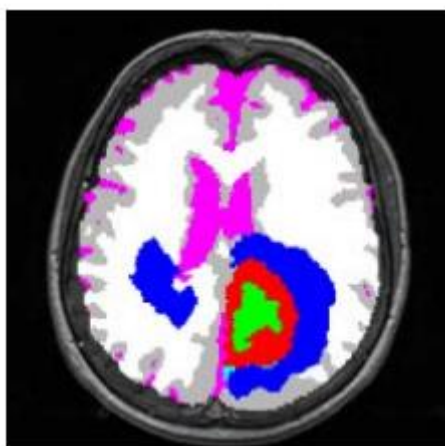




## *BraTumIA*



## **Installation Guidelines**

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## 1. Introduction

The **Neuroimaging Informatics Tools and Resources Clearinghouse** (NITRC) is a neuroimaging informatics knowledge environment for MR, PET/SPECT, CT, EEG/MEG, optical imaging, clinical neuroinformatics, imaging genomics, and computational neuroscience tools and resources.

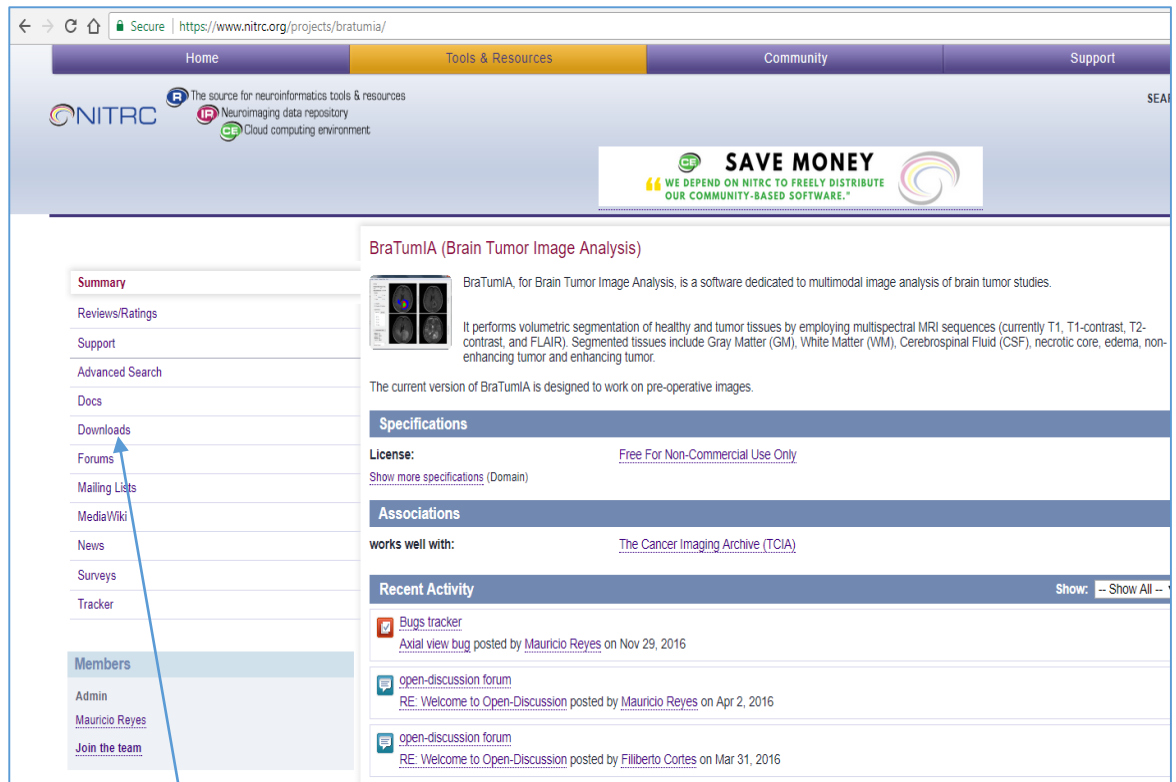
BraTumIA is a software tool for automatic brain tumor image analysis developed by NITRC[1]. BraTumIA works using a pipeline consisting of skull-stripping, multi-modal registration, tissue classification and segmentation of subcortical structures are carried out sequentially. A brain mask is generated by skull-stripping the given images, followed by registration. Registration ensures voxel-to-voxel correspondence between the different MRI sequences. Segmentation of healthy and tumor tissues are done based on combined classification and regularization. This produces a label map and quantitative information about tissue volumes. Healthy subcortical structures are segmented using a deformable registration of an atlas to the patient image. The label maps can be converted back into the original space of each image sequence. They are shown as an overlay on the original images [2].

## 2. System Requirements

- Windows 7 or Windows 8 (64bit version)
- 16 GB of RAM memory (or above)
- 2 GB of hard disk space

## 3. Installation guidelines

1. Go to :<https://www.nitrc.org/projects/bratumia/>



2. Click on downloads
3. User gets a requirement form for downloading BraTumIA ,as shown below:

**Requirement Form for BraTumIA**

First name:

Last name:

Institution:

Country:

E-Mail:

Reason for the request:

4. Fill the requirement form and click request. User will get a status message as shown below:

**Request State for BraTumIA**

First name	Last name	Institution	Country	Email	Comment	Created	Request State
Mudathir	Bakht	Fukushima Medical University	Japan	m-bakht@fmu.ac.jp	Brain tumor segmentations	2017-08-02 10:23:36	Your request will processed as soon as possible
seema	bhat	Dayananda Sagar College of Engineering	India	seemasbhat@gmail.com	research	2017-08-07 08:21:52	Your request will processed as soon as possible

5. User will receive an acceptance mail to the specified email id in the requirement form. The following link:

<http://istb-software.unibe.ch/bratumia/MIA/BraTumIA.html> is provided for downloading the software.

6. Click on: [BraTumIA-1.2.1-MS-Windows-Installer.zip](#)

7. Unzip the folder and click on setup.exe for installing the BraTumia software.

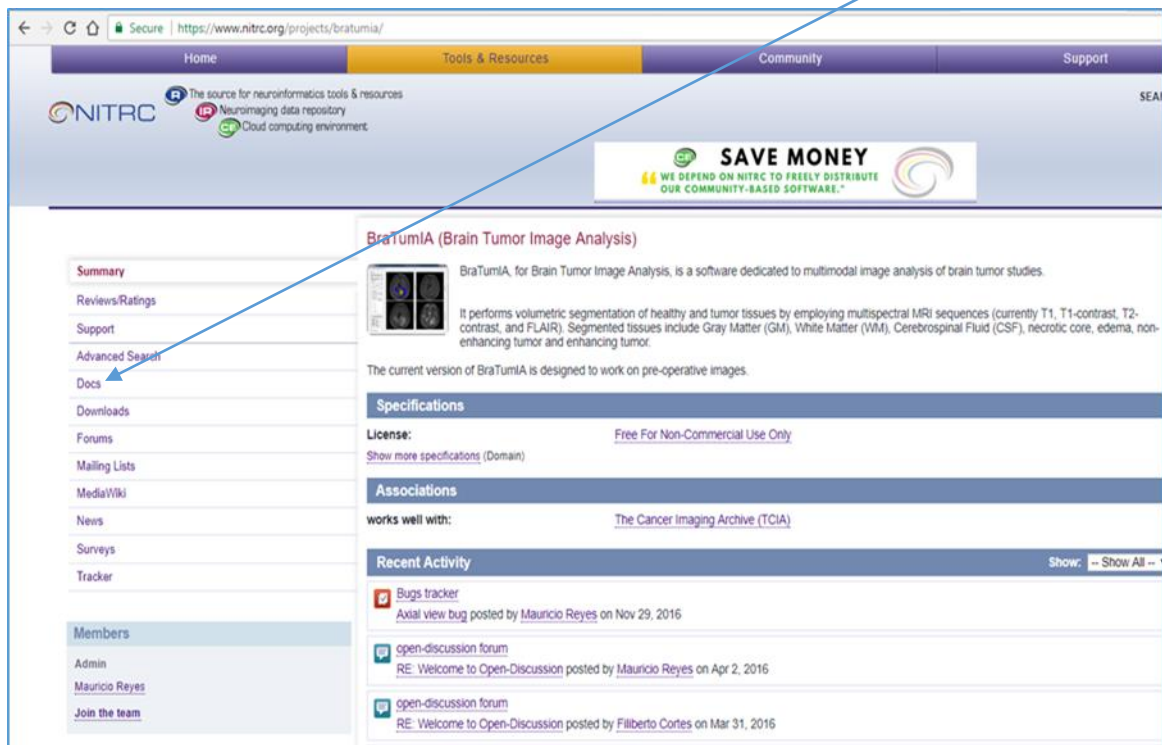
#### 4. The main window of BraTumIA



The main window of BraTumIA contains menu buttons for loading and unloading images at the top. On the left panel, the user can find different options for processing and visualizing the data. The largest part of the main window contains four visualization sub-windows, where the image data and the label overlay can be shown. The different sub-windows can either show different MRI sequences or one sequence in different orientations.

## 5. Loading the data

1. To load the standard data set for BraTumia trail run, click on Docs



2. Click on Test Case for BraTumia.



3. Download and unzip the folder.

Test data has: T<sub>1</sub>, T<sub>1</sub>contrast, T<sub>2</sub> and FLAIR images.

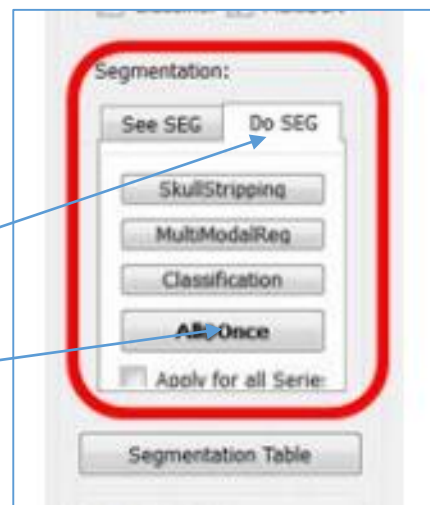
BraTumIA supports volumetric images in the meta image format (.mha), the Nifti format (.nii) and Dicom series (.dcm). If the format is Dicom, the different modalities have to be located in different folders and the location of the folder for 4 each modality has to be selected. The directory tree has to be selected in the left sub-window and the final folder/image in the right sub-window.



The user can start to load the patient images by clicking on the Load button and add the sequences.

## 6. Processing the data

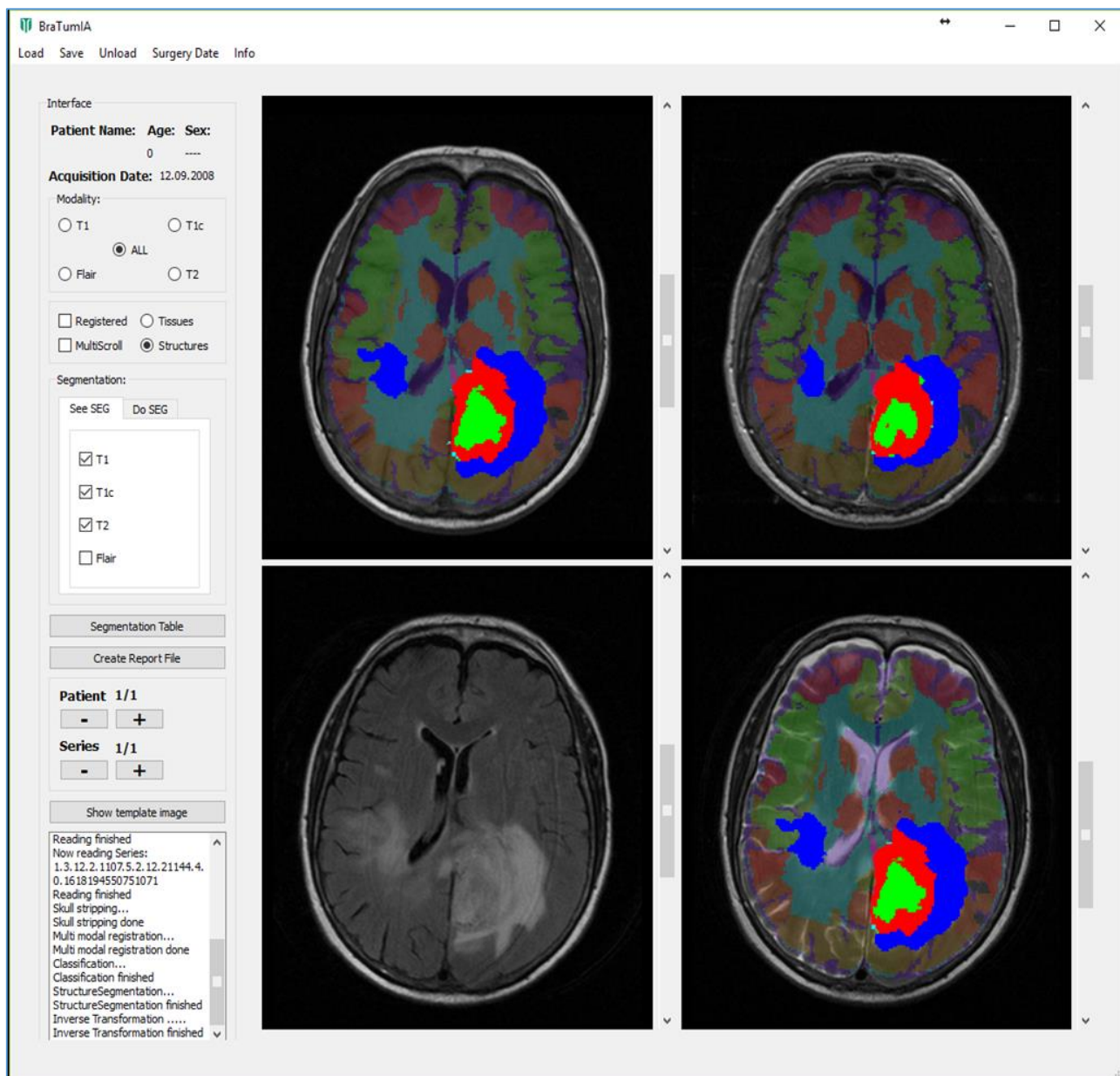
The user can call each module separately (skullstripping, multi-modal registration, classification) or he can press the All@Once button for a completely automatic processing in the Do Seg tab, located on the left panel. The classification button and also the All@Once button will perform both segmentation of tissues and subcortical structures. The progress can be seen in the command line window.



## 7. Visualizing and analyzing the results

The visualization sub-windows can be used in two ways: when all is ticked in the modality selection panel on the left, then all four modalities are displayed in clock-wise direction, starting with T<sub>1</sub> on the top left, T<sub>1</sub>contrast top right, T<sub>2</sub> bottom right and FLAIR bottom left. If only one specific modality is ticked, then this modality is displayed in axial, coronal and sagittal view in 3 sub-windows and the fourth sub-window shows the T<sub>1</sub>contrast image.

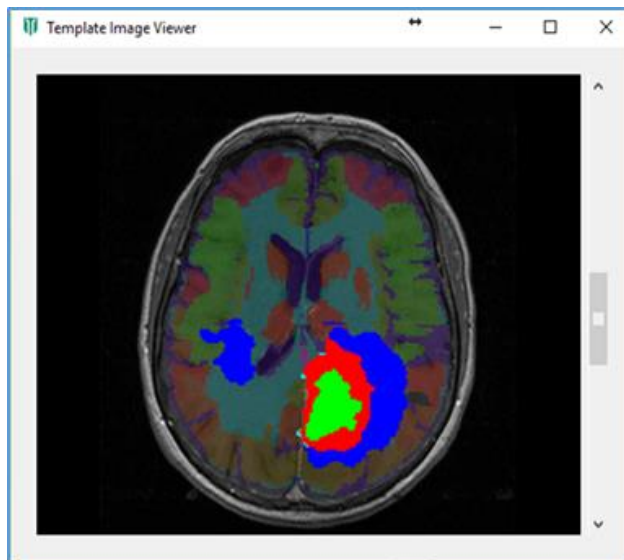




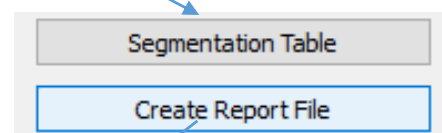
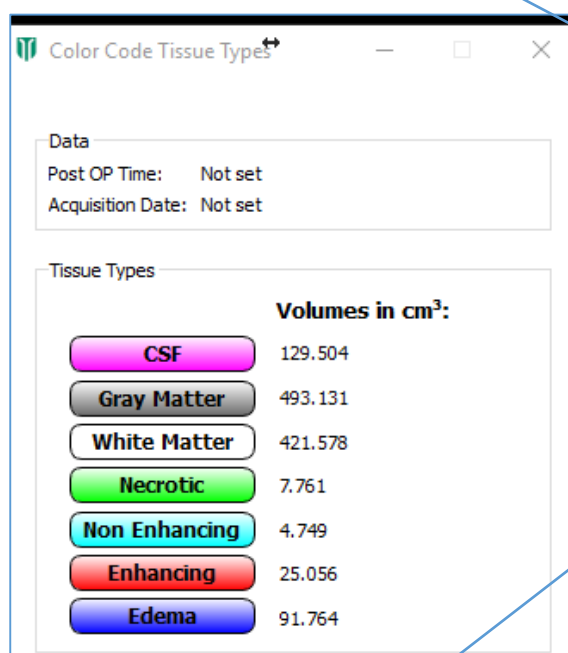
If the *show template window* button is clicked, the template image is shown in a separate pop-up window.







The *segmentation table* is a pop-up window that shows the volumes for each segmented tissue compartment. From this window user can switch on and off certain layers of the color label overlay by clicking on the individual tissue.








By pressing the *Create Report File* button, a .csv file is created that contains a longitudinal volumetric analysis of the active patient. It is stored in the output folder of the first baseline scan.

```
AcquisitionDate::Fri Sep 12
2008
CSF::3.33096e+006
Gray Matter::129504
White Matter::493131
Necrotic::421578
Edema::7761
Non Enhancing::91764
Enhancing::4749
```





## 7. Locating the output for external use

All the results are stored in an output folder which has been chosen by the user when loading the data. The output folder will contain: *SkullStripped* folder, *Registration* folder, *classification* folder and *structures* folder.



The *Registration* folder contains all registered image sequences, skull-stripping in .mha format and the transformation parameters used for each sequence in the .tfm files.

New Volume (G:) > SEEMA_BHAT > Registration > META			
Name	Date modified	Type	Size
 Flair-1.3.12.2.1107.5.2.12.21144.4.0.161713...	07-08-2017 14:49	MHA File	617 KB
 T1-1.3.12.2.1107.5.2.12.21144.4.0.1616270...	07-08-2017 14:49	MHA File	579 KB
 T1c-1.3.12.2.1107.5.2.12.21144.4.0.161819...	07-08-2017 14:49	MHA File	581 KB
 T2-1.3.12.2.1107.5.2.12.21144.4.0.1616226...	07-08-2017 14:49	MHA File	625 KB
 Template-1.3.12.2.1107.5.2.12.21144.4.0.1...	07-08-2017 14:49	MHA File	596 KB

New Volume (G:) > SEEMA_BHAT > Registration > DATA			
Name	Date modified	Type	Size
 Flair-Transform_1.3.12.2.1107.5.2.12.2114...	07-08-2017 14:49	TFM File	1 KB
 T1c-Transform_1.3.12.2.1107.5.2.12.2114...	07-08-2017 14:49	TFM File	1 KB
 T1-Transform_1.3.12.2.1107.5.2.12.2114...	07-08-2017 14:49	TFM File	1 KB
 T2-Transform_1.3.12.2.1107.5.2.12.2114...	07-08-2017 14:49	TFM File	1 KB

The *SkullStripped* folder contains the brain mask of the T<sub>1</sub> contrast image and the skull-stripped T<sub>1</sub> contrast image in .mha format.

New Volume (G:) > SEEMA_BHAT > Skullstripped > META			
Name	Date modified	Type	Size
 T1c-1.3.12.2.1107.5.2.12.21144.4.0.161819...	07-08-2017 14:44	MHA File	59 KB
 T1c-1.3.12.2.1107.5.2.12.21144.4.0.161819...	07-08-2017 14:44	MHA File	2,772 KB

The *classification* folder and the *structures* folder contain the label image in the registered image space and the label images which have been transformed back into the original space of each modality. The classification folder also contains a report file in .txt format. The report file lists the segmentation volumes for all the healthy and pathologic tissue. subcompartments. The conventional 2D Response Assessment in Neuro-Oncology (RANO) diameter measurements can be automatically extracted from the segmentation result.

#### Volumes

0 3.33096e+006

1 129504

2 493131

3 421578

4 7761

5 91764

6 4749

7 25056

#### Legend:

-1: Initial value for labels and volumes. Appears if not all labels were found or some got merged

0 Background

1 CSF

2 Gray Matter

3 White Matter

4 Necrotic

5 Edema

6 Non Enhancing

7 Enhancing

Units [mm<sup>3</sup>]

Conventional 2D measures

SPD: 1318.03 mm<sup>2</sup>

lesion 1: 42.7563 mm \* 30.8265 mm

lesion 2: 0 mm \* 0 mm

lesion 3: 0 mm \* 0 mm

The subcorticalStructures.txt file in the *structures* folder provides information which structure is represented by which number.

New Volume (G:) > SEEMA\_BHAT > Structures

Name

Date modified

Type

Size

DICOM

META

subcorticalStructures.txt

subcorticalStructures.txt - Notepad

File Edit Format View Help

4 necrosis

5 edema

6 non-enhancing tumor

7 enhancing tumor

150 everything else inside brain

450 CSF

0Background0000000255

181Precentral\_L255128255255

182Precentral\_R17718255255

183Frontal\_Sup\_L4525547255

184Frontal\_Sup\_R106209255255

185Frontal\_Sup\_Orb\_L122255158255

186Frontal\_Sup\_Orb\_R25587186255

187Frontal\_Mid\_L18315054255

188Frontal\_Mid\_R216255159255

189Frontal\_Mid\_Orb\_L18116980255

190Frontal\_Mid\_Orb\_R2551520255

11Frontal\_Inf\_Oper\_L42255255255

12Frontal\_Inf\_Oper\_R11625577255

13Frontal\_Inf\_Tri\_L6253234255

14Frontal\_Inf\_Tri\_R218108255255

15Frontal\_Inf\_Orb\_L24255108255

## 8. Reference

- 1.S. Bauer, T. Fejes, R. Meier, M. Reyes, J. Slotboom, N. Porz, A. Pica, and R. Wiest, “BraTumIA – A software tool for automatic Brain Tumor Image Analysis,” 2013.
- 2.N. Porz, S. Bauer, A. Pica, P. Schucht, J. Beck, R. K. Verma, J. Slotboom, M. Reyes, and R. Wiest, “Multi-Modal Glioblastoma Segmentation: Man versus Machine,” *PLoS One*, vol. 9, no. 5,p.e96873,2014.
3. <https://www.nitrc.org/projects/bratumia/>