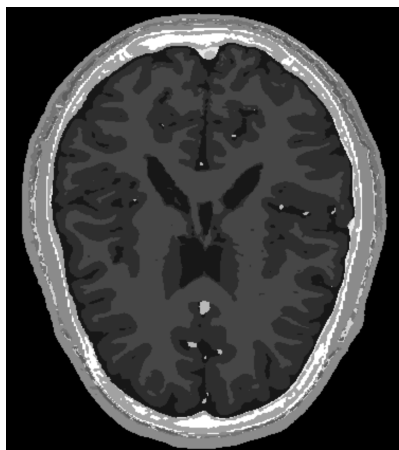# MedVis1 Project: Comparative Visualization of Brain Anatomy Variability

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(a) Segmented cranial scan. The labels are visualized as certain gray values.

(b) Shape of the segmented white and grey matter.

Figure 1: Image of a segmented cranial scan. We defined the shape of a brain as the union of the labels for white and grey matter.

1 Motivation & Problem Statement

This work aims to visualize the variability of brain anatomy over a multitude of brain scans. Therefore we use a dataset provided by McGill University[1]. Figure 1a shows an image of the given data. The dataset provides 20 cranial MRI scans that are labeled per voxel (see the documentation for details). We define the shape of a brain as the union of gray matter and white matter labels. Figure 1b shows a binary image which defines the shape of the brain shown in figure 1a. A particular challenge of this work is to enable the user to compare multiple

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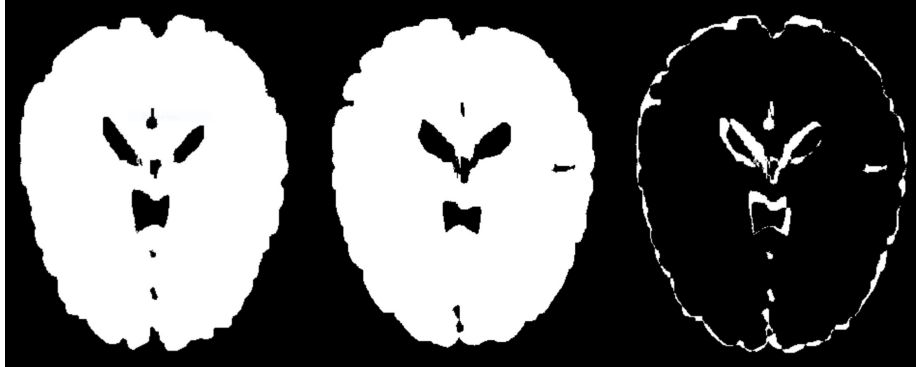[1] https://brainweb.bic.mni.mcgill.ca/anatomic_normal_20.html

Figure 2: (left) shape of b_{ref}. (middle) shape of a specific b_j. (right) absolute difference $d = |b_{ref} - b_j|$

brains against each other. Therefore, we define two deviation metrics, the *sum of errors* metric and the *boxplot deviation* metric to quantify the variability. In the following sections, we describe both metrics in more detail and present our results.

2 Deviation Metrics

2.1 Sum of Errors Metric

Consider a set of segmented brains shapes $B = \{b_1, ..., b_n\}$ as shown in figure 1b, where n is the number of brains. The sum of errors metric compares the shape of a reference brain $b_{ref} \in B$ against the shapes of all brains in B. More precisely, the absolute difference d between b_{ref} and every other brain b_j is computed. This results in n binary images which are 1 at every point in space where the shape of b_{ref} and the shape of b_j differ. Summing over these images and normalizing them leads to a deviation map M with respect to b_{ref}:

$$M(b_{ref}) = \frac{1}{n} \sum_{j=1}^{n} |b_{ref} - b_j|. \tag{1}$$

Figure 2 shows b_{ref}, a specific b_j and their absolute difference. Figure 3 shows a 2D visualization of the normalized deviation map $M(b_{ref})$. This metric is one way to quantify the brain variability. However, it is always relative to a certain reference brain.

2.2 Boxplot Deviation Metric

This approach aims to create a kind of continuous 2D-boxplot regarding the shapes of the brains, in order to display a "mean brain shape" and the level of local deviation. Since a geometrically exact averaging of the available shapes
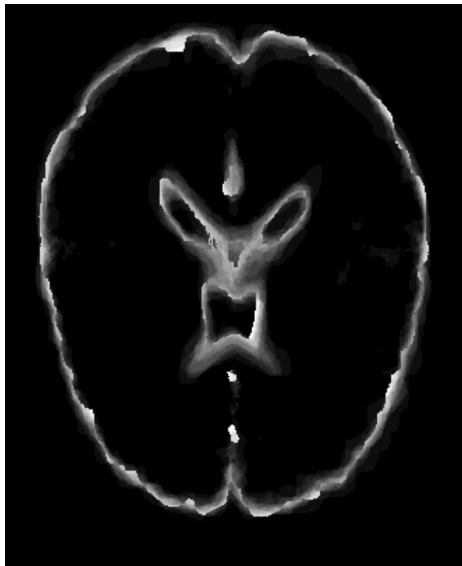
Figure 3: Image of the normalized sum of errors deviation map $M(b_{ref})$

would have required vertex mapping, we could only approximate the average shape. To do this, the binary segmentation masks are summed up:

$$I(x, y, z) = \frac{1}{20} \sum_{1}^{20} I_n(x, y, z) \qquad (2)$$

Thus, the resulting intensities $I(x, y, z)$ are normalized sums over the corresponding voxel values of the 20 base scans.

The contour of the iso-value 0.5 (implemented as range [0.45, 0.55] for better visibility) represents the mean border of the brain and is color-coded in white. The other colors represent the deviations up to quartiles, 10%/90%-percentiles and outliers in different shades of blue (see figure 4).

In general, the 0.5 iso-contour does not guarantee a meaningful approximation of a mean shape. However, two factors support the reasonability of such an approach in this specific case:

- The scans are all aligned in scale and position and they are overall homogeneous in their shapes.

- If mappable vertices for the different brain shapes existed, it would be a fair assumption that individual vertices varied (approximately) only along a straight line. Hence, the variation is rather structured than chaotic.

As noise does not contribute to mean estimation, the original brain scans are smoothed by a Gauss filter with $\sigma = 6.0$ before the normalized sum is computed.
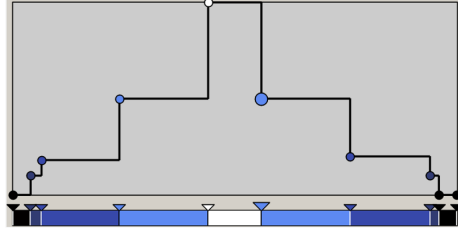
Figure 4: Color and opacity coding of intensity values for the boxplot deviation visualization

3 Results

3.1 2D Visualizations

Both metrics are visualized as scrollable 2D-slices of the volume, with representative slices for coronal, axial and sagittal axis displayed in figure 5. Figure 5a shows the deviations of the sum of errors metric, color-coded in shades of red and yellow. Figure 5b shows the mean border in white and boxplot-like deviations in shades of blue. While the boxplot deviation visualization does not have a background, the pre-segmented cranial MRI scan 04 serves as background for the sum of errors visualization. For clear visibility of the colored metric overlay, white & grey matter of the background scan are color-coded dark while skull, muscle, marrow and other segments are displayed in light colors. This visualization method does not take transparencies into account, i.e. all colors of the overlay are opaque.

3.2 3D Visualizations

In this section, we describe how we map both deviation maps onto 3D data and create meaningful visualizations. Figure 6 two 3D visualization showing one specific deviations map respectively. Figure 6a shows the segmented cranial MRI scan 04 (*subject04_crisp*) and the sum of error deviation map, with b_{ref} computed from *subject04_crisp*, projected onto the scan. We defined a color map that assigns every value in the deviation map a color value and an alpha value. Red indicates areas of high variability, yellow represents areas of medium variability. Completely transparent regions, where only the dataset is visible, indicate no variability. Figure 6b shows the boxplot deviation map projected onto the *subject04_crisp*. The white line indicates the shape of the mean brain. The blue colors with decreasing intensity show the regions of the respective quartiles, the 10%/90%-percentiles and the 5%/95% percentiles, respectively. It is possible to interactively slice through the dataset, using clipping planes. To preserve spatial context a ghosted envelope of the brain shape is rendered (see figure 7).

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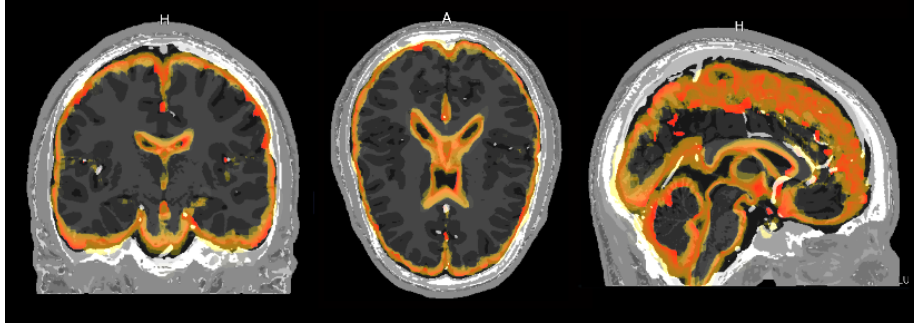
(a) 2D visualization of the sum of errors metric on a representative brain slice for each axis, including background.
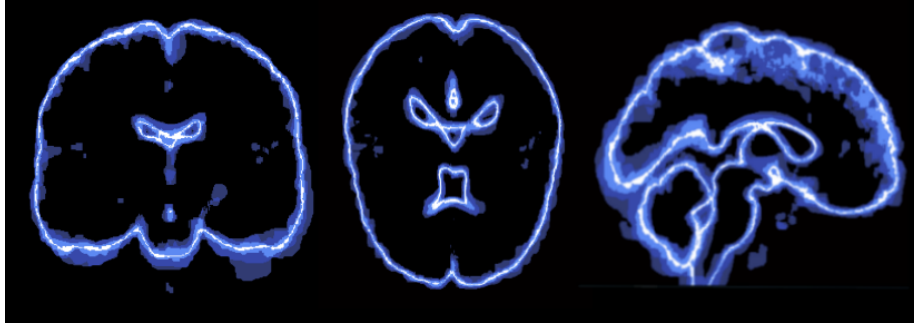
(b) 2D visualization of the boxplot deviation metric on a representative brain slice for each axis, without background.
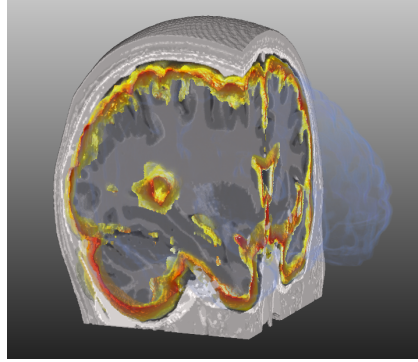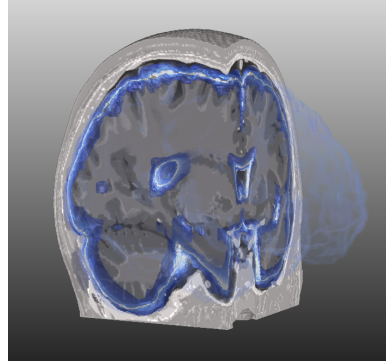
Figure 5: 2D visualizations

4 Limitations

This approach just compares the shape of the brains, but not the differences of the chosen labels among each other. The method could be further extended to also be able to analyze the differences between white and gray matter respectively.

5 Distribution of Work

Marian Stoschitzky computed the boxplot deviation metric from the dataset. He was responsible for all 2D visualizations. Jakob Troidl computed the Sum of Errors deviation metric from the dataset. He was also responsible for all 3D visualizations.

(a) Visualization of the sum of errors deviation metric.

(b) Visualizations of the boxplot deviation metric.

Figure 6: 3D visualizations of both deviation metrics. A ghosted envelope of the brain shape is rendered to preserve spatial context.
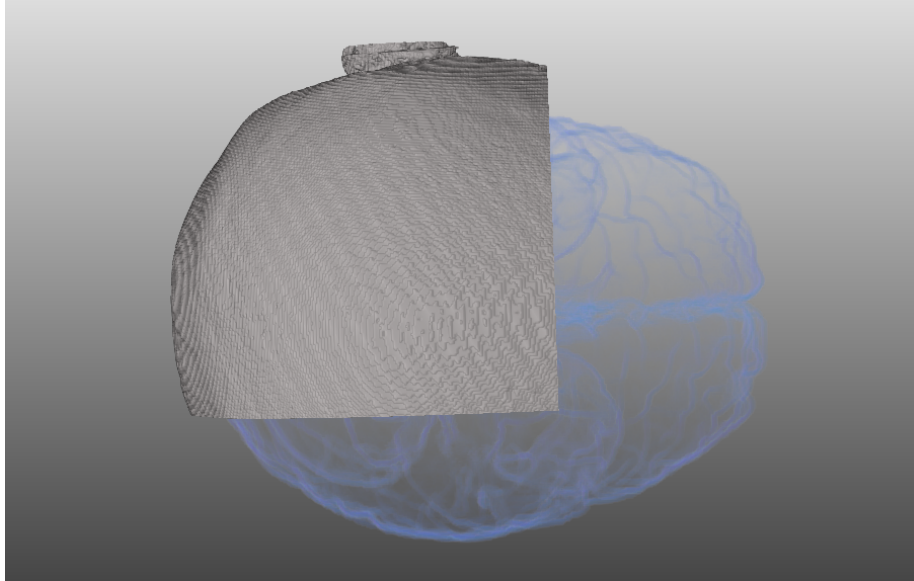

Figure 7: A transparent envelope of the brain shape is rendered to preserve the spatial context when cutting through the volume.