Preliminary Development of an Automated Analysis Tool for Intracranial MRA

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Introduction

In recent years intracranial MRA has developed to where high quality, high resolution images of the vasculature are routinely obtained. These high resolution images may be of sufficient quality for automated quantification of disease status. Towards this end we have been developing an automated analysis tool for intracranial MRA images. The analysis uses the Z-buffer segmentation (ZBS) algorithm to extract the vascular voxels from the image and mathematical morphology operators to group the voxels into distinct vascular segments for which centerlines are computed using least squares splines. We report here on our initial experience with this method.

Methods

Our automated analysis consists of the following steps: 1) segmentation of the vasculature with the ZBS algorithm; 2) detection of bifurcations; 3) trimming segments created from false bifurcation detection; 4) assigning parent child relationships to each vascular segment; 5) computing the vessel centerline for each segment; 6) measuring segment properties.

Image Acquisition: Images were acquired on a 512x192x64 grid covering a 220x165x58 mm3 imaging volume. Central k-space MT was used to suppress background signal. Images were reconstructed with zero-filled interpolation [3] to a 1024x768x128 matrix and subregioned to a 512x512x120 matrix centered around the Circle of Willis.

ZBS Segmentation: The ZBS segmentation is a simple vascular segmentation algorithm developed by Parker et al. [Parker, 2000] which makes minimal assumptions about the nature of the vasculature. As such the segmentation is ideally suited for segmenting vascular images with pathology, where objects of interest may not meet the tubular criteria assumed by many other segmentation techniques (e.g. [Sato, 1997], [Frangi, 2001]). Default parameters as described in [Parker, 2000] were used to generate the segmented data.

Bifurcation Detection: To detect the vascular bifurcations within the segmented data we apply the algorithm of Matsutani et al [Matsutani, 1998]. Assuming a binary mask (B) of the vasculature, we start with a seed within the mask (X_0). The seed is dilated by a structuring element (K). This dilated structure is then intersected with the original mask to get the next structure (X_1). To generate the mask at step X_N we apply the following operation: $X_N = (X_{N-1} \bullet K) \cap B$. If the dilation step occurs at a bifurcation then when we subtract mask X_{N-1} from mask X_N there are multiple discontiguous structures with the same parent, indicating a bifurcation. This process is repeated until $X_N = X_{N-1}$ (that is no new voxels have been added to the structure).

Trimming False Bifurcations: Because MRA data is discrete and noisy, it may include bumpy structures mimicking a bifurcation but not actually of interest. How sensitive the algorithm is to these false structures depends on the size of the structuring element used: structures smaller than the radius of the structuring element will not be detected. However, larger structuring elements result in poorer localization of the bifurcation. Inevitably some false bifurcations will be detected. We delete these structures if the child segment has fewer than 20 voxels.

Parent/Child Relationships: Starting with endpoint segments (segments with no children), we trace back the segments identifying the parents of each segment until all segments have been assigned a parent/child relationship.

Segment Vessel Centerline: For each segment we compute the vessel centerline using a least squares spline. In order to fit the spline we need a parameterized list of points. After the application of the bifurcation detector, each vascular segment consists of the group of points added in the dilation/intersection step. These groups are naturally parameterized and we identify the center-of-mass (COM) of the maximum of distance from edge values. These COM values form the parameterized list of points for the fit. Once the centerline is fit the segment is re-parameterized into groups of points based on the minimum perpendicular distance to the centerline for each voxel in the segment. This process is applied iteratively until a stopping criteria is met. The amount of smoothing applied is adaptively adjusted to insure that the centerline tracks the vessel and does not cut outside of it.

Morphological Characterization: The centerline can be used as a basis for morphological characterization of the vessels. Because of the discrete nature of the data, we compute quantities such as mean vessel radius using a moving average window.

Results

Figure 1 shows examples of the segmentation, detected bifurcations, an extracted vessel path, an extracted centerline and estimated vessel radius for a vascular segment. Note that the extracted path for the posterior element traced back to the right ICA (bifurcation seed point) and not to the basilar tip (physiological origin).

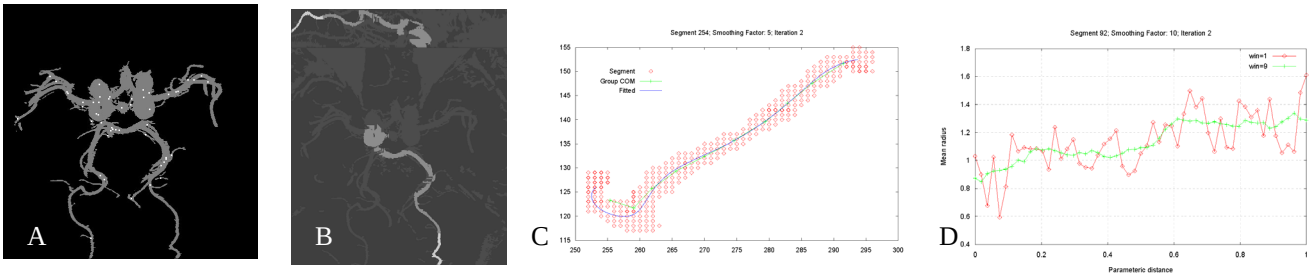

Figure 1.A, Axial projection of the segmented mask with bifurcation points highlighted. B. Identified vessel path traced from terminating segment (bright) to the seed point. On the top is a lateral projection, on the bottom is an axial projection. C. Axial projection of centerline fit through a vascular segment. The piecewise linear line is the centerline determined from the initial distance from edge values while the smooth line is the least squares spline estimate. D. Mean vessel radius by position along centerline for a different vessel segment. The jagged line is the radius estimate based on single centerline point calculations. The Smoother line is the radius estimate using a moving average window.

Discussion:

We have found that this preliminary vascular analysis system works quite well on our MRA images. However, there are still improvements needed. First, we currently have some fragmentation of large vessels during the bifurcation detection. Second, we need to recognize vascular beds, so that vessel paths can proceed to their physiological origin, not simply the root of the bifurcation detection process. The developed techniques should form a useful basis for future quantitative analysis of vascular disease processes, content based image retrieval, phenotype cataloging of the vasculature and computer aided detection.

References:

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