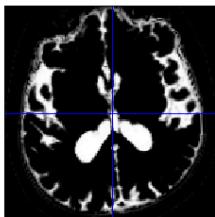
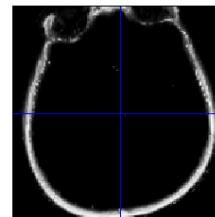
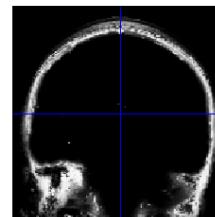
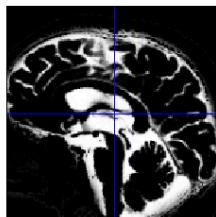
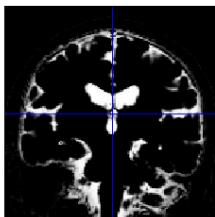
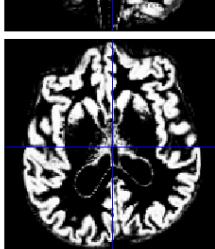
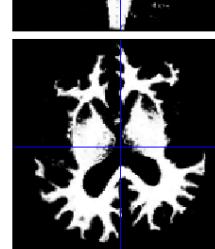
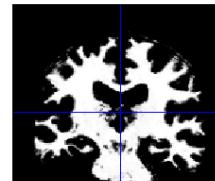
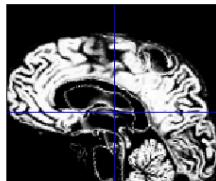
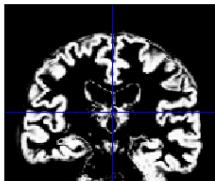
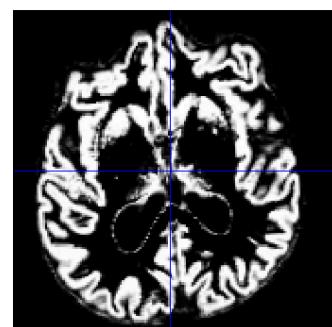
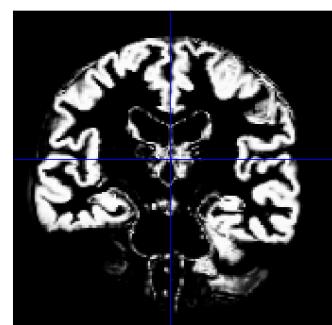
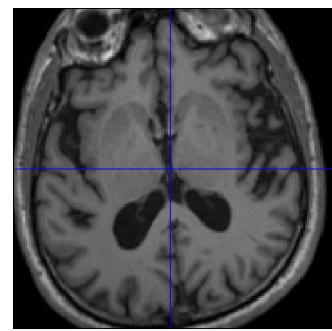
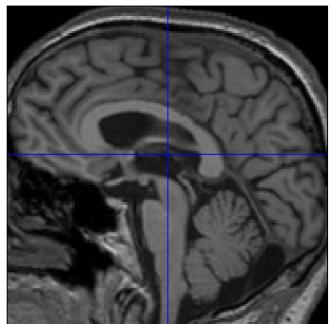
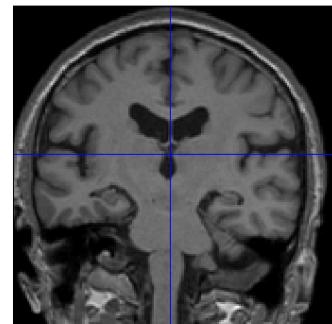


**ICBM Tissue Probabilistic Atlases.** These tissue probability maps are kindly provided by the International Consortium for Brain Mapping, John C. Mazziotta and Arthur W. Toga.

# Tissue Probability Maps for “New Segment”

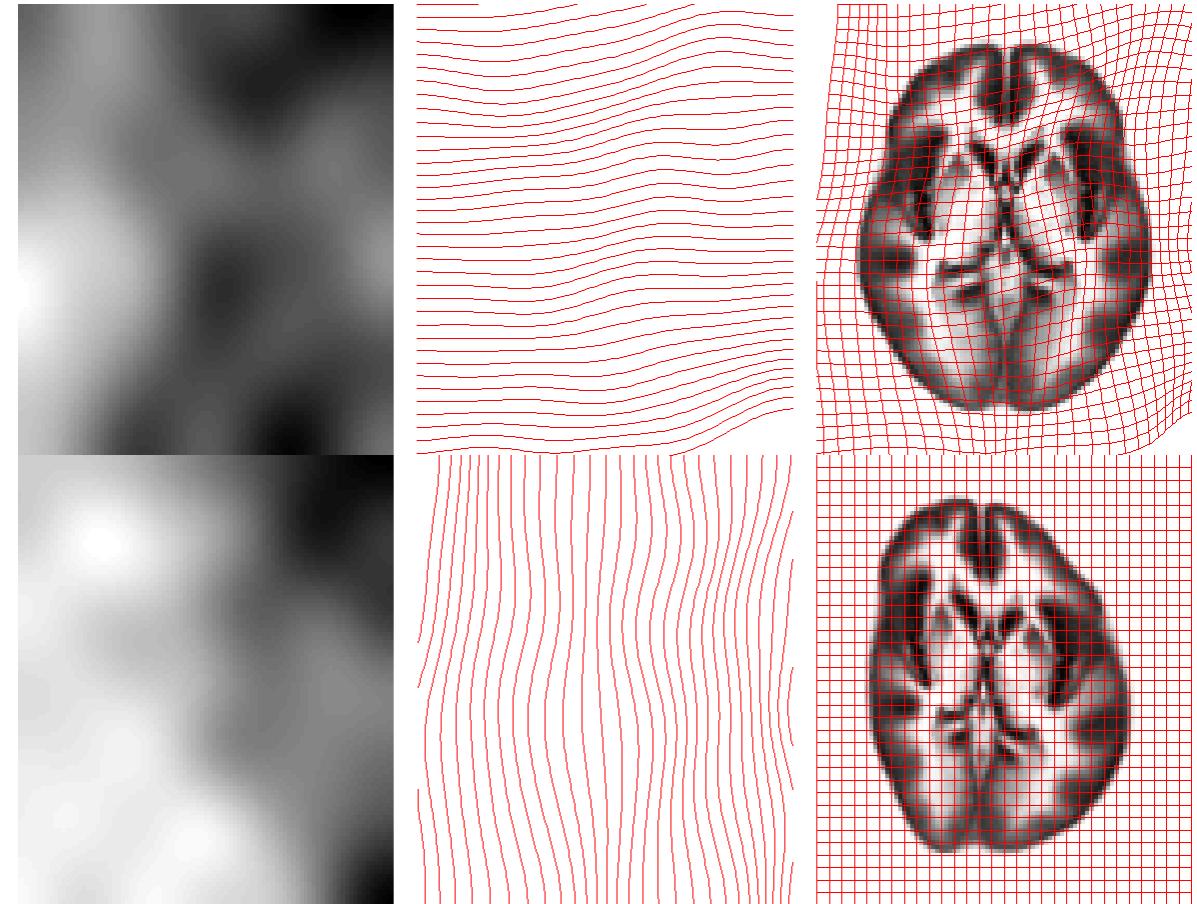
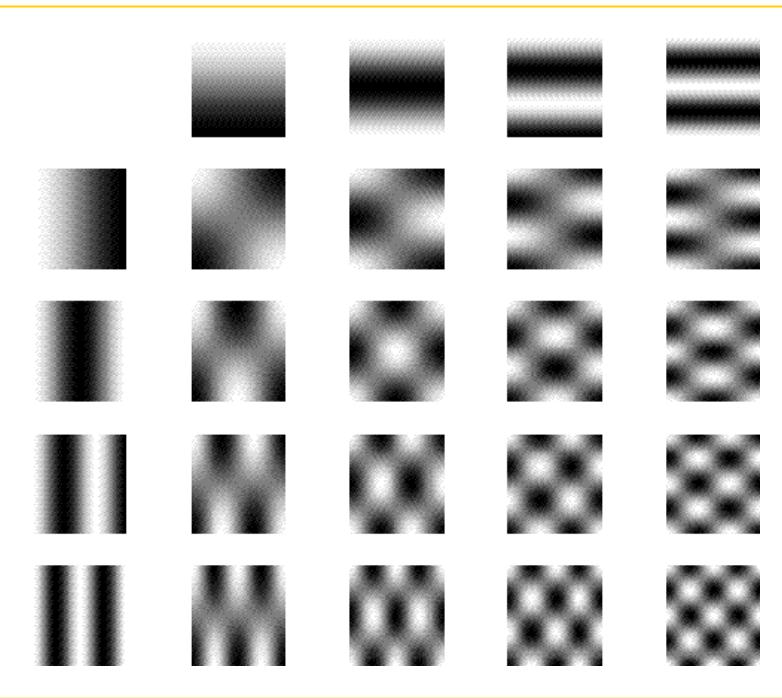
Includes additional non-brain tissue  
classes (bone, and soft tissue)





# Deforming the Tissue Probability Maps

- \* Tissue probability images are warped to match the subject
- \* The inverse transform warps to the TPMs

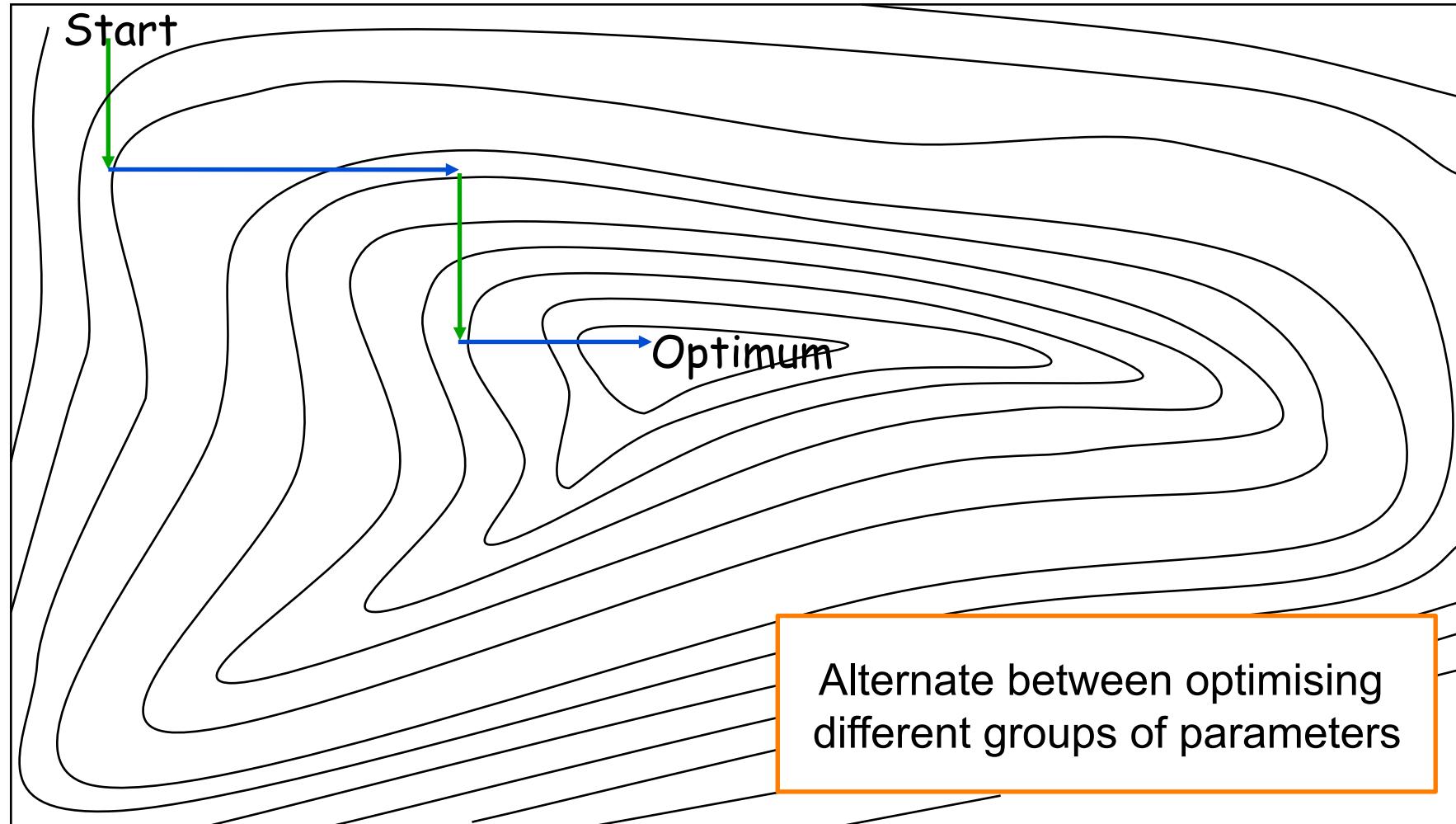


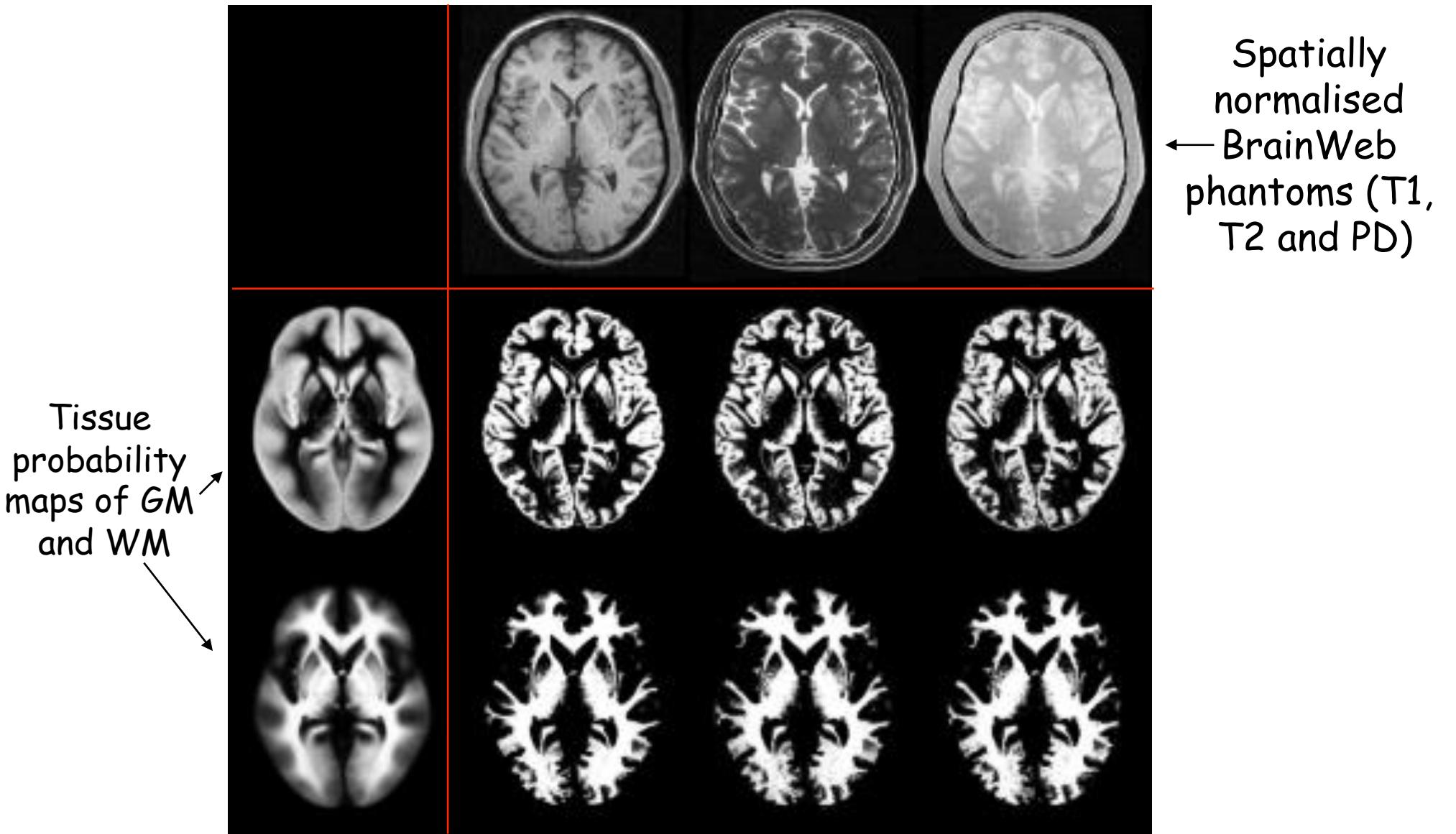
# Fitting the unified model

- \* Model fitting involves optimising an objective function as with respect to its parameters
- \* Begin with starting estimates, and repeatedly change them so that the objective function decreases each time
- \* The unified model has one overall objective function
- \* Sets of parameters are repeatedly optimised in turn

$$E = -\sum_{i=1}^I \log \left[ p_i(\beta) \sum_{k=1}^K \frac{\gamma_k b_{ik}(\alpha)}{\sum_{j=1}^K \gamma_j b_{ij}(\alpha)} \frac{1}{\sqrt{2\pi\sigma_k^2}} \exp \left( -\frac{(o_i(\beta)y_i - \mu_k)^2}{2\sigma_k^2} \right) \right]$$

# Steepest Descent



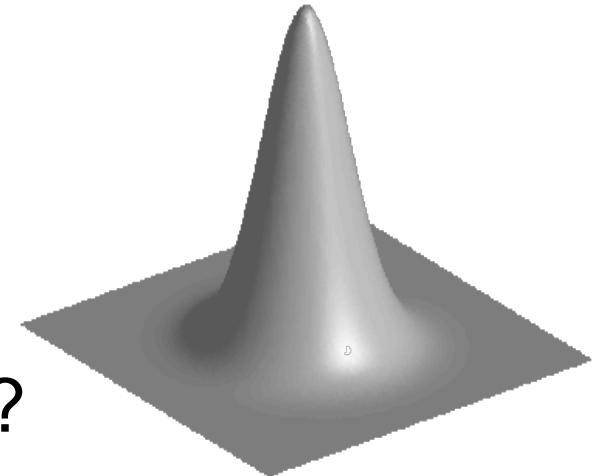


Cocosco, Kollokian, Kwan & Evans. "BrainWeb: Online Interface to a 3D MRI Simulated Brain Database". NeuroImage 5(4):S425 (1997)

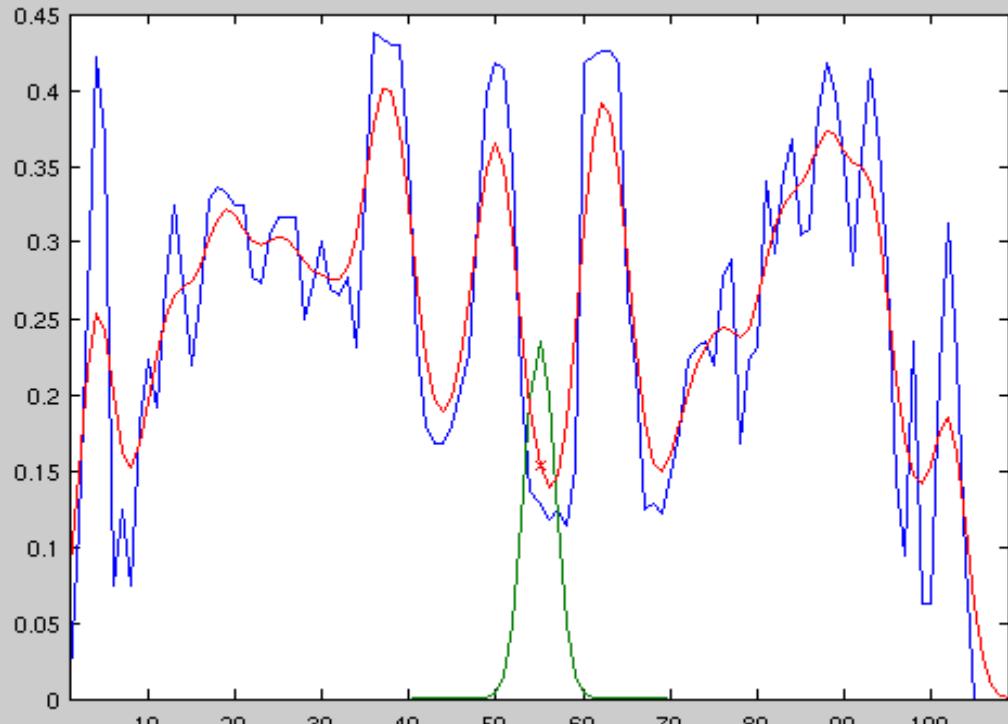
# Contents

1. Registration basics
2. Motion and realignment
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4. Spatial normalisation
5. Unified segmentation
6. **Gaussian smoothing**

# Smoothing



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

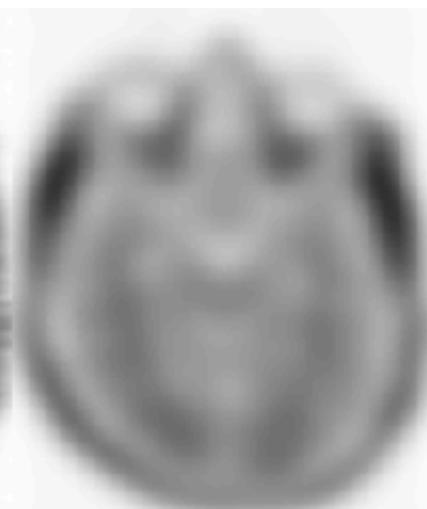
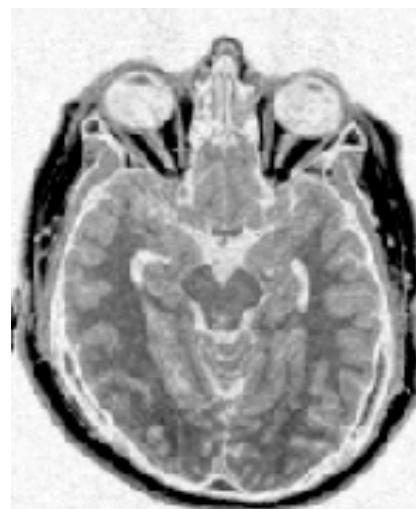
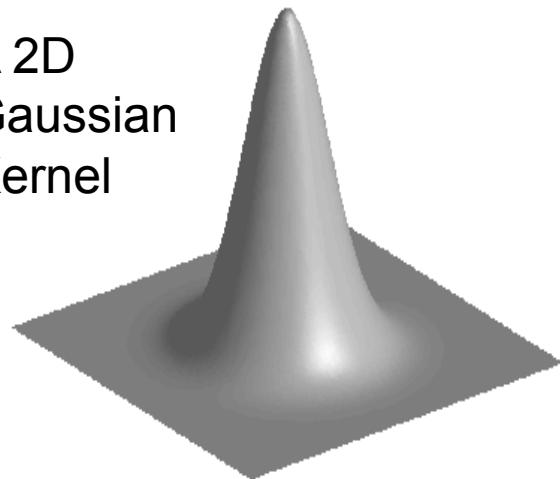


## Example of Gaussian smoothing in one-dimension

The Gaussian kernel is **separable** we can smooth 2D data with two 1D convolutions.

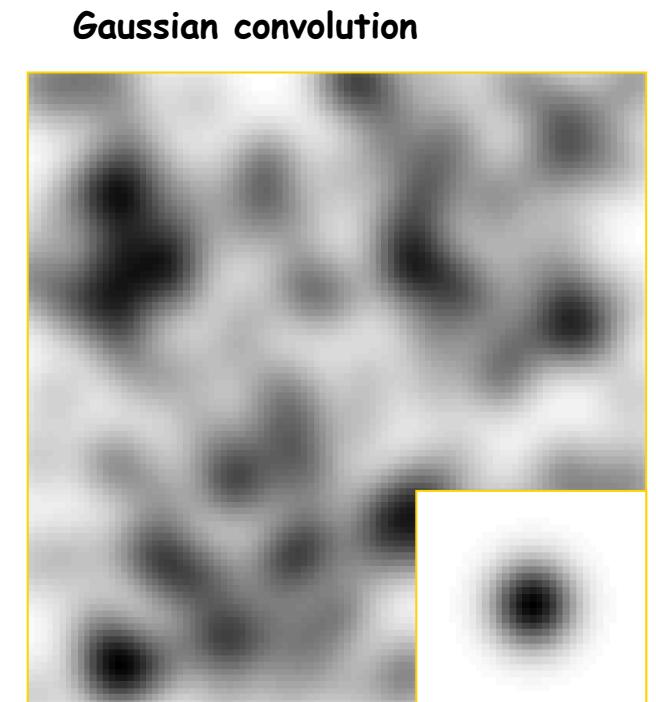
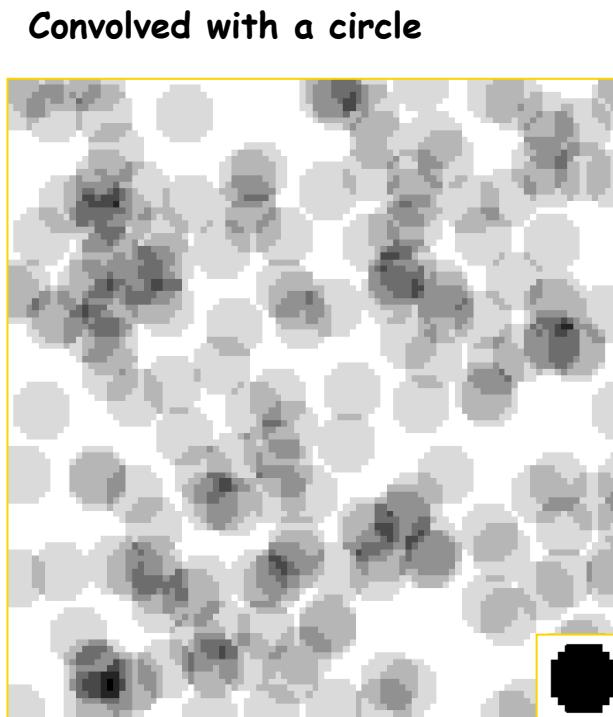
Generalisation to 3D is simple and efficient

A 2D Gaussian Kernel



# Smoothing – a link to ROI analysis

Each voxel after smoothing effectively represents a weighted average over its local region of interest (ROI)

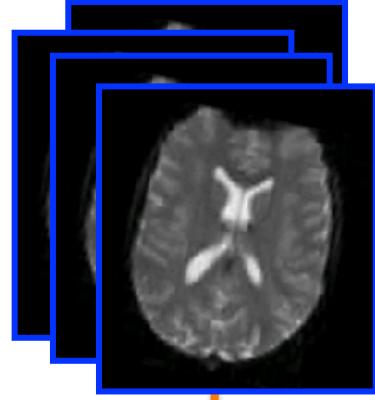


# References

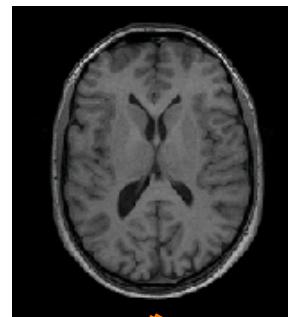
- \* Friston et al. *Spatial registration and normalisation of images.* Human Brain Mapping 3:165-189 (1995).
- \* Collignon et al. *Automated multi-modality image registration based on information theory.* IPMI'95 pp 263-274 (1995).
- \* Ashburner et al. *Incorporating prior knowledge into image registration.* NeuroImage 6:344-352 (1997).
- \* Ashburner & Friston. *Nonlinear spatial normalisation using basis functions.* Human Brain Mapping 7:254-266 (1999).
- \* Thévenaz et al. *Interpolation revisited.* IEEE Trans. Med. Imaging 19:739-758 (2000).
- \* Andersson et al. *Modeling geometric deformations in EPI time series.* NeuroImage 13:903-919 (2001).
- \* Ashburner & Friston. *Unified Segmentation.* NeuroImage 26:839-851 (2005).
- \* Ashburner. *A Fast Diffeomorphic Image Registration Algorithm.* NeuroImage 38:95-113 (2007).

# Preprocessing overview

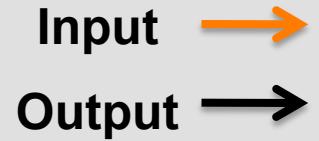
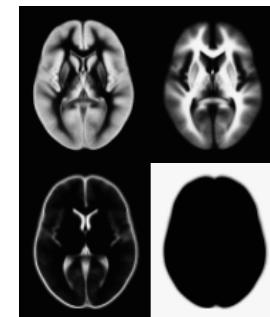
Func. time-series



Anatomical MRI

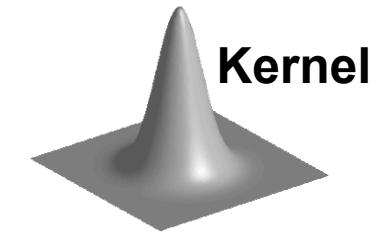


TPMs

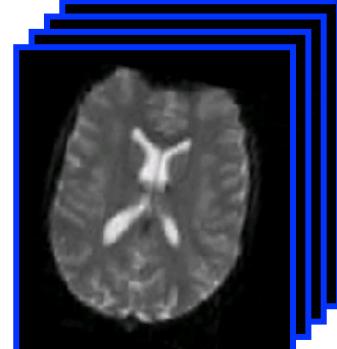


Segmentation

Transformation  
(seg\_sn.mat)



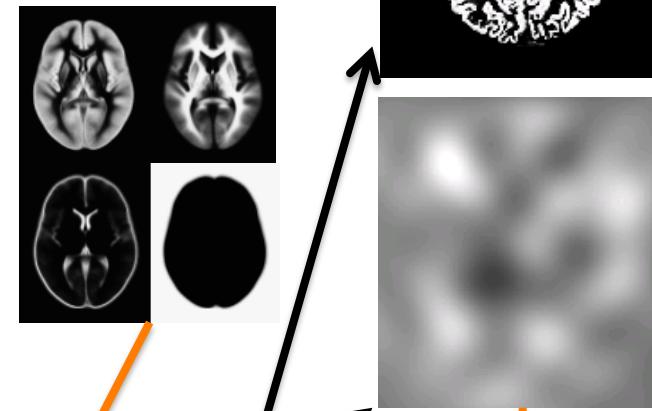
REALIGN



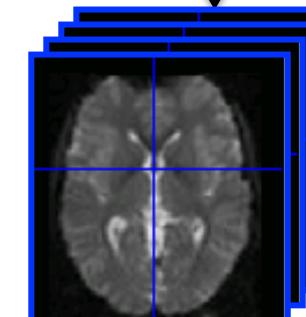
COREG



SEGMENT



NORM  
WRITE



Motion corrected

Mean  
functional

(Headers  
changed)

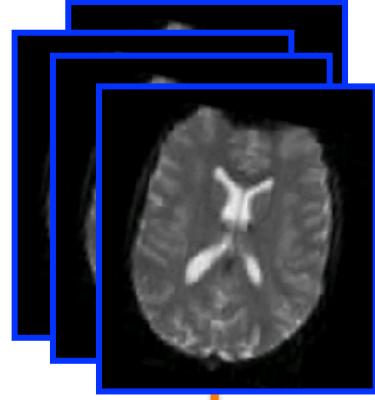
ANALYSIS

$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

MNI Space

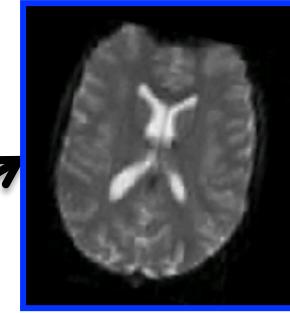
# Preprocessing (func. only)

Func. time-series

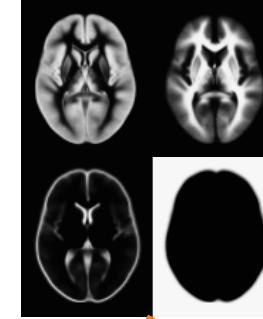


REALIGN

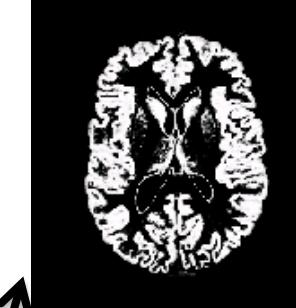
Mean  
functional



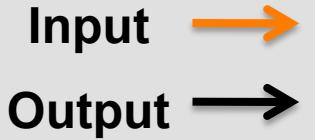
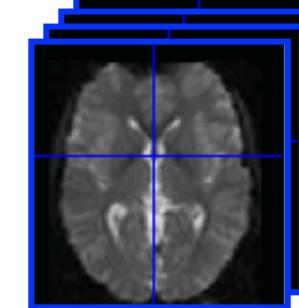
TPMs



SEGMENT

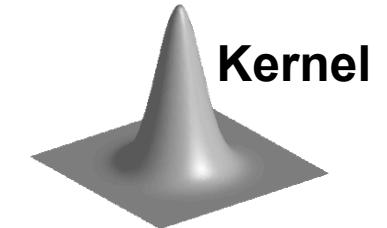


NORM  
WRITE

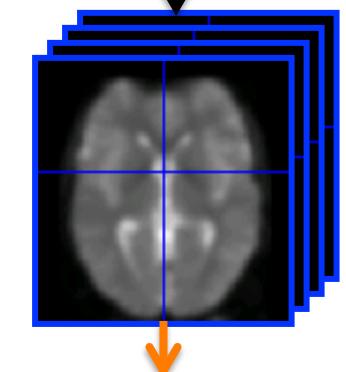


Segmentation

Transformation  
(seg\_sn.mat)



SMOOTH



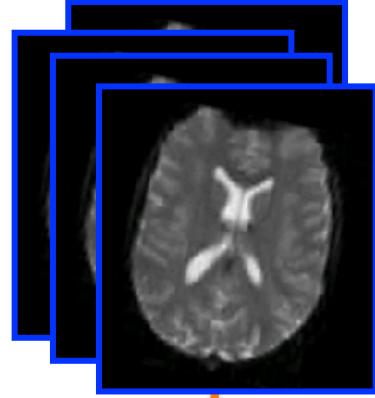
Motion corrected

MNI Space

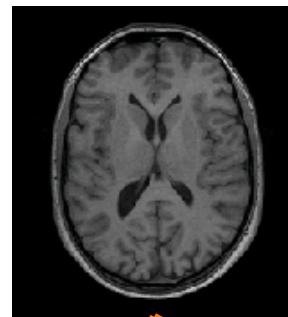
ANALYSIS

# Preprocessing overview

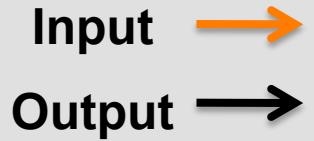
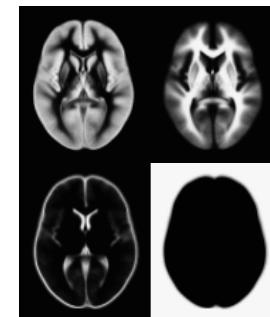
Func. time-series



Anatomical MRI

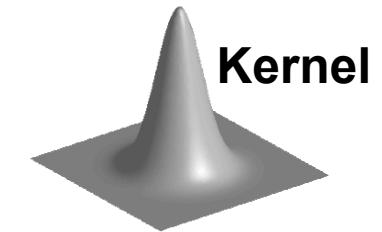


TPMs

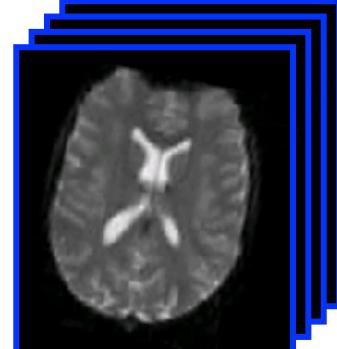


Segmentation

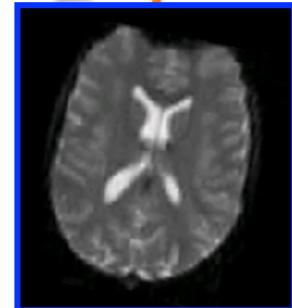
Transformation  
(seg\_sn.mat)



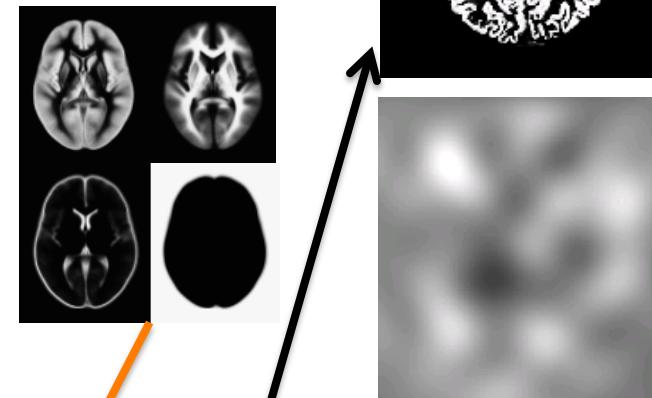
REALIGN



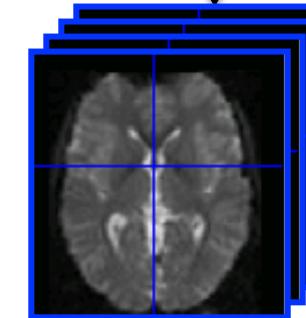
COREG



SEGMENT



NORM  
WRITE



Motion corrected

Mean  
functional

(Headers  
changed)

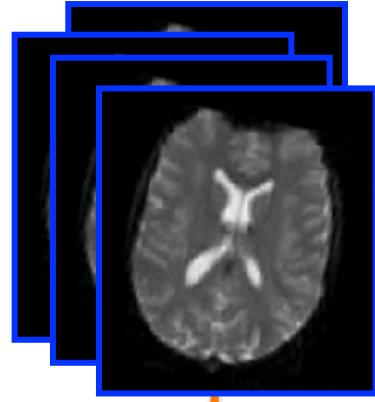
ANALYSIS

$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

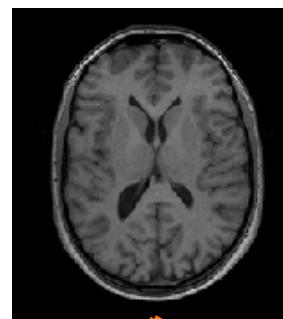
MNI Space

# Preprocessing with Dartel

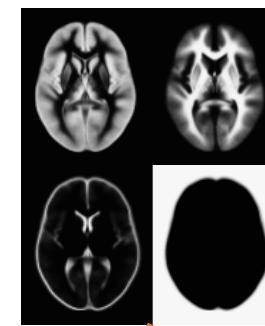
Func. time-series



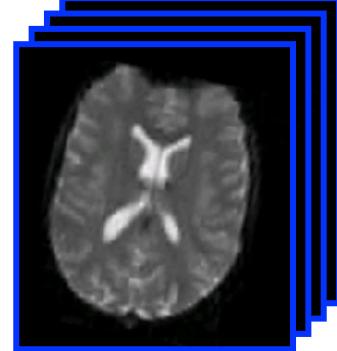
Anatomical MRI



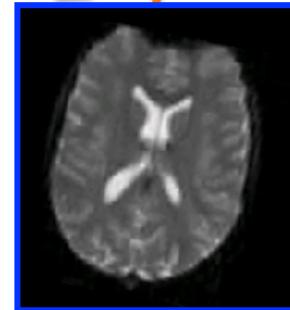
TPMs



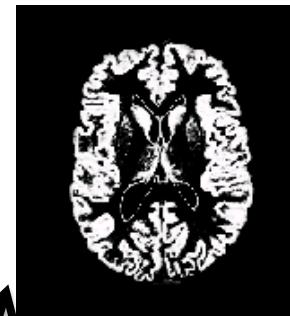
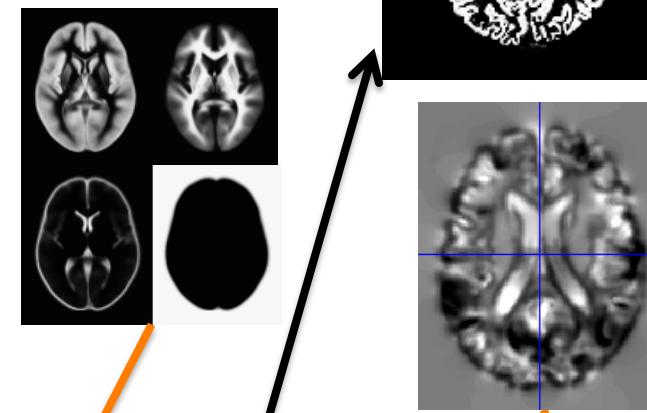
REALIGN



COREG

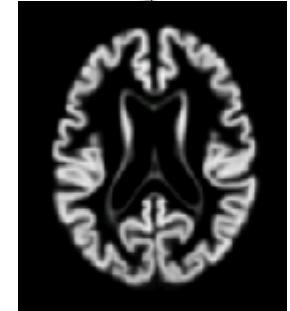


SEGMENT



DARTEL  
CREATE  
TEMPLATE

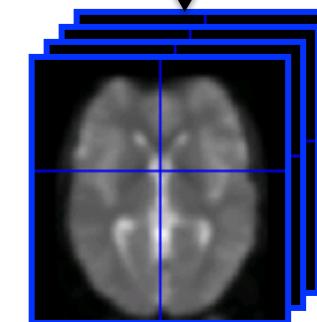
DARTEL  
NORM 2 MNI  
& SMOOTH



Motion corrected

Mean  
functional

(Headers  
changed)



ANALYSIS

$$\begin{pmatrix} m_{11} & m_{12} & m_{13} & m_{14} \\ m_{21} & m_{22} & m_{23} & m_{24} \\ m_{31} & m_{32} & m_{33} & m_{34} \\ 0 & 0 & 0 & 1 \end{pmatrix}$$