Chapter 8

Pipelines: Large Scale Automatic Analysis of 3D Brain Data Sets

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Introduction

Recently, the demand for the automatic quantitative analysis of large medical image data sets (hundreds or thousands of scans) has been growing, particularly in the brain mapping community. Typical examples are the construction of probabilistic atlases of the adult and pediatric brain [4, 6], the analysis of pathology in the context of clinical research and clinical trials [12], and the statistical analysis of functional imaging studies [this conference]. The data analysis for such studies is often a daunting task which puts substantial demands on the available computational resources. In order to address this issue, we have developed PCS (Production Control System), which allows the rapid implementation and parallel execution of an analysis 'pipeline,' a term used here to describe a sequence of processing stages applied to a collection of input data.

Methods

In the UNIX environment, it is common practice to develop software which performs an elementary task and which is executed in a command-line fashion. Most image analysis tasks can be decomposed into a sequence of such elementary operations, which, in combination with a distributed network of workstations, allows for a high degree of parallelization at minimal programming cost.

Given a processing pipeline where each of the processing 'stages' is performed by a single command, PCS allows the user to specify this command with its options, input and output files, and dependencies on other stages in the pipeline using a simple script language. Efficient course-grain parallelism is achieved by distributing the individual jobs over a network of workstations via a load-balancing queue. PCS monitors the status of each job and submits a new job when the prerequisites for its submission have been satisfied (typically the completion of all stages on whose output data the stage depends).

At the McConnell Brain Imaging Centre (BIC), a typical pipeline for the analysis of 3D brain image data includes processing stages such as registration with a stereotaxic coordinate system [2], correction for intensity non-uniformities [9], intensity normalization [11], noise reduction [5], cortical surface extraction [7], and atlas matching using non-linear brain deformation [1, 3]. Also as a standard procedure, a number of composite verification images is produced during processing, to allow the rapid visual inspection of the results for a large number of data sets (see Figure 8.1).

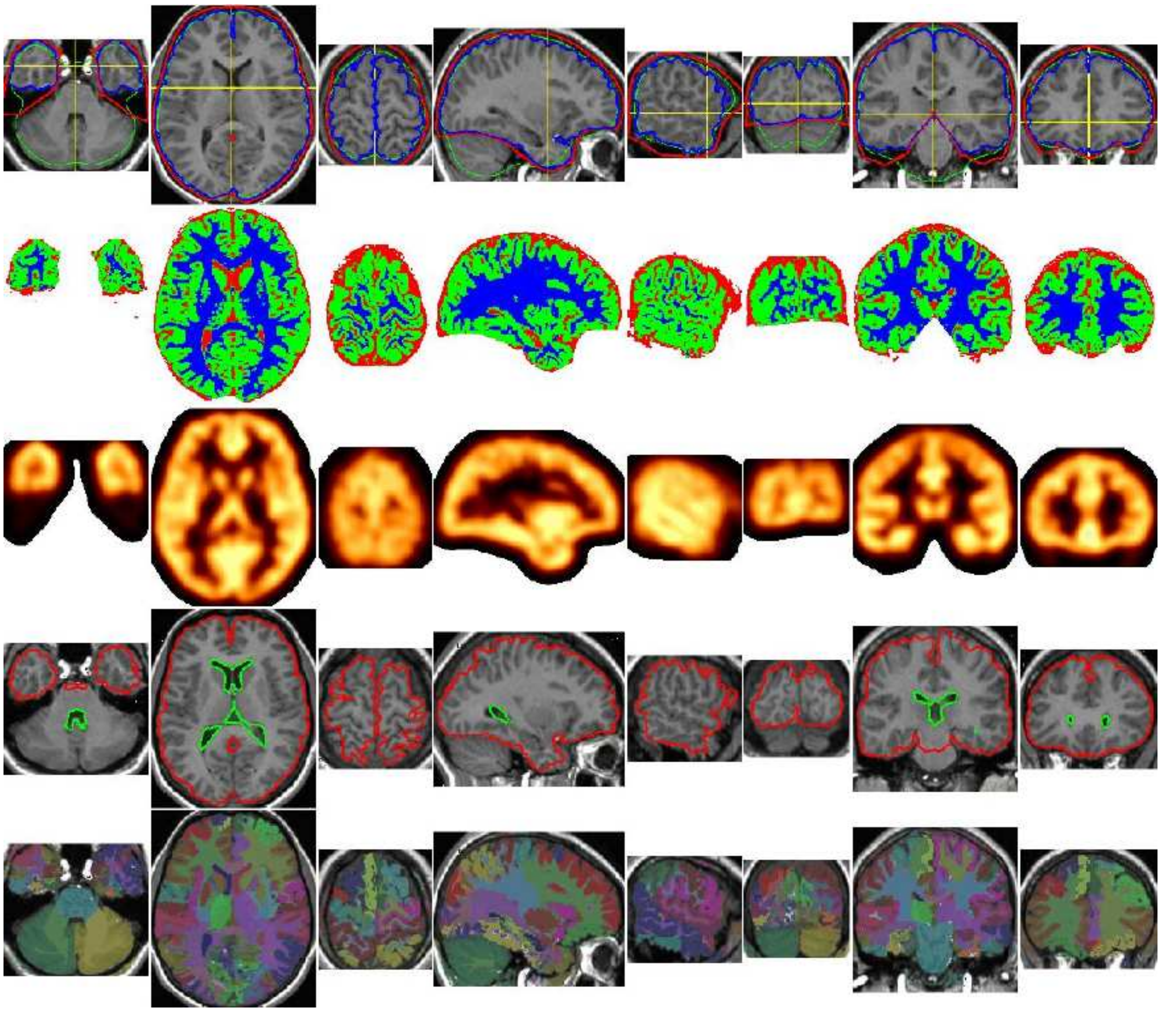

Figure 8.1: Example of a single-subject pipeline verification image (see text).

Pipeline Examples

Two of the pipelines which are currently in use at the BIC are illustrated in montreal/insect/figures 8.2 and 8.3. Figure 8.2 shows an incarnation of INSECT (Intensity Normalized Stereotaxic Environment for Classification of Tissues [12]), a pipeline designed for the classification of tissues in MRI. INSECT was used to automatically quantify multiple sclerosis (MS) lesions in over 2000 scans, a process that took less than 2 months using PCS and a network of 12 SGI workstations. Figure 8.3 shows the analysis pipeline designed for the automatic analysis of normal human brain, which has so far been applied to brain MRIs obtained from about 150 healthy adults [8, 3] and more than 100 healthy children and adolescents [13].

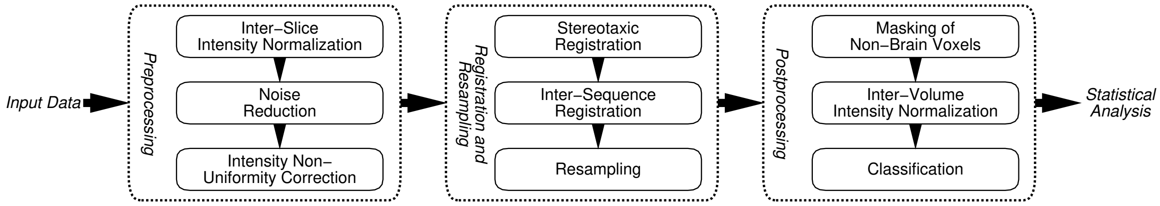

Figure 8.2: Flow diagram of the INSECT [12] pipeline.

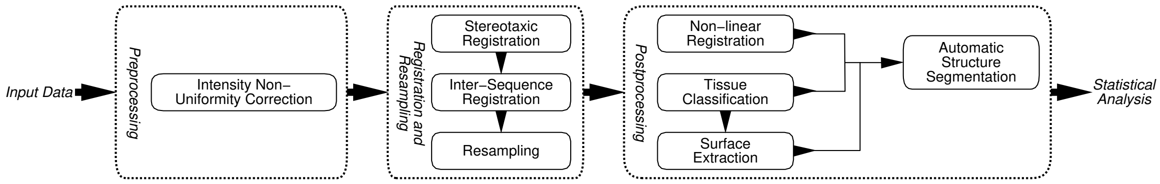

Figure 8.3: Flow diagram of the ICBM [8] pipeline.

Results

Figure 8.1 shows an example of a verification image, obtained from the analysis of the brain of a healthy child. Each column of this image shows a different slice through stereotaxic (Talairach) space, while each row shows different intermediate and final products of the automatic analysis. Top row: T_1-weighted volume with several contours, showing the axes of Talairach space (yellow), the outline of the MNI 305 average brain (green), and a low- and high-resolution cerebral surface [7] (red and blue, respectively). Second row: 3-class INSECT classification [12]. Third row: smoothed (FWHM=10) gray matter classification [10]. Fourth row: T_1-weighted image, non-linearly deformed at low resolution to match a model brain, shown with its cerebral (red) and ventricular (green) contours. Bottom row: T_1-weighted image with the automatic (ANIMAL+INSECT [3]) segmentation transparently overlaid.

montreal/insect/figures 8.4-8.7 show examples of composite image data, such as average MRI scans and Statistical Probability Anatomy Maps (SPAMs) obtained using the PCS-driven, automatic analysis of MRI data in the context of various ongoing projects.

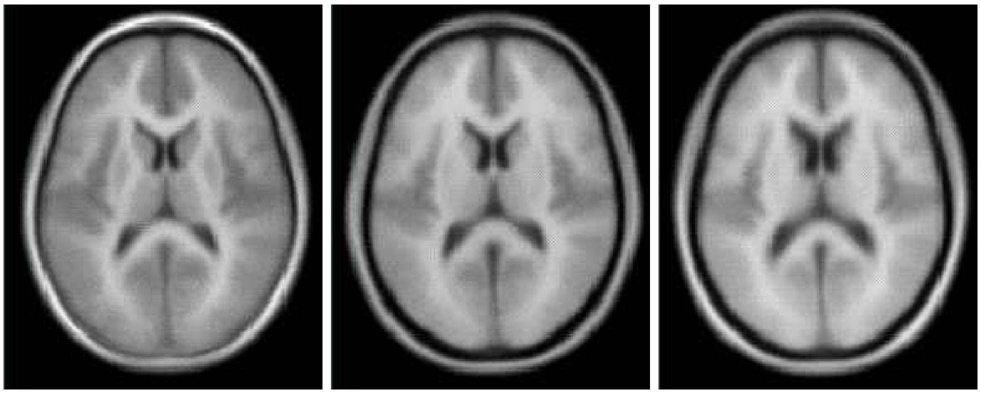

Figure 8.4: Average T_1-weighted MRIs of, from left to right, a pediatric population (n=130), healthy adults (n=151), and MS patients (n=460).

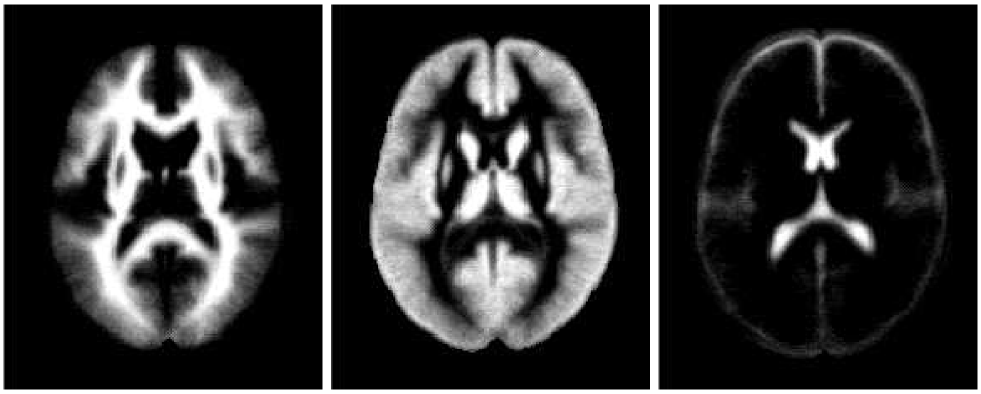

Figure 8.5: SPAMs of white matter, gray matter, and CSF, automatically derived from 151 healthy adults.

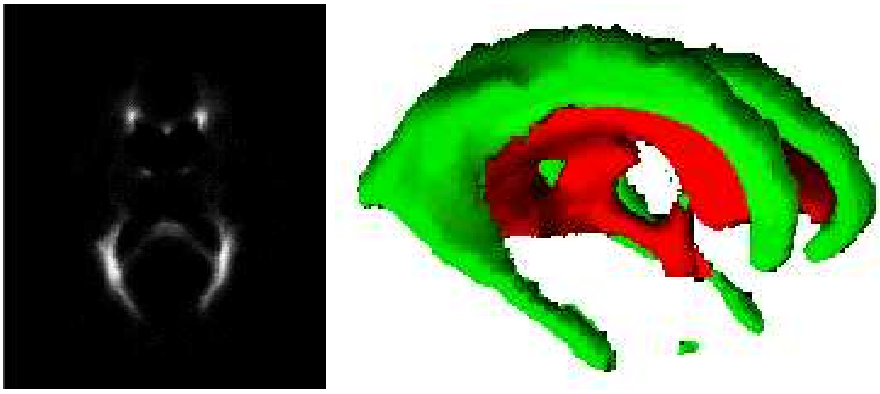

Figure 8.6: MS lesion SPAM (n=460), shown in transverse cross-section and rendered with the CSF SPAM shown in Figure 8.5.

Conclusion

The Production Control System (PCS) that we have developed allows the rapid implementation and efficient parallel execution of processing pipelines on large amounts of data. PCS has shown its usefulness in a number of application areas, and it is currently in routine use at the BIC for the automatic analysis of MRI data in a multi-center, mass production setting.

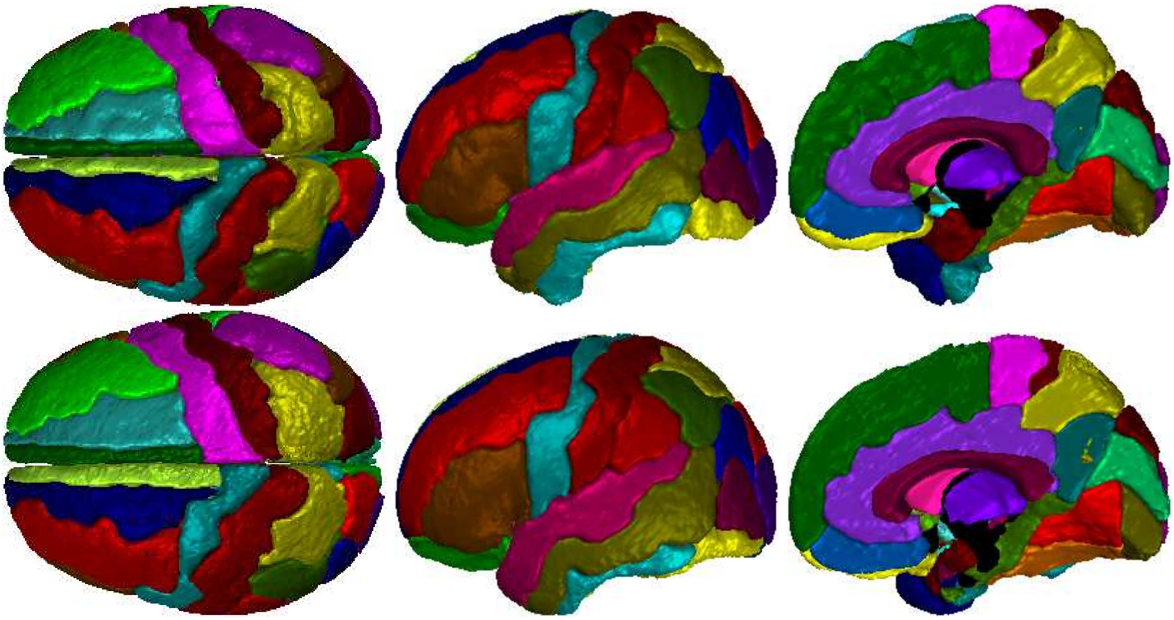

Figure 8.7: 3D renderings of structure SPAMs, automatically generated from (top) 152 healthy adults (age 24.6 ± 4.8) and (bottom) 110 children and adolescents (age 11.2 ± 3.6). From left to right: top view, lateral view of left hemisphere, medial view of right hemisphere.

Bibliography

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