

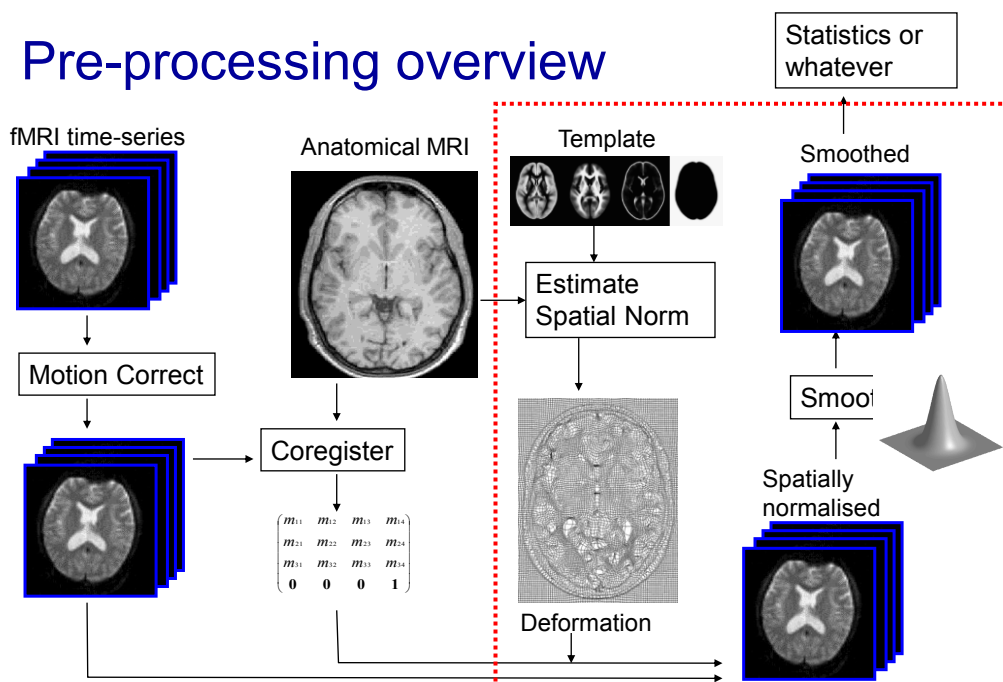


# Preprocessing II: Between Subjects

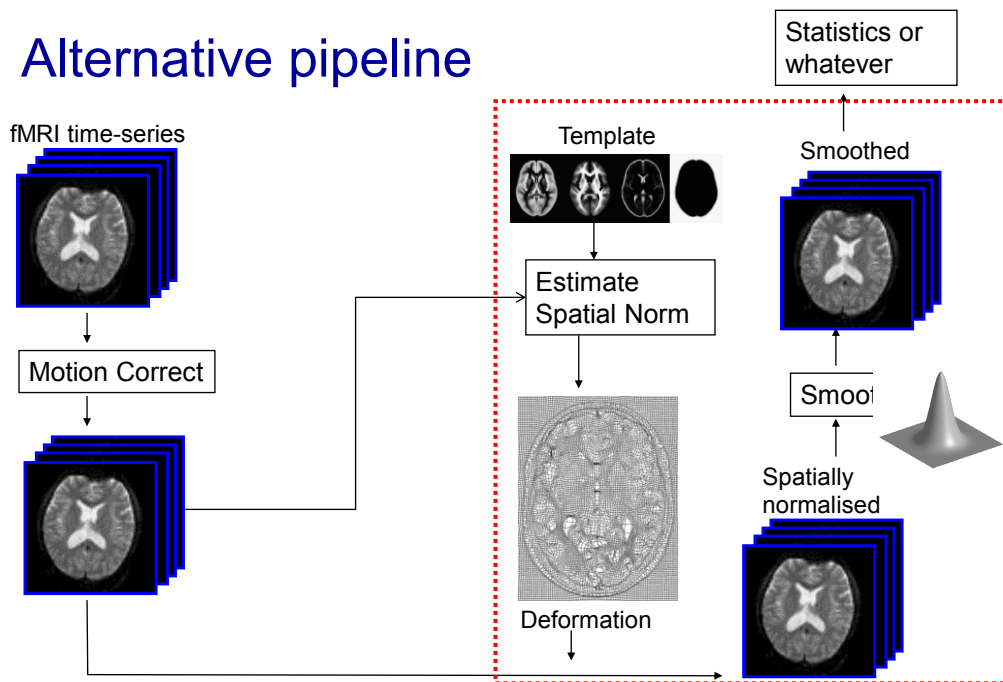
John Ashburner

Wellcome Trust Centre for Neuroimaging,  
12 Queen Square, London, UK.

## Pre-processing overview



## Alternative pipeline



## Contents

### \* Normalise/Segment

Use segmentation routine for spatial normalisation

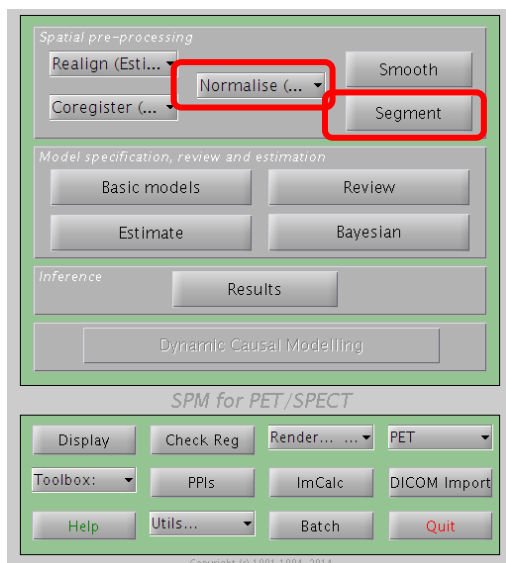
- \* Gaussian mixture model
- \* Intensity non-uniformity correction
- \* Deformed tissue probability maps
- \* Dartel
- \* Smoothing

## Spatial normalisation

- \* Brains of different subjects vary in shape and size.
- \* Need to bring them all into a common anatomical space.
  - \* Examine homologous regions across subjects
    - \* Improve anatomical specificity
    - \* Improve sensitivity
  - \* Report findings in a common anatomical space (eg MNI space)
- \* In SPM, alignment is achieved by matching grey matter with grey matter and white matter with white matter.
  - \* Need to segment.

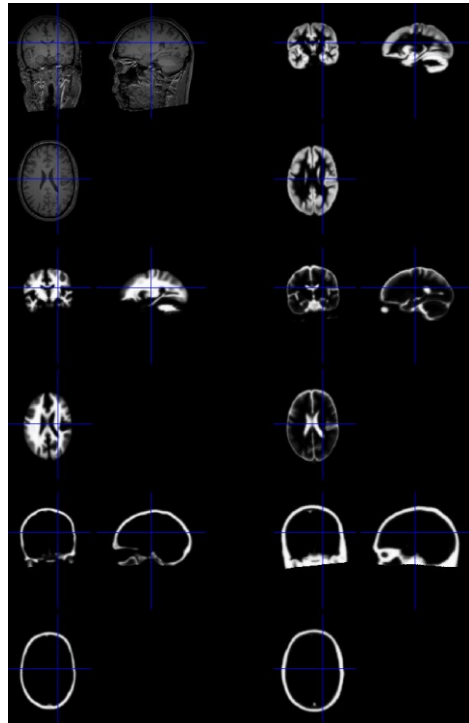
## Normalise/Segment

- \* This is the same algorithm as for tissue segmentation.
- \* Combines:
  - \* Mixture of Gaussians (MOG)
  - \* Bias Correction Component
  - \* Warping (Non-linear Registration) Component



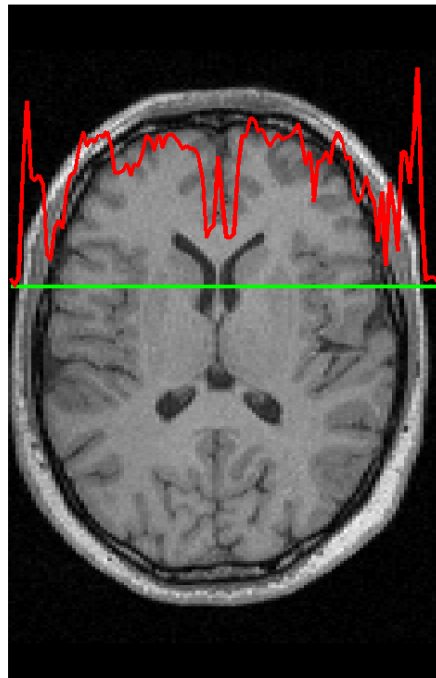
## Spatial normalisation

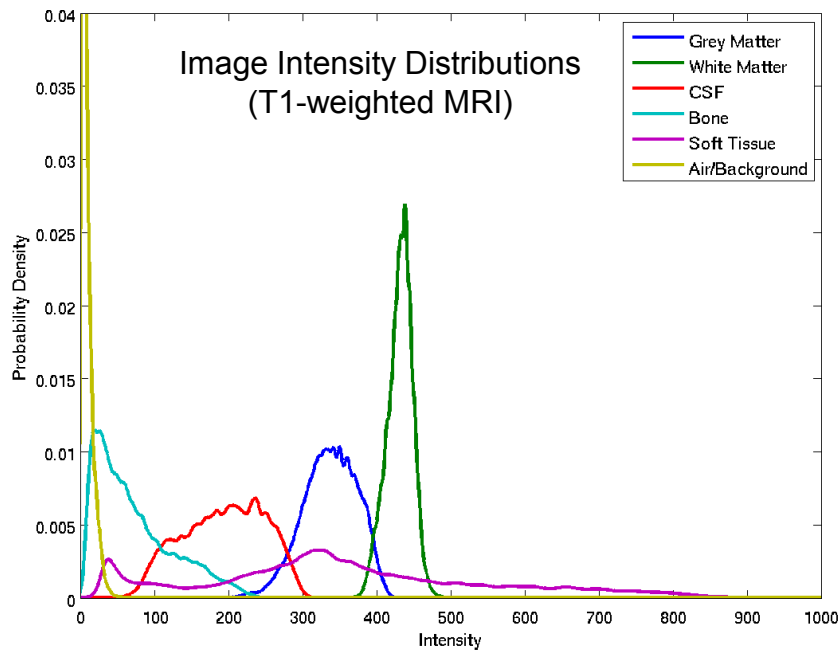
- \* Default spatial normalisation in SPM12 estimates nonlinear warps that match tissue probability maps to the individual image.
- \* Spatial normalisation achieved using the inverse of this transform.



## Segmentation

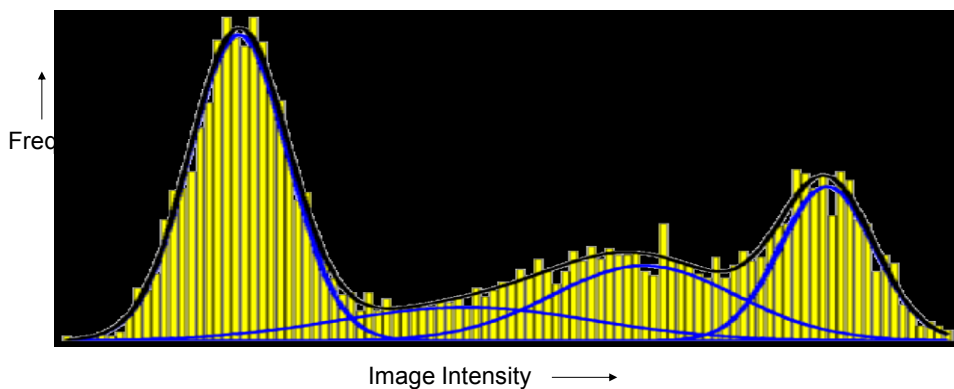
- \* Segmentation in SPM12 also estimates a spatial transformation that can be used for spatially normalising images.
- \* It uses a **generative model**, which involves:
  - \* Mixture of Gaussians (MOG)
  - \* Warping (Non-linear Registration) Component
  - \* Bias Correction Component



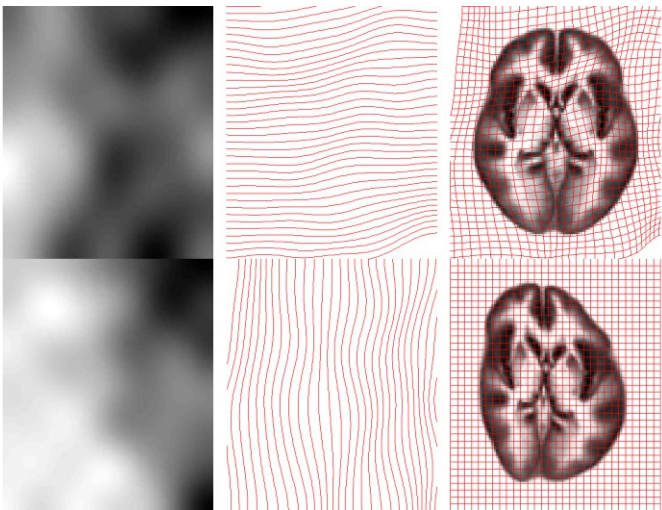


## Modelling tissue intensities

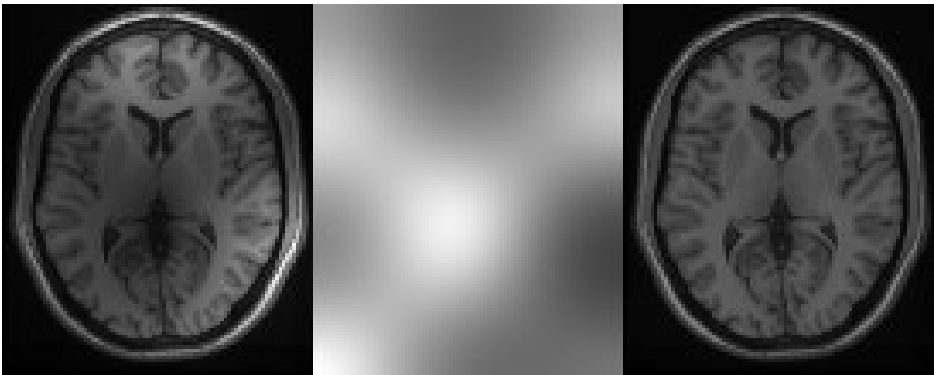
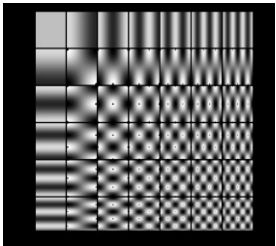
- \* Classification is based on a **Mixture of Gaussians** model (MOG), which represents the intensity probability density by a number of Gaussian distributions.



# Modelling deformations



# Modelling a bias field

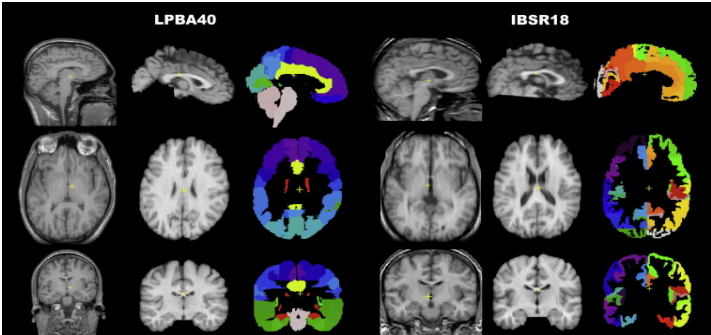
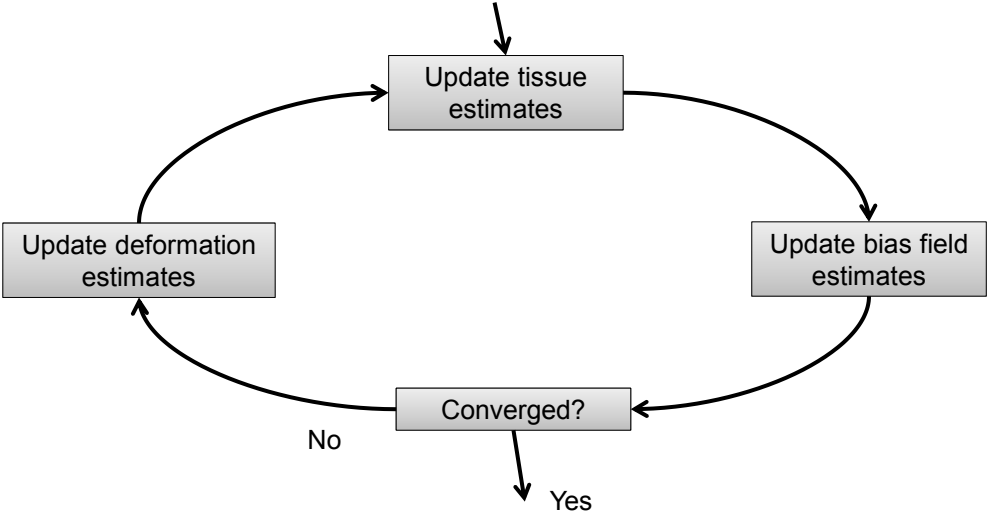


Corrupted image

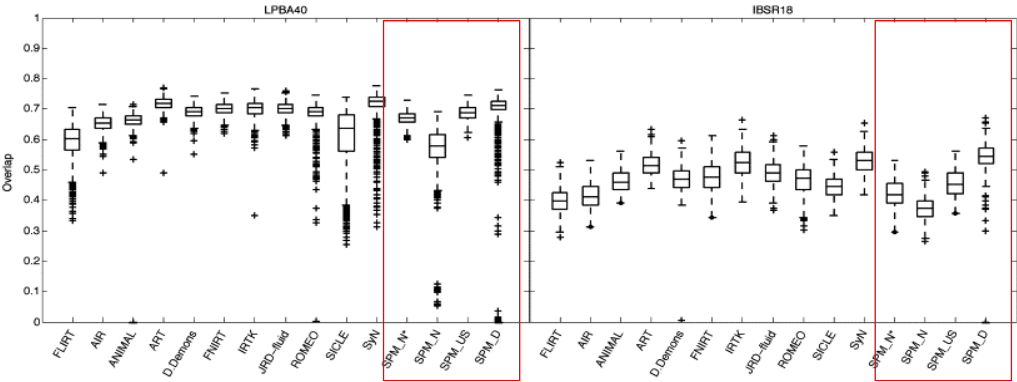
Bias Field

Corrected image

# Iterative optimisation scheme

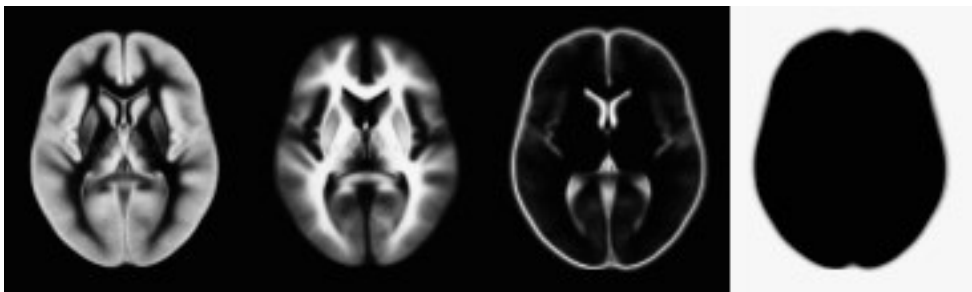


Evaluations of nonlinear registration algorithms



# Old tissue probability maps

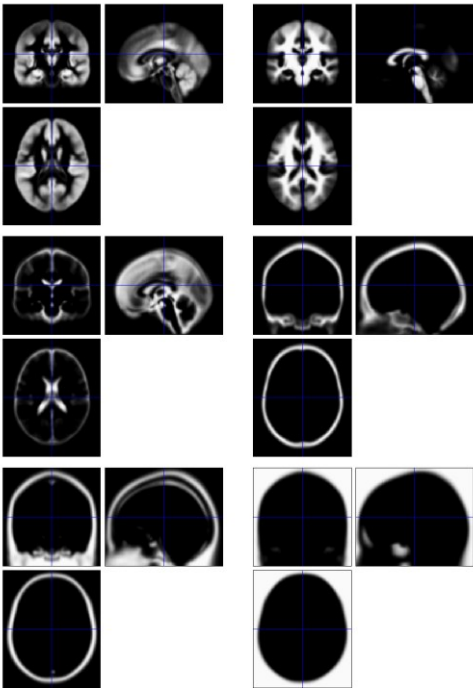
- \* Tissue probability maps (TPMs) are used instead of the proportion of voxels in each Gaussian as the prior.



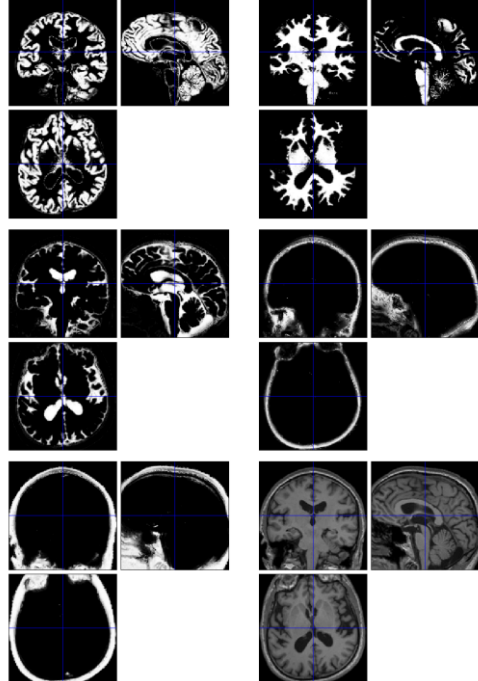
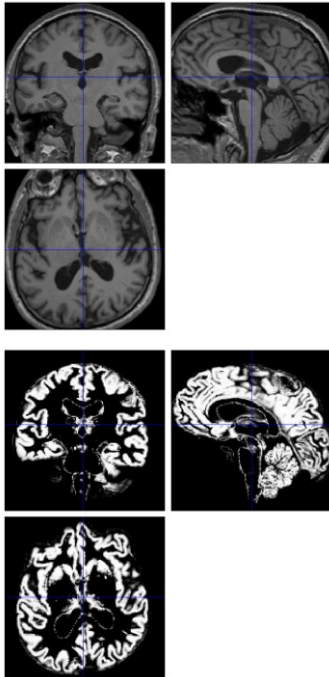
**ICBM Tissue Probabilistic Atlases.** These tissue probability maps are kindly provided by the **International Consortium for Brain Mapping**, John C. Mazziotta and Arthur W. Toga.

## Tissue probability maps in SPM12

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







## Contents

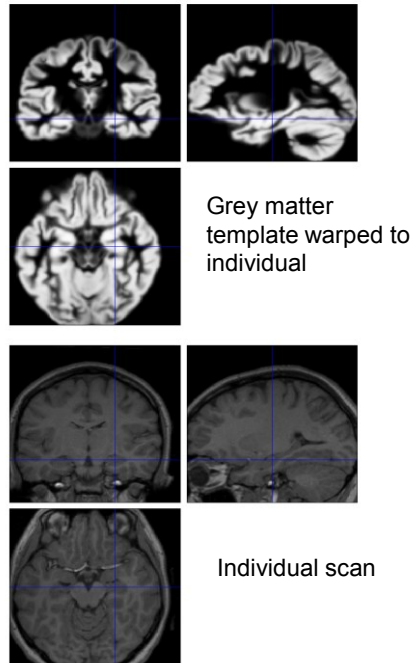
- \* Normalise/Segment

## \* Dartel

- \* Velocity field parameterisation
- \* Objective function
- \* Template creation
- \* Examples
- \* Smooth

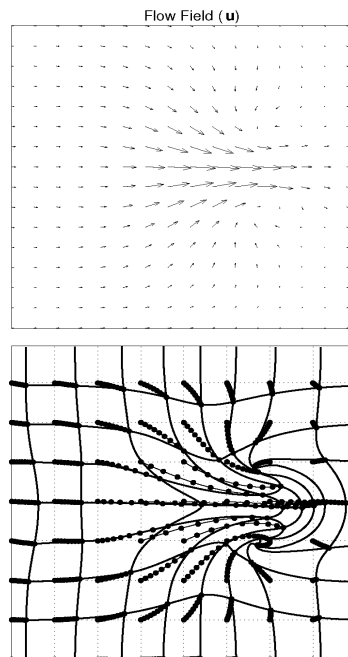
## Dartel image registration

- \* Uses fast approximations
  - \* Deformation integrated using scaling and squaring
- \* Uses Levenberg-Marquardt optimiser
  - \* Multi-grid matrix solver
- \* Matches GM with GM, WM with WM etc
- \* Diffeomorphic registration takes about 30 mins per image pair (121×145×121 images).

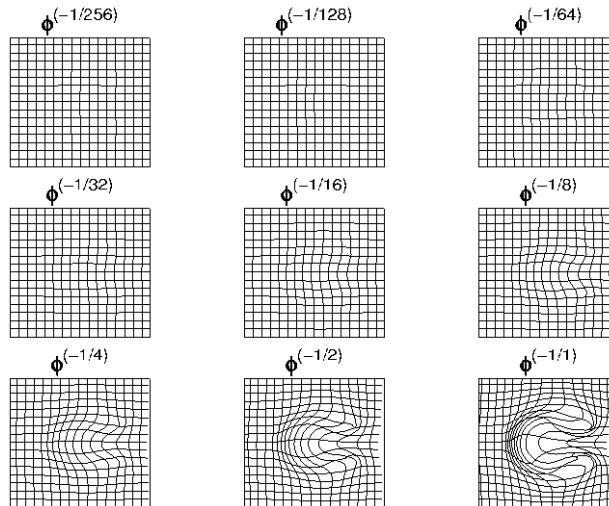


## Dartel

- \* Parameterising the deformation
- \*  $\boldsymbol{\phi}^{(0)} = \text{Identity}$
- \*  $\boldsymbol{\phi}^{(1)} = \int_{t=0}^1 \mathbf{v}(\boldsymbol{\phi}^{(t)}) dt$
- \*  $\mathbf{V}$  is an estimated velocity field.
- \* Scaling and squaring is used to generate deformations.



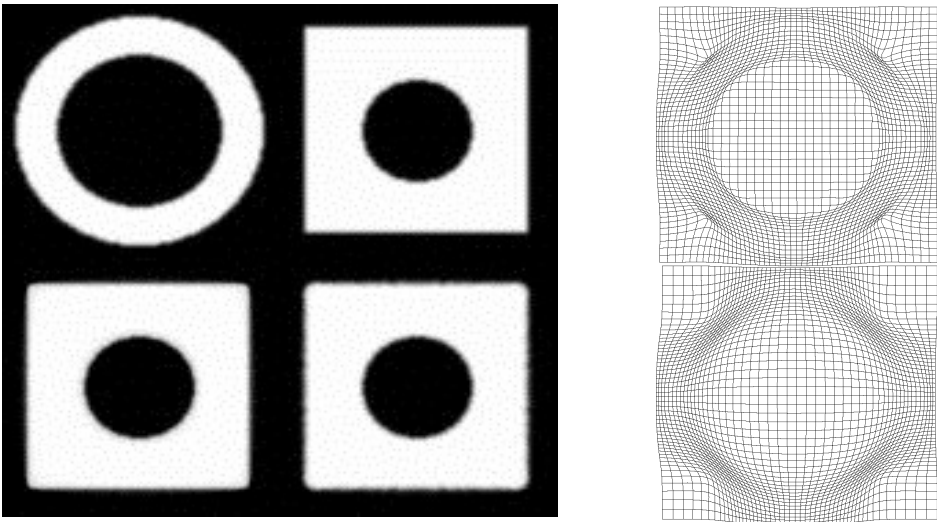
## Scaling and squaring example



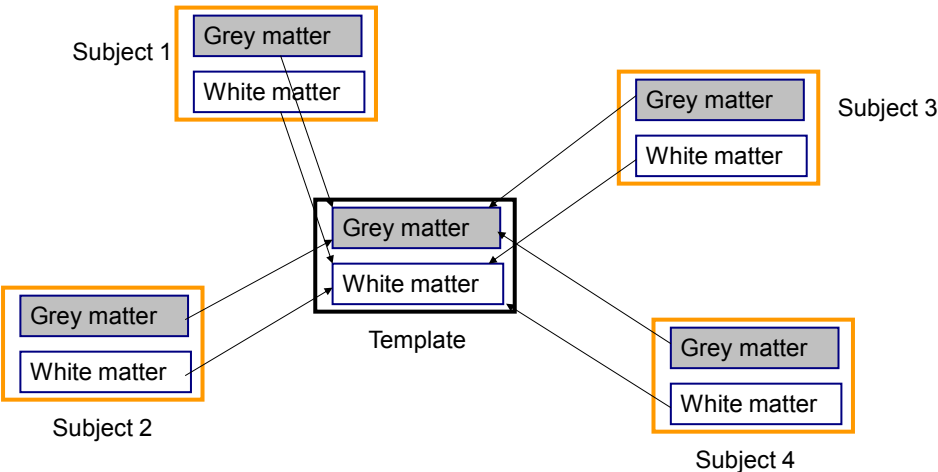
## Registration objective function

- \* Simultaneously minimize the sum of:
  - \* **Matching Term**
    - \* Drives the alignment of the images.
    - \* Multinomial assumption
  - \* **Regularisation term**
    - \* A measure of deformation roughness
    - \* Keeps the warps spatially smooth.
- \* A balance between the two terms.

# Effect of different forms of regularisation



# Simultaneous registration of GM to GM and WM to WM



# Template

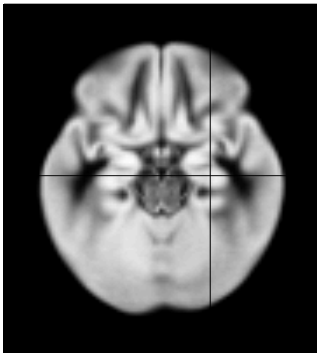
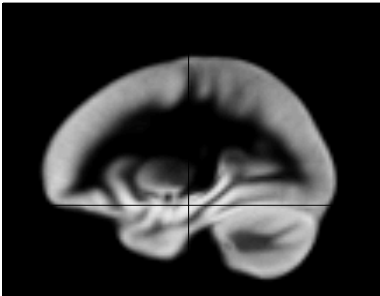
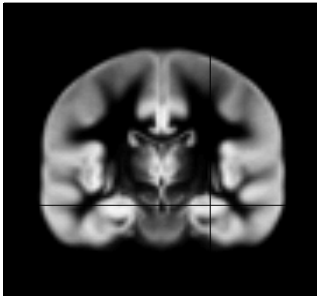
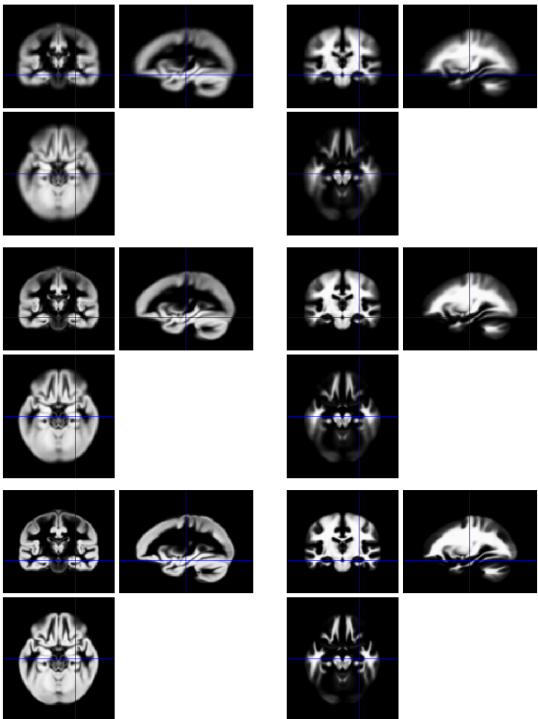
Iteratively generated  
from 471 subjects

Began with rigidly  
aligned tissue  
probability maps

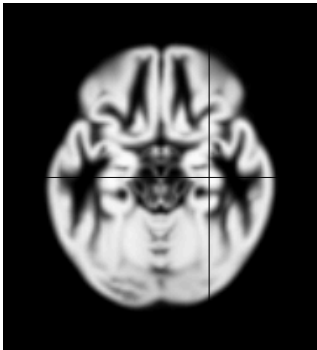
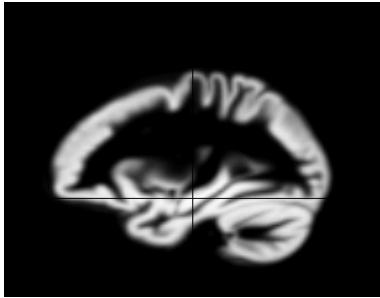
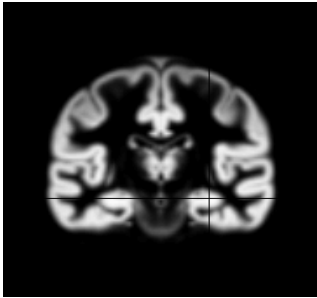
Initial  
Average

After a few  
iterations

Final  
template

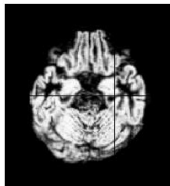
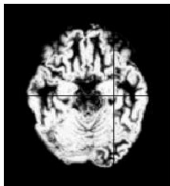
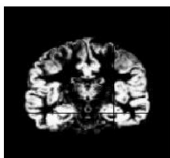
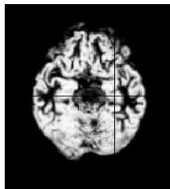
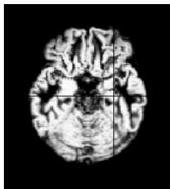
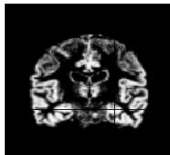
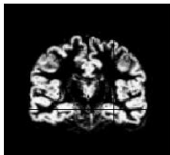


Grey matter  
average of 452  
subjects – affine

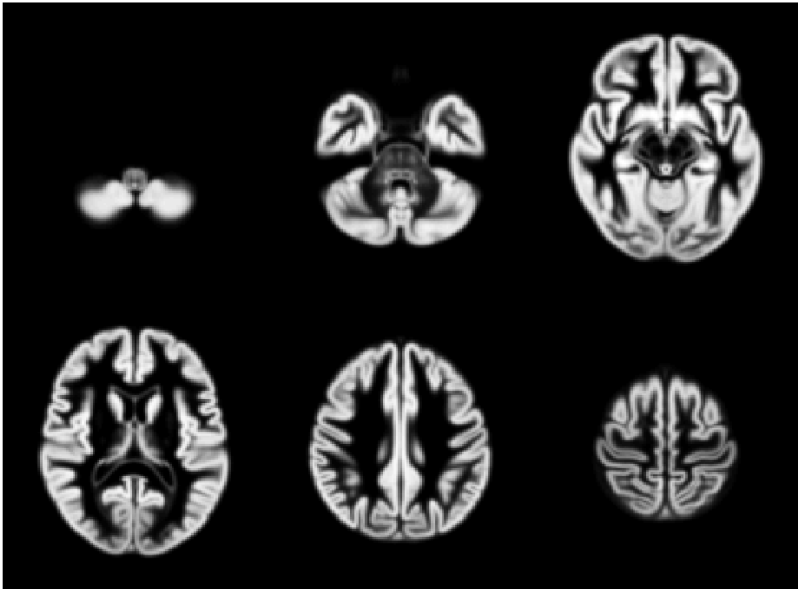
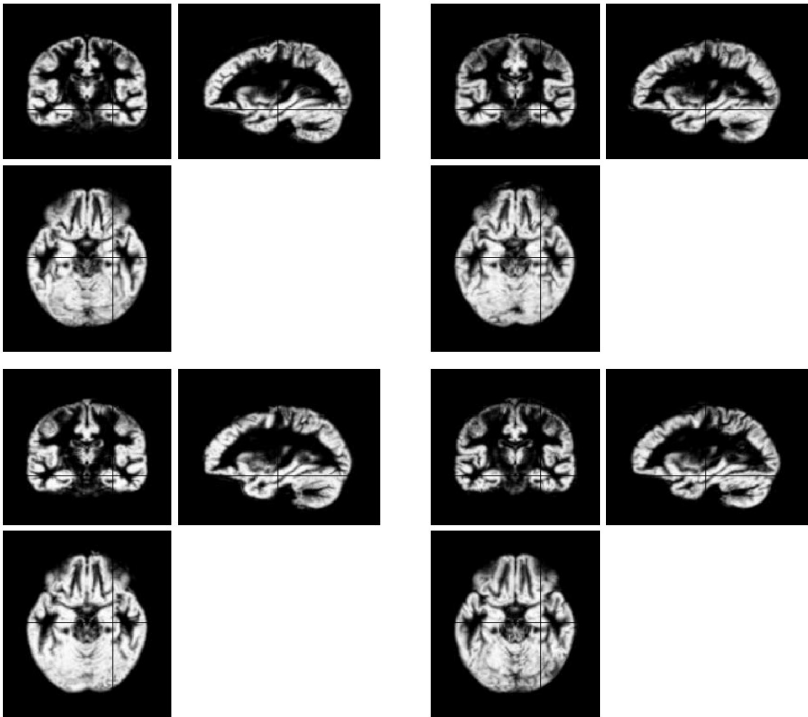


Grey matter  
average of 471  
subjects

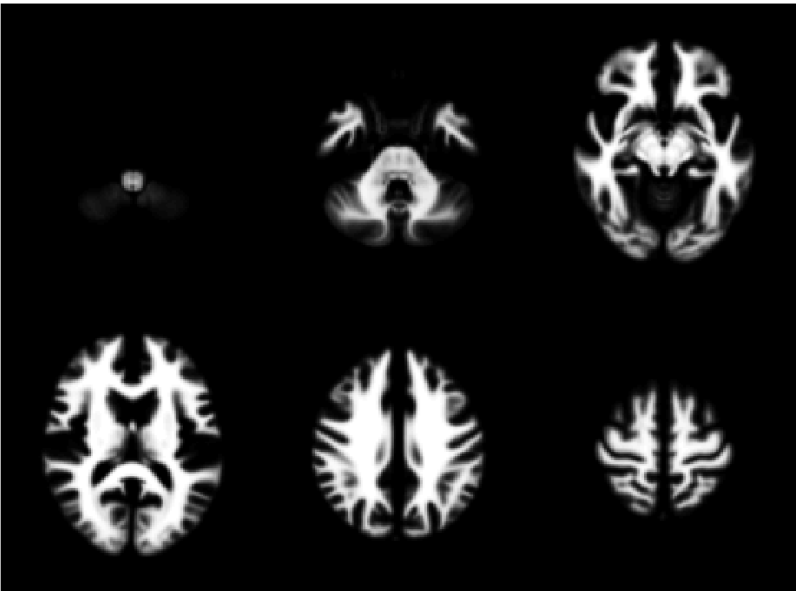
Initial  
GM images



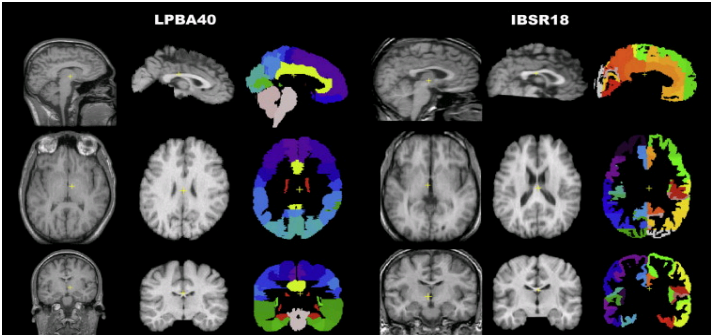
Aligned  
GM images



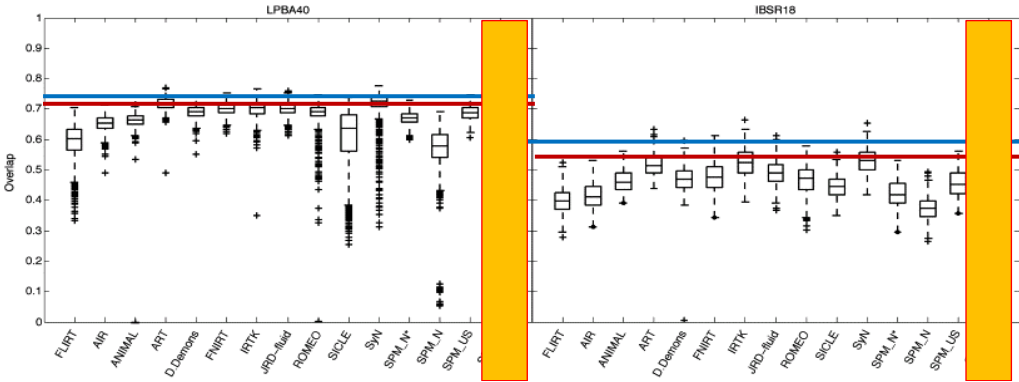
471 Subject Average



471 Subject Average



Evaluations of  
nonlinear  
registration  
algorithms





# Contents

- \* Normalise/Segment
- \* Dartel

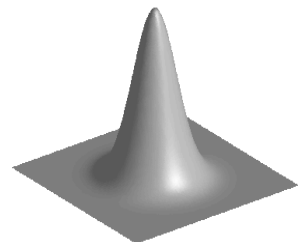
## \* Smoothing

- \* Compensating for inaccuracies in inter-subject alignment

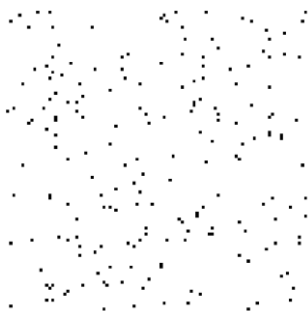
## Smooth

Blurring is done by [convolution](#).

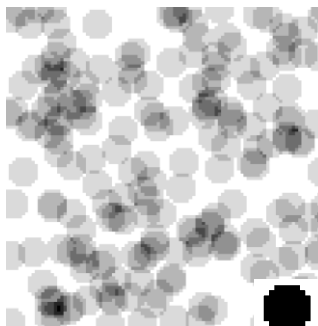
Each voxel after smoothing effectively becomes the result of applying a weighted region of interest (ROI).



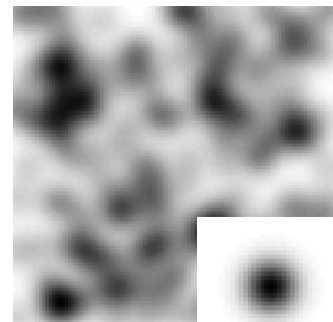
Before convolution



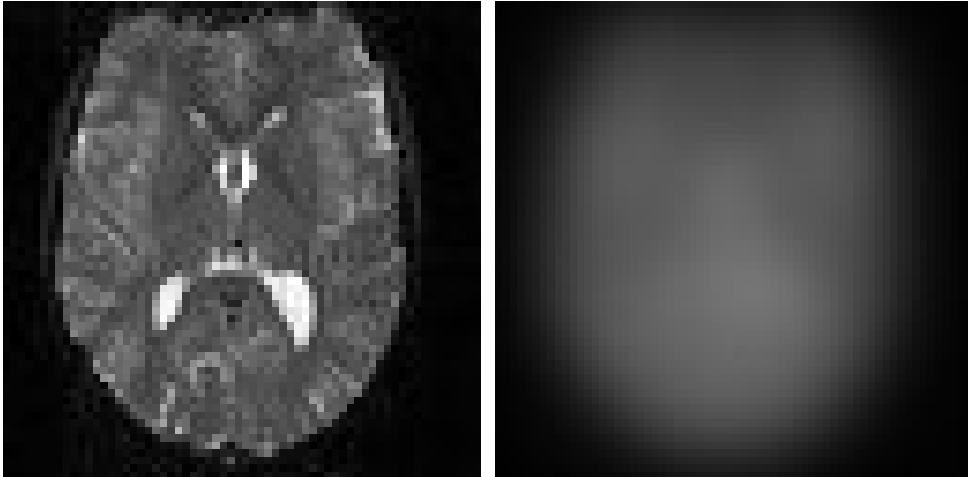
Convolved with a circle



Convolved with a Gaussian



## Smooth



## References

- \* [Ashburner & Friston](#). *Unified Segmentation*. NeuroImage 26:839-851 (2005).
- \* [Ashburner](#). *A Fast Diffeomorphic Image Registration Algorithm*. NeuroImage 38:95-113 (2007).
- \* [Ashburner & Friston](#). *Computing average shaped tissue probability templates*. NeuroImage 45(2): 333-341 (2009).
- \* [Klein et al.](#) *Evaluation of 14 nonlinear deformation algorithms applied to human brain MRI registration*. NeuroImage 46(3):786-802 (2009).