Experimenting with Segmentation in ITK

Release 0.01

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Abstract

This document describes some experiments for segmentation using the Insight Toolkit ITK www.itk.org. The code of the experiment is written following the ITK CodingStyle as described in the directory Insight/Documentation/Style.pdf.

Segmentation is still an open problem and there are quite a lot of algorithms specific to application domains and data being used. In this experiment I've used a 3-D MRA scan of Brain retrieved from MIDAS website.

The paper is accompanied with the source code, input data, parameters and output data that the author used for experimenting with the algorithm.

Contents

At the very least region growing algorithms need a seed point, so we need to visualize the data to decide on the coordinates of that seed point. ImageViewer application is pretty handy for that purpose and can be accessed from InsightApplications directory.

1 Software Requirements

To run the experiment you need to have the following software installed:

- Insight Toolkit 3.2.
- CMake 2.4
- ImageViewer or ParaView.

Note that you dont actually need to have ImageViewer to run the program. The only use of ImageViewer is to examine the image and pick up some parameters for the segmentation.

2 Experiment

I've used the Normal-061 MRA scan image which can be get from http://insight-journal.org/dspace/handle/1926/942. Before the experiment the 67th z slice looks like figure 1.

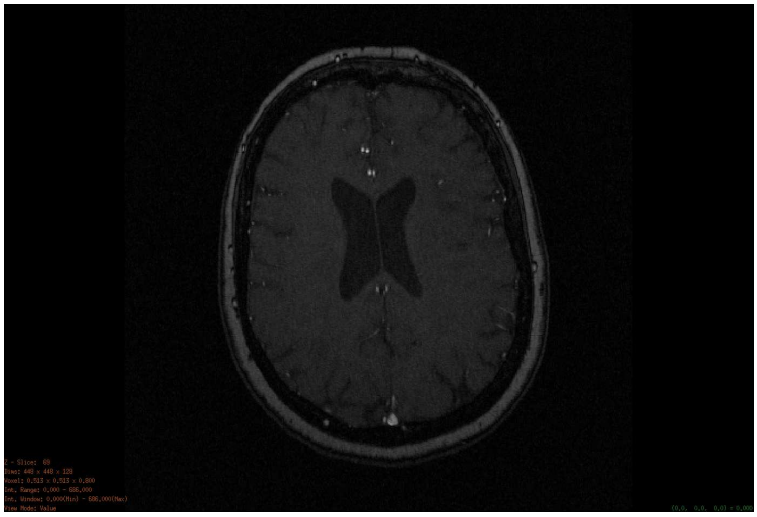

Figure 1: The 69th z slice before segmentation

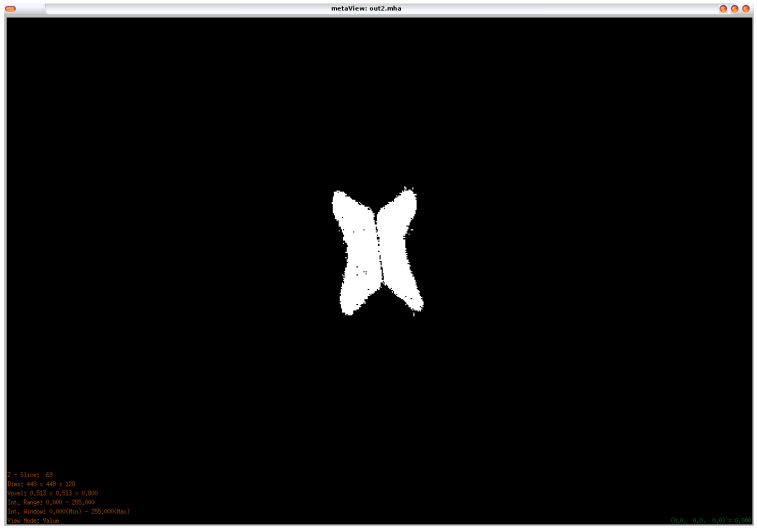

Figure 2: The 69th z slice after segmentation

The method used to segment the image is Connected Threshold (itk::ConnectedThresholdImageFilter). The method expects seed values for x,y,z coordinates a lower value and an upper value as the thresholds.

Playing around with lower threshold and upper threshold, having a threshold value bigger than 87 seems to get unrelated regions. The lower threshold was not as important as the upper one, so the choice of 0 for lower and 87 for upper seemed fine. For these parameters the 69th z slice of the resulting segmentation is given in figure 2.

To replicate this result run the provided code by:

```
BrainSegmentation Normal061-MRA.mha res.mha 210 199 69 0 87
```