Image Segmentation

Release 1.0

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RPI

Abstract

This document describes an algorithm implemented using the Insight Toolkit ITK www.itk.org. This paper is accompanied with the source code, input data, parameters and output data that the authors used for validating the algorithm described in this paper. This adheres to the fundamental principle that scientific publications must facilitate reproducibility of the reported results.

Contents

Using image filters from the Insight Toolkit and example code for 2D image segmentation, I developed an algorithm for segmenting regions in 3D images.

Experiment

The motivation behind this experiment was to expose students to the concepts of Open Data, Open Source and Open Access which are the three pillars of Open Science. It also demonstrated the characteristics of medical image segmentation and how it is applied to clinical problems by using MRI data of a human brain as the input. The experiment used Connected Threshold to segment 3D medical images, segmenting the ventricles of a normal human brain, or tumors. The input used was an MRI scan of a healthy, normal human brain from the MIDAS collection at Kitware, specifically Normal012.

Method

The method used for image segmentation was the Connected Threshold method. This method is a particular type of region growing algorithm which starts from a seed region that are located “inside” the object to be segmented. The pixels neighboring this seed are evaluated to determine if they are also part of the object. The process continues until the neighboring pixels are no longer considered to be a part of the region based on the criteria for the particular algorithm. The criterion used for the Connected Threshold method is to evaluate the intensity within a specific interval. To specify this interval, the user gives an upper and lower bound for the intensity of the region to be segmented.

Instructions

To reproduce the example, the Normal-012 MRI image with the title T2 from the Designed Database of MR Brain Images of Healthy Volunteers in the MIDAS collection needs to be downloaded. Using cmake and the CMakeLists.txt provided, ConnectedThresholdImageFilter.cxx needs to be compiled. Once compiled, the program can be run using the following command line arguments to get the desired output:

```
./ConnectedThreshold Normal012-T2.mha Normal012-T2-output.mha 103.5 127.0 71.0 94.5 125.0 71.0 1200 2000
```

The program takes two seeds, one for each each ventricle in the brain. The first seed is (103.5, 127.0, 71.0) and the second seed is (94.5, 125.0, 71.0). The lower bound for the intensity is 1200 while the upper bound for the intensity is 2000. The input file is Normal012-T2.mha and the output file is Normal012-T2-output.mha.

Results

The resulting image shows the segmented ventricles of the brain. If viewing the image in ImageViewer, the segmented region should be seen around slice 71 in the output file.