Structural Segmentation

- FAST tissue-type segmentation
- FIRST sub-cortical structure segmentation
- BIANCA segmentation of white matter lesions
- FSL-VBM voxelwise grey-matter density analysis
- SIENA/SIENAX global atrophy estimation
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FAST
FMRIB’s Automated Segmentation Tool
generic tissue-type segmentation and bias field correction
FAST: Input

- First use BET to remove non-brain. All volumetric results are highly sensitive to errors here. For bias-field correction alone the errors do not matter that much.

- Input is normally a single image (T1, T2, proton-density....)

- Or several inputs ("multichannel")
- For multi-channel, all must be pre-aligned (FLIRT)
Intensity Model

tissue intensity distributions

• Histogram = voxel count vs. intensity

• Model = mixture of Gaussians

• If well separated, have clear peaks; then segmentation easy

• Overlap worsened by:
  • Bias field
  • Blurring
  • Low resolution
  • Head motion
  • Noise
Probability Model

- Histogram = probability distribution function
- Model = mixture of Gaussians
- Probability determined for each tissue class

For example:
Voxel near WM/GM border

P(CSF) near zero
P(GM) low
P(WM) moderate

Intensity = 17203
Bias Field Correction

- MRI RF (radio-frequency field) inhomogeneity causes intensity variations across space.
- Causes problems for segmentation.
- Need to remove bias field before or during segmentation.
- Becomes more common and problematic at high field.
Bias Field Correction

Original

Bias

Restored

Histograms
Use Spatial Neighbourhood Information (MRF)

- Neighbourhood information: “if my neighbours are grey matter then I probably am too”

- Simple classifiers (like K-means) do not use spatial neighbourhood information

- More robust to noise

- Need the right balance between believing neighbours or intensity

Likely configuration
High probability

Unlikely configuration
Low probability
Use Spatial Neighbourhood Information (MRF)

Combine with probability based on Gaussian Mixture Model:

$$\text{Final log probability} = \log p(\text{intensity}) + \beta \log p(\text{MRF})$$

Final result depends on $\beta$ value

This is user-adjustable
Effect of MRF Weighting

\[ \beta = 0 \]

\[ \beta = 0.1 \]

\[ \beta = 0.3 \]

\[ \beta = 0.5 \]
Effect of MRF Weighting

β = 0

β = 0.1

β = 0.3

β = 0.5
Partial Volume Modelling

- A better model is what fraction of each voxel is tissue X?
- “partial volume” = fraction of CSF, GM or WM

This substantially improves accuracy of volume estimation
FAST - The Overview

• Initial (approximate) segmentation
  • Tree-K-means

• Iterate
  • Estimate bias field
  • Estimation segmentation; iterate
    • Update segmentation (intensity + MRF)
    • Update tissue class parameters
      (mean and standard deviation)

• Apply partial volume model
  • MRF on mixel-type (how many tissues)
  • PV Estimation
Optional Use of Priors (tissue probability maps)

- Segmentation priors = average of many subjects’ segmentations
- Can use priors to weight segmentation, but can skew results (e.g. due to misalignment)
- FAST does not use priors by default
- If bias field is very bad, priors can be turned on to help initial segmentation (alternatively, do more iterations)
- Can also be turned on to feed into final segmentation (e.g. to aid segmentation of deep grey .... but see FIRST)

<table>
<thead>
<tr>
<th>Mean $T_1$-wt</th>
<th>GM</th>
<th>Priors</th>
<th>WM</th>
<th>CSF</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1.png" alt="Image" /></td>
<td><img src="image2.png" alt="Image" /></td>
<td><img src="image3.png" alt="Image" /></td>
<td><img src="image4.png" alt="Image" /></td>
<td><img src="image5.png" alt="Image" /></td>
</tr>
</tbody>
</table>
Other Options

**FAST:**

- **Bias field smoothing (-l)**
  - vary spatial smoothing of the bias field

- **MRF beta (-H)**
  - vary spatial smoothness of the segmentation

- **Iterations (-I)**
  - vary number of main loop iterations

**fsl_anat:**

- This is an alternative tool that performs brain extraction and bias field correction (along with other things) in a different way and so is worth trying out too
FAST
FMRIB’s Automated Segmentation Tool

Summary
- Typically use a single T1-weighted image
- Multichannel is an option
- Segments into three main tissue-types:
  - Grey Matter, White Matter and CSF
- Models and corrects for bias field
  - Can be used just for bias field correction
- Combines intensity and neighbourhood information
- Partial Volumes Estimates (PVE) are most useful and more accurate for volume calculations
- Can use priors, but can cause bias, so not the default
- Have several adjustable parameters to optimise output
FIRST
FMRIB’s Integrated Registration & Segmentation Tool
Segmentation of subcortical brain structures
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Segmentation of subcortical brain structures
Sub-Cortical Structure Models

Incorporate prior anatomical information via explicit shape models
Have 15 different sub-cortical structures (left/right separately)

- Thalamus
- Caudate
- Putamen
- Accumbens
- Hippocampus
- Pallidum
- Amygdala
- Brainstem
Training Data

• Manual segmentations courtesy of David Kennedy, Center for Morphometric Analysis (CMA), Boston

• 336 complete data sets

• T₁-weighted images only

• Age range 4 to 87
  - Adults: Ages 18 to 87, Normal, schizophrenia, AD
  - Children: Ages 4 to 18, Normal, ADHD, BP, prenatal cocaine exposure, schizophrenia.
Model Training: Alignment to MNI152 space

- All CMA data affine-registered to MNI152 space
  - 1mm resolution, using FLIRT

- 2-stage process:
  - Whole head 12 DOF affine
  - 12 DOF affine with MNI-space sub-cortical mask
Deformable Models

- Model: 3D mesh
- Use anatomical info on shape & intensity (from training)
- Deformation: iterative displacement of vertices
- Maintain point (vertex) correspondence across subjects
The Model: Shape

- Model average shape (from vertex locations)

- Also model/learn *likely variations* about this mean
  - modes of variation of the population; c.f. PCA
  - also call eigenvectors

- Average shape and the modes of variation serve as prior information (known before seeing the new image that is to be segmented)
  - formally it uses a Bayesian formulation
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\[ X = \mu_X + U \Sigma b_X \]

- mean
- Eigenvectors (modes)
- Singular values
- Shape parameters
• Intensity is then sampled along the surface normal and stored

• Learn average intensity and “modes of variation”

• Aside: the intensities are re-scaled to a common range and the mode of the intensities in the structure is subtracted
FIRST - Model

- **Model**: 3D mesh
- **Training the model**: learn average shape/intensity and likely variations ("modes of variation") about both
- **Fitting the model**: Find the "best" shape by searching along modes of variation and uses intensity match to judge fitting success
Boundary Correction

• FIRST models all structures by meshes

• Converting from meshes to images gives two types of voxels:
  - boundary voxels
  - interior voxels

• Boundary correction is necessary to decide whether the boundary voxels should belong to the structure or not

• Default correction uses FAST classification method and is run automatically (uncorrected image is also saved)
  - ensures that neighbouring structures do not overlap
Vertex Analysis

- Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects)
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Controls

Disease

Consider each vertex in turn
Vertex Analysis

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Controls

Disease

Consider each vertex in turn

Do a test on distance of these vertices to average shape
Vertex Analysis

• Use a univariate test at each vertex to measure difference in location (e.g. between means of two groups of subjects) using distance along surface normals.

• Results are now given as images and statistics done with randomise.

• Can do analysis in MNI space or native structural space.

• MNI space analysis normalises for brain size.
Running FIRST

• Inputs:
  - $T_1$-weighted image
  - Model (built from training data) - provided with FSL

• Applying FIRST
  - A single command: `run_first_all`
    1. registers image to MNI152 1mm template
    2. fits structure models (meshes) to the image
    3. applies boundary correction (for volumetric output)

• Analysis:
  - Use command: `first_utils`
    • volumetric analysis (summary over whole structure)
    • vertex analysis (localised change in shape and/or size)
    • randomise (with multiple comparison correction)
FIRST
FMRIB’s Integrated Registration & Segmentation Tool

Summary

• Specific to certain deep grey structures
• Uses broad training set - very general demographics
• Can only work with T1-weighted images
• Models average and variations of shape and intensity
• Represents the boundary as a set of points
• Separate boundary correction step to get voxel labels

• Can perform vertex analysis to look at changes in shape and size