



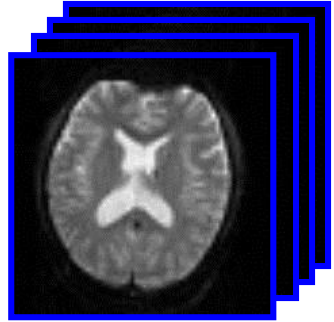
# Preprocessing II: Between Subjects

John Ashburner

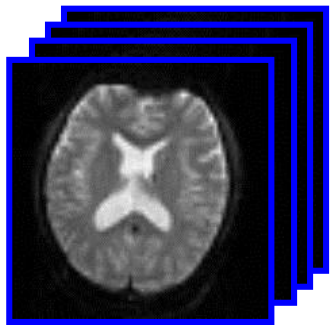
Wellcome Trust Centre for Neuroimaging,  
12 Queen Square, London, UK.

# Pre-processing overview

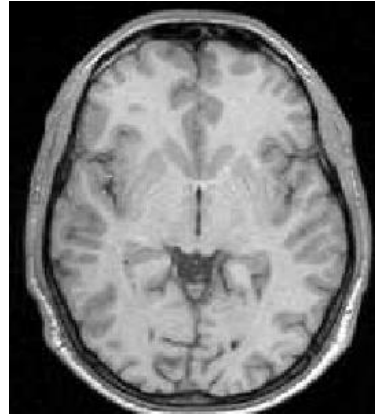
fMRI time-series



Motion Correct



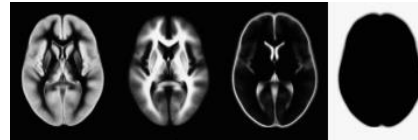
Anatomical MRI



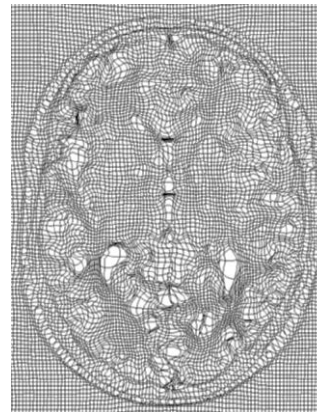
Coregister

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

Template



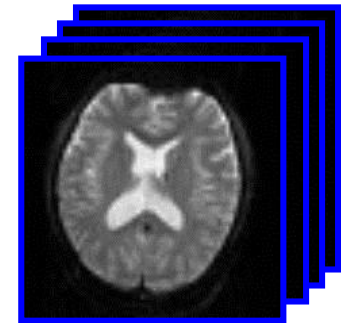
Estimate  
Spatial Norm



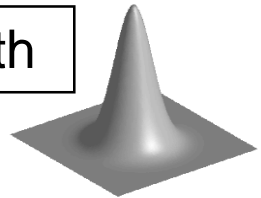
Deformation

Statistics or  
whatever

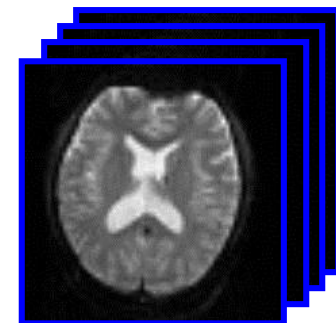
Smoothed



Smooth

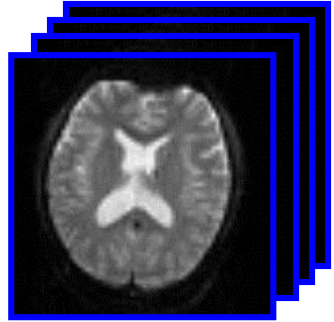


Spatially  
normalised

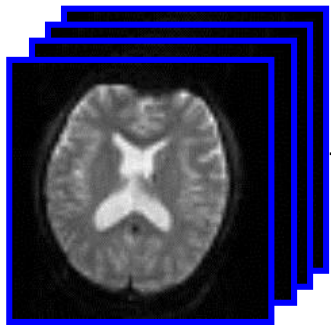


# Alternative pipeline

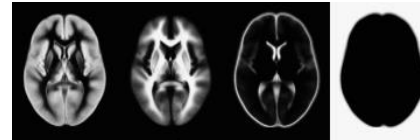
fMRI time-series



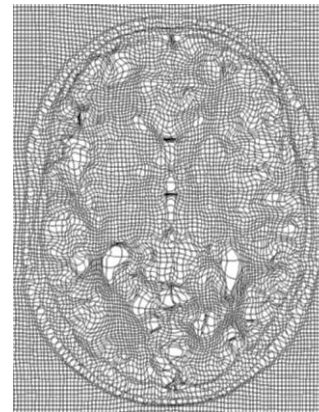
Motion Correct



Template



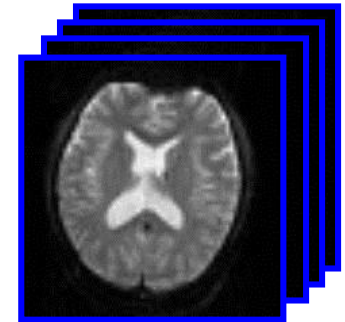
Estimate  
Spatial Norm



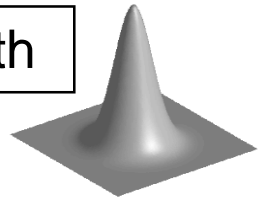
Deformation

Statistics or  
whatever

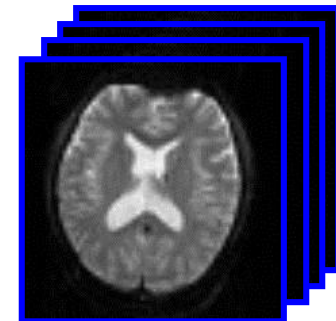
Smoothed



Smooth



Spatially  
normalised



# Contents

## \* **Normalise/Segment**

**Use segmentation routine for spatial normalisation**

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

\* Dartel

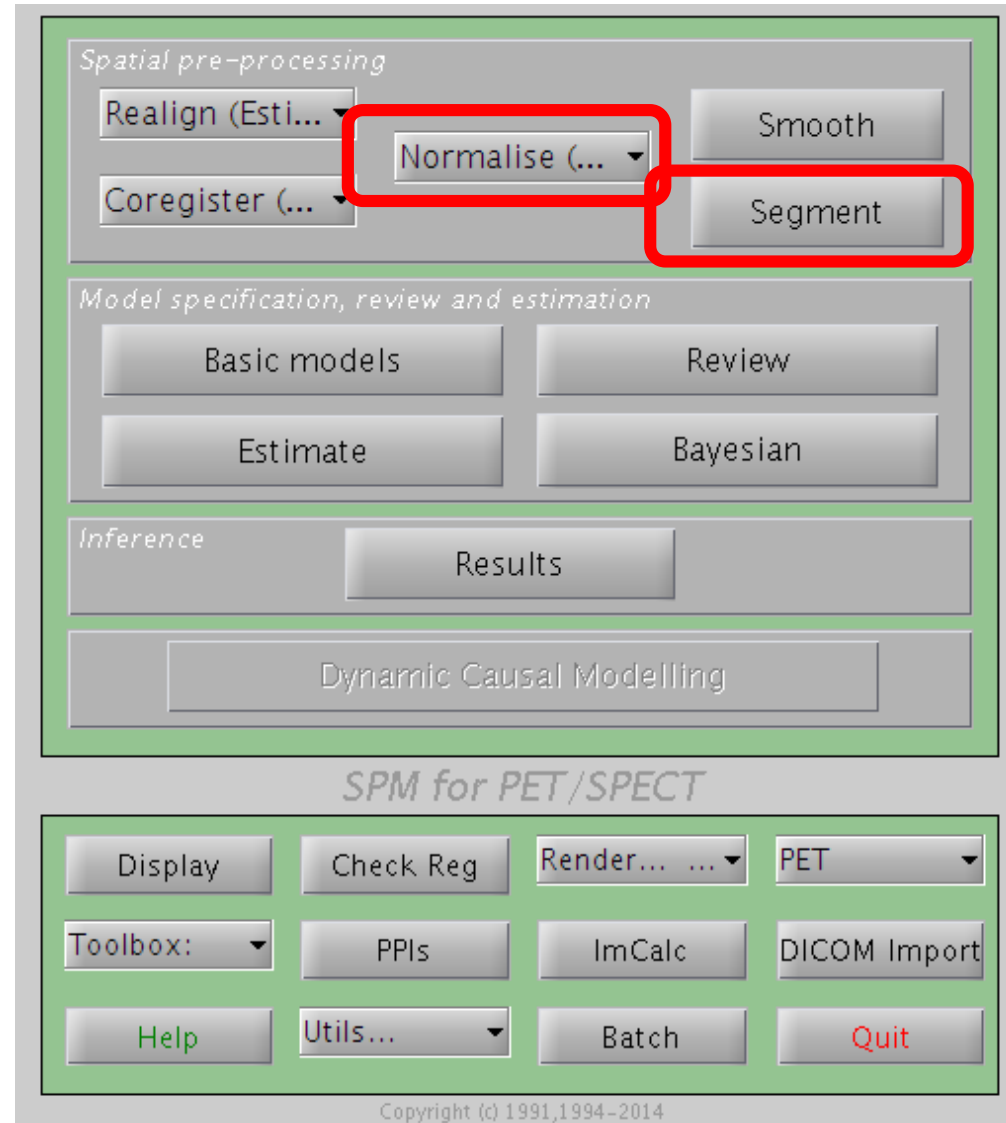
\* Smoothing

# 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.

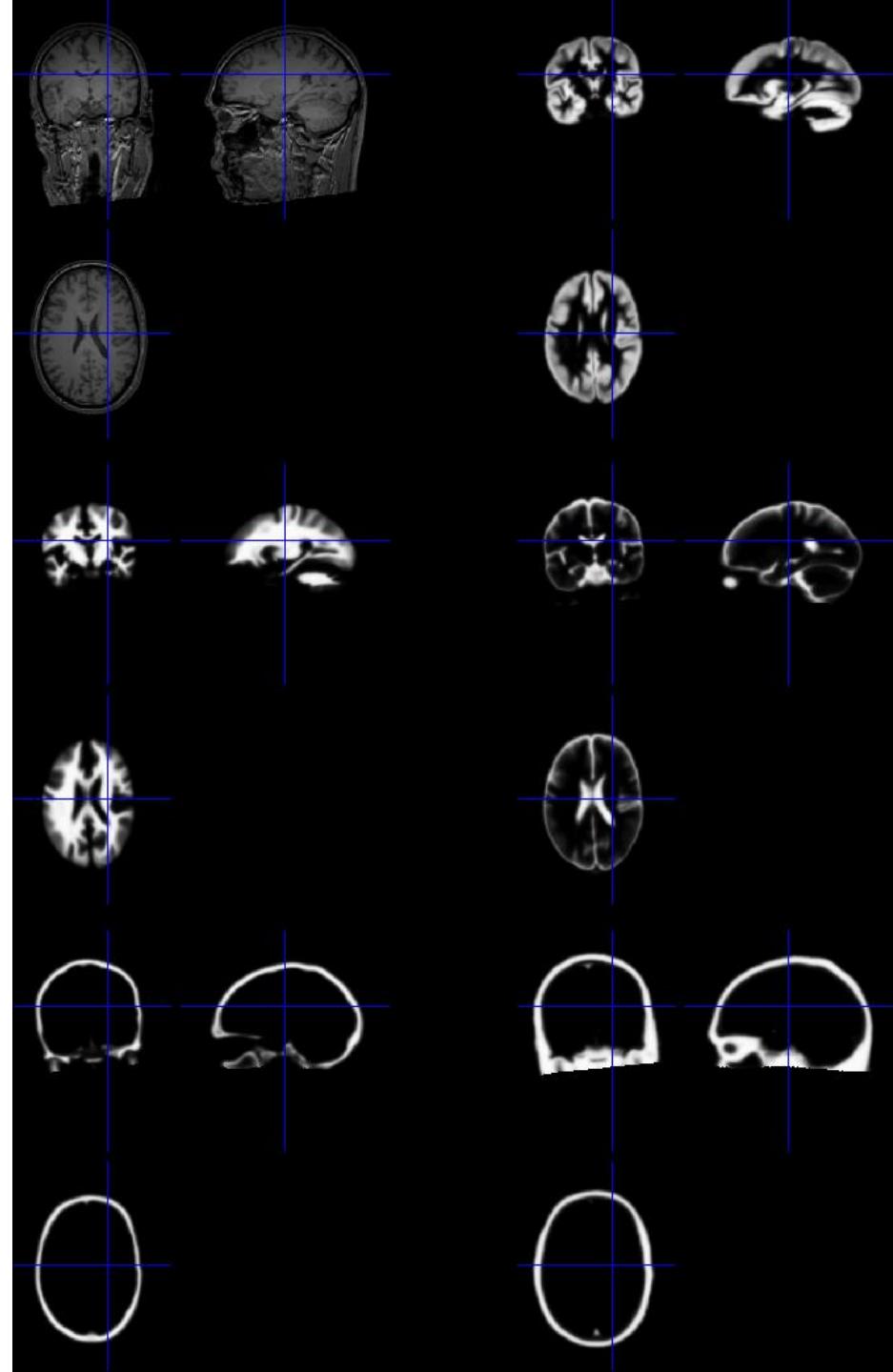
# Normalise/Segment

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



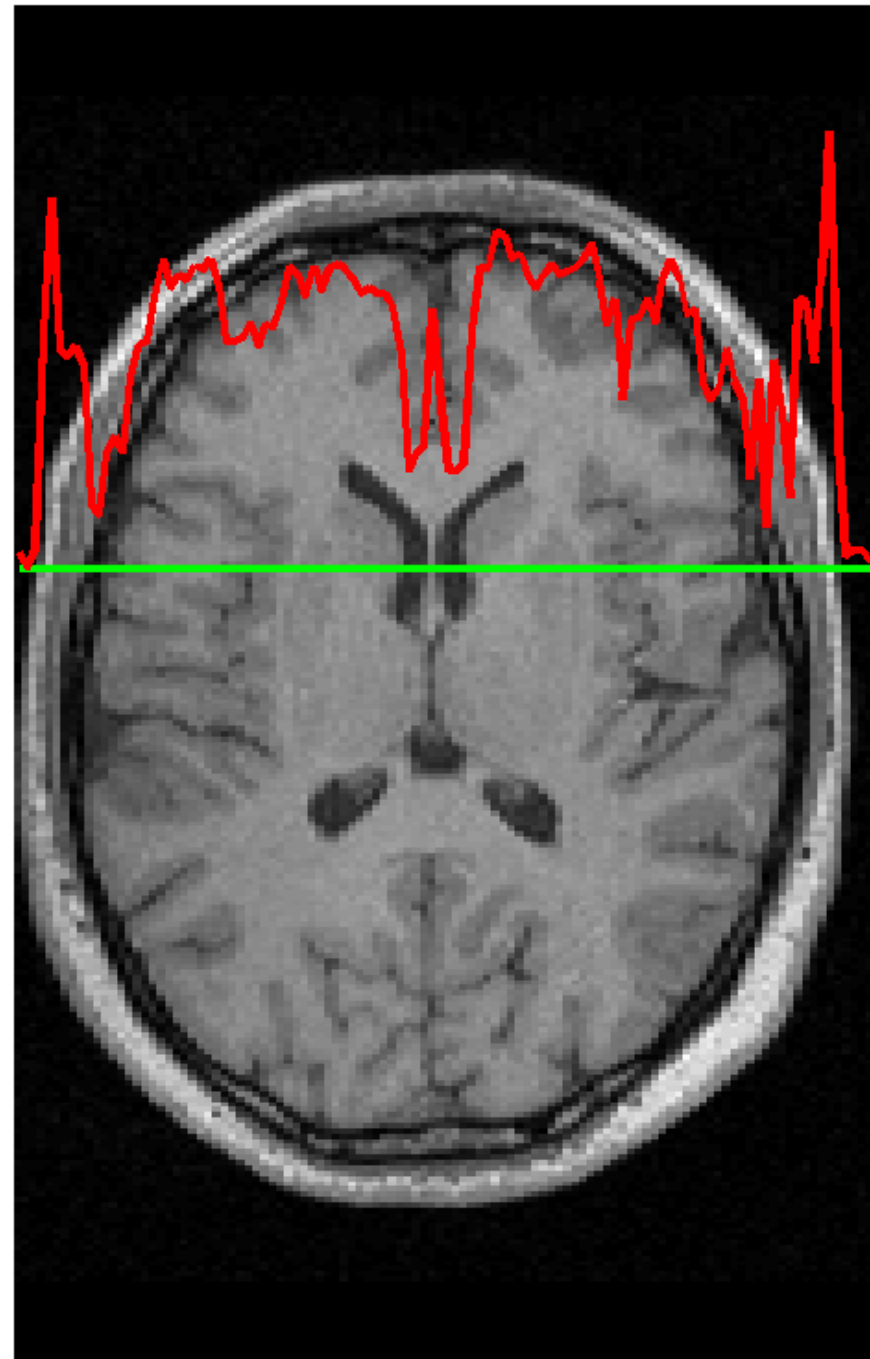
# Spatial normalisation

- \* 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.

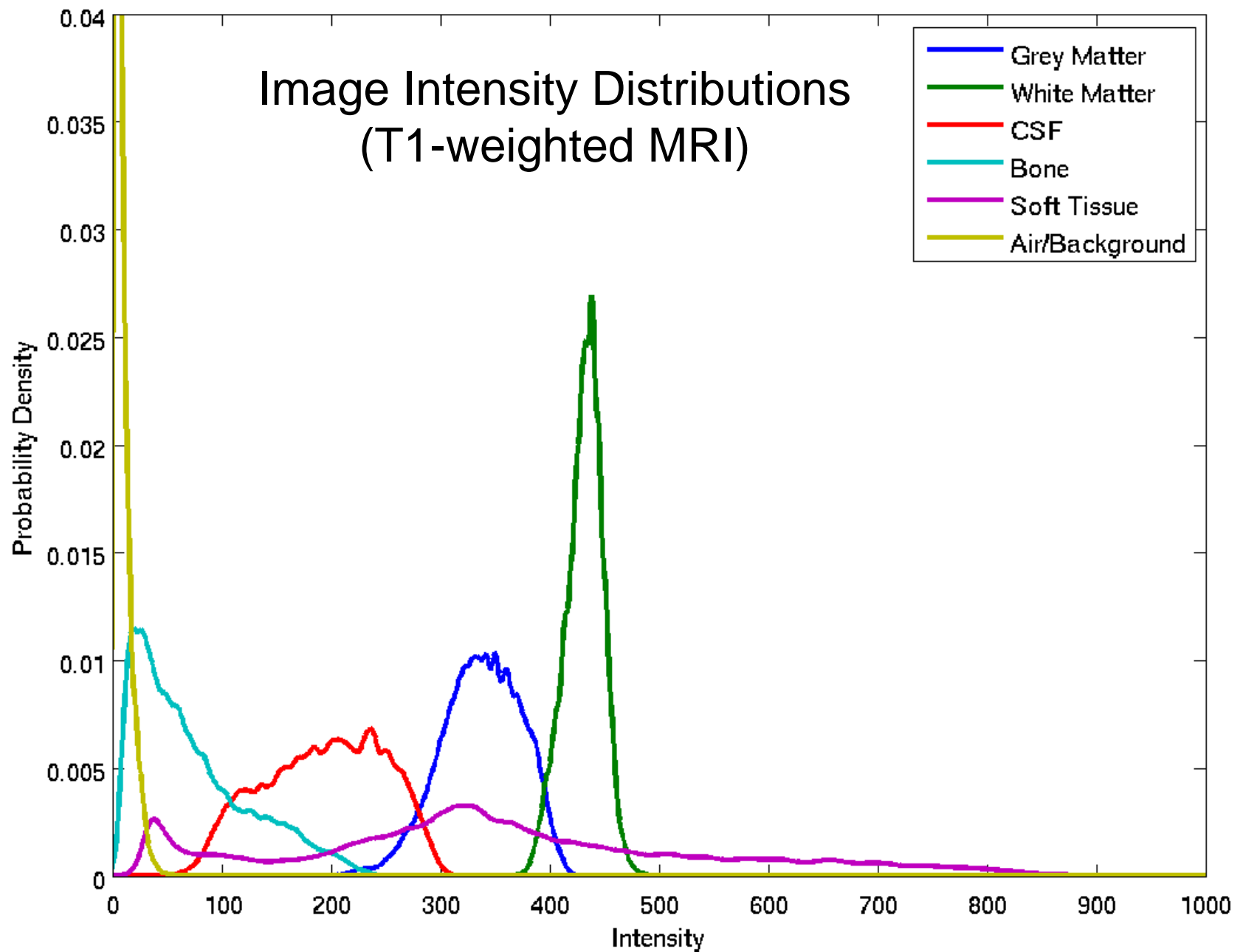


# Segmentation

- \* 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

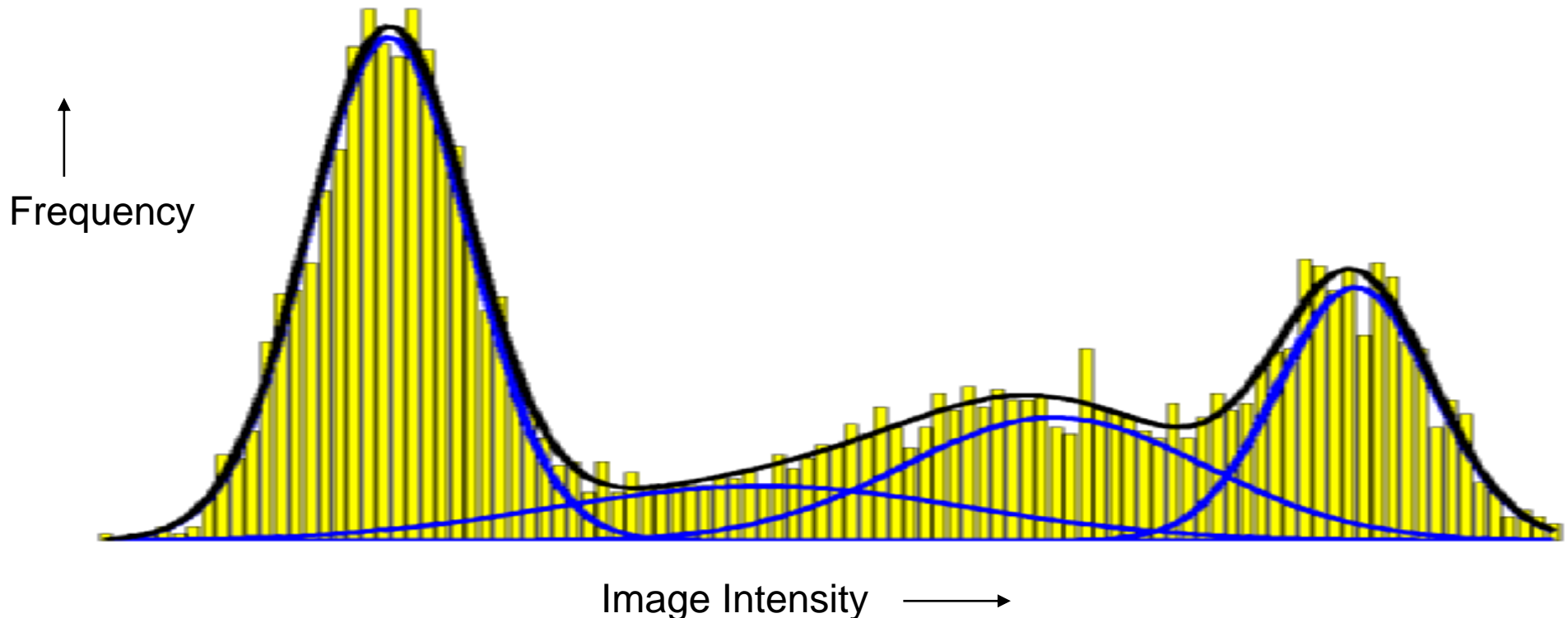




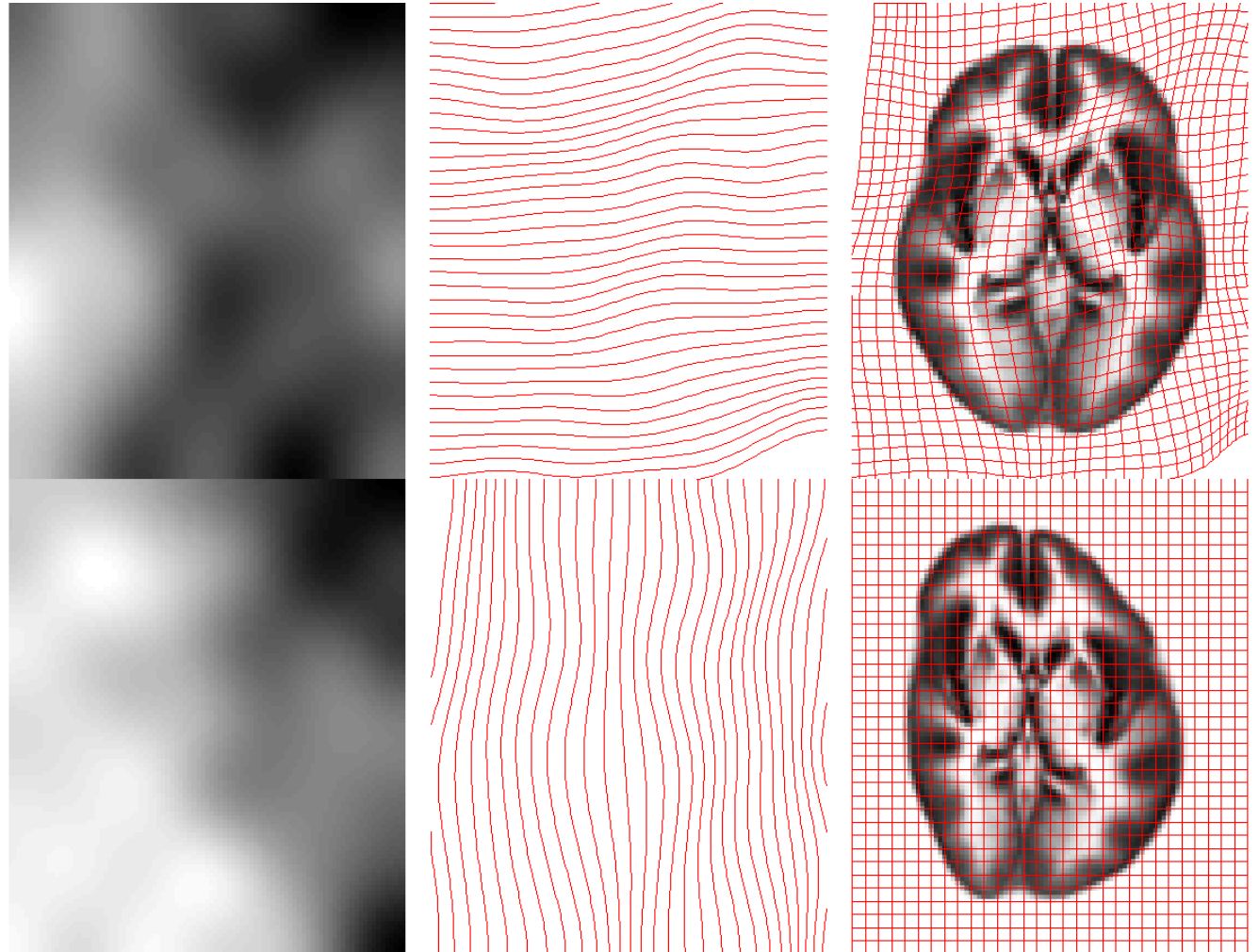


# Modelling tissue intensities

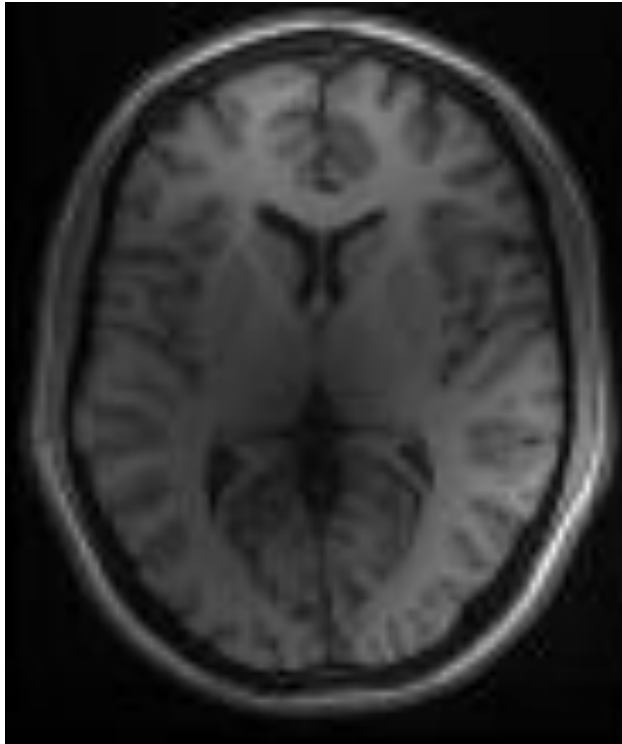
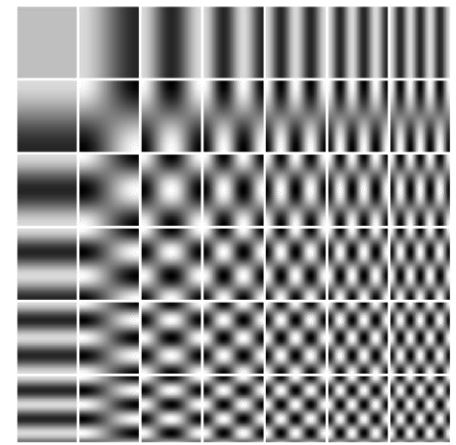
- \* Classification is based on a ***Mixture of Gaussians*** model (MOG), which represents the intensity probability density by a number of Gaussian distributions.



# Modelling deformations



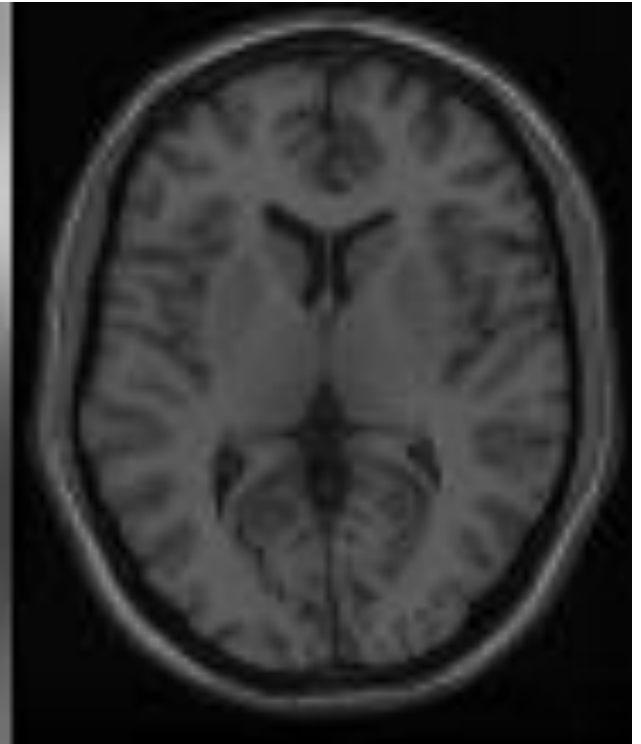
# Modelling a bias field



**Corrupted image**

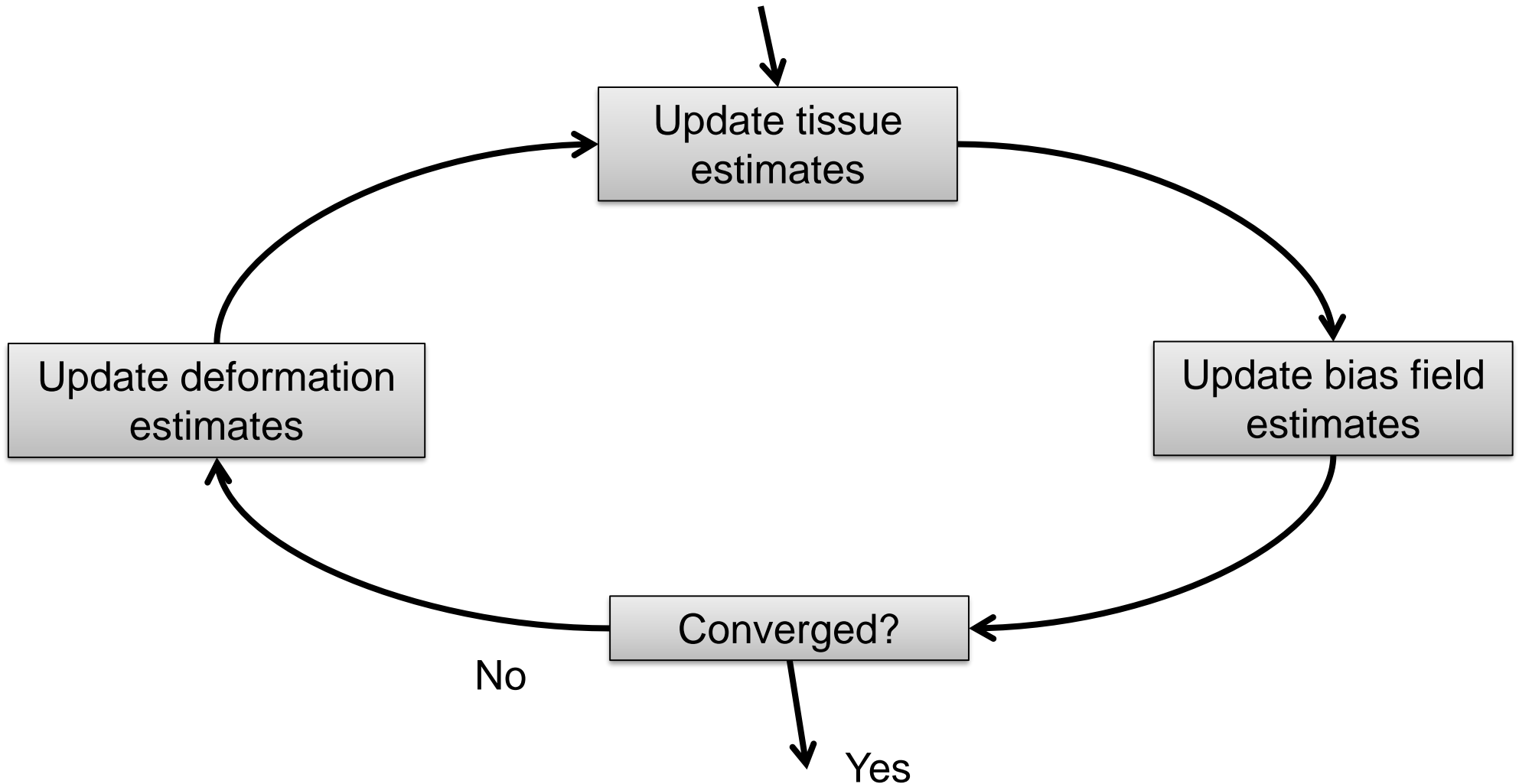


**Bias Field**

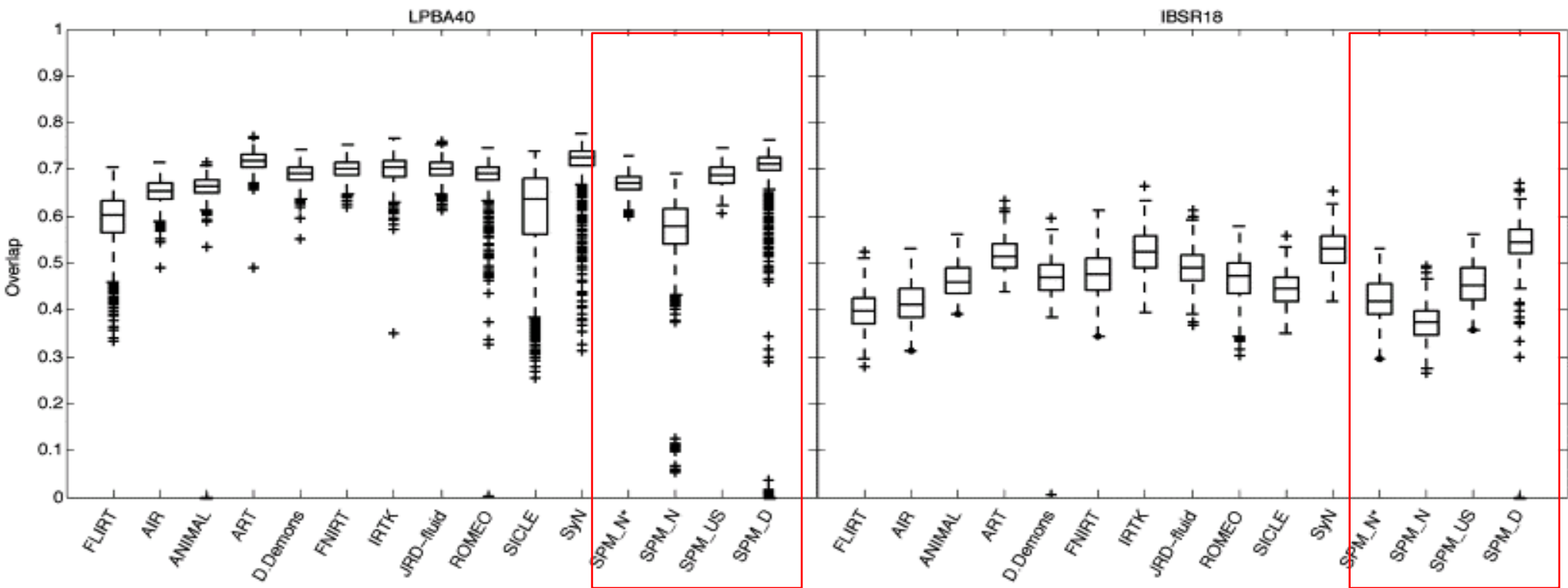
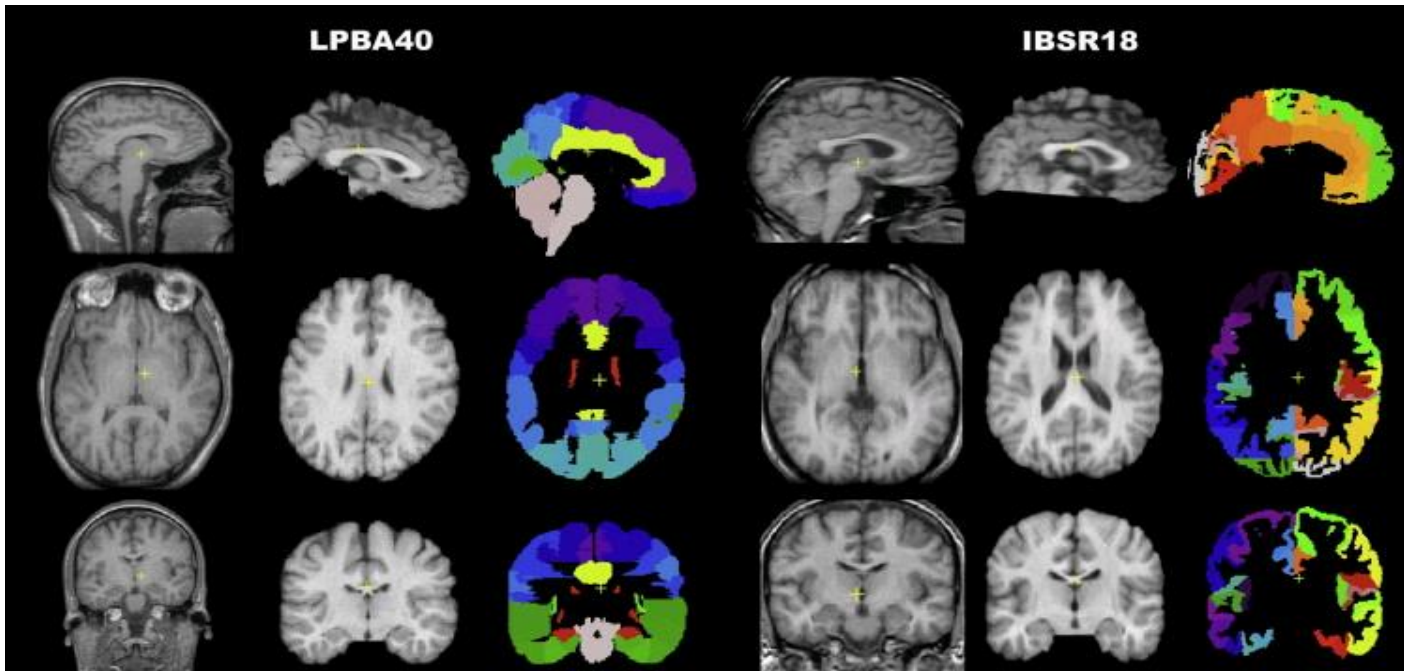


**Corrected image**

# Iterative optimisation scheme

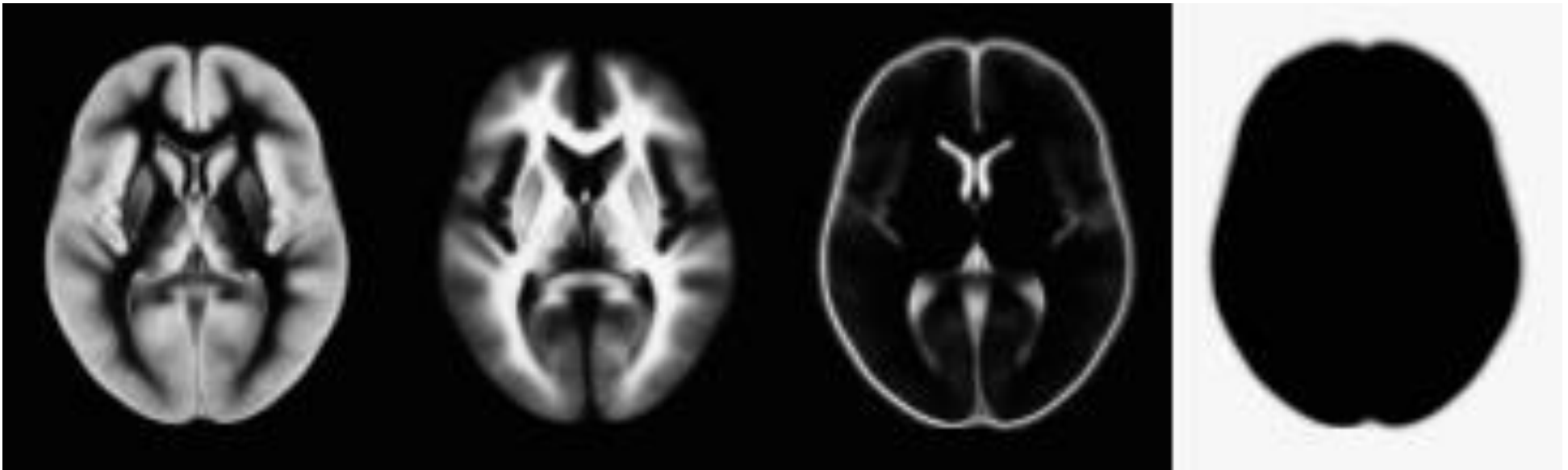


# Evaluations of nonlinear registration algorithms



# Old tissue probability maps

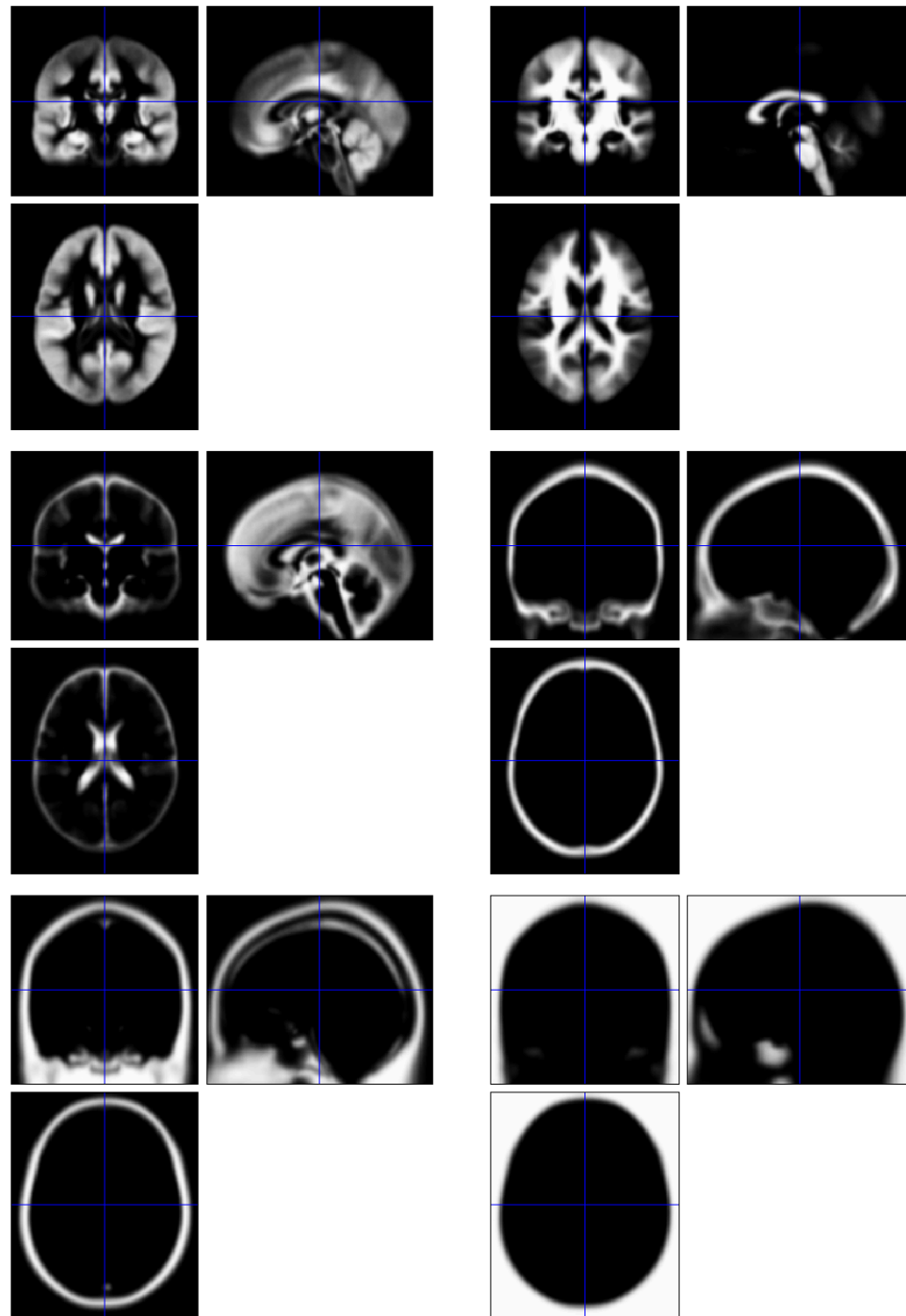
- \* Tissue probability maps (TPMs) are used instead of the proportion of voxels in each Gaussian as the prior.



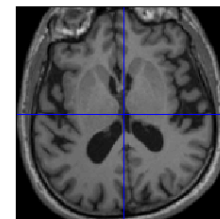
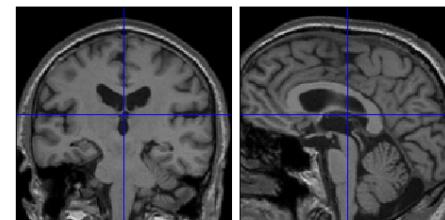
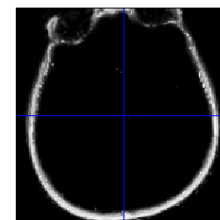
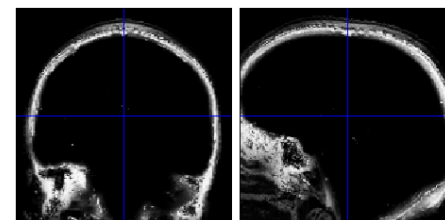
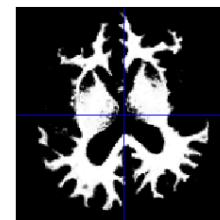
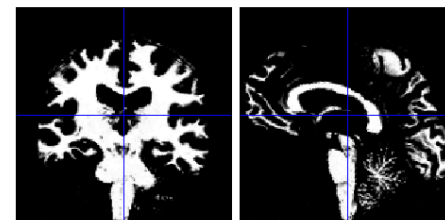
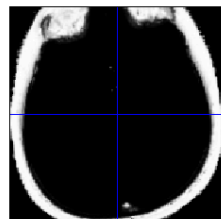
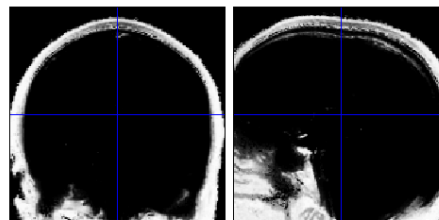
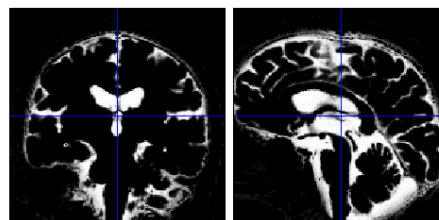
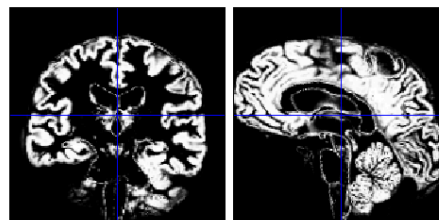
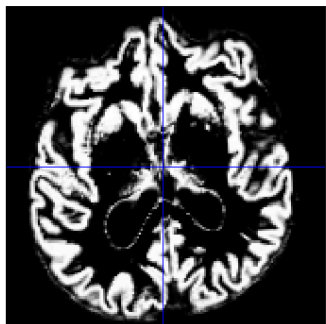
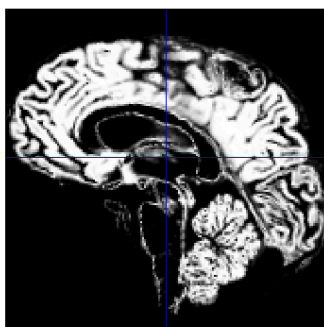
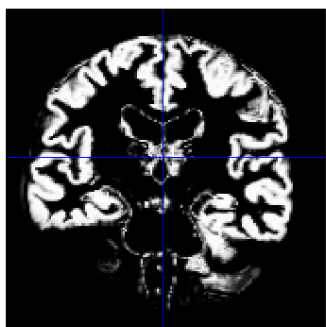
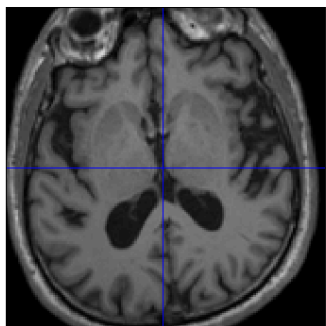
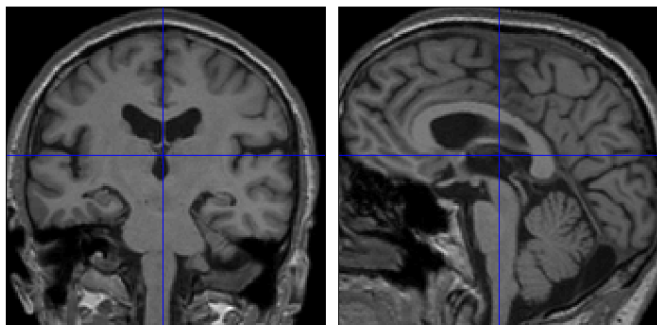
**ICBM Tissue Probabilistic Atlases.** These tissue probability maps are kindly provided by the **International Consortium for Brain Mapping**, John C. Mazziotta and Arthur W. Toga.

# Tissue probability maps in SPM12

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







# Contents

- \* Normalise/Segment

- \* **Dartel**

  - \* **Velocity field parameterisation**

  - \* **Objective function**

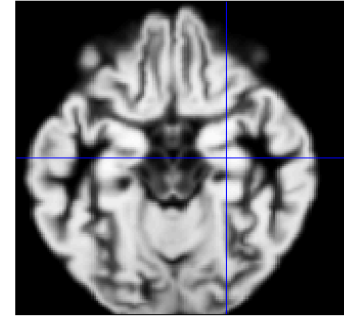
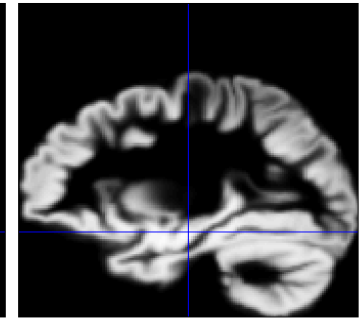
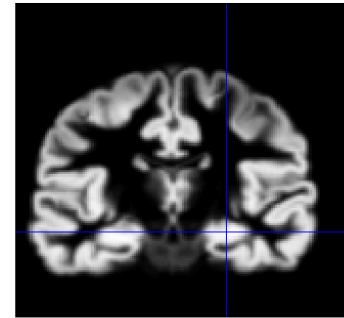
  - \* **Template creation**

  - \* **Examples**

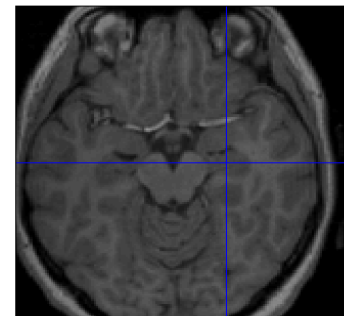
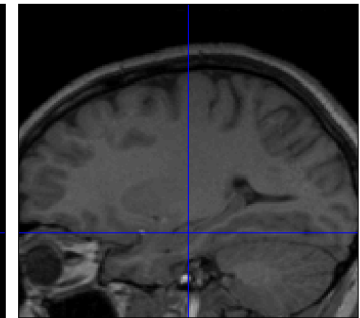
- \* Smooth

# 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).



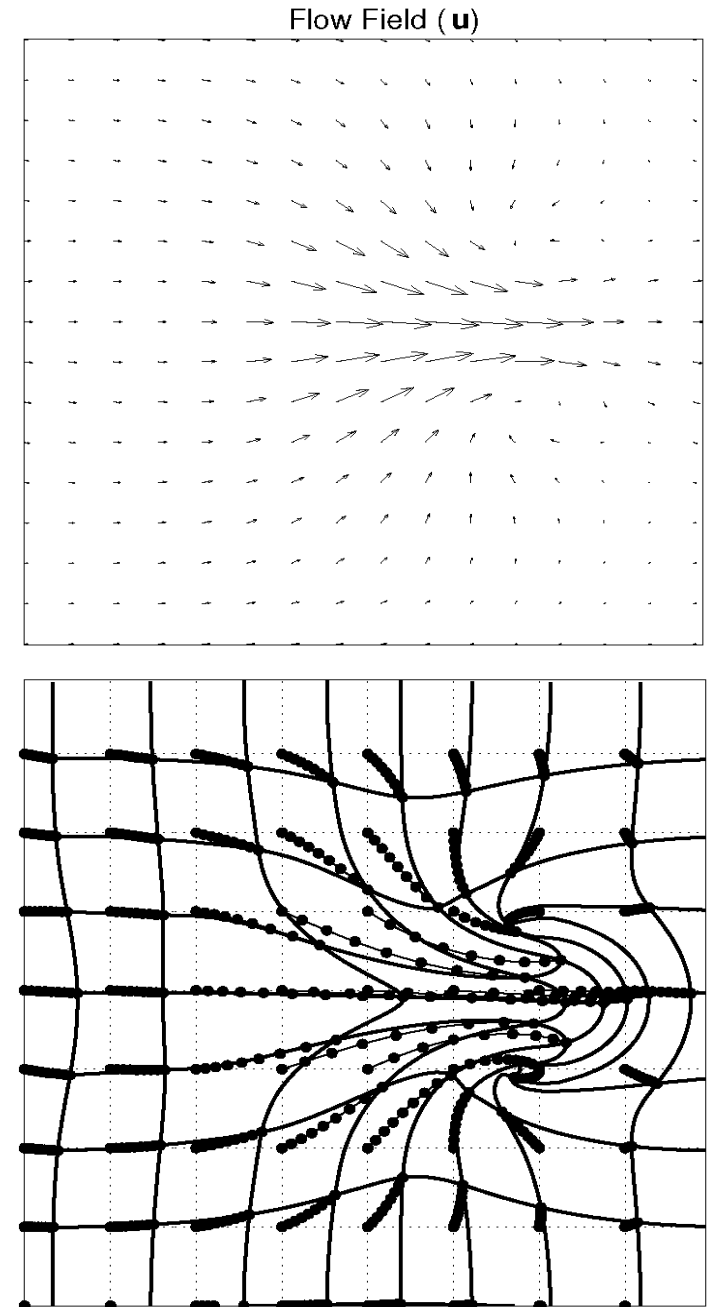
Grey matter  
template warped to  
individual



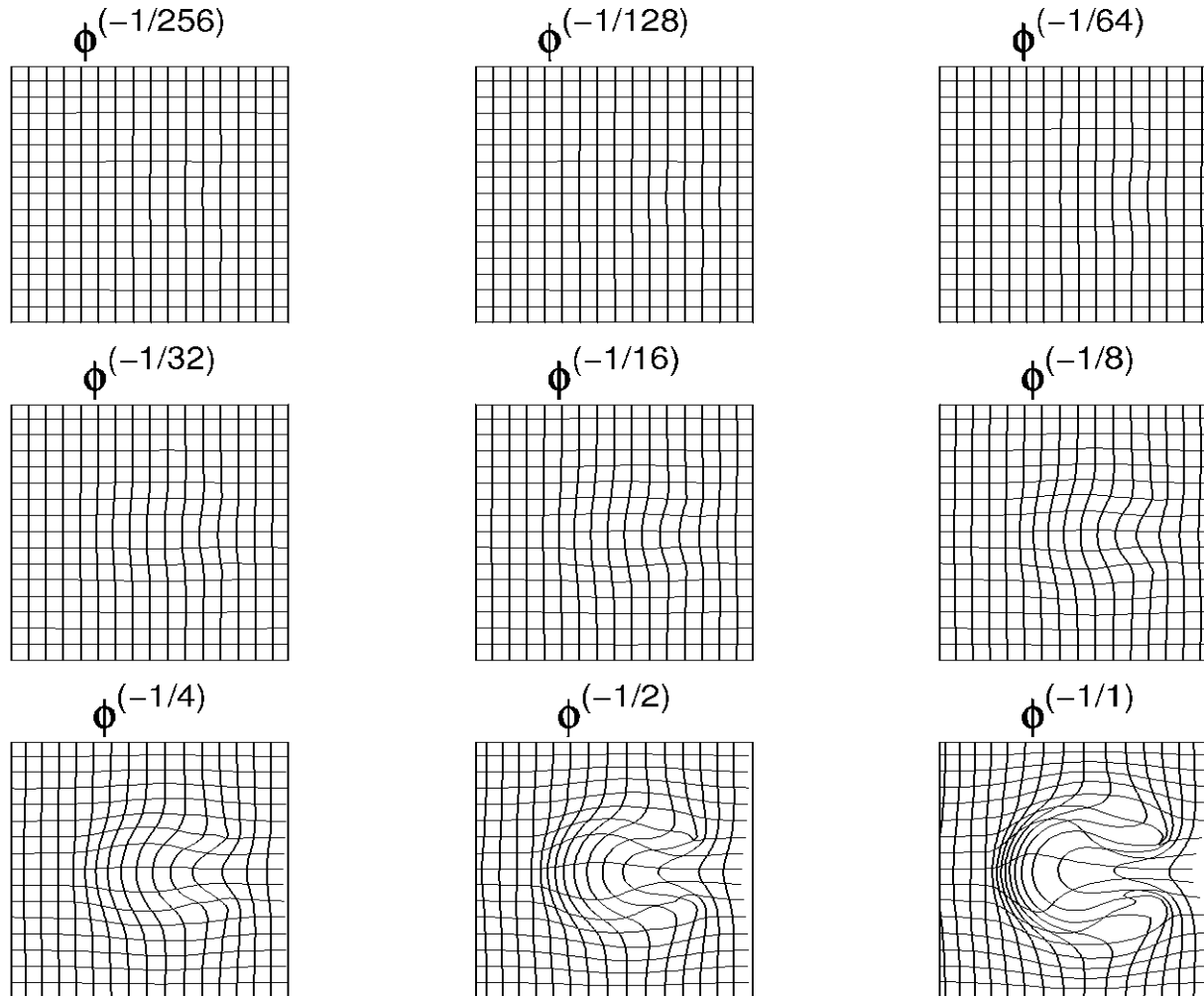
Individual scan

# Dartel

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



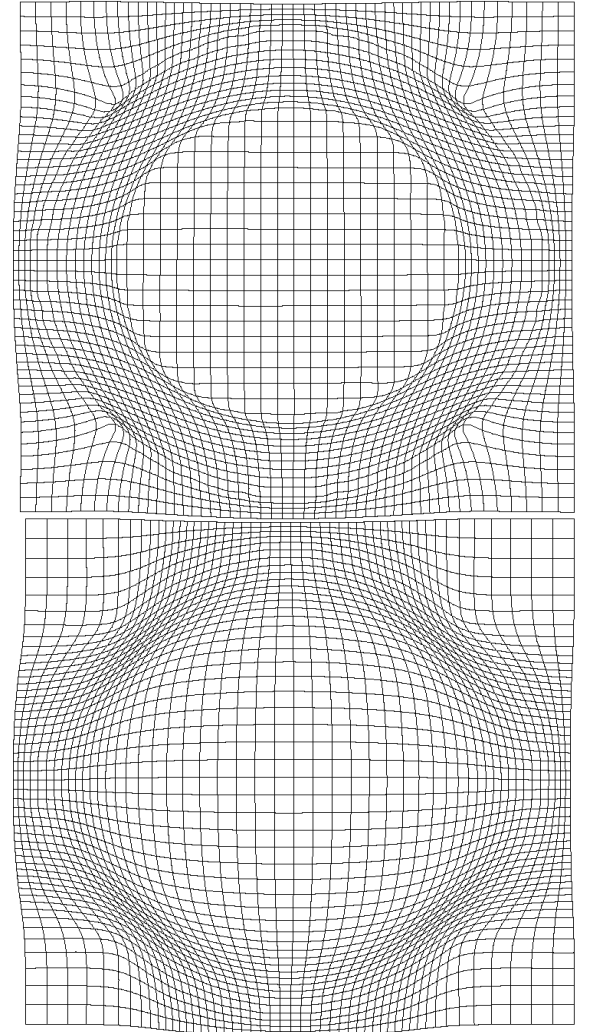
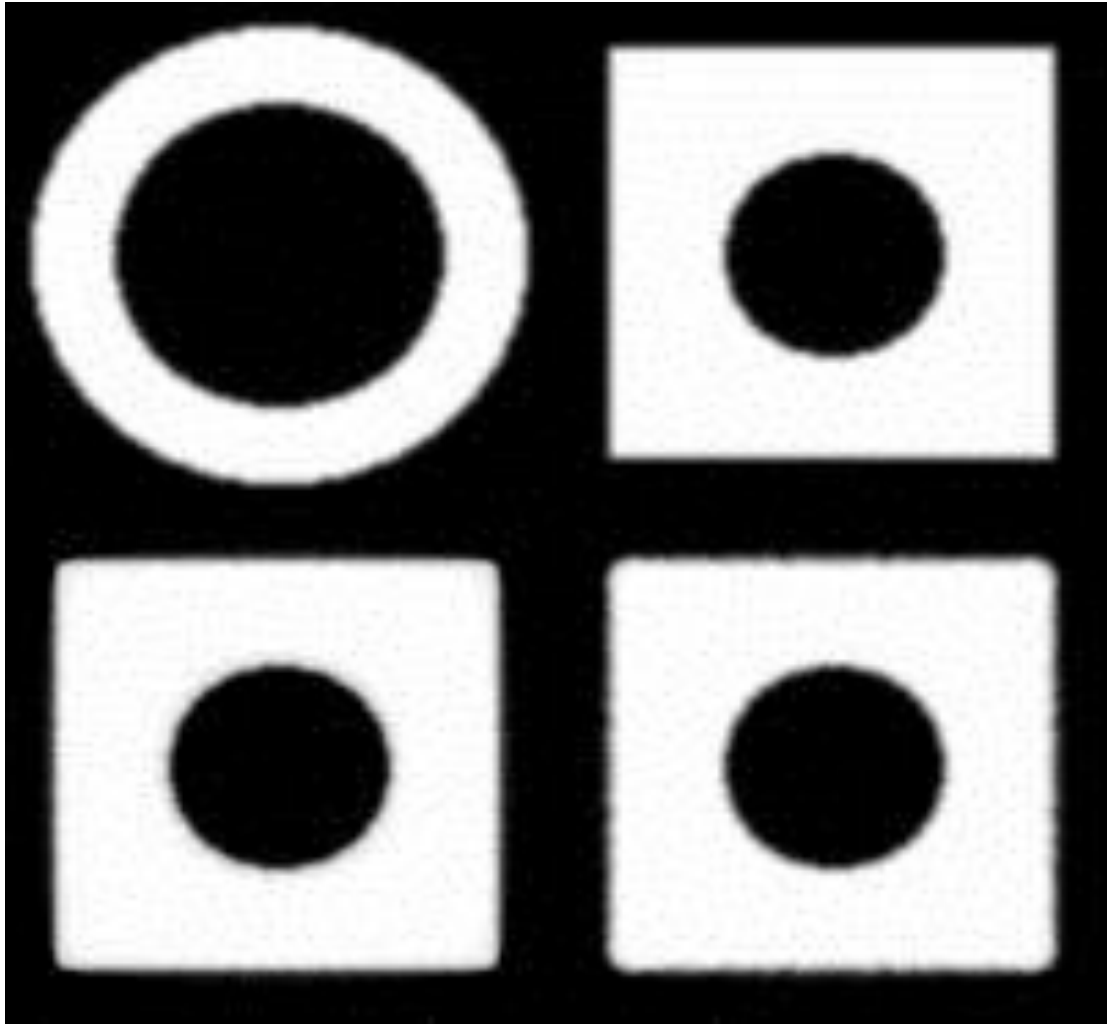
# Scaling and squaring example



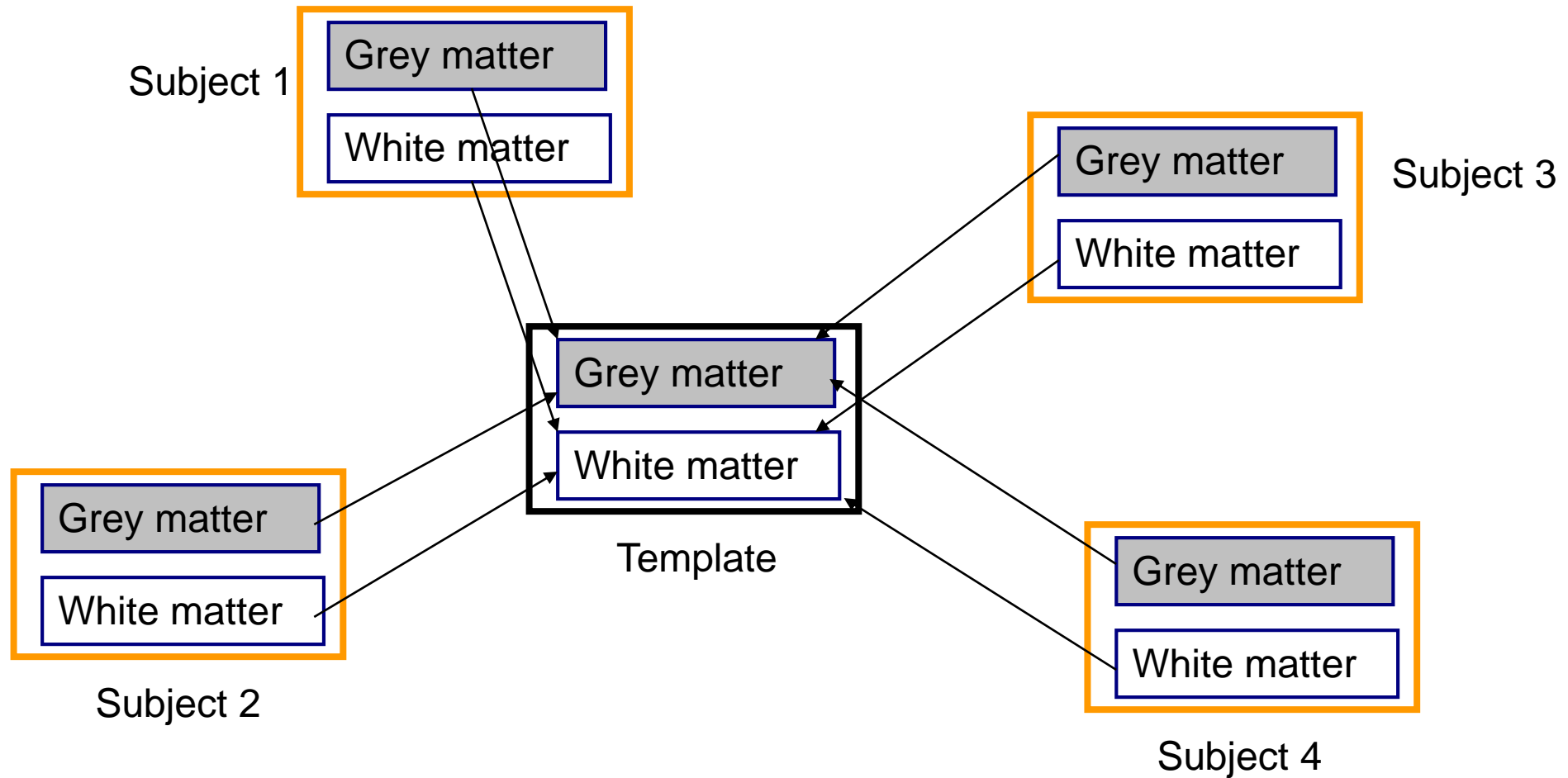
# Registration objective function

- \* 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



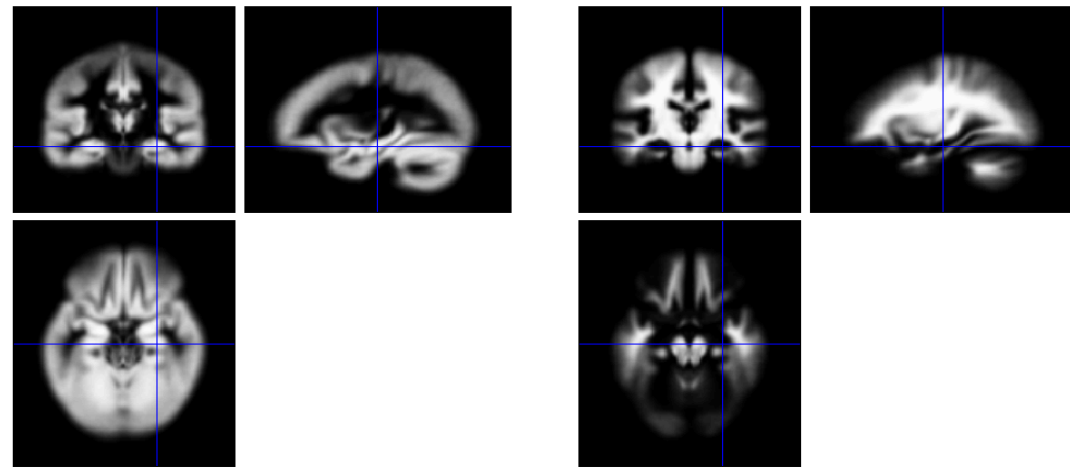


# Template

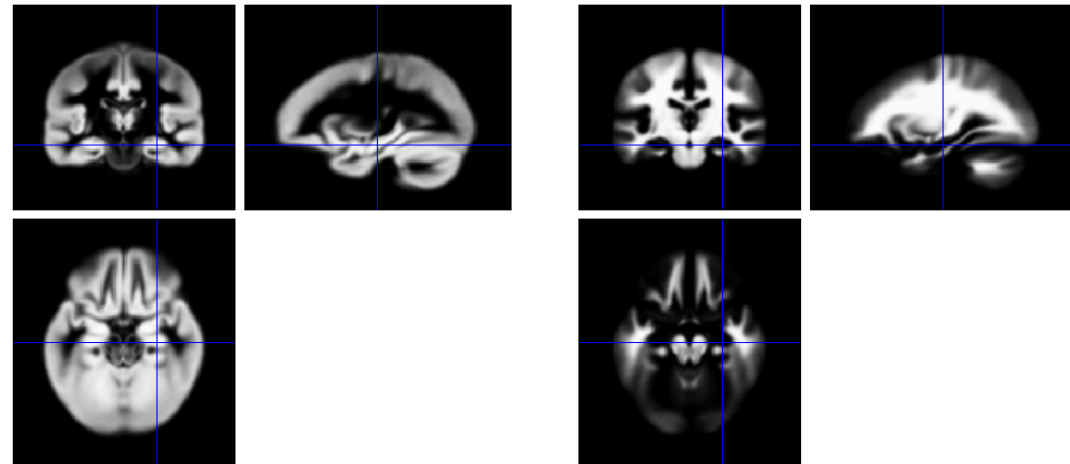
Iteratively generated  
from 471 subjects

Began with rigidly  
aligned tissue  
probability maps

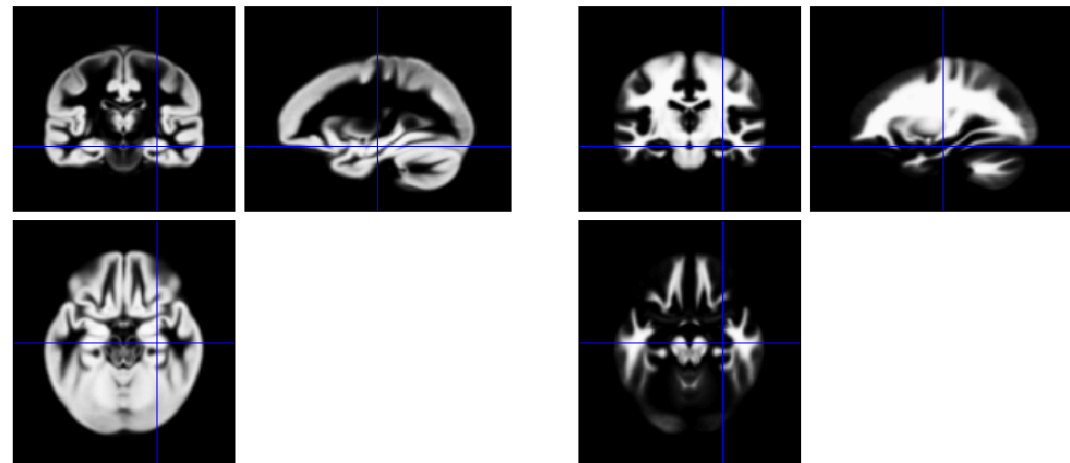
Initial  
Average

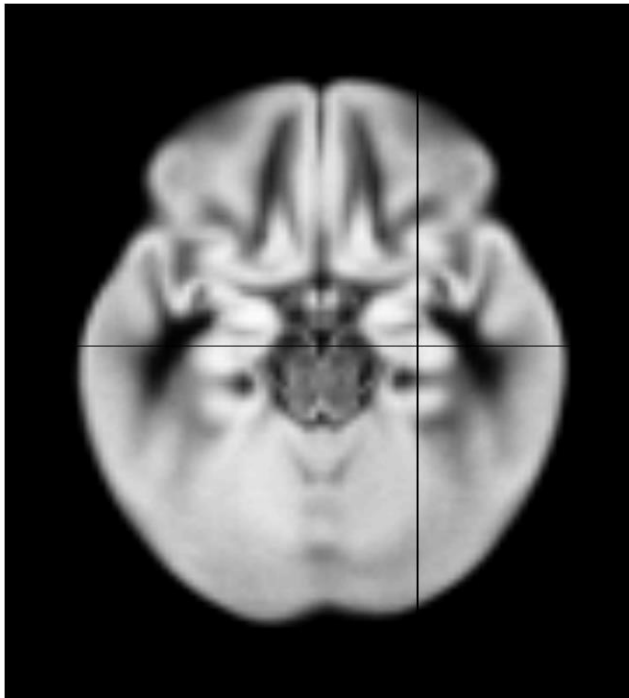
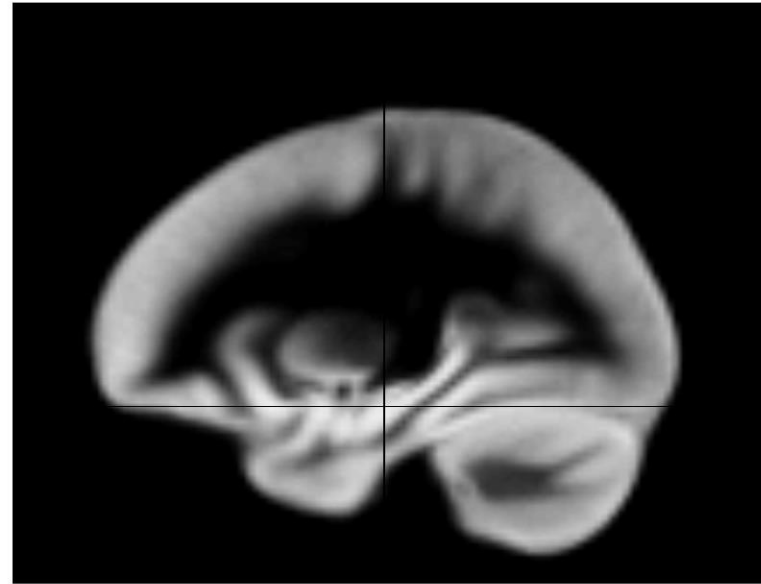
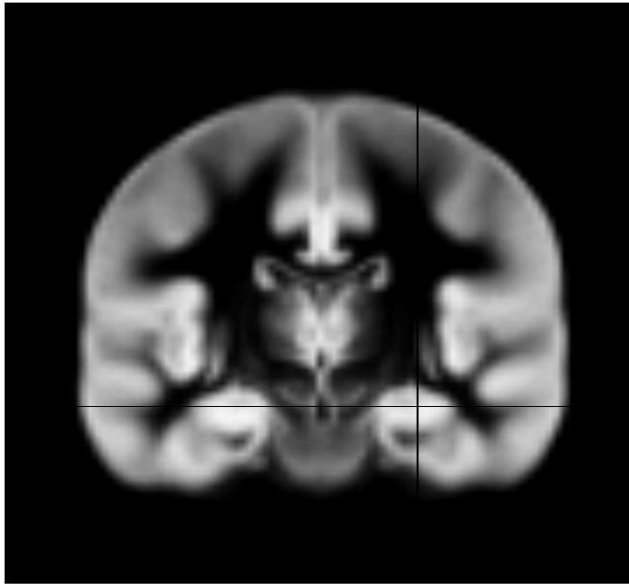


After a few  
iterations

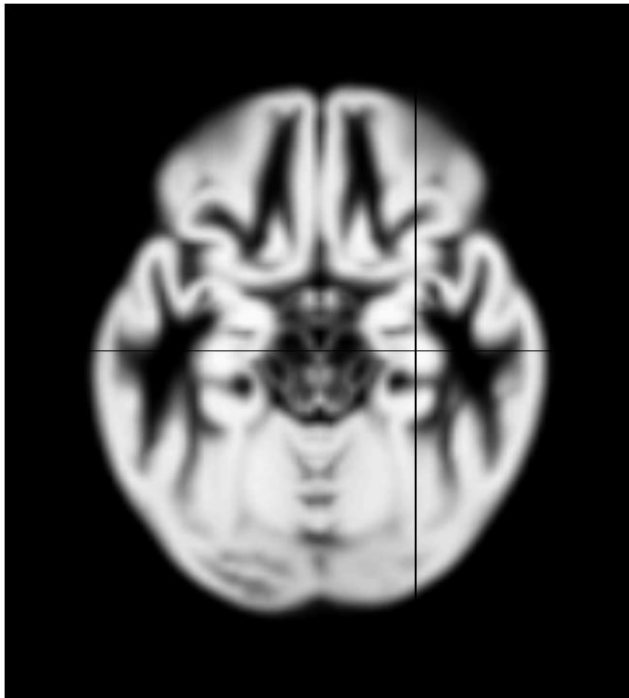
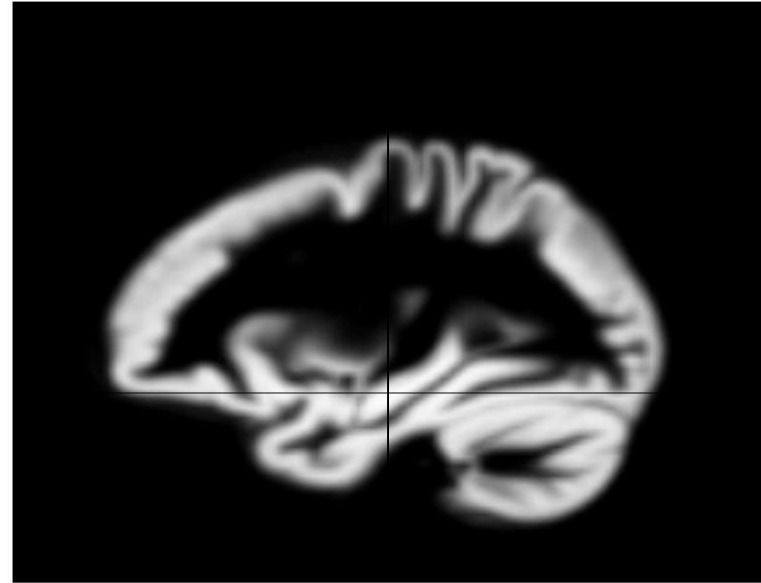
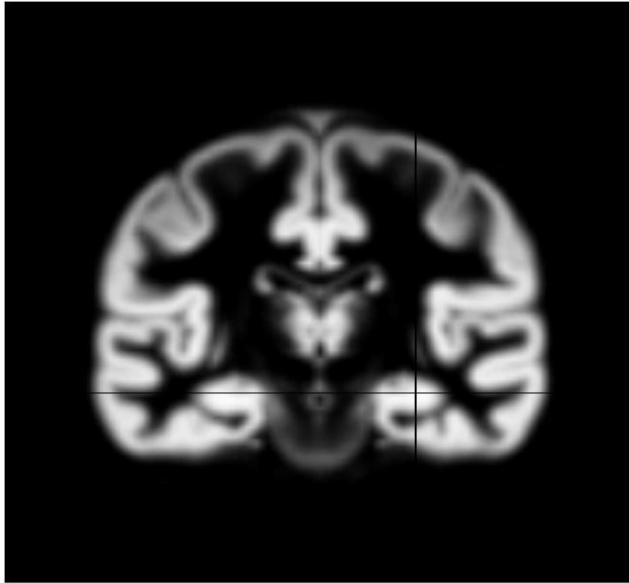


Final  
template



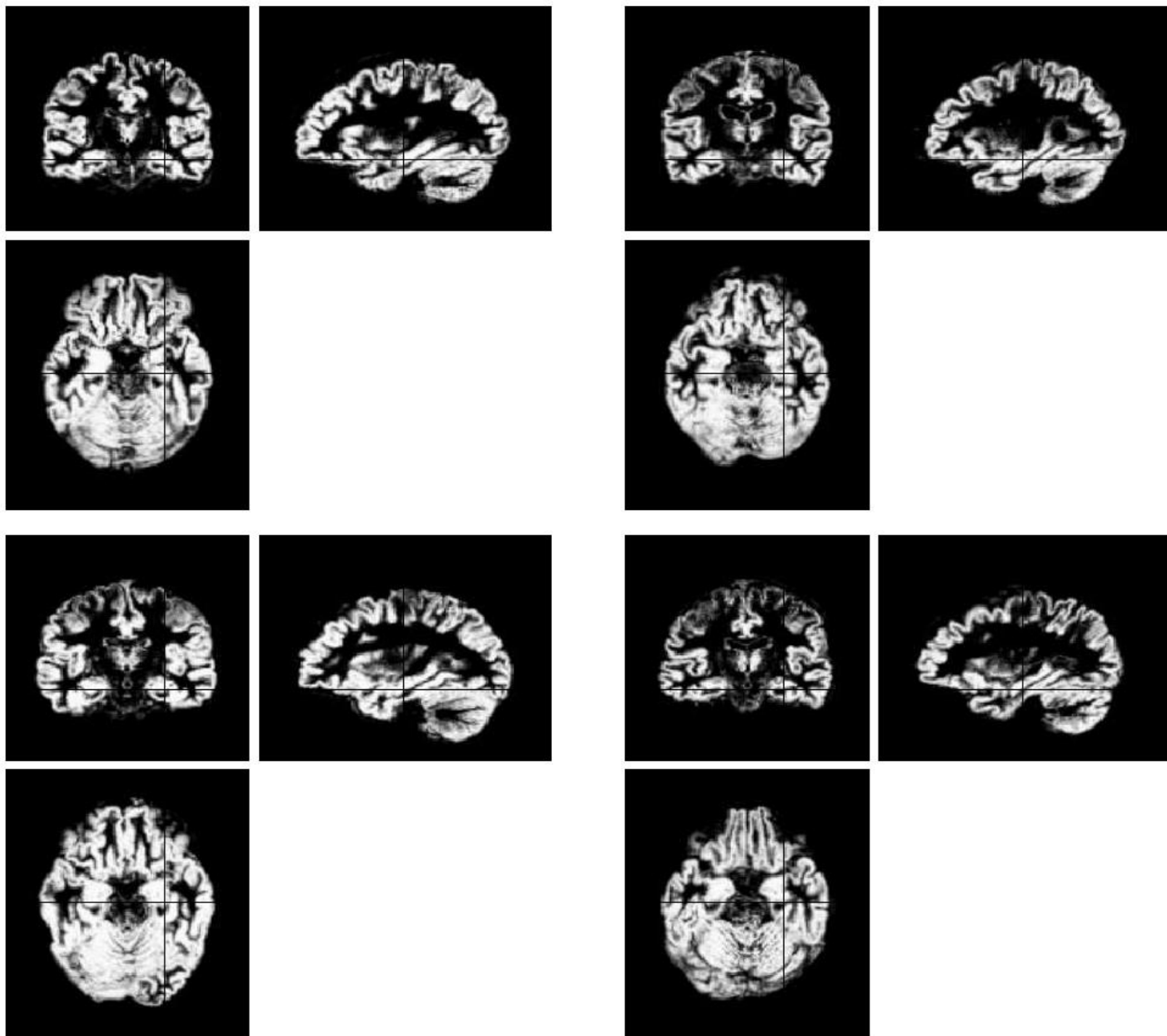


Grey matter  
average of 452  
subjects – affine

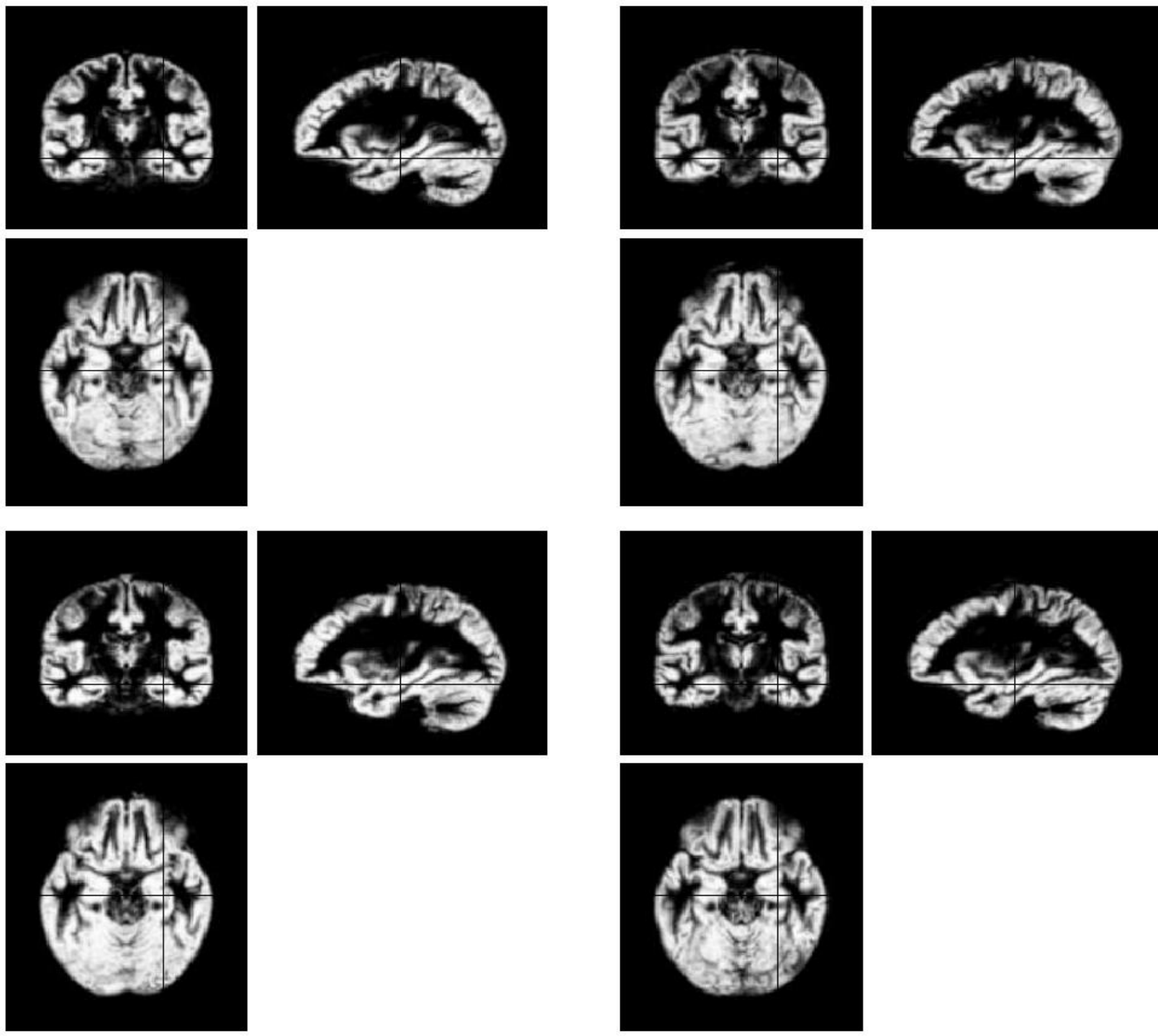


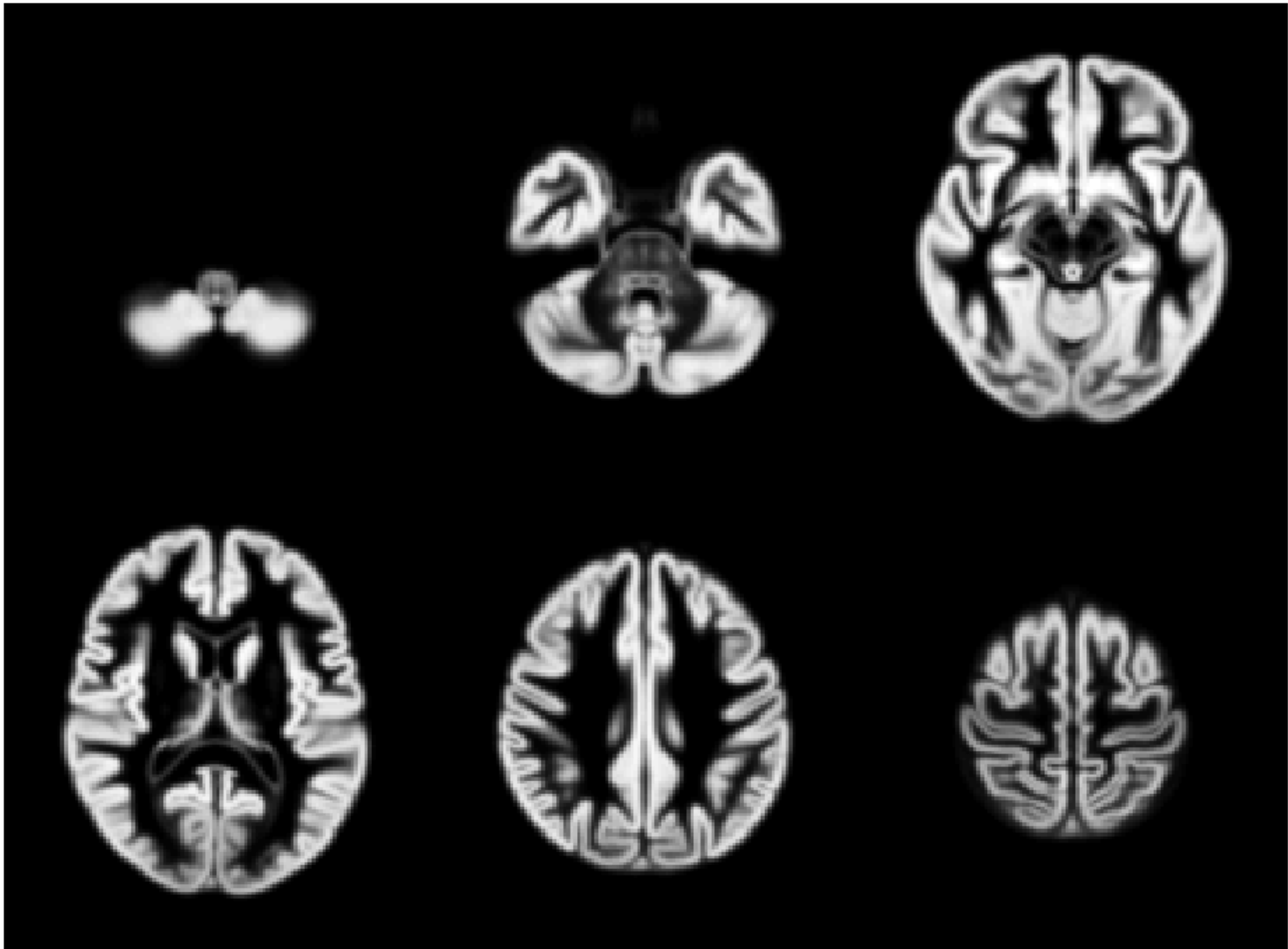
Grey matter  
average of 471  
subjects

Initial  
GM images

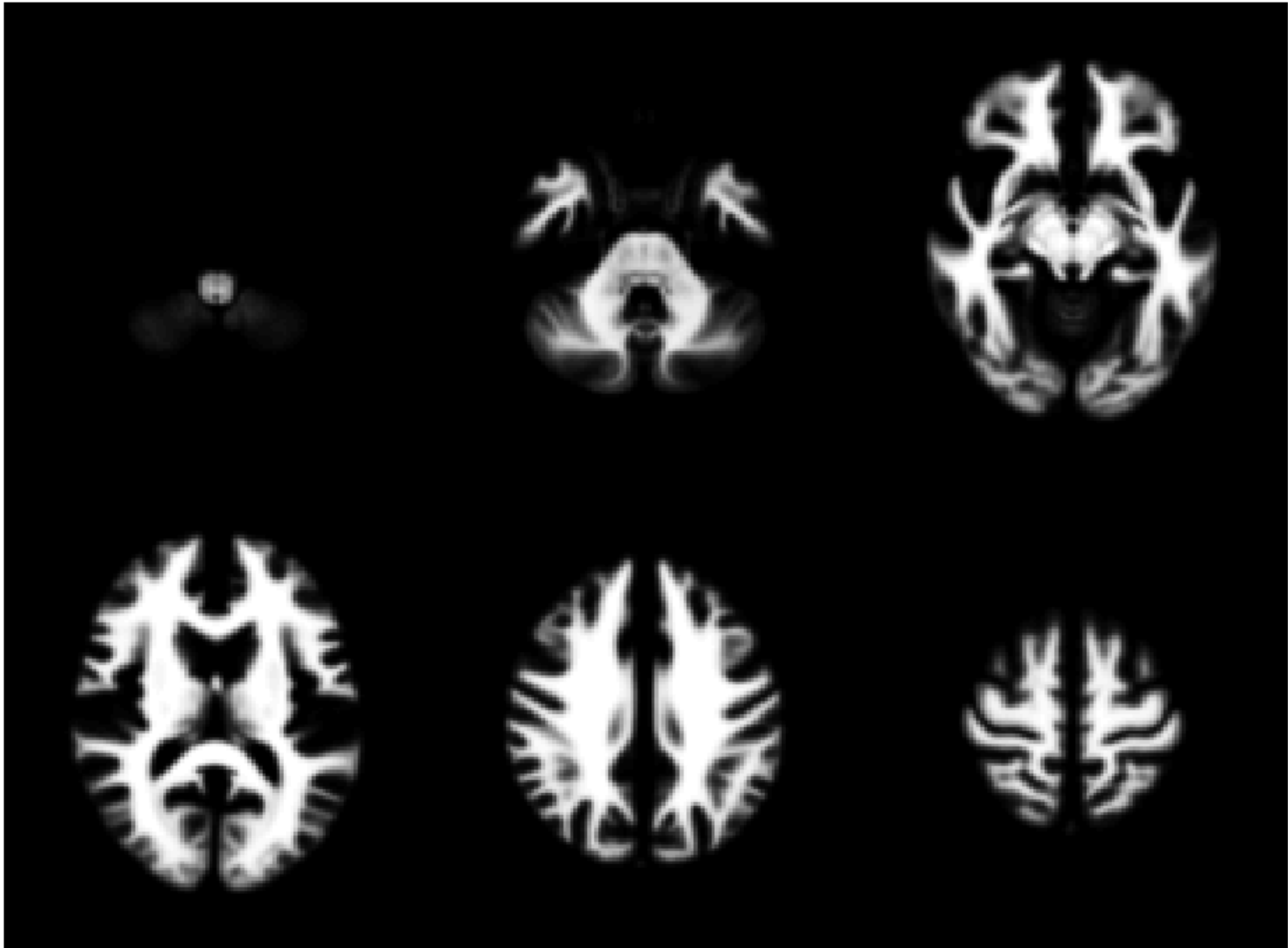


Aligned  
GM images

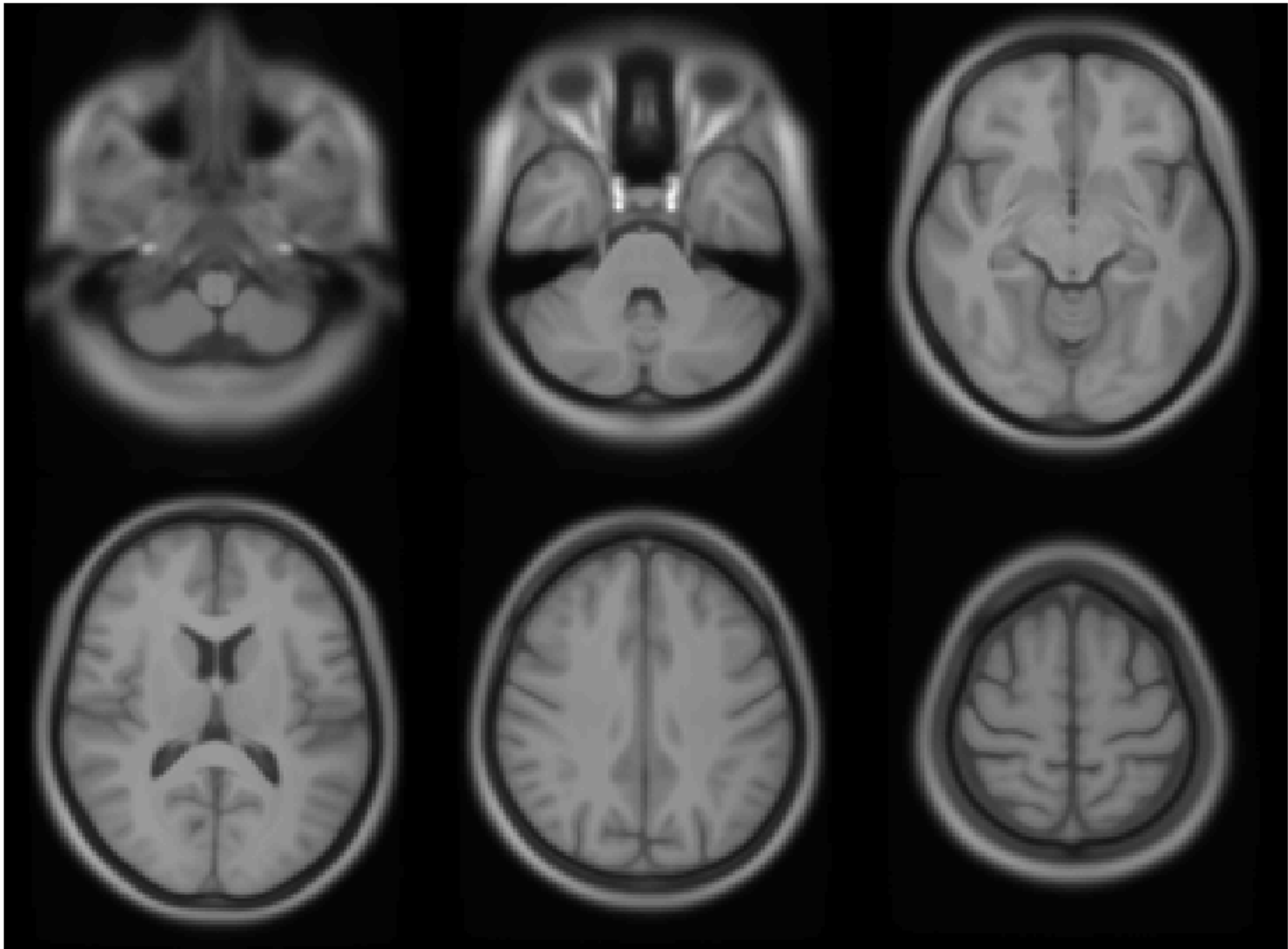




471 Subject Average

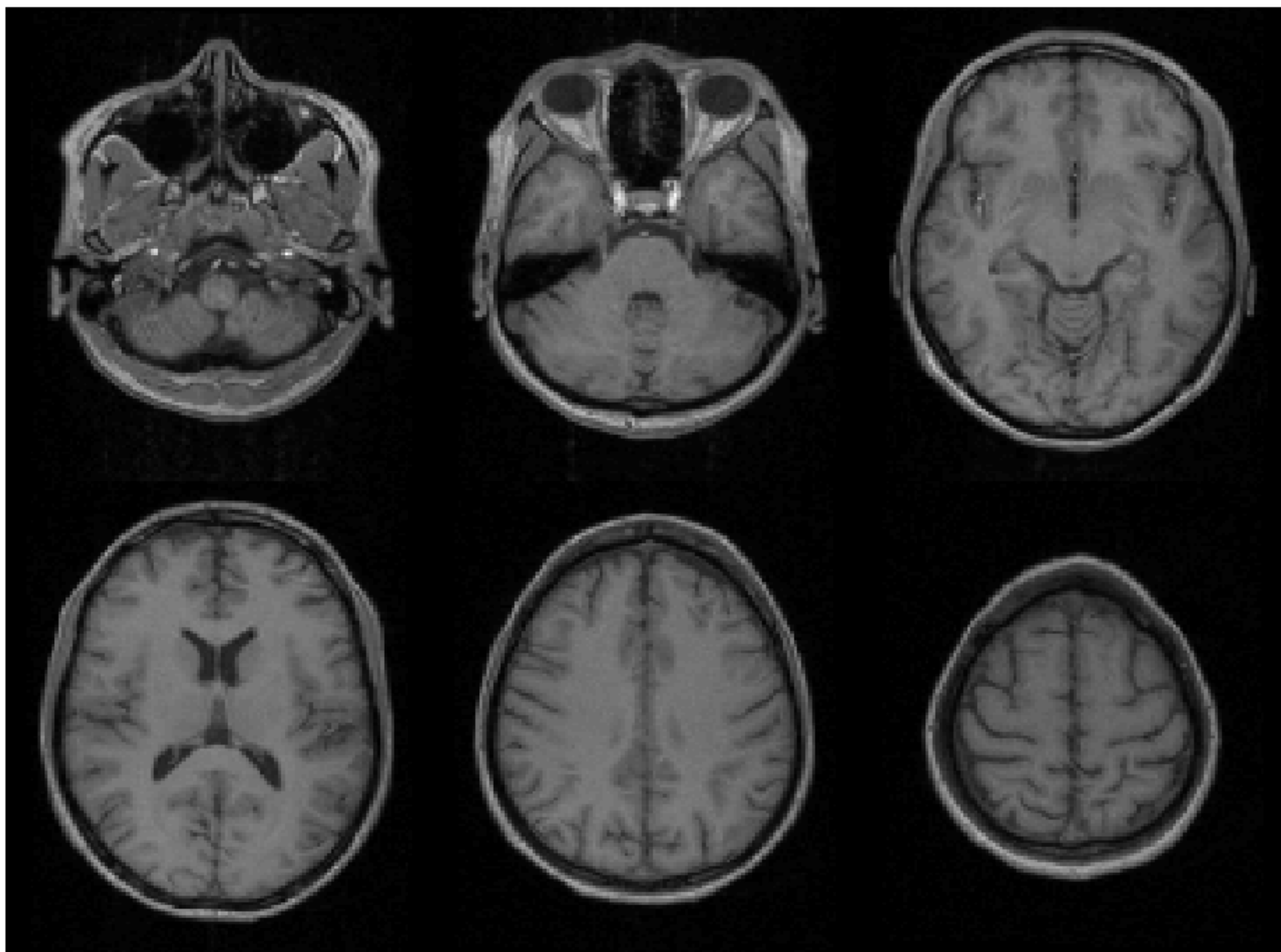


471 Subject Average

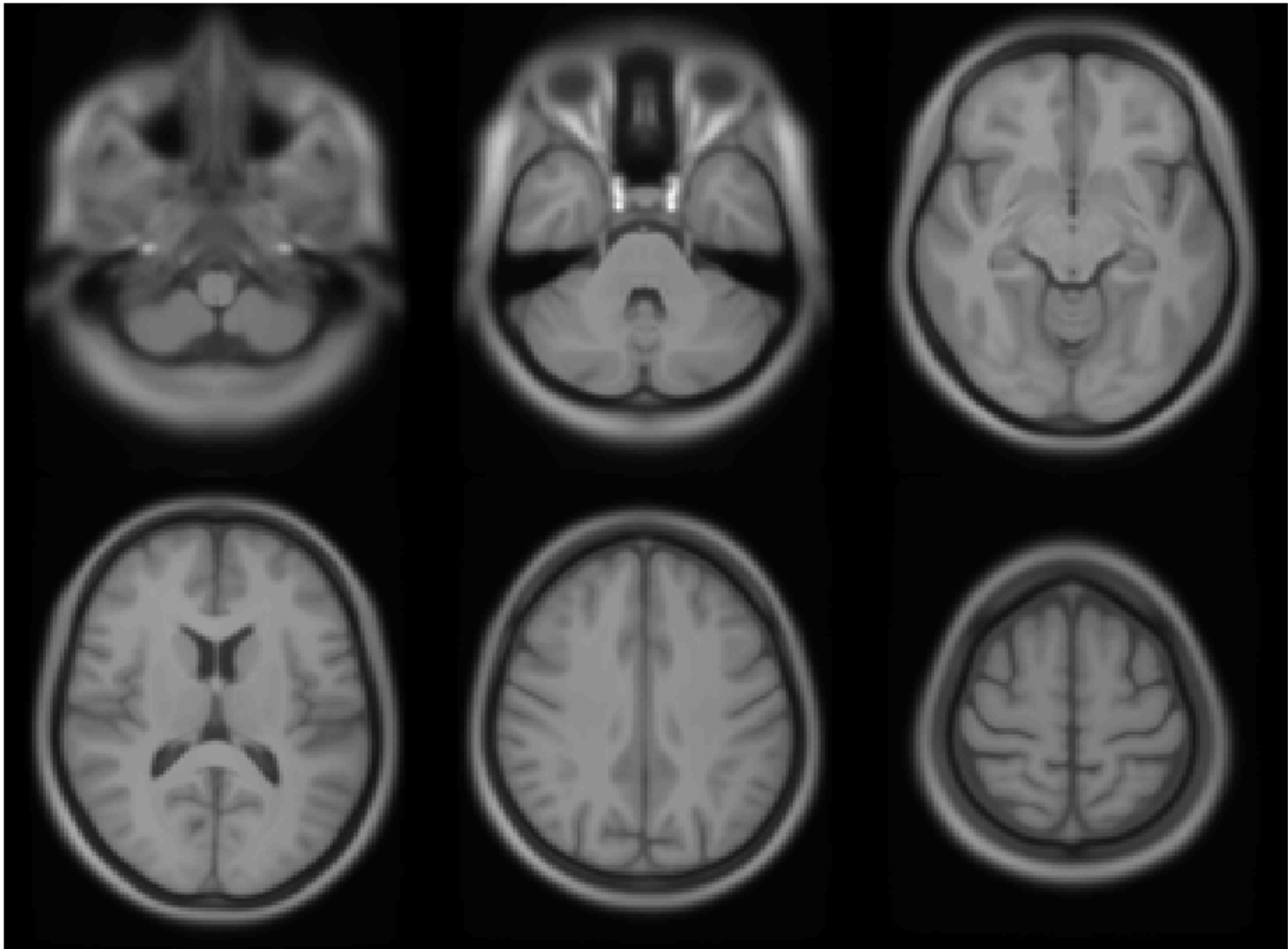


471 Subject Average

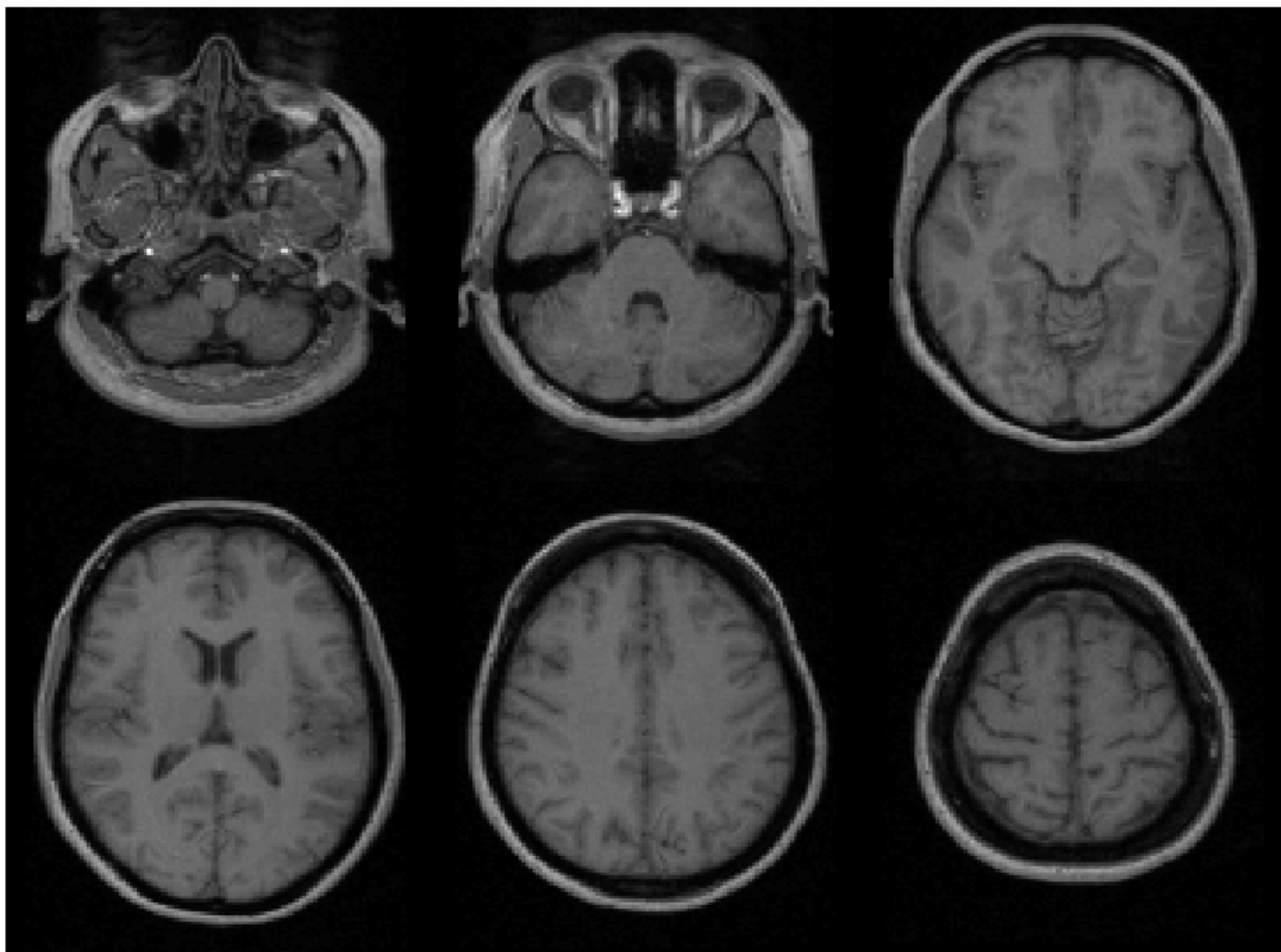




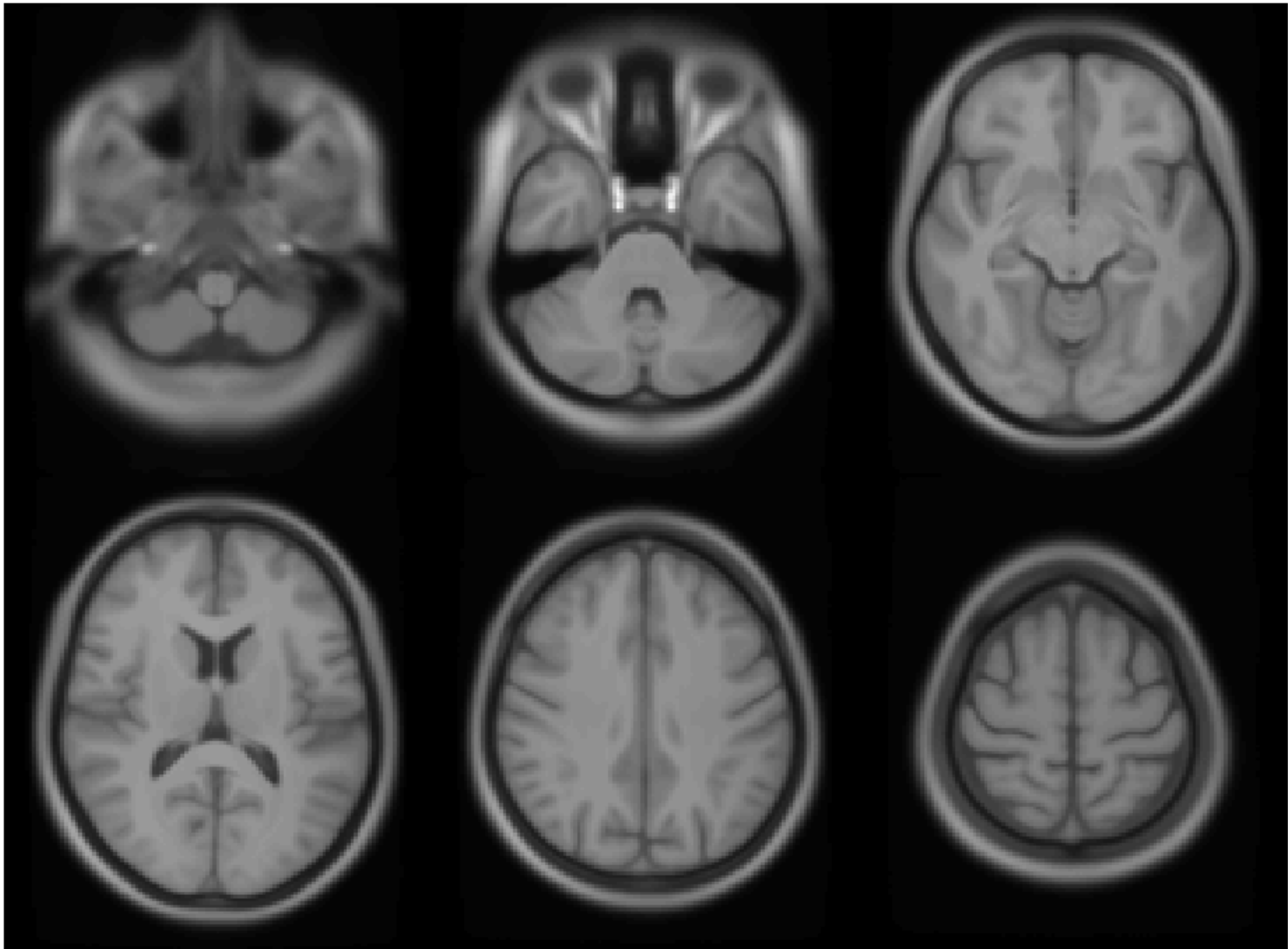
Subject 1



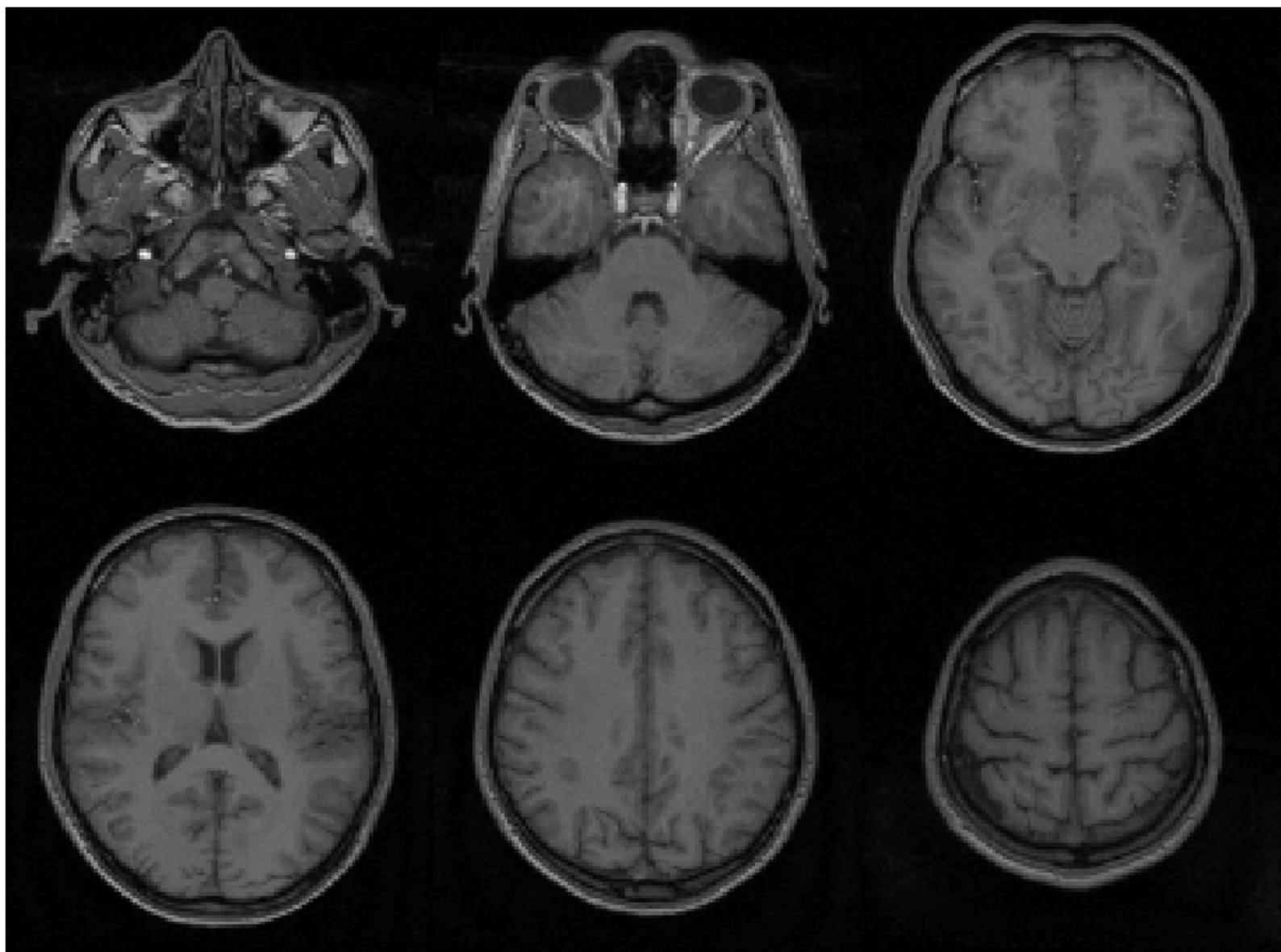
471 Subject Average



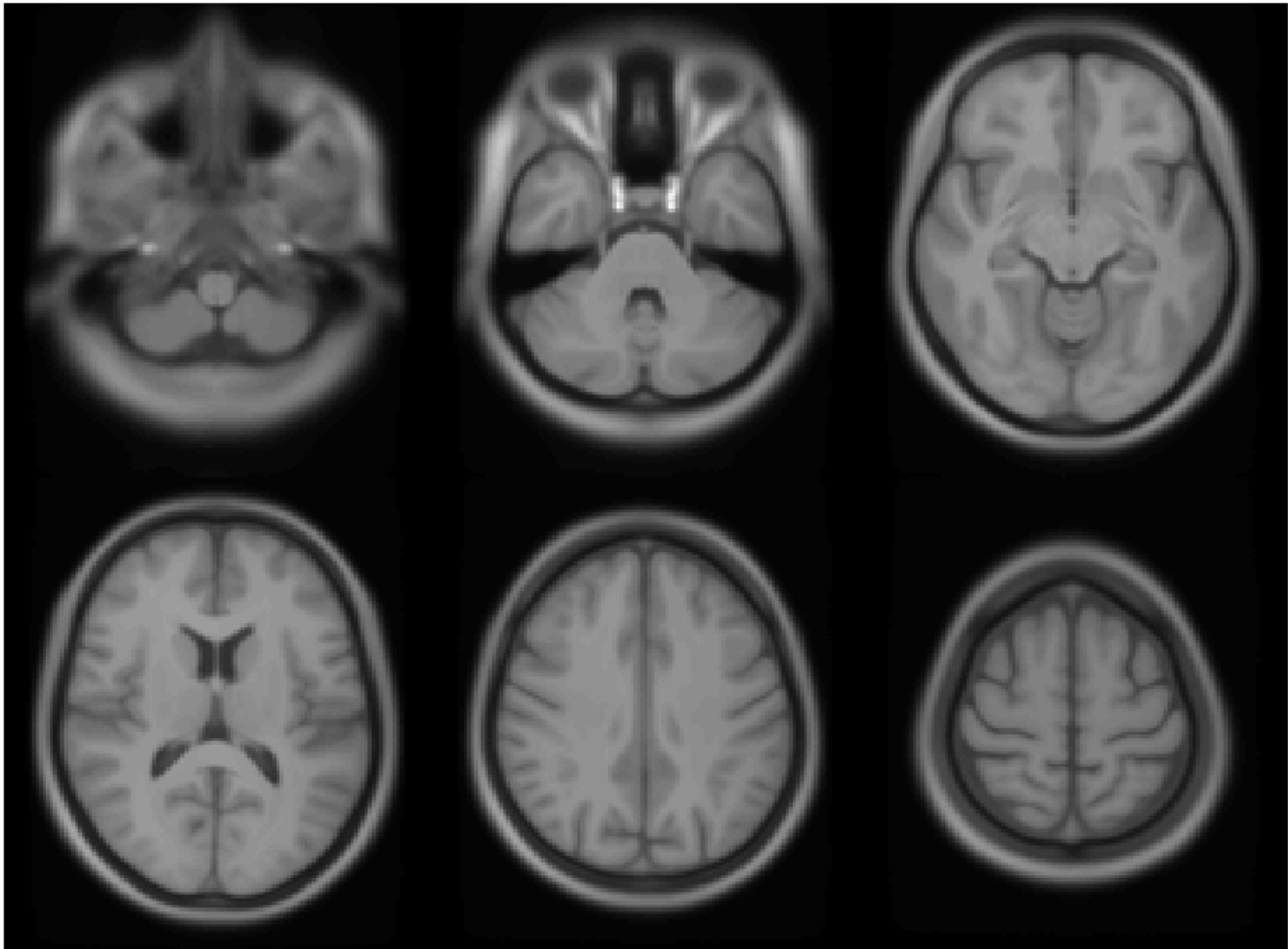
Subject 2



471 Subject Average



Subject 3

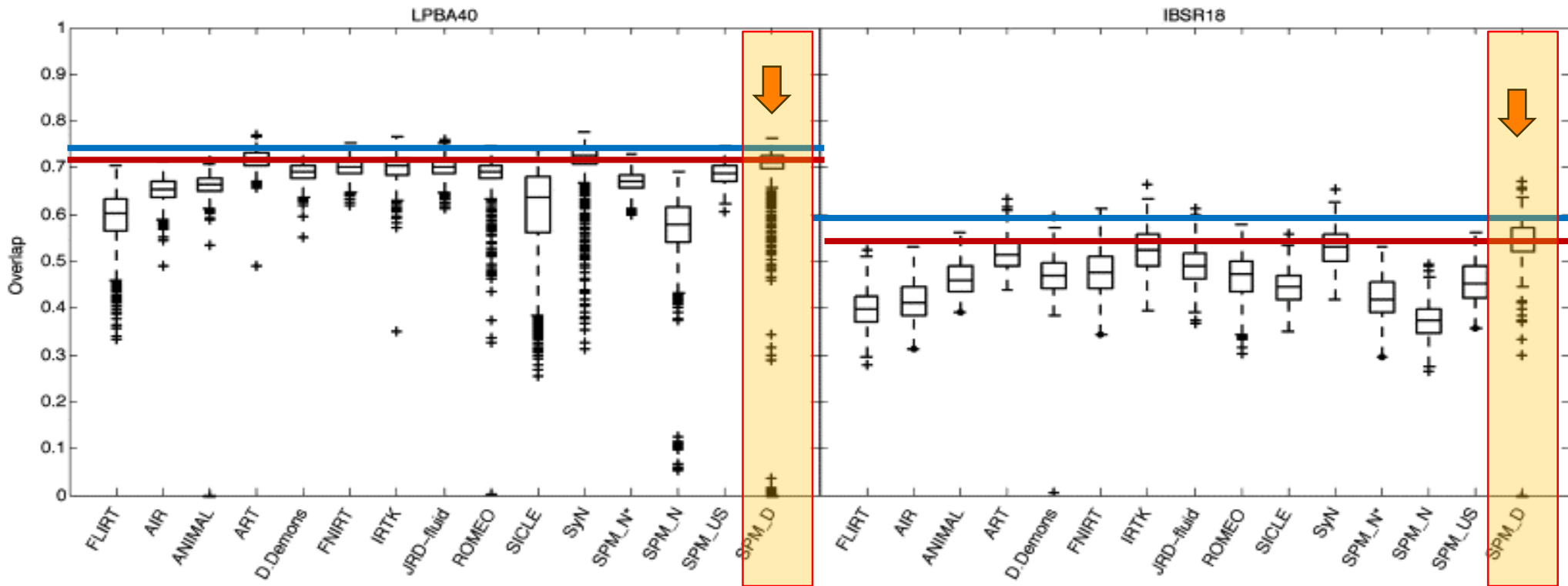
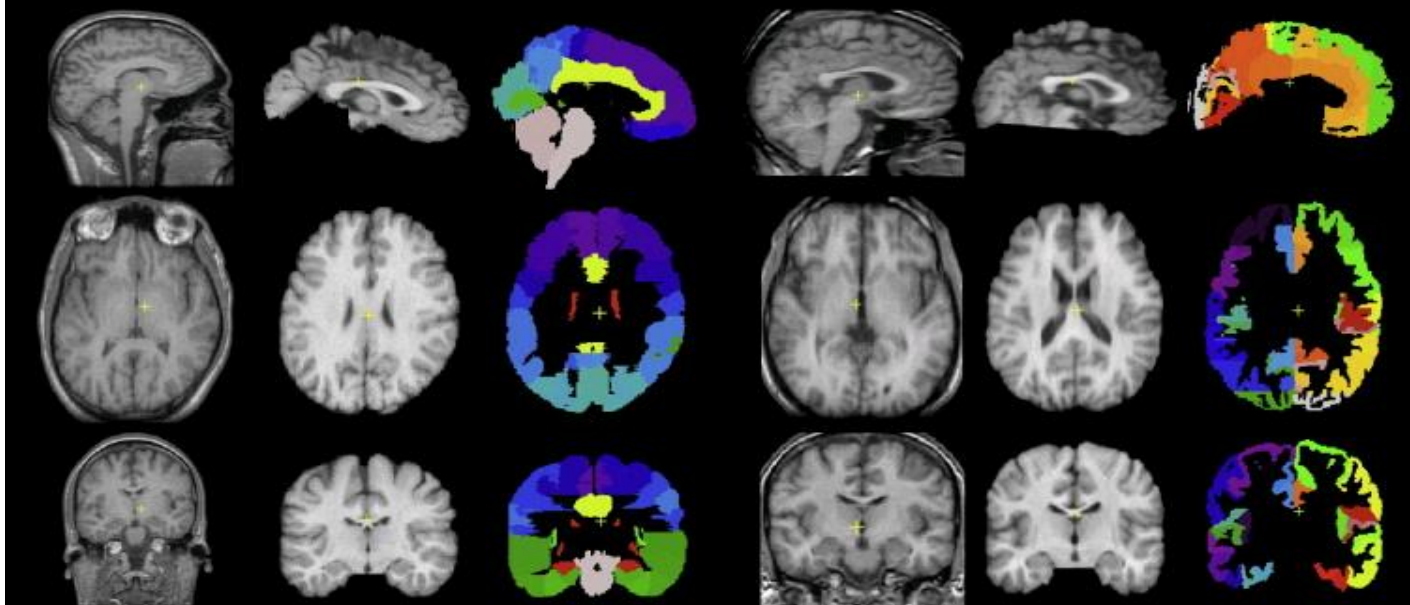


471 Subject Average

LPBA40

IBSR18

# Evaluations of nonlinear registration algorithms



# Contents

- \* Normalise/Segment

- \* Dartel

- \* **Smoothing**

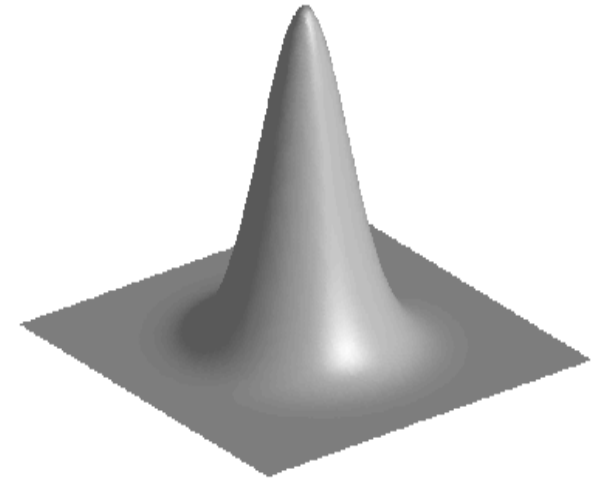
  - \* **Compensating for inaccuracies in inter-subject alignment**



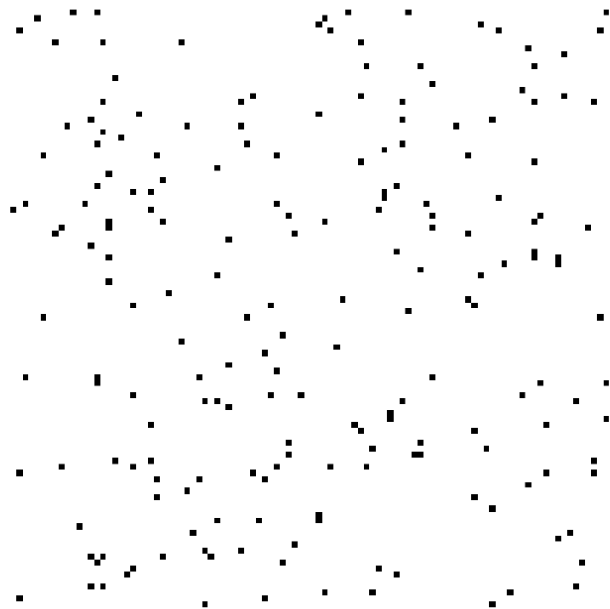
# Smooth

Blurring is done by **convolution**.

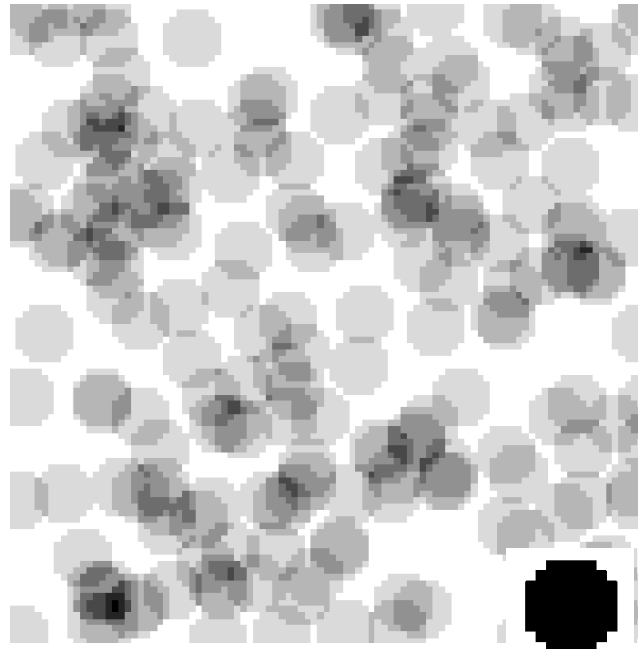
Each voxel after smoothing effectively becomes the result of applying a weighted region of interest (ROI).



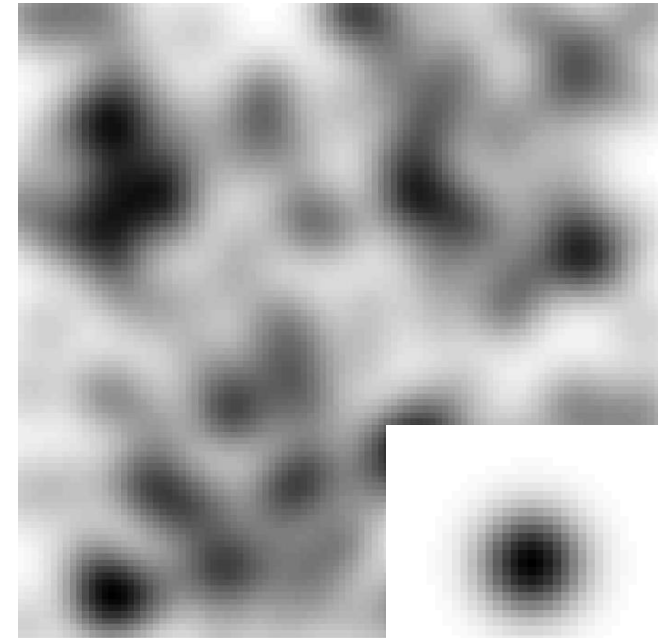
Before convolution



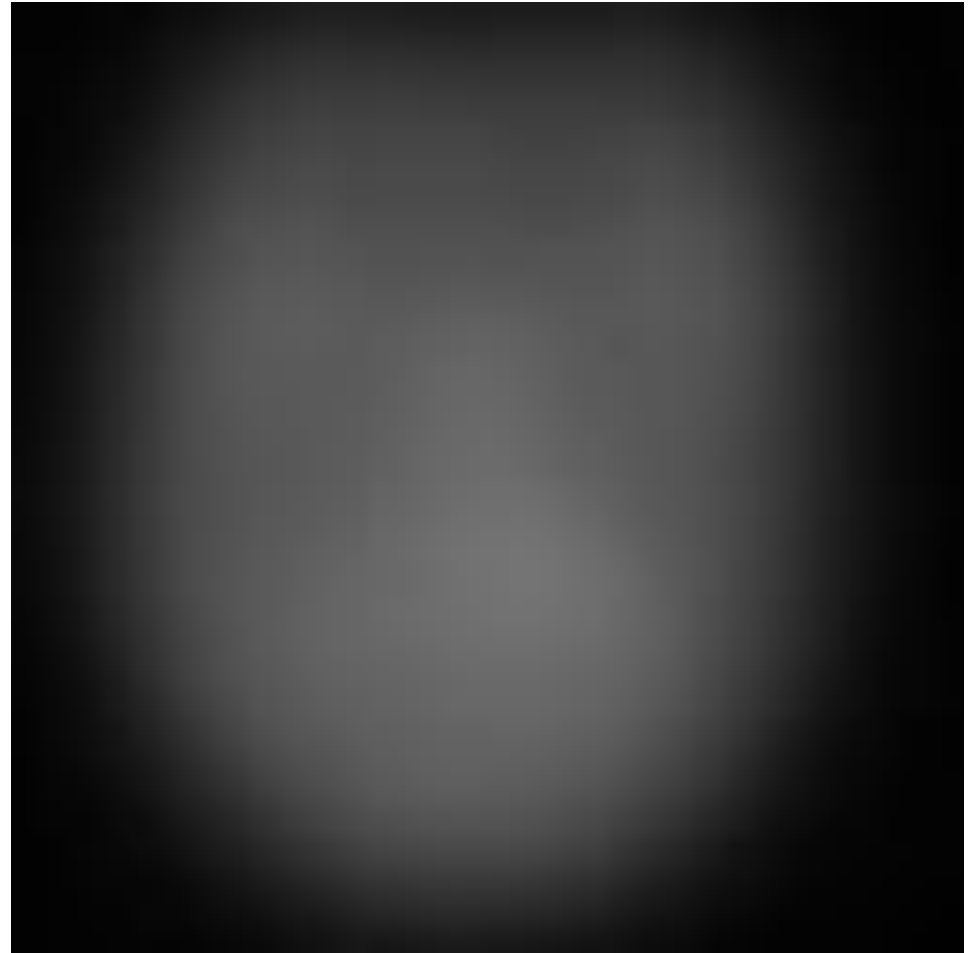
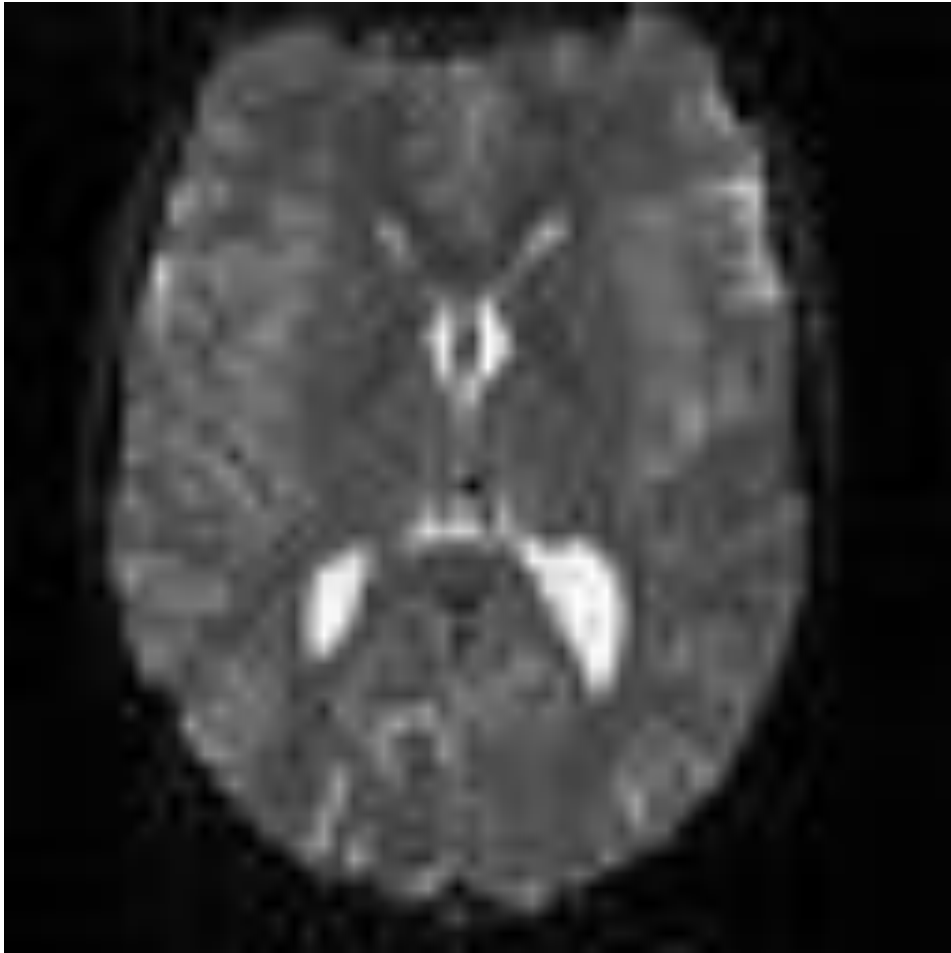
Convolved with a circle



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).