



# BrainVisa Plugin for Automated Measurements of Sulcal Length and Depth.

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## Introduction

There is a growing need for computational methods capable of providing regionalized measurements of the features of cortical morphology. These measurements are needed for studies of genetic control over gyrogenesis; normal and abnormal regional variability of cerebral cortex; changes in cortical atrophy with age and others. We developed a plugin for a popular image analysis package BrainVISA, to calculate average sulcal lengths and depth (ASLD) for individual sulci. This method was used to perform a genetic analysis of the average sulcal depth and length in a translational genetic study in a population of genetically mapped baboons.

## Methods

### Automated measurements of sulcal length/ depth

We developed an automated method to measure regional sulcal length and depth. This method is implemented as an extension to the BrainVISA (BV) framework and works as plug-in for BV anatomy pipeline. The sulcal length and depth measurement are performed on a labeled graph of the cortical folds.



Figure 1. Convex Junction (top), Bottom Junction (bottom), outliers (red circles) and B-spline curves produced to measure sulcal length

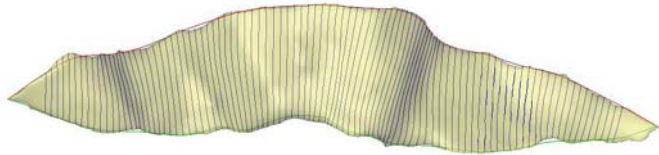


Figure 2. Measurement of regional sulcal depth along the surface of the sulcus

The algorithm consists of the in the following steps (Figure 1)

- 1.Extract "hull junction" points e.g. locations where a sulcus joins with the convex hull of the brain
- 2.Extract "bottom junction" point e.g. the points with the highest curvature on the floor of a sulcus
- 3.Extract sulcal mesh e.g. the mesh representing the body of the sulcus. If sulcus is interrupted, meshes for two or more segments are joined.
4. Outliers are filtered out by removing junction points that are not in the proximity of either sulcal edge
5. Top line is created by parametrizing hull junction points using a B-spline curve
6. Bottom line is created by parametrizing bottom junction points using a B-spline curve
7. Regional sulcal depth is measured by fitting B-spline curves along the sulcal mesh at equidistant.
8. The output data are presented for
  - Average sulcal length/depth
  - Sulcal length for top/bottom curves
  - Regional depth measurements, including
    - Location along the parametrized curve
    - Image-coordinates for the start and finish point
    - Whether the depth is fitted along the sulcal mesh or between sulcal segments

This algorithm is implemented as a plug in for BranVisa (<http://brainvisa.info>) (Figure 2). This algorithm can be executed on a single/multiple subjects as long as their data were processed with BrainVisa anatomical pipeline and subjected to manual/automated sulcal identification and labeling

## Methods (continued)

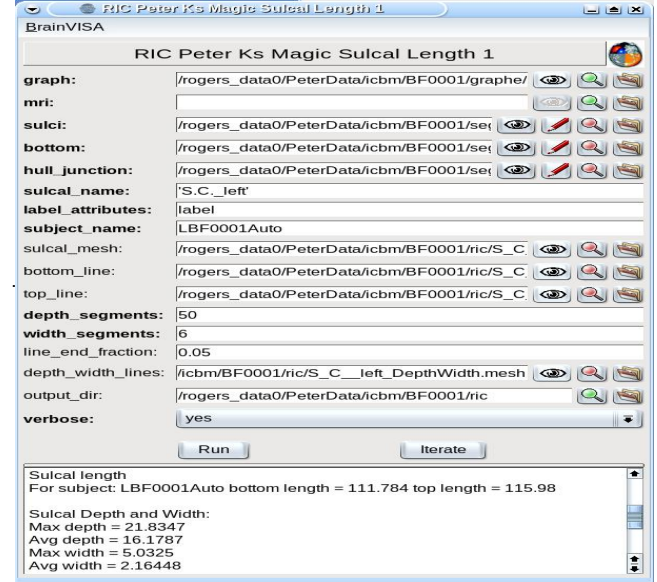


Figure 3. BrainVisa interface for sulcal length/depth measurements

### Genetic analysis of central sulcus length and depth in extended human pedigrees

**Subjects:** Data was analyzed for 255 (93 males) participants in Genetics Of Brain Structure (GOBS) project.

**Processing:** All subjects were pre-processed using BrainVisa anatomical pipeline. Average sulcal length and depth were subjected to heritability analysis using variance component methods implemented in Solar.

## Results

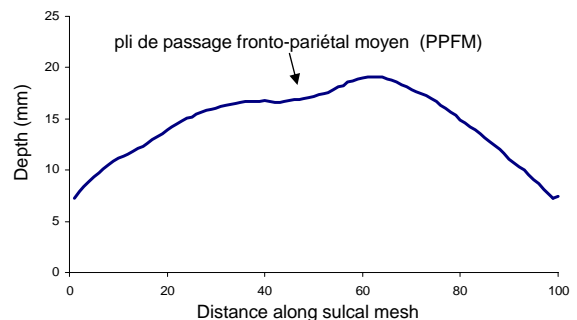


Figure 4. Average depth profile for central sulcus

The average depth profile for the central sulcus is shown in Figure 4. The PPFM point is clearly visible.

Heritability analysis reported that: 63% of variability in sulcal area was attributed to genetics ( $h^2=0.63\pm0.14$ ); 57% of variability in sulcal length was attributed to genetics ( $h^2=0.57\pm0.13$ ); and 34% of variability in sulcal depth was attributed to genetics ( $h^2=0.34\pm0.12$ );

## Availability

<http://ric.uthscsa.edu/personalpages/petr/>

## Acknowledgements

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