



A MIPAV Plug-in For the Visual And Quantitative Comparison Of FreeSurfer Sub-cortical Segmentation Results

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ABSTRACT

FreeSurfer is an automated structural brain imaging pipeline that includes the segmentation of subcortical structures. Factors such as scanner manufacturer, magnetic field strength, head placement relative to isocenter, and pulse sequence have been shown to affect the reliability of the subcortical segmentation. Reliability of segmentation results is often measured using intra-class correlations. These correlations, however, do not provide any information as to where the subcortical structures differ.

A new MIPAV plugin was created to enable visual comparison of segmentations of a specified subcortical structure across multiple MRI sessions. The plugin provides an automatic segmentation, registration and overlap comparison pipeline for specified pairings of a selected subcortical structure across sessions. Parallel processing on a multi-core CPU node is implemented in Java. The local based registration algorithm is multi-threading enabled and allows a user specified number of parameters (6, 9, 12). In addition, MIPAV's command line interface enables the plugin to run simultaneously over hundreds of nodes on a cluster computer (Biowulf). The clustering, local based multithreading, and efficient memory management build a powerful computing infrastructure to run the pipeline on large MRI datasets.

Once scanner test-retest reliability has been established, the technique can be used to measure longitudinal brain changes.

Methods

1. MRI Brain Sub-cortical Images Segmentation, Registration, and Comparison Pipeline

The protocol objective is to apply the auto-segmentation, registration and comparison pipelining against the children's pediatric database in order to conduct analyses to detect the brain related diseases, which include autism, schizophrenia, Alzheimer, etc. Clinical groups will make observations by comparing the subtle structural differences associated with disease.

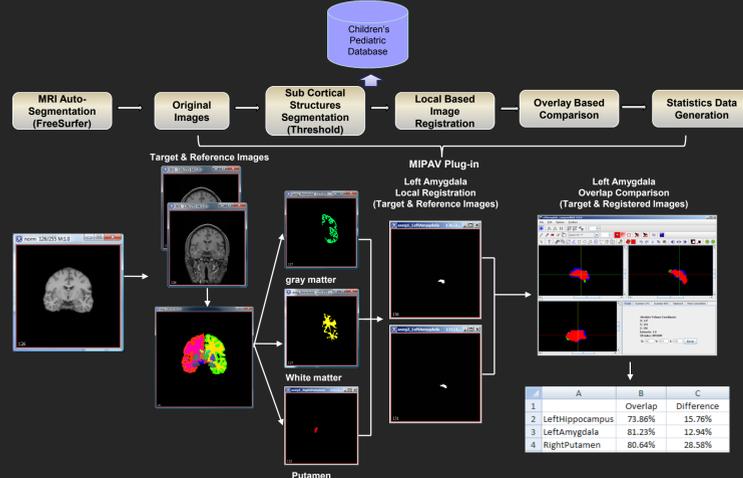


Fig 1 MIPAV plug-in Segmentation, Registration, Comparison Pipeline

The basic pipelining operations consists of

- 1) Automated segmentation of MRI brain scans to obtain the sub-cortical regional structures. Automatic labeling on sub-cortical sections is shown in the first brain image. The automatic segmentation is processed by the FreeSurfer software as a pre-processing step.
- 2) MIPAV threshold based segmentation to single out each sub-cortical structure.
- 3) Sub-cortical based local image registration. Register the target and reference images. Users have the options to specify degree of freedom, 7 DOF, 9 DOF, 12 DOF.
- 4) Overlay based comparison: the overlay comparison can be 2.5D based color wise comparison or 3D surface overlay comparison (transparency view). On the tri-planar images, the red color presents the similarity, the blue and green color present the difference between the registered and target images.
- 5) Automatic generation of a comma separated spreadsheet of the comparison data.

2. Parallelized Registration Algorithm

Multi-threading enabled Automatic Registration (Powell Algorithm)

From Level 8 to Level 1, each level performs Powell search based cost function computation with multi-threading enabled. It utilizes the multi-tasking parallelism on the modern multi-core computers. It chunks the datasets into small kernels, and each kernel in turn computes the minimum cost. Powell's search algorithm creates multiple instances of Powell's search based on the coarse sampling rate. For example, each search has a constant value for rotation X and rotation Y, and a set of rotations in Z. The Powell instances can run as separate threads or sequentially. If they run sequentially, the Powell algorithm will use threads internally.

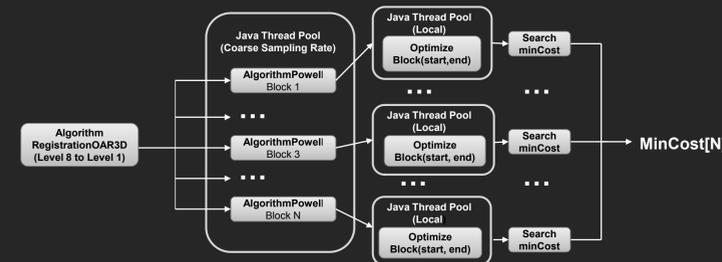


Fig 2 Multi-threading Automatic Registration

3. Biowulf Clustering

The whole pipeline is implemented as a MIPAV plug-in, and it can run from the MIPAV command line. We use SWARM console to run multiple pipeline instances on Biowulf cluster. Clinical researchers can simply create a script to run SWARM command line, and hit run to let the whole registration programs run for days. By taking the advantage of parallel processing power on Biowulf clusters, GPU nodes, and multi-cores, we create a novel implementation that runs MIPAV image processing algorithms on large clinical database.

4. Efficient Memory Management

One single segmentation, registration, and comparison pipeline instance only consumes up to 1 GB memory. Efficient Java based garbage collection mechanism clear up the memory after each run. So, even a laptop computer that supports JVM up to 1 GB can run the program.

Case Study

Hippocampal Atrophy: Alzheimer's Patient

T1-weighted MRI brain scans were acquired every two years over a 12-year period. The chart in Figure 3 shows a progressive reduction in left and right hippocampal volumes as measured by FreeSurfer subcortical segmentation. Figures 4 and 5 show the reduction in volume from years one to three and years ten to twelve, respectively. This allows the practitioner to see the portions of the hippocampus that are most affected at each stage of the disease.

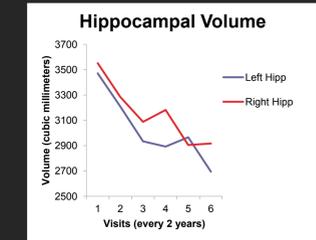


Fig 3 Reduction in volume

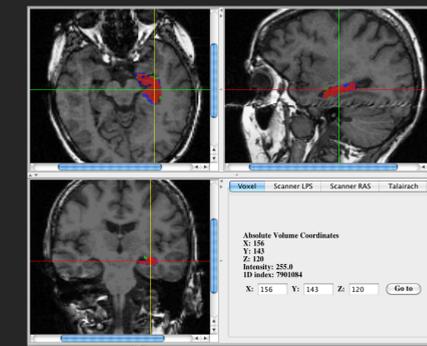


Fig 4 Reduction in left hippocampal volume from year 1 to year 3 after diagnosis.

(Color code: blue = year 1; green = year 3; red = overlap)

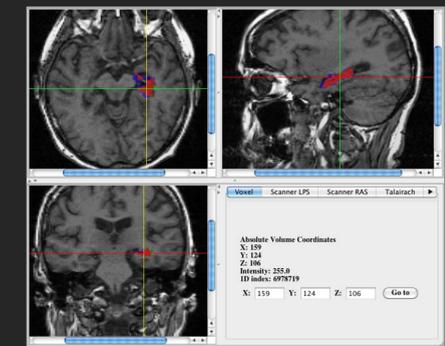


Fig 5 Reduction in left hippocampal volume from year 10 to year 12 after diagnosis.

(Color code: blue = year 10; green = year 12; red = overlap)

Conclusions

1. This MIPAV plug-in enables the quantification and visualization of changes in subcortical structures as measured by FreeSurfer.
2. The plug-in takes advantage of multi-threading, GPU (not discussed here), and cluster computing capabilities to provide rapid results.
3. Easily obtained visual comparison of changes in brain structures can prove to be a useful tool in clinical practice.

References

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