

MRI Image Analysis

User Manual



Image by Harry Sieplinga, HMS/Getty Images

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Overview

Project Background

The MRI Image Analysis program was developed for our client, Dr. Jaffar Ali Shahul Hameed, Ph.D, Associate Professor of Mathematics at Florida Gulf Coast University. The program was developed for a project to determine tumor growth and tumor projection as part of a model that theorizes that growth during treatment may not always be from the failure of treatment and that the growth operates on a dampened oscillation.

Developed By



This program was developed by Hands of Gold—David Bryce, Brian Paxson, Elliot Hutchinson, and Justin Nunn (as pictured) as part of a class project for CEN 3073 Software Specifications at FGCU. It was developed using Java and JavaFX.

Download the source code at github.com/postsneakernet/MRI

Getting Started

Using Valid Data

MRI Image Analysis software expects data for a patient to be in a specific format:

```
patientDirectory > monthDirectories > mrImages
```

Where each patient directory contains only directories for the months containing the MRI images and each month contains exactly 8 MRI images. The MRI images should be jogs and conform to an alphabetical naming so that the first image comes before the second image and so on. Additionally, the images should not contain a “.” in the filename other than the one before the file extension. A suggested file name for the first month and first image:

```
mri-m1i1.jpg
```

Data Created by MRI Image Analysis

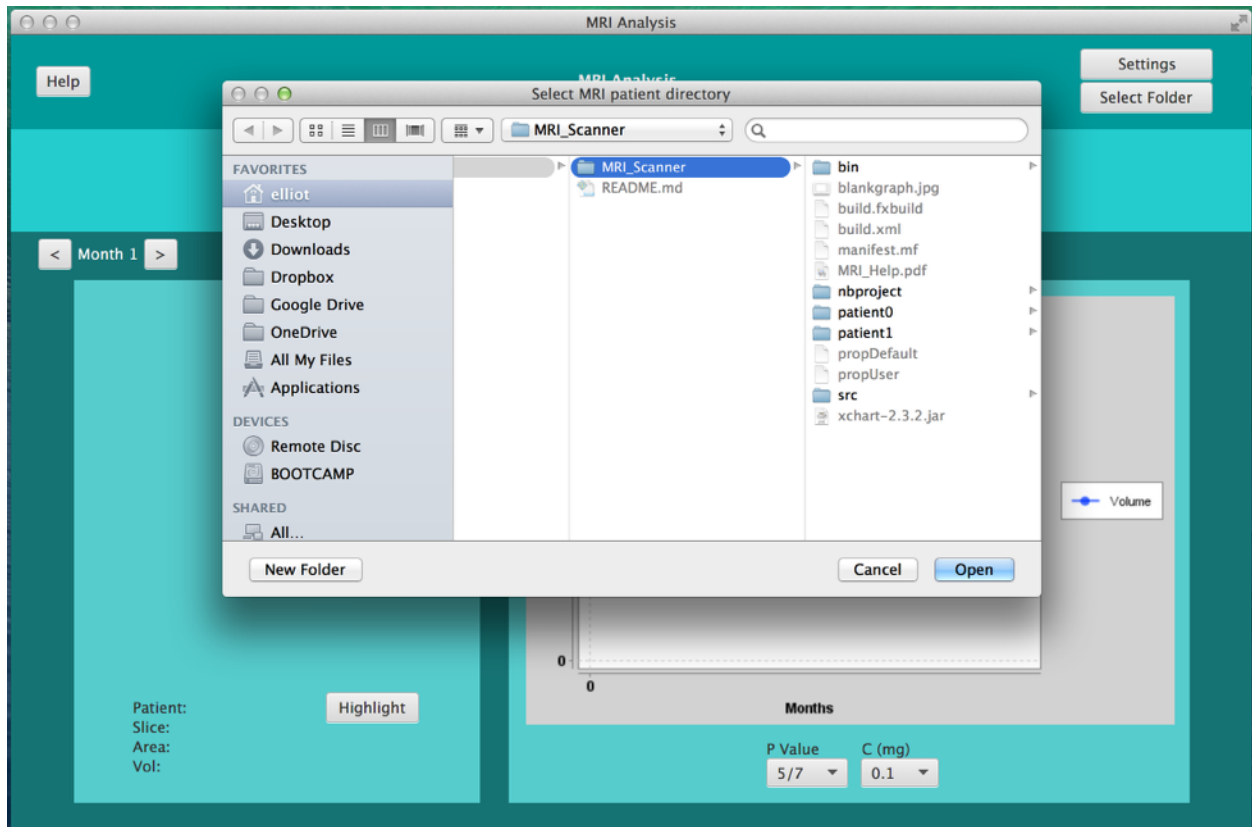
The area calculated from each month for each image is saved in the month’s folder in an area.dat file. This file will be used on subsequent analysis for the patient if present in the month directory. The last highlighted image is saved in the month directory that with “last-image.” prepended to the filename as in:

```
last-image.mri-m1i1.jpg
```

A settings “propUser” file is generated, as well, and is stored in the root of the program directory.

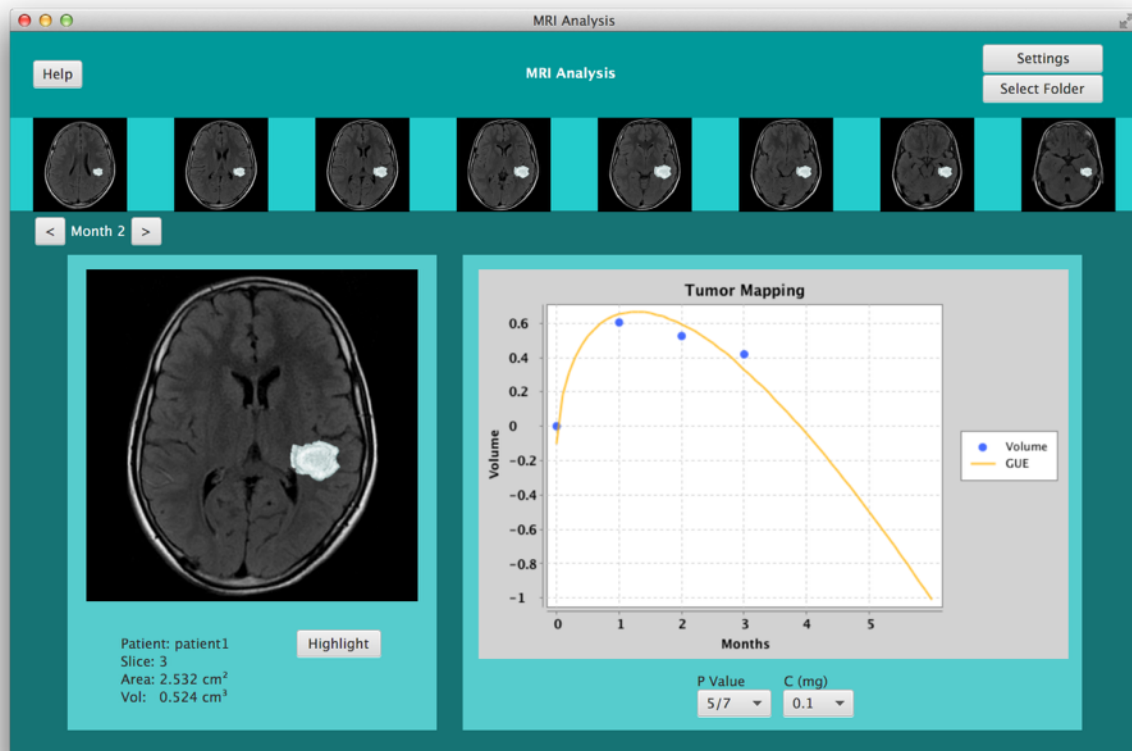
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Selecting Patient Directory



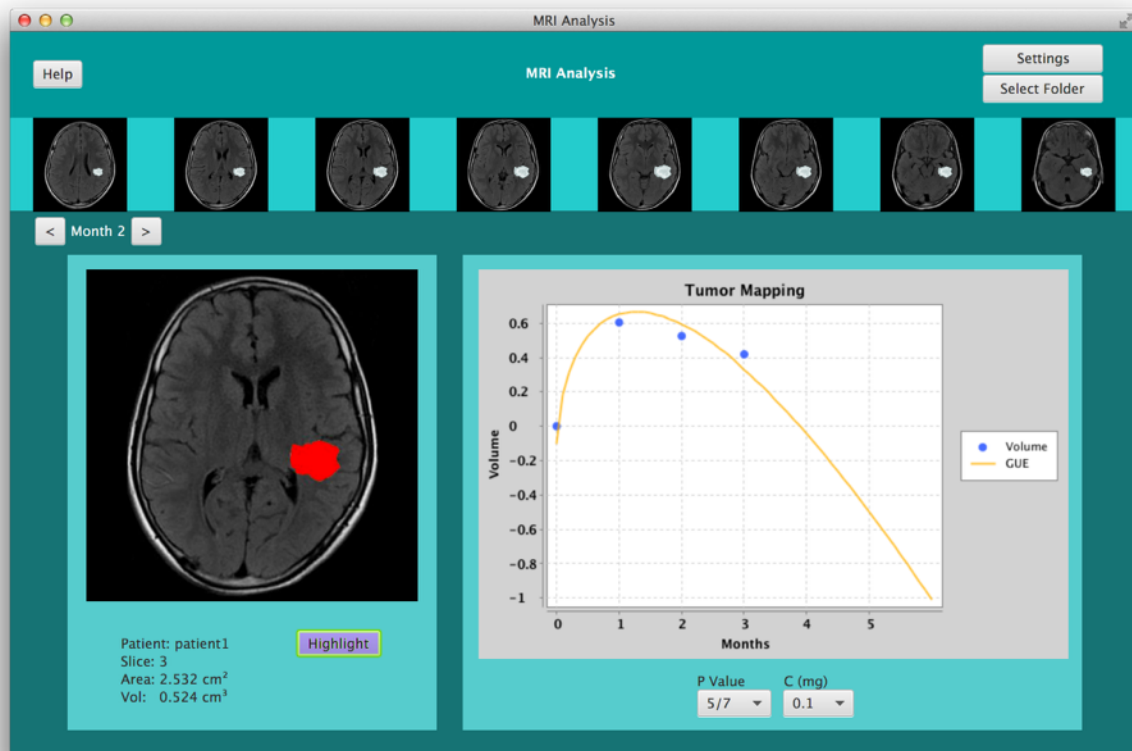
Click the Select Folder button in the upper-right corner of the program. A directory chooser opens, defaulting to the root of the program folder. Navigate to the patient directory and select open. The area for each image for all months will be calculated, as well as the volume, and the graph will be updated reflecting the information.

Selecting Patient Months and Images



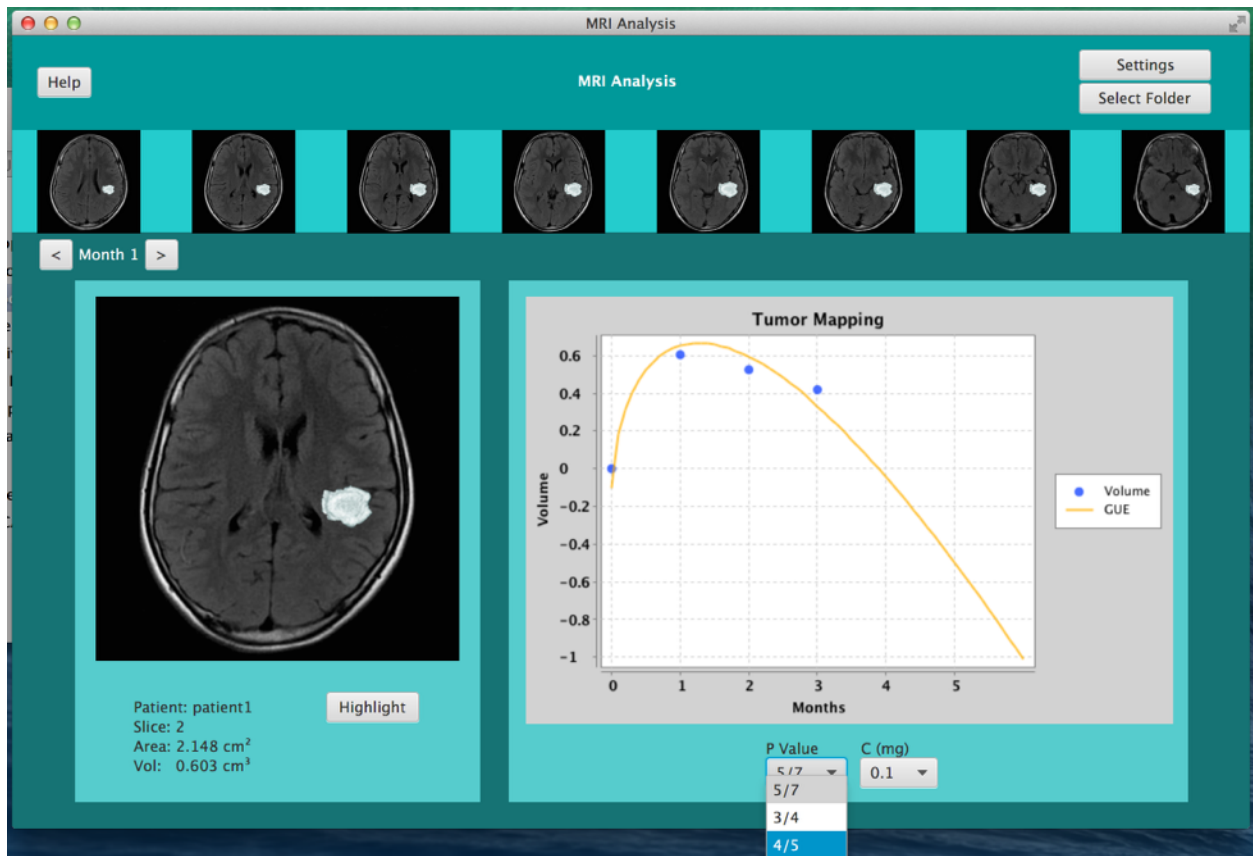
Months can be navigated by clicking the left and right arrows under the image thumbnails in the upper-left of the program. Click on a thumbnail to view a larger version of the image as well as the area of the tumor at that slice.

Highlighting Tumor Area



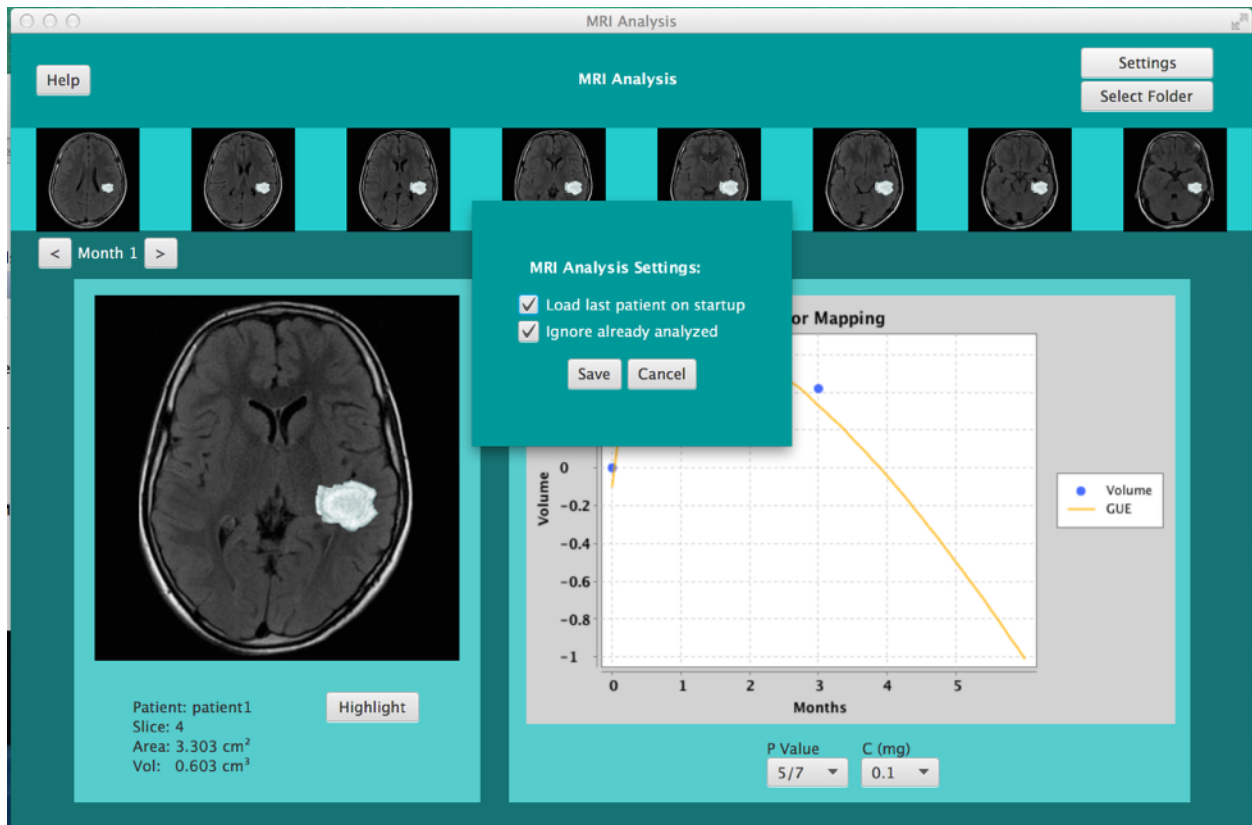
Click the Highlight button to toggle tumor highlighting. The location of the tumor will show in red on the image.

Changing P and C Values



Click on the drop down menu under the graph for P Value and C Value to change the values for P and C, respectively. The graph will automatically update with the new value.

Adjusting Settings



Behavior of the program can be changed by clicking the Settings button in the upper-right corner of the program. The last patient directory is loaded on program start. To change this setting, uncheck the load last patient on startup box. By default, the area is not recalculated again for months that were already stored. This can be changed by unchecking the box for ignore already analyzed. Click Save to save the changes or Cancel to discard the changes.

Known Issues

Area and Volume of Tumors

Due to HIPAA laws, this program was not developed and tested using real patient data. The program was tested with data modified in Photoshop and might not correspond to accurate values. Since the physical, real-world values are not known, area is calculated using a pixel-to-centimeter conversion and the volume is calculated from the the sum of each area slice for the month and then converted from pixels to centimeters.