Abstract

Reference for segmentation in neuroimaging are collected. Both tissue segmentation and parcellation is included.

This structured bibliography is part of a larger collection of bibliographies see http://www.imm.dtu.dk/~fn/bib/Nielsen2001Bib/. The bibliography is written in \LaTeX and \BibTeX and should be available both as HTML and PostScript.

The bibliography is probably far from complete, but new references are added whenever the author finds new material and has the time to add them. You can email the author if corrections are required or you have found some reference that you fell ought to be included: fn@imm.dtu.dk.

Thanks to Jürgen Hänggi, Jonathan Bailleul and Arno Klein who provided information. Much of the information in this bibliography is from the SPM mailing list posted by numerous researchers.

This work is or has been funded by the European Union project MAPAWAMO, the International Neuroimaging Consortium (INC) American Human Brain Project, Danish Research Councils through THOR Center for Neuroinformatics and the Villum Kann Rasmussen Foundation.

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1 General references

A list of references is available from http://neuro-www.mgh.harvard.edu:16080/cma/seg/references.html

1.1 Unclassified

(Harris et al., 2001) parcellation of cortex with brain warping and manual atlas. PMID: 8978636, PMID: 9786148, PMID: 11185422

2 Inhomogeneity correction

MRI intensity non-uniformity can have a substantial impact on the performance of the segmentation results (Sled et al., 1997a) and the image should be bias field corrected. Table 1 shows a number of the tools in use. (Ashburner and Friston, 1998) describes a combination of tissue classification with inhomogeneity correction. (Arnold et al., 2001; Schaper et al., 2001) compares six algorithms for inhomogeneity correction (N3, hum, eq, bfc, cma and SPM99). Other references in relation to bias field estimation is (Guillemaud and Brady, 1997).

<table>
<thead>
<tr>
<th>Name</th>
<th>Method and Description</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>cma</td>
<td>Polynomial basis functions. Part of segmentation program</td>
<td>Center for Morphometric Analysis, Massachusetts General Hospital</td>
</tr>
<tr>
<td>EMS *</td>
<td>“FMRIB’s Automated Segmentation Tool”. A segmentation tool including inhomogeneity correction</td>
<td>(Van Leemput, 2001, p. 15–19), (Van Leemput et al., 1999a)</td>
</tr>
<tr>
<td>eq</td>
<td></td>
<td>(Cohen et al., 2000)</td>
</tr>
<tr>
<td>FAST *</td>
<td>Implemented in the mri_normalize program. Can be executed from csurf GUI.</td>
<td><a href="http://www.fmrib.ox.ac.uk/fsl/fast-index.html">http://www.fmrib.ox.ac.uk/fsl/fast-index.html</a></td>
</tr>
<tr>
<td>FreeSurfer *</td>
<td>The “itk::MRIBiasFieldCorrectionFilter” class in the National Library of Medicine Insight Segmentation and Registration Toolkit (ITK) based on Legendre polynomial</td>
<td>(Dale et al., 1999; Fischl et al., 1999a; Fischl et al., 1999b; Fischl and Dale, 2000; Fischl et al., 2001; Busa, 2002) <a href="http://surfer.nmr.mgh.harvard.edu/">http://surfer.nmr.mgh.harvard.edu/</a></td>
</tr>
<tr>
<td>hum</td>
<td></td>
<td>(Brinkmann et al., 1998)</td>
</tr>
<tr>
<td>ITK *</td>
<td>Implemented in the mri_normalize program. Can be executed from csurf GUI.</td>
<td><a href="http://www.itk.org/-HTML/MRIBiasCorrection.htm">http://www.itk.org/-HTML/MRIBiasCorrection.htm</a>, (Styner et al., 2000; Styner and Gerig, 1997)</td>
</tr>
<tr>
<td>N3 *</td>
<td></td>
<td>(Sled et al., 1998; Sled et al., 1997b; Sled, 1997) <a href="http://www.bic.mni.mcgill.ca/software/N3/">http://www.bic.mni.mcgill.ca/software/N3/</a></td>
</tr>
<tr>
<td>PABIC *</td>
<td>“PArametric BIas field Correction”. Included in ITK.</td>
<td>(Styner et al., 2000; Styner and Gerig, 1997)</td>
</tr>
<tr>
<td>SPM *</td>
<td>Available in the functions with prefix spm_bias.</td>
<td>(Ashburner and Friston, 2000)</td>
</tr>
</tbody>
</table>

Table 1: MRI Inhomogeneity correction tools.
3 Stripping

“Stripping”, “skull-stripping”, “brain/non-brain segmentation”, “brain surface extraction”, “brain extraction” or “brain extraction algorithms (BEA)” remove the skull and scalp and maintains the “brain” which usually includes white and grey matter as well as CSF. Table 2 is a list of the tools for this operation. A study showed that McStrip was much slower than BSE and BET, but that it was the most precise (Boesen et al., 2003). Another algorithm is described in (Atkins and Mackiewich, 1998). The AFNI and FreeSurfer packages also enable skull stripping.

Table 2: Stripping

<table>
<thead>
<tr>
<th>Name</th>
<th>Impl.</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>3dIntracranial *</td>
<td>AFNI</td>
<td>Brain extraction included in</td>
<td>(Ward, 1999), <a href="http://afni.nimh.nih.gov/afni/-">http://afni.nimh.nih.gov/afni/-</a></td>
</tr>
<tr>
<td></td>
<td></td>
<td>“Brain extraction meta-algorithm”</td>
<td>doc/help/3dIntracranial.html</td>
</tr>
<tr>
<td>BEMA</td>
<td></td>
<td>“Brain extraction meta-algorithm”</td>
<td>(Rex et al., 2004)</td>
</tr>
<tr>
<td>BET *</td>
<td></td>
<td>“Brain Extraction Tool” by Stephen Smith. Conveniently included in FSL, MRIcro and mri3dX</td>
<td>(Smith, 2002; Smith, 2000),</td>
</tr>
<tr>
<td></td>
<td></td>
<td>“Brain Surface Extraction” part of BrainSuite. Interactive GUI version exists with the X/Motif-based xbse</td>
<td><a href="http://www.fmrib.ox.ac.uk/fsl/bet/">http://www.fmrib.ox.ac.uk/fsl/bet/</a>, MRIcro: <a href="http://www.psychology.nottingham.ac.uk/staff/crl/mricro.html">http://www.psychology.nottingham.ac.uk/staff/crl/mricro.html</a></td>
</tr>
<tr>
<td>McStrip *</td>
<td>IDL, C</td>
<td>“Minneapolis Consensus Strip” (MCS). Consensus/hybrid based method relying on AIR5.0 and BSE</td>
<td>(Shattuck et al., 2001; Sandor and Leahy, 1997), <a href="http://neuroimage.usc.edu/BSE/">http://neuroimage.usc.edu/BSE/</a></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Can be executed from csurf GUI.</td>
<td>(Rehm et al., 2004; Rehm et al., 1999),</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><a href="http://www.neurovia.umn.edu/incweb/McStrip_download.html">http://www.neurovia.umn.edu/incweb/McStrip_download.html</a></td>
</tr>
<tr>
<td>FreeSurfer *</td>
<td></td>
<td></td>
<td>(Dale et al., 1999; Fischl et al., 1999a; Fischl et al., 1999b; Fischl and Dale, 2000; Fischl et al., 2001; Busa, 2002)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><a href="http://surfer.nmr.mgh.harvard.edu/">http://surfer.nmr.mgh.harvard.edu/</a></td>
</tr>
</tbody>
</table>
4 Brain tissue segmentation

4.1 Methods for segmentation


<table>
<thead>
<tr>
<th>Input Output</th>
<th>I</th>
<th>A</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>T1, T2, PD GM, WM, CSF</td>
<td>-</td>
<td>-</td>
<td>Selection of a training classes for the segmentation</td>
<td>(Harris et al., 1999)</td>
</tr>
<tr>
<td>T1, T2, PD WM, GM, CSF, outliers</td>
<td>✓</td>
<td>✓</td>
<td>Gaussian mixture estimated robustly. Lesions detected as outliers. Bias field modeled with polynomials. Markov random field for prior volumes</td>
<td>(Van Leemput et al., 2001; Van Leemput et al., 2000)</td>
</tr>
</tbody>
</table>

4.2 Tools

Table 4: Tools for segmentation

<table>
<thead>
<tr>
<th>Name</th>
<th>Input</th>
<th>Output</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>EMS</td>
<td>GM, WM, CSF, ...</td>
<td></td>
<td>‘Expectation-Maximization Segmentation’ implemented as an SPM plugin</td>
<td>(Van Leemput et al., 2001; Van Leemput et al., 1999b; Van Leemput et al., 1999a; Maes et al., 1997; Van Leemput et al., 2000) <a href="http://bilbo.esat.kuleuven.ac.be/web-pages/downloads/ems/ems.html">http://bilbo.esat.kuleuven.ac.be/web-pages/downloads/ems/ems.html</a></td>
</tr>
<tr>
<td>FAST *</td>
<td>GM, WM, CSF, ...</td>
<td></td>
<td>FMRIB’s Automated Segmentation Tool, Hidden Markov model with inhomogeneity correction</td>
<td>(Zhang et al., 2001a; Zhang et al., 2000; Zhang et al., 2001b) <a href="http://www.fmrib.ox.ac.uk/fsl/fast/">http://www.fmrib.ox.ac.uk/fsl/fast/</a></td>
</tr>
<tr>
<td>INSECT</td>
<td></td>
<td>GM, WM and CSF segmentation with an artificial neural network with 9-parameter spatial normalization</td>
<td>(Kollokian, 1996; Collins et al., 1994)</td>
<td></td>
</tr>
<tr>
<td>IRIS *</td>
<td></td>
<td></td>
<td>Visualization program with manual drawing by Guido Gerig and Sean Ho. One of the versions is called IRIS2000</td>
<td><a href="http://www.cs.unc.edu/~ru%C2%B1n/iris/">http://www.cs.unc.edu/~ru±n/iris/</a></td>
</tr>
<tr>
<td>Name</td>
<td>Input</td>
<td>Output</td>
<td>Description</td>
<td>Reference</td>
</tr>
<tr>
<td>------------</td>
<td>-------------</td>
<td>-------------</td>
<td>--------------------------------------</td>
<td>----------------------------------------</td>
</tr>
<tr>
<td>MIDAS</td>
<td></td>
<td>WM, GM, CSF, Lesion</td>
<td>“Medical Image Display and Analysis Software”. Interactive Unix/X program, with thresholding, region growing and morphological operations</td>
<td>(Freeborough et al., 1997)</td>
</tr>
<tr>
<td>SEAL</td>
<td></td>
<td></td>
<td>“Sulcal Extraction and Automated Labelling”</td>
<td>(Goualher et al., 1999)</td>
</tr>
<tr>
<td>SEGRAS WM, GM, CSF, Lesion</td>
<td></td>
<td></td>
<td>Trained artificial neural network used as classifier</td>
<td>Alan Rene Rasmussen, Hvidovre Hospital</td>
</tr>
<tr>
<td>SPM *</td>
<td></td>
<td></td>
<td>Segments into GM, WM, CSF and other. Implemented in versions SPM99 and SPM2.</td>
<td>(Ashburner and Friston, 1997; Ashburner and Friston, 2000; Ashburner and Friston, 2003)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Combined manual/automatic</td>
<td>(Zavaljevski et al., 2000)</td>
</tr>
</tbody>
</table>

### 4.3 Labeled brains

Probabilistic volumes for background, CSF, grey matter, white matter, fat, muscle/skin, skin, skull, glial matter, and “connective” are available in connection with the BrainWeb web-service/database from the URL http://www.bic.mni.mcgill.ca/brainweb/anatomic_normal.html.

“ICBM tissue probabilities” with gray matter, white matter and CSF are available from http://www.loni.ucla.edu/ICBM/ICBM_TissueProb.html.

The Internet Brain Segmentation Repository (IBSR), http://www.cma.mgh.harvard.edu/ibsr/, has simulated and real MRI data with gray/white/other expert segmentations.

Gray, white and CSF and brain mask are also distributed with the SPM2 package (in the `apriori` subdirectory).

### 4.4 Unclassified

(Ashburner and Friston, 2005)
Cortical surface extraction

“Cortical surface extraction” or “Cortical surface reconstruction”.

The “marching cubes” algorithm (Lorensen and Cline, 1987) can extract the cortical surface but with a bad results. The algorithm is implemented in Matlab, IDL, VTK and polyr (Jensen, 1995; Nielsen, 1998).

(Mohlberg and Zilles, 2000) obtains somewhat better results by combining surface warping, marching cubes and a fluid membrane model. (Zeng et al., 1999; MacDonald et al., 2000) use coupled inner and outer surface of the cortex. (Goldenberg et al., 2002) describes an other method. None of these seem to be publicly available. The MacDonald program seems to be available internally at MNI and able to handle MINC files, see http://www.bic.mni.mcgill.ca/~david/FAQ/How_to_extract_cortical_surfaces.txt.

FreeSurfer traces the white matter (Dale et al., 1999). A poor man’s method with a MRI T1 along this line is first to do skull-stripping, then threshold on a sufficiently high value to only incorporate the white matter and lastly make an ordinary marching cubes.

**Table 5: Cortical surface extraction**

<table>
<thead>
<tr>
<th>Name</th>
<th>Impl.</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>BrainVoyager</td>
<td></td>
<td></td>
<td><a href="http://www.brainvoyager.com">http://www.brainvoyager.com</a></td>
</tr>
<tr>
<td>FreeSurfer *</td>
<td></td>
<td>Can be executed from csurf GUI.</td>
<td>(Dale et al., 1999; Fischl et al., 1999a; Fischl et al., 1999b; Fischl and Dale, 2000; Fischl et al., 2001; Busa, 2002) <a href="http://surfer.nmr.mgh.harvard.edu/">http://surfer.nmr.mgh.harvard.edu/</a></td>
</tr>
<tr>
<td>SureFit *</td>
<td></td>
<td></td>
<td><a href="http://brainvis.wustl.edu/~resources/surefitnew.html/">http://brainvis.wustl.edu/~resources/surefitnew.html/</a></td>
</tr>
<tr>
<td>SurfRelax *</td>
<td></td>
<td></td>
<td>(Larsson, 2001), <a href="http://www.cns.nyu.edu/~jonas/software.html">http://www.cns.nyu.edu/~jonas/software.html</a></td>
</tr>
</tbody>
</table>
6 Parcellation

IBASPM (“Individual Brain Atlases using Statistical Parametric Mapping software”, http://www.thomaskoenig.ch/Lester/ibaspm.htm) is an SPM2 plugin that utilizes the normalization and brain tissue segmentation parts of SPM2 together with the AAL atlas for the construction of parcellation of the brain in individuals. Programs by Claus Svarer and others (http://nru.dk/software/) provide similar capabilities (Svarer et al., 2005; Svarer et al., 2002) using, e.g., MRIWarp (Kjems et al., 1999a; Kjems et al., 1999b).

Rview contains a number of interactive drawing functions http://www.colin-studholme.net/software/software.html

6.1 Labeled brains

Table 6: Labeled brains. The second column with the ‘#’ heading indicates the number of labels. ‘*’ denotes that the labeled brain is readily available on the Internet. Entries above the line is digitized and paper atlases are below the line.

<table>
<thead>
<tr>
<th>Name</th>
<th>#</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>AAL</td>
<td></td>
<td>See Tzourio-Mazoyer</td>
<td>Van Essen, Drury. Included in MRICro as brodmann.hdr/brodmann.img.gz</td>
</tr>
<tr>
<td>Brodman *</td>
<td>41+1</td>
<td>Brodmann areas. Non-space filling, non-probabilistic.</td>
<td>(Applied Medical Imaging, 1994; Seitz et al., 1990; Greitz et al., 1991; Thurfjell et al., 1994; Thurfjell et al., 1995; Bohn et al., 1986; Bohn et al., 1989; Bohn et al., 1991)</td>
</tr>
<tr>
<td>CBA</td>
<td>“almost 400”</td>
<td>Atlas incorporated in a commercial program. “Greitz atlas”. Brodman areas, gyri, central structures</td>
<td>(Nowinski et al., 2001; Nowinski et al., 1997; Nowinski et al., 1995b; Nowinski et al., 1995a)</td>
</tr>
<tr>
<td>Cerefy</td>
<td>2 x 19</td>
<td>Segmentation of MNI single subject Non-probabilistic, space-filling, Non-hierarchical.</td>
<td>(Hammers et al., 2002)</td>
</tr>
<tr>
<td>Hammers</td>
<td>3(?) 43</td>
<td>Commercial digitized versions of the Talairach and Schaltenbrand atlases and Windows/MacIntosh program.</td>
<td>(Nowinski et al., 2001; Nowinski et al., 1997; Nowinski et al., 1995b; Nowinski et al., 1995a)</td>
</tr>
<tr>
<td>IBSR “18”</td>
<td>43</td>
<td>“18 Scans: T1-weighted MR Image data with expert segmentations of 43 individual structures”</td>
<td><a href="http://www.cma.mgh.harvard.edu/ibsr/data.html">http://www.cma.mgh.harvard.edu/ibsr/data.html</a></td>
</tr>
<tr>
<td>ICBM Kabani</td>
<td>90/91(?)</td>
<td>Parcellation of MNI single subject in accordance with NeuroNames</td>
<td>(Kabani et al., 1998)</td>
</tr>
<tr>
<td>Iowa’ (frontal)</td>
<td>11</td>
<td>Parcellations of the frontal cortex by two human raters</td>
<td>(Crespo-Facorro et al., 1999)</td>
</tr>
<tr>
<td>Iowa’ (temporal)</td>
<td>16</td>
<td>Parcellation of the temporal neocortex</td>
<td>(Kim et al., 2000)</td>
</tr>
<tr>
<td>Name</td>
<td>#</td>
<td>Description</td>
<td>Reference</td>
</tr>
<tr>
<td>-------------------------</td>
<td>----</td>
<td>------------------------------------------------------------------------------</td>
<td>--------------------------------------------------------------------------</td>
</tr>
<tr>
<td>‘Iowa’ (cerebral cortex)</td>
<td>41</td>
<td>Based on 10 subjects. Previously ‘The Whole Brain Atlas’ transformed to MNI-space</td>
<td>(Crespo-Facorro et al., 2000)</td>
</tr>
<tr>
<td>Mindboggle *</td>
<td>?</td>
<td>MNI-space, probabilistic, space-filled, hierarchical. Approximate volumes based on labeling in the BrainMap database.</td>
<td>(Evans et al., 1996; Collins et al., 1999)</td>
</tr>
<tr>
<td>Jerne, “Volumes of Interest”) *</td>
<td>100+</td>
<td>Probability map of selected cytoarchitectonic areas from Jülich: 1, 3a, 3b, 4a, 4b, 6, 17 (V1), 18 (V2), 41, 44, 45</td>
<td>(Eickhoff et al., 2005c; Eickhoff, 2005; Geyer et al., 1996; Amunts et al., 1999; Amunts et al., 2000; Morosan et al., 2001; Rademacher et al., 2001; Amunts et al., 1998; Morosan et al., 1996; Eickhoff et al., 2005b; Eickhoff et al., 2005a), <a href="http://www.fz-juelich.de/ime/spm_anatomy_toolbox">http://www.fz-juelich.de/ime/spm_anatomy_toolbox</a>, <a href="http://www.fz-juelich.de/ime-ProbabilityMaps_eng.html">http://www.fz-juelich.de/ime-ProbabilityMaps_eng.html</a></td>
</tr>
<tr>
<td>PMaps *</td>
<td>18</td>
<td>A program that contains two brain templates: A digitized Talairach atlas and MNI</td>
<td>(Lancaster et al., 2000b; Lancaster et al., 1997a; Lancaster et al., 1997b; Lancaster et al., 2000a). The labeling is used by the WFU PickAtlas program.</td>
</tr>
<tr>
<td>Talairach Daemon *</td>
<td>2 × 45(?)</td>
<td>MNI-space, non-probabilistic, non-space filled, semi-hierarchical. This is sometimes referred to as “automated anatomical labeling” or “AAL”. The labeled volume is distributed with MRCro as MNI-space, labeled with 116 different labels</td>
<td>(Tzourio-Mazoyer et al., 2002a; Tzourio-Mazoyer et al., 2002b), <a href="http://www.cyceron.fr/freeware/">http://www.cyceron.fr/freeware/</a>. The labeled volume is distributed with MRCro as mricro/aal.img(.gz) and aal.txt</td>
</tr>
<tr>
<td>Tzourio-Mazoyer *</td>
<td>116</td>
<td>Commercial program with atlas</td>
<td>(Höhne et al., 1992; Höhne, 1997; Höhne, 2001)</td>
</tr>
<tr>
<td>VOXEL-MAN *</td>
<td>?</td>
<td>Book with simple drawings of cytoarchitectonic areas.</td>
<td>(Brodmann, 1994)</td>
</tr>
<tr>
<td>Brodmann</td>
<td></td>
<td>Book with labeled brain in stereotaxic space</td>
<td>Duvernay 1992</td>
</tr>
<tr>
<td>Mai</td>
<td></td>
<td>Book that describe sulcal variability</td>
<td>(Mai et al., 1997)</td>
</tr>
<tr>
<td>Ono</td>
<td></td>
<td>Book</td>
<td>(Ono et al., 1990)</td>
</tr>
<tr>
<td>Schaltenbrand</td>
<td></td>
<td>Book</td>
<td>(Schaltenbrand and Wahren, 1977)</td>
</tr>
<tr>
<td>Talairach ‘Many’</td>
<td></td>
<td>Book with a labeled brain in stereotaxic space</td>
<td>(Talairach and Tournoux, 1988; Talairach and Szikla, 1967)</td>
</tr>
</tbody>
</table>

Brodmann area labeling has been developed using descriptions from the Caret package on the Colin27 atlas and a cortical surface matching method (Rasser et al., 2004): Individual subject’s structural MRI are deformed to an atlas.

An Internet service with the MNI SPAM probability volumes was announced with (Kim et al., 2002) with the URL http://nm.snu.ac.kr/SPAM/ but it does not seem to work.

6.2 Unclassified

(Bajcsy et al., 1983; Bailleul et al., 2004)

7 Validation and comparison

<table>
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<tr>
<th>Type</th>
<th>Description</th>
<th>Reference</th>
</tr>
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Table 7: Validation methods

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