ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Human Atlas.

Human Atlas

Human Cryo Dataset
76 year old normal female human cadaver. The specimen was prepared for sectioning by perfusing with 8% formalin, cryoprotecting with 10% glycerol, freezing in isopentane and dry ice and blocking in green tempera paint and 3% sucrose solution. The brain was cryosectioned at -20 ˚C through the horizontal plane in 100 µm increments on a heavy duty cryomacrotome (PMV Stockholm, Sweden). The cryomacrotome was equipped with a high resolution camera for digital image capture of serial images (1024, 24-bit) collected from the cryoplaned specimen blockface at every 600 µm. The actual image size was measured at 18.5 cm. Data were assigned real value coordinate values in micrometers for width, height, and depth and reconstructed to a single 3D data volume. In order to place the brain into the Talairach system, different amounts of scaling were imposed on 12 rectangular regions of brain defined by vectors from the AC-PC line and the extrema.

Human MRI Dataset
Whole brain MRI was performed on a 1.5 Tesla Phillips ACSIII Scanner. The sequence was T1 spoiled grass (SPGR) with a slice thickness of 1mm (TR=18 ms, TE=10 ms). Images were acquired in the saggital plane.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the ICBM 452 T1 Atlas.

ICBM 452 T1 Atlas

Affine AIR 12 Atlas
The atlas was created using AIR5.0 and exists in two formats (Analyze/IMG/HDR & MINC). The atlas is based on linear transforms of the subjects into the atlas space using a 12-parameter affine transformation (the air12 atlas). This atlas uses chirp-z interpolation for reslicing the voxel intensities.

Warp 5 Atlas
The second atlas is based on a 5th order polynomial transformation into the atlas space (the warp5 atlas). This atlas uses a 3D-sinc interpolation with half-windows of 6 voxels in each dimension. It has a more accurate alignment then the linear atlas and shows more detail.

Additional information about this atlas is available at the following resources:
http://dx.doi.org/10.1006/nimg.1995.1012
http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1088516/
http://www.ncbi.nlm.nih.gov/pubmed/11522763
http://www.ncbi.nlm.nih.gov/pubmed/17266101

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the ICBM Probabilistic Atlases.

ICBM Probabilistic Atlases

ICBM Probabilistic Tissue Atlas
All 452 ICBM subject T1-weighted scans were aligned with the atlas space, corrected for scan inhomogenities, and classified into gray matter, white matter, and cerebrospinal fluid. The 452 tissue maps were separated into their separate components and each component was averaged in atlas space across the subjects to create the probability fields for each tissue type. These fields represent the likelihood of finding gray matter, white matter,or cerebrospinal fluid at a specified position for a subject that has been linearly aligned to the atlas space.

ICBM Lobular Probabilistic Atlas
Fifty-three ICBM subjects were linearly aligned with the atlas space and each subject's lobes were manually delineated (specifically frontal, parietal, temporal, occipital, insular cortex, and cerebellum were delineated). These delineations were averaged across the subjects and used to create probability maps for the likelihood of finding the specified lobe at a given position in a young adult normal subject's brain that has been linearly aligned with the atlas.

ICBM Deep Nuclei Probabilistic Atlas
Fifty-three ICBM subjects were linearly aligned with the atlas space and each subject's caudate, thalamus, and putamen was manually delineated. Each delineation was averaged and used to create a probability map for the structure of interest in the atlas space. The probability maps represent the chances of finding the nucleus of interest at a specified location in the atlas for a subject that has been linearly aligned to the atlas space.

ICBM Sulcal Probabilistic Atlas
Fifty-nine T1-weighted MRI scans from ICBM subjects cross-matched for gender (30 males, 29 females), laterality (30 right-handed, 29 left-handed), and age (avgerage = 24.3 years) were processed to produce surface meshes representing the cerebral cortex of each subject. Twenty sulci were delineated bilaterally on each cortical mesh.* Subjects brains were then aligned with an affine transformation and a 5th-order polynomial transformation to the atlas space. The transforms were used to resample all sulci to the atlas space in a linear and a non-linear fashion and probability fields for each sulcus were created for the affine and 5th-order polynomial cases.

* Bilaterally defined sulci included: the central sulcus, precentral sulcus, postcentral sulcus, middle frontal sulcus, inferior frontal sulcus, ascending branch of the sylvian fissure, horizontal branch of the sylvian fissure, sulcus triangularis, olfactory sulcus, collateral sulcus, occipital-temporal sulcus, sylvian fissure, main branch of the superior temporal sulcus, ascending branch of the superior temporal sulcus, posterior branch of the superior temporal sulcus, inferior temporal sulcus, intraparietal sulcus, primary intermediate sulcus, secondary intermediate sulcus, and the transverse occipital sulcus for a total of 40 sulci per subject.

http://dx.doi.org/10.1006/nimg.1995.1012
http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1088516/
http://www.ncbi.nlm.nih.gov/pubmed/11522763
http://www.ncbi.nlm.nih.gov/pubmed/17266101

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the ICBM T2 Atlas.

ICBM T2 Atlas

Affine AIR 12 Atlas

The atlas was created using AIR5.0 and exists in two formats (Analyze/IMG/HDR & MINC). The atlas is based on linear transforms of the subjects into the atlas space using a 12-parameter affine transformation (the air12 atlas). This atlas uses chirp-z interpolation for reslicing the voxel intensities.

Additional information about this atlas is available at the following resources:

http://dx.doi.org/10.1006/nimg.1995.1012
http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1088516/
http://www.ncbi.nlm.nih.gov/pubmed/11522763
http://www.ncbi.nlm.nih.gov/pubmed/17266101

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the ICBM Template.

ICBM Template

The high definition structural brain template is the average of 27 T1 weighted MRI acquisitions from a single subject (from Montreal Neurological Institute database). The template is aligned within the stereotaxic space of the ICBM average template derived from that of Talairach and Tournoux (1988). Cortical gyri, subcortical structures and the cerebellum have been delineated from the structural brain template and assigned a unique label.

The 3-D set of labels can be imported and registered onto the structural MRI of any individual subject through a fully automatic implementation of diverse software assembled in the specific module of the LONI Pipeline. The Pipeline is designed to be used in a connection with the LONI Pipeline Server. Please obtain an account for the Pipeline Server and connect to it before using this Pipeline. To request an account please go to: http://resource.loni.usc.edu/collaboration/collaborator-application/.

Additional information about this atlas is available at the following resources:

http://dx.doi.org/10.1006/nimg.1995.1012
http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1088516/
http://www.ncbi.nlm.nih.gov/pubmed/11522763
http://www.ncbi.nlm.nih.gov/pubmed/17266101

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the LPBA40 Atlas.

LPBA40 Atlas

Delineation

MRI data from 40 subjects were preprocessed according to existing LONI protocols to produce skull-stripped brain volumes. These volumes were aligned to the ICBM305 atlas using rigid-body transformation to correct for head tilt and reduce bias in the delineation process. This produced a transform from native space to delineation space and an associated inverse transform. In each of the 40 subjects, 58 structures were delineated manually according to protocols developed for this project (see LPBA40 Protocols) using BrainSuite.

Image processing

Brain masks were constructed from the manual delineations and projected back to the native delineation space. The MRI volumes in native space were masked to produce brain-only MRI volumes. These volumes were then corrected for non-uniformity using BrainSuite's Bias Field Corrector. The bias-corrected brain data were processed with the Partial Volume Classifier software to produce maps of grey matter, white matter, and cerebrospinal fluid for each subject volume. The brains were then aligned to atlas targets using 3 widely used methods. The atlas targets were chosen based on the method.

LPBA40.AIR (ICBM452 Warp 5 Atlas)

Each corrected brain volume was aligned from its native space to the ICBM-452 Warp 5 T1 average using AIR align_warp. This produced a native space to ICBM452 space transform. Volumes were cropped prior to registration (pad: 8); the cropped volumes were aligned to the ICBM-452 atlas (settings: −m 12 −t1 1 −t2 1). The corrected brain volumes were resliced into the ICBM452 space using chirp-Z interpolation (AIR).

LPBA40.FLIRT

Using FLIRT with the default settings, each corrected brain was aligned, each brain was aligned to the avg152T1_brain.

LPBA40.SPM5

Using SPM5's unified segmentation method with the default settings, each whole-head scan in the native space was aligned to the avg152T1 target.

Atlas construction

For each of the three atlas variants, we constructed a series of maps from the transformed data.

- Intensity atlas (LPBA40intensityavg) - a voxel-wise average of the skull-stripped MRI volumes in ICBM452 space

LPBA40 Atlas continued

- Tissue class probabilistic atlas (LPBA40tissue) - three volumes, where each voxel contains a count of the number of subject volumes that had that voxel labeled as a the associated tissue type (GM, WM, or CSF)
- Structure probability maps (LPBA40structure) - 56 volumes, each of which contains the voxel-wise count of the number of subjects that had that voxel labeled as the given structure
- Grey matter masked structure probability maps (LPBA40GMstructure) - 56 volumes, each of which contains the voxel-wise count of the number of subjects that had that voxel labeled as the given structure and also as GM
- Maximum likelihood atlas (LPBA40) - for each voxel, we computed the most likely tissue type based on the 40 delineated subject volumes; in the case of a tie, the tissue type was chosen at random from the equilikely labels. This data set contains both the maximum likelihood label volume and a volume composed of the maximum count at each voxel
- Maximum likelihood grey matter atlas (LPBA40) - This is similar to LPBA40, above, but the tissue labels were pre before performing the maximum likelihood computation

Data Distribution
Each variant of the atlas can be downloaded as a zip file containing the above data. The LPBA40.AIR atlas is available in either NIFTI or Analyze format (note that we use a right-handed coordinate system to be consistent with the ICBM452 atlas downloads). The LPBA40.SPM5 and LPBA40.FLIRT atlases are available in NIFTI format, since both SPM5 and FLIRT support NIFTI. All files are gzipped to reduce the size of the total dataset.

Each zip file contains the following directories:
PDF: the estimated probability density functions for each structure
PDFGM: the estimated GM probability density functions for each structure
avg: the LPBA40 average intensity brain in that space
maxprob: the most likely label and highest probability value at each voxel
tissue: the CSF, GM, and WM probability density maps

Each component file is stored using the following naming convention:
lpba40.{registration method}.{atlas target}.{description}.nii.gz

(for the Analyze version of the LPBA40.ICBM452 variant, .img.gz is used). For example, lpba40.flirt.avg152T1_brain.wm.pdf.nii.gz is the density map for white matter in the LPBA40.FLIRT atlas.:

The dataset also includes a text file which provides the name of each structure and the integer ID number used in the label volumes.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Monkey Atlas.

Monkey Atlas

Cryo

Closely spaced (50 mm) images of the specimen blockface were digitally acquired and modified to produce whole head and brain only 3D image sets. The resulting data sets were organized into a digital volume and repositioned into a stereotaxic coordinate system defined by Horsley and Clark (1908). From the rotated data sets, orthogonal images were obtained by digitally resampling the volume in order to produce a full set of coronal, sagittal, and horizontal images. Stereotaxic reference grids were applied to each image indicating the A/P, M/L, or Hc (depending on orientation of cut) position within the digital volume. Specific anatomic structures were outlined from the cryosection data set and 3D surface models reconstructed. Structural labels indicating nuclei, tracts, and other neuroanatomical features were incorporated into coronally sliced cryosection images spaced at 500 mm. Labels applied to the images used the abbreviations found in the Winters, Kado, and Adey (1969) atlas. The CT, PET, and MRI data sets were reconstructed into a digital volume and co-registered (CT and MRI by landmark matching and fiducials, PET by an automated ratio method) to the cryosection volume.

MRI

MRI was performed on a GE 1.5 Tesla Signa scanner. Both T1-wieghted (TR=600, TE=11) and T2-weighted (TR=3000, TE=80) scans were performed. Fifteen MR images were collected through the specimen's head with an interslice distance of 4mm, and a calculated in-plane resolution of 3mm.

CT

CT was performed on a General Electric (GE) High Light Advantage scanner. Fifty three slices were obtained with an interslice distance of 1mm, and calculated in-plane resolution of 1mm.

PET

PET was performed by intravenous injection of [18F] -deoxyglucose on a Siemens 831 tomographic system. Thirty slices were produced with an interslice distance of 2mm and an in-plane resolution near 6mm.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Mouse Atlas.

MAP 2003 Atlas

In vivo MRI
Twelve week-old male C57BL/6 mice (Jackson Laboratories) were initially anesthetized with ketamine/xylzaine and then maintained on isofluorane for the duration of the imaging experiment. Diffusion-weighted uMRI images were acquired over several hours in a high-field magnet. Diffusion-weighted volumes show a great deal of anatomical detail and good contrast between gray and white matter.

Ex vivo MRI
Twelve week-old male C57BL/6 mice were sacrificed by an overdose of halothane (Sigma) according to procedures approved by the UCLA Animal Research Committee. The animals were intracardially perfused using a Minipuls II peristaltic pump (Gilson) at very low pressure with chilled PBS for approximately two minutes and FormaldeFresh (Fisher) for 15 minutes. The animals were decapitated, soft tissue removed, and the skulls were post-fixed in FormaldeFresh for 16 hours and then scanned.

Blockface and Histology
The brains were removed from post-fixed skulls and further post-fixed in FormaldeFresh for 16 hours. After post-fixation the brains were dipped in a mixture of india ink (Pelikan) and 5% gelatin (Sigma) to simplify segmentation of tissue from background later. The brains were cryoprotected in a solution of 20% sucrose for 16 hours to prevent freezing artifacts. The brains were then embedded in OCT compound (Sakura) at 4° C and snap-frozen at -70° C in a 2-methylbutane/ dry ice bath. Blockface imaging is a colorimetric imaging modality free of many of the spatial artifacts that affect serially stained sections: shatter, tears, bubbles, and other mechanical distortions. High-resolution color images of the blockface are acquired as it is sectioned, relying on the inherent contrast of white and gray matter to discriminate anatomical boundaries. Nissl-stained sections provide a wealth of information about cortical lamination and the topography of subcortical nuclei.

MAP 2001 Atlas

Mice:
Twelve week-old male C57BL/6 mice (Jackson Laboratories) were sacrificed by an overdose of halothane (Sigma) according to procedures approved by the UCLA Animal Research Committee.

Cryostat:
A CM3050S cryostat (Leica) was modified to include a micrometer (Heidenhain) that allowed the blockface to be returned to its original position (within 0.5um) and a camera mount for a DMCIe

digital camera (Polaroid) that would image the blockface prior to each section at a resolution of 1600x1200(approximately 10um/pixel).

Cryosection:
Brains were removed without perfusion or post-fixation and embedded in OCT compound (Sakura). The samples were cut serially in 50um thick coronal sections on a modified CM3050S cryostat (Leica) and images taken prior to each section. The images were acquired at a large aperture setting in combination with a short exposure time to minimize signal outside the plane of section.

Sample Preparation:
Mice were intracardially perfused using a Minipuls II peristaltic pump (Gilson) at very low pressure with PBS for approximately two minutes, FormaldeFresh (Fisher) for ten minutes, 10% sucrose in FormaldeFresh for ten minutes and finally 20% sucrose for ten minutes. The brain was removed and cryoprotected in a series of increasing sucrose concentration culminating in 30% sucrose (10% FormaldeFresh) overnight.

Histology:
Brains were cut serially in 50um thick coronal sections on a modified CM3050S cryostat (Leica) and images taken prior to each section. Sections 200um apart were Nissl-stained (Thionin) as described (LS) and alternating sections 200um apart were myelin-stained using a modified myelin impregnation stain (Gallyas 79).

Immunohistochemistry:
Image Processing. Stained preparations were digitized using a 1.25X macro objective and a 0.63X C-mount on an AX70 microscope (Olympus) with a DMCIe digital camera (Polaroid) at a resolution of 1600x1200 (approximately 10um/pixel). The digitized images were linearly registered to the blockface images using Automated Image Registration (RW) and non-linear warping was adjusted using a continuum mechanic warping algorithm (T&T 1998, 1999) based on the Cauchy-Navier operator of linear elasticity. Processing was done on an Onyx 200 supercomputer (SGI). The two-dimensional images were then reconstructed into a three-dimensional volume and quantitatively transformed into a defined and common coordinate system.

Anatomic Delineations:
Anatomic delineations were made on the digitized images of the Nissl stained sections using Illustrator 8.0 (Adobe) on a Macintosh computer (Apple). Delineations were verified with various paper atlases (GP).

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Mouse Magnetic Resonance Microscopy Atlas.

Mouse Magnetic Resonance Microscopy Atlas

MRM

Mice were anesthetized initially with ketamine/xylzaine and then maintained on isofluorane for the duration of the imaging experiment. Magnetic resonance imaging was done at 37 C using an 89 mm vertical bore 11.7 T Bruker Avance imaging spectrometer with a micro-imaging gradient insert and 30 mm birdcage RF coil (Bruker Instruments). Typical imaging parameters were as follows: T2-weighted RARE 3D imaging protocol (8 echoes), matrix dimensions = 256 x 256 x 256; FOV = 3 cm x 1.5 cm x 1.5; repetition time (TR) = 1500 ms; effective time (TE) = 10 ms; number of averages = 4. The images were padded with zeros to double the number of time domain points in each dimension, the Fourier transformed to yield a matrix of 512 x 256 x 256. This procedure is commonly called zero-filling and is a well known interpolation method (Farrar and Becker, 1971; Fukushima and Roeder, 1981). Typical spatial resolution was approximately 60 um3 per voxel.

Nomenclature and Delineations

Neural structures (including cell groups, fiber tracts and gross anatomical features such as the ventricles) were determined under the microscope from the histologically stained sections. 3D label volumes were painted onto coregistered MRM, Nissl-, myelin-, and acetylcholine esterase-stained volumes using BrainSuite (Shattuck and Leahy, 2002). The delineations depict asymmetries present in the sections, making them more immediately useful than if they were stylized. Delineation of brain nuclei requires an expert neuroanatomist to draw on high-level knowledge, accumulated over a lifetime of careful study of disparate materials (Swanson, 1998). Consequently, manual input was necessary for even approximate parcellation of brain in its fine details. In the development of a comprehensive, standardized, and mutually exclusive nomenclature (Bowden and Martin, 1995; Bard et al., 1998) and anatomic delineation, our primary reference was the mouse brain atlas of Paxinos and Franklin (Paxinos and Franklin, 2001).

Usage

This atlas volume can be viewed using the Mouse BIRN Atlasing Tool (MBAT) or SHIVA. See the respective manuals for these programs.

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ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Mouse Minimum Deformation Atlas.

Mouse Minimum Deformation Atlas

MRM

Mice were anesthetized initially with ketamine/xylzaine and then maintained on isofluorane for the duration of the imaging experiment. Magnetic resonance imaging was done at 37° C using an 89 mm vertical bore 11.7 T Bruker Avance imaging spectrometer with a micro-imaging gradient insert and 30 mm birdcage RF coil (Bruker Instruments). Typical imaging parameters were as follows: T2-weighted RARE 3D imaging protocol (8 echoes), matrix dimensions = 256 x 256 x 256; FOV = 3 cm x 1.5 cm x 1.5; repetition time (TR) = 1500 ms; effective time (TE) = 10 ms; number of averages = 4. The images were padded with zeros to double the number of time domain points in each dimension, the Fourier transformed to yield a matrix of 512 x 256 x 256. This procedure is commonly called “zero-filling” and is a well known interpolation method (Farrar and Becker, 1971; Fukushima and Roeder, 1981). Typical spat Nomenclature and Delineations
Neural structures (including cell groups, fiber tracts and gross anatomical features such as the ventricles) were determined under the microscope from the histologically stained sections. 3D label volumes were “painted” onto coregistered MRM, Nissl-, myelin-, and acetylcholine esterase-stained volumes using BrainSuite (Shattuck and Leahy, 2002). The delineations depict asymmetries present in the sections, making them more immediately useful than if they were stylized. Delineation of brain nuclei requires an expert neuroanatomist to draw on high-level knowledge, accumulated over a lifetime of careful study of disparate materials (Swanson, 1998). Consequently, manual input was necessary for even approximate parcellation of brain in its fine details. In the development of a comprehensive, standardized, and mutually exclusive nomenclature (Bowden and Martin, 1995; Bard et al., 1998) and anatomic delineation, our primary references were the mouse brain atlas of Paxinos and Franklin (Paxinos and Franklin, 2001) and the rat brain atlas of Swanson (Swanson, 2004).

Usage

This atlas volume can be viewed using the Mouse BIRN Atlasing Tool (MBAT) or SHIVA. See the respective manuals for these programs.

For more information about SHIVA, see http://www.loni.usc.edu/Software/SHIVA

Download

Data are compressed and combined into a single tar for download. Unzip these before viewing. Mac users can automatically unzip these files, or a program may be used such as winzip (http://www.winzip.com/index.htm) for Windows or gzip (http://www.gzip.org/) for Unix. To view volumes in MBAT, select “Open Data” and select the file in the Open dialogue. To view .atlas or .keg files in MBAT select the “Open Atlas” option and select the file in the Open dialogue.

Mouse Minimum Deformation Atlas continued

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ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Neonatal (P0) Mouse Nissl Brain Atlas.

Neonatal (P0) Mouse Nissl Brain Atlas

A full-color Nissl-stained volume with resolution of 6.6 x 50 x 6.6 μm3 was constructed. A sub-sampled version of this volume (with resolution of 13.3 x 50 x 13.3 μm3) was co-registered to a standard anatomical space defined by an averaged geometry of C57BL/6J P0 mouse brains. A hundred and forty-five anatomical structures were delineated based on the histological images. Anatomical relationships of delineated structures were established based on the hierarchical relations defined in the atlas of adult mouse brain so the P0 atlas can be related to the database associated with the adult atlas.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Neonatal (P0) MRI Mouse Brain Atlas.

Neonatal (P0) MRI Mouse Brain Atlas

Image acquisition for the subjects used to define the atlas
Eight mice from two sets of littermates were sacrificed hypothermally within 24 hours after birth, perfused intracardially with 10ml of phosphate-buffered saline (PBS) and then 10ml 2% paraformaldehyde (PFA). Animals were decapitated and the heads post-fixed with 2% PFA for 24hr before MR scans. Heads were soaked in 5% ProHance for 5 days then immersed in Fomblin for the MR scans. T2 weighted 3D spin-echo MRI images were acquired using an 11.7 T BrukerAvance imaging spectrometer with a micro-imaging gradient insert and 20 mm birdcage RF coil (Bruker Instruments). The following data acquisition parameters were used: TR/TE=300ms/6.8ms, 2 averages, FOV=12.8mm x 9mm x 9mm, matrix size= 256x128x128, T=288.1-K. The mice weighed between 1.4 and 1.5 g before being sacrificed. All animals were housed and treated in accordance with the UCLA Animal Research Committee guidelines.

Anatomical labeling
Each MR brain image volume was firstly segmented into olfactory bulbs, cerebrum, diencephalon, midbrain-hindbrain and cerebellum. The basal ganglia (caudate putamen + globus pallidus), mammillary bodies, superior and inferior colliculi, substantia nigra, and white matter tracts anterior commissure (temporal limb) and fimbria of hippocampus, were then labeled digitally.

Constructing the standard atlas space
Each image volume was registered to a common space with four steps. Initial alignment employed a 6-parameter linear rigid body transformation to fix the location of the origin (interpeduncular fossa) and oriented the brain. The secondary registration was accomplished with a 12-parameter affine transformation calculated using an automatic registration algorithm that maximizes 3D cross-correlation of the image intensity (1). The image volume that retained the best structural integrity and the best image contrast was selected as the registration target for the other seven image volumes. Regions outside the brains were masked before the automatic registration step was performed. This second registration step normalized the global scale. Histogram equalization was performed on the resulting images. The intensity average brain of these eight co-registered images was then created. Histogram equalization prevented an average image from being biased toward the brighter image, and thus represents an average space of the co-registered brains. This average brain then served as the new target for registration step three. Here, a 30-parameter non-linear warping was used to reduce regional variations between subjects. Finally, a feature-based registration was performed to maximize the mutual information between the anatomical label volume of each subject and the label volume drawn on the intensity average volume from the eight co-registered brains. Retrieved displacement fields were then used to resample each image volume (2). A newly averaged image of these eight revised co-registered brain forms the standard atlas space.

Neonatal (P0) MRI Mouse Brain Atlas continued

Defining the probability maps
The anatomical label volumes were forced to adapt to a stereotactic space. Each voxel in the probability map for a given anatomical structure describes the probability that the voxel belongs to this anatomical structure. The label volume retrieved from a given threshold is the collection of voxels with probabilities greater than the threshold.

Labeling the average brain
The anatomical labels were firstly retrieved from the probability map with the threshold that retrieved volumes close to, but less than the population average. These labels were smaller than actual sizes of the corresponding structures, resulting in gaps along the boundaries between neighbor structures. These gaps were filled manually based on the intensity average image. If the boundary could not be easily discriminated on the image, delineations were made along the midpoints between boundaries defined by labels retrieved from the probability map.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Rat Atlas.

Rat Atlas

A three dimensional (3D) computerized map of rat brain anatomy was generated using six male Sprague-Dawley rats, weighing 270-320 g. Their heads were frozen and closely spaced cryosectional images were digitally captured every 50 microns at 1024 x 1024 resolution. Each serial data set was organized into a digital volume, re-oriented into a flat skull position, nd brought into register with each other. A volume representative of the group following registration was chosen based on its anatomic correspondence with the other specimens as measured by image correlation coefficients and landmark matching. Mean positions of lambda, bregma and the interaural plane of the group within the common coordinate system were used to transform the representative volume into a 3D map of rat neuroanatomy.

The LONI Rat Brain Atlas is available in 2 ways - as an interactive web Java applet showing 2D slices of the atlas in axial, sagittal and coronal views, or as a downloadable 3D stereotactic brain atlas in Analyze, Mnc and Nifti file formats. The dimensions of the atlas are 1024x1024y21z and its resolution is (0.05, 0.05, 2.5) mm3.

ATLAS METHODS

The following paragraphs describe the methods that were used on the different version(s) of the Vervet Atlas.

Vervet Atlas

A manuscript detailing construction of the atlas is in preparation. Cyromacrotome data collection has been described in abstract form:

Rubins DJ, Ambach K, Toga AW, Melega WP, Cherry SR. Development of digital brain atlas of the vervet monkey. J Cereb Blood Flow Metab. 1999;19 (suppl):S781

and MRI data collection is described in:

Fears SC, Melega WP, Service SK, Lee C, Chen K, Tu Z, Jorgensen MJ, Fairbanks LA, Cantor RM, Freimer N, Woods RP (2009) Identifying heritable brain phenotypes in an extended pedigreee of vervet monkeys. J Neurosci 29:9:2867-75.

ATLASES

Web-Viewers

The Human, Monkey, Mouse and Varvet 2D Atlas viewers are web-based 2D slice viewers that visualize single slices at a time. The user selects a modality and an orientation from the panels on the left. At the bottom of the viewer is a graphical representation of the brain with a bar through it and a thumbnail image. Dragging the bar will scroll through the images, and releasing it will update the main panel on the right with a high-resolution image of the selected slice.

- Human Atlas - view in web viewer (requires Java)
- Monkey Atlas - view in web viewer (requires Java)
- Mouse Atlas - view in web viewer (requires Java)
- Vervet Structural Atlas
- Vervet MRI Atlas

Downloads

- [ ] Alzheimer's Disease Template (minc format)
- [ ] Alzheimer's Disease Template (analyze format)
- [ ] Chinese_56 (analyze format)
- [ ] Fetal Atlas 15-22 GW
- [ ] Fetal Atlas Jacobian
- [ ] Fetal Atlas Local Shape Analysis
- [ ] Fetal Atlas Surface
- [ ] Human CRYO Dataset
- [ ] Human MRI Dataset (analyze format)
- [ ] Human MRI Dataset (minc format)
- [ ] ICBM 452 T1 Affine Transformations Atlas
- [ ] ICBM 452 T1 5th Order Polynomial Warps Atlas
- [ ] ICBM DTI-81 Atlas Color (raw)
- [ ] ICBM DTI-81 Diffusion Weighted (raw)
- [ ] ICBM DTI-81 Fractional Anisotropy (raw)
- [ ] ICBM DTI-81 T2 (raw)
- [ ] ICBM DTI-81 White Matter Parcellation Map (raw)
- [ ] ICBM Probabilistic Tissue Atlas
- [ ] ICBM Lobular Probabilistic Atlas
- [ ] ICBM Deep Nuclei Probabilistic Atlas
- [ ] ICBM Sulcal Probabilistic Atlas
- [ ] ICBM T2 Atlas
- [ ] ICBM Single Subject MRI Anatomical Template
- [ ] ICBM Single Subject MRI Anatomical Template for use in MBAT software version 3.0+
- [ ] LPBA40/AIR atlas (analyze format)
- [ ] LPBA40/AIR atlas (NIFTI format)
- [ ] LPBA40/FLIRT atlas (NIFTI format)
- [ ] LPBA40 Subjects FLIRT: Transforms from delineation and native_radiological spaces to the LPBA40/FLIRT atlas
- [ ] LPBA40/SPM5 atlas (NIFTI format)
- [ ] LPBA40 Subjects ICBM452: Transforms from delineation and native spaces to the LPBA40/AIR atlas
- [ ] LPBA40 Subjects SPM5: Transforms from delineation and native spaces to the LPBA40/SPM5 atlas
- [ ] LPBA40 Subjects Delineation Space: MRI and label files in delineation space
- [ ] LPBA Subjects Delineation Space Surfaces: Surface models in delineation space
- [ ] LPBA40 Subjects Native Space: MRI data and brain masks in native space
- [ ] LPBA40 Subjects Native Radiol. Space: MRI and brain masks in native_radiological space
- [ ] LBPA40 Atlas, for use with MBAT software version 3.0+
- [ ] Monkey Atlas CRYO Dataset
- [ ] Monkey Atlas MRI Dataset
- [ ] Monkey Atlas CT Dataset
- [ ] Monkey Atlas PET Dataset
- [ ] Mouse Atlas Project (MAP) 2003 Atlas
- [ ] Archived MAP 2001 Atlas
- [ ] Mouse Atlas Project (MAP) 2003 Dataset
- [ ] Mouse Magnetic Resonance Microscopy Atlas for use with MBAT software version 3.0+
- [ ] Mouse Magnetic Resonance Microscopy Atlas Data
- [ ] Mouse Minimum Deformation Atlas (MDA), for use with MBAT software version 3.0+
- [ ] Mouse Minimum Deformation Atlas (MDA) Surfaces, for use with BrainSuite software
- [ ] Mouse Minimum Deformation Atlas (MDA) Data
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Full color Nissl-stained volume in sample space - 1024 x 150 x 1024
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Full color Nissl-stained volume in atlas space - 752 x 200 x 752
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Gray-level Nissl-stained volume in sample space - 1024 x 150 x 1024
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Gray-level Nissl-stained volume in atlas space - 752 x 200 x 752
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Gray-level Nissl-stained sub-sampled isotropic volume - 1024 x 150 x 1024
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Anatomical label volume in sample space - 1024 x 150 x 1024
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Anatomical label volume in atlas space - 752 x 200 x 752
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Atlas package in sample space - 1024 x 150 x 1024
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas Atlas package in atlas space - 752 x 200 x 752
- [ ] Neonatal (P0) Mouse Nissl Brain Atlas, for use with MBAT software version 3.0+
- [ ] Mouse Minimum Deformation Atlas
- [ ] Neonatal (P0) MRI Mouse Brain Atlas 0.625 Probability
- [ ] Neonatal (P0) MRI Mouse Brain Atlas 0.75 Probability
- [ ] Neonatal (P0) MRI Mouse Brain Atlas 0.825 Probability
- [ ] Neonatal (P0) MRI Mouse Brain Atlas 1.00 Probability
- [ ] Neonatal (P0) MRI Mouse Brain Atlas 0.50 Probability without labeled brain
- [ ] P0 Mouse Brain MRI Atlas, for use with MBAT software version 3.0+
- [ ] Rat Atlas 1024 x 1024 Gridded and Gridded & Labeled CRYO Dataset
- [ ] Rat Atlas 512 x 512 Gridded and Gridded & Labeled CRYO Dataset
- [ ] Rat Atlas 1024 x 1024 y 21 z 3D Rat Brain Atlas Volume (reconstructed from the coronally labeled 2D atlas slices)
- [ ] Vervet Atlas Cryo Dataset
- [ ] Vervet Atlas MRI Dataset
- [ ] Vervet Atlas NIfTI 1.1 formatted .nii file
- [ ] Vervet Atlas NIfTI 1.1 formatted .hdr and .img file

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ATLASES

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RESEARCH

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Current Research Initiatives

The goal of LONI research is on the development of deformation strategies, warping algorithms, and quantitative data analyses to create a set of brain atlases that characterize the normal brain through development, to adulthood and on to old age, the Alzheimer's brain, and the brains of other patient populations.developed to train medical students and neuroanatomists. It is accessible to the public.

Alzheimer's Disease | Development | Optical Signals | Schizophrenia

Atlases | INRIA - Epidaure | Related Sites | Research Manual

Overview | Methods | Download | Available Atlases

Chinese_56 | Fetal Brain | Human | ICBM 452 T1 | ICBM DTI-81 | ICBM Probabilistic

ICBM T2 | ICBM Template | LPBA40 | Monkey | Mouse | Mouse MR

Microscopy | Mouse Min Def | Neonatal Mouse | Neonatal Mouse MR | Rat | Varvet

Chinese_56 Atlas

Chinese brain Atlas is an average brain template composed of high quality brain MRI data from 56 Chinese young subjects. Seven additional Chinese brains were registered to both ICBM152 and the Chinese_56 atlas. It is found that there is more deformation required to register the additional Chinese brains to the ICBM152 than to the Chinese_56. Thus the Chinese brain template (Chinese_56) better represents the shape and size of the Chinese population.

Methods (pdf)

View and Download