

User Manual

Brain Tumor Detection and Classification is an application build to classify an MRI scan of the brain into malignant types of Glioblastoma Multiforma and High-Grade Glioma and benign types of Meningioma and Pituitary Adenoma. To help the user, we have created a User Manual to make using the application simple and straightforward. Follow the steps given below:

- 1) Open MATLAB.
- 2) In the “Command Window” type “guide”. A dialog box will appear.

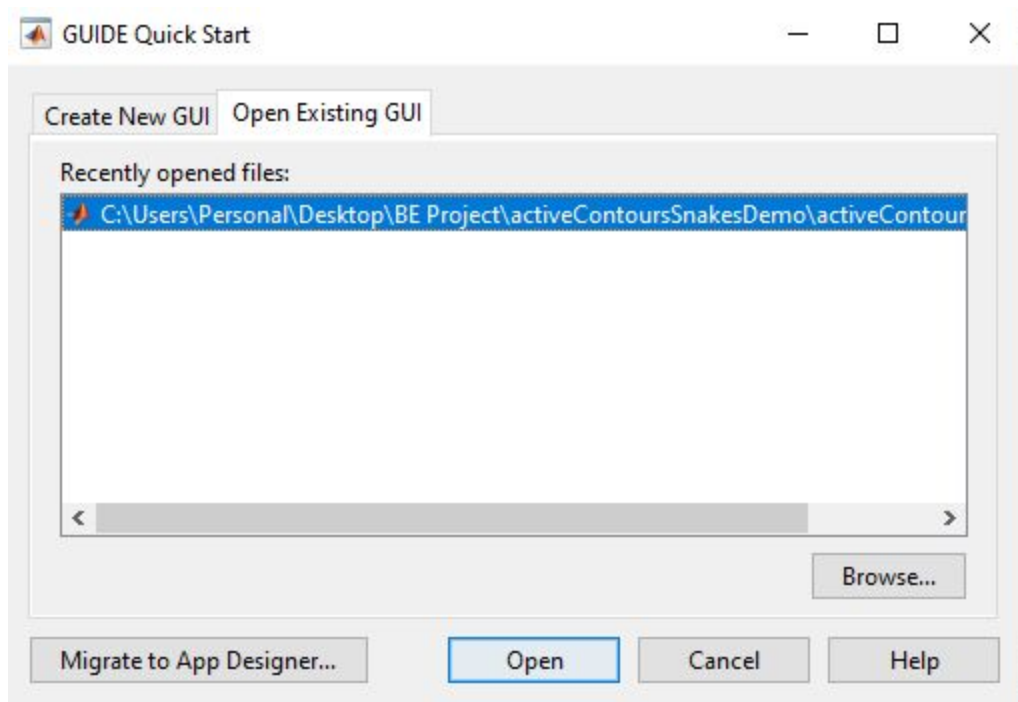


Figure 1: Guide Quick Start

- 3) If you are a first time user, the recently opened files will be empty. Click on Create new GUI and browse your project folder to find “snk.fig” i.e. the .fig file of our GUI. Once you open this, when you open this Guide dialog box again, this option will be available in your “Open Existing GUI” window. When you open this you will see the dialog box as shown in figure 2.

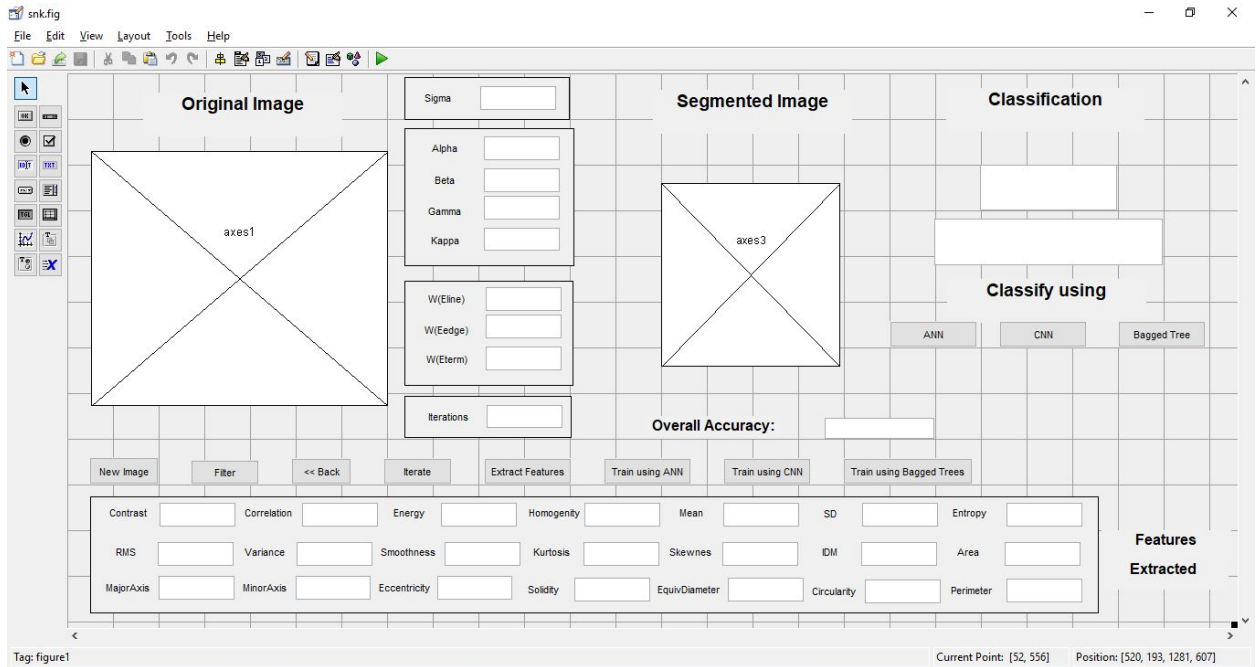


Figure 2: GUI window

- 4) User can make any changes to the GUI if required on this window. Once the changes are done, click on the green arrow at the top to run the application.

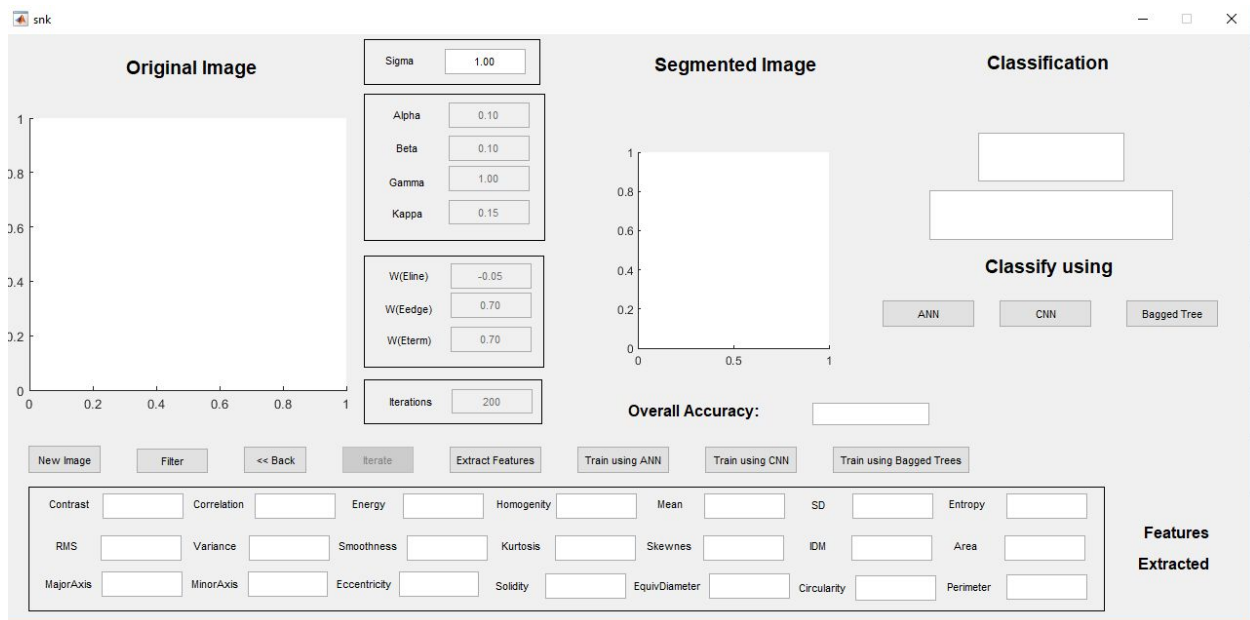


Figure 3: Application Window

- 5) To upload a new MRI scan click on “New Image”. A browsing window will open. Select any new MRI scan from your computer.

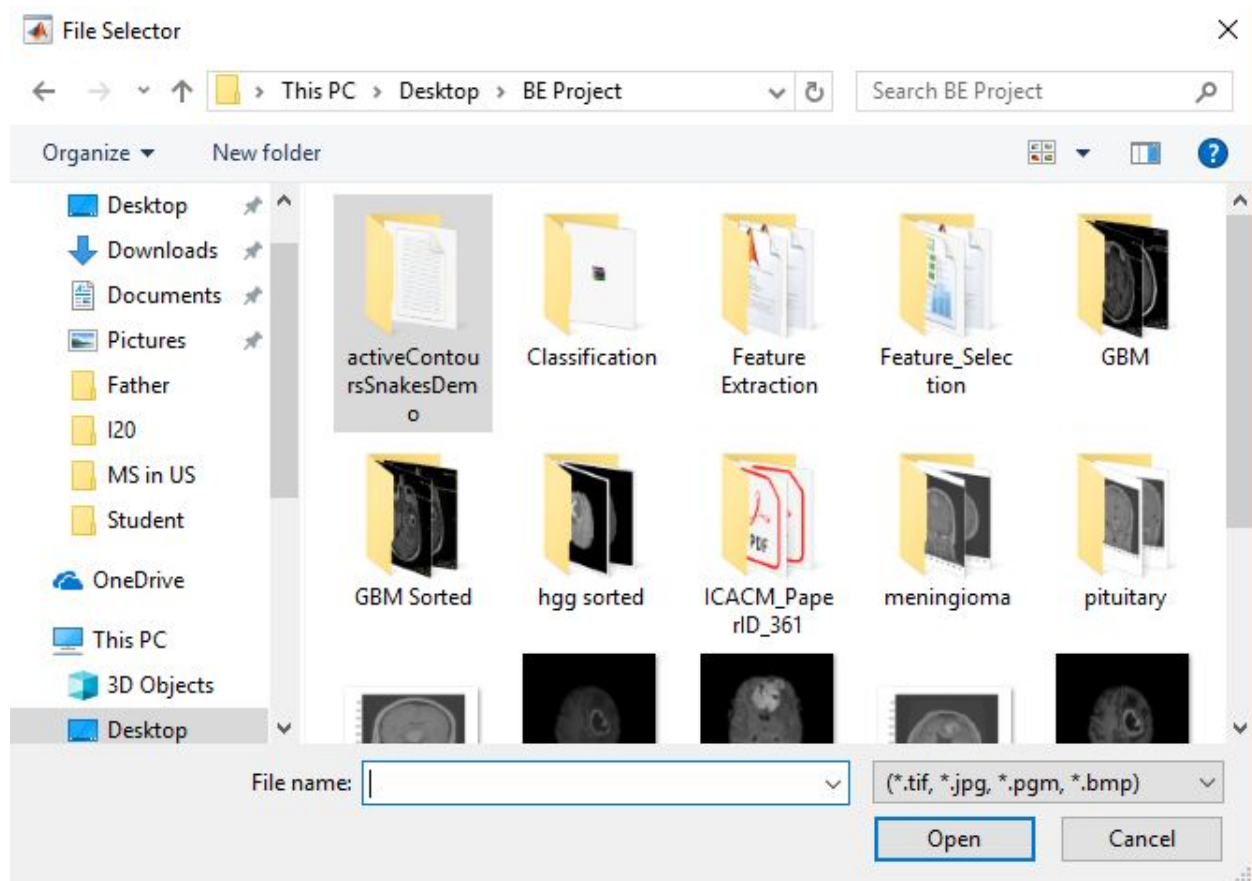


Figure 4: File Selector

- 6) Once the image is uploaded, it will be displayed in the section below “Original Image”. Now click on “Filter”. Pre-processing will be done and a crosshair will appear to take initial input of points.
- Note: You can increase or decrease the value of sigma to smoothen the image accordingly.

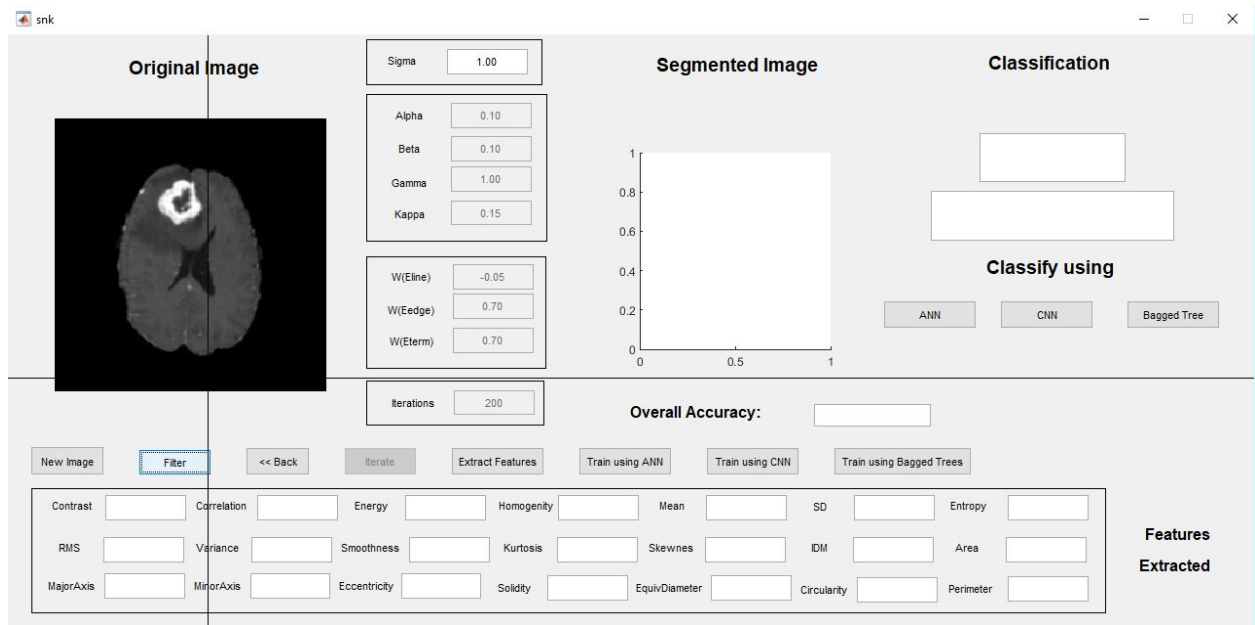


Figure 5: Image input

- 7) Give the initial input of points around the tumor. These points help the Snakes: Active Contour algorithm to slither down to the tumor region. You can use your left mouse click to mark the points and your right mouse click to mark your final point. You can mark any number of points. It is advisable to not mark the points very far away from the tumor region because it will become difficult for the algorithm to converge down to the tumor.



Figure 6: Points Selection

- 8) Click on Iterate to start the segmentation algorithm which is Active Contours: Snakes. The following parameters are used with the algorithm, the details of which are provided below. User can change the values of any of these parameters. The segmented image will be displayed in the section below “Segmented Image”.

α (alpha): Specifies the elasticity of the snake. This controls the tension in the contour by combining with the first derivative term.

β (beta): Specifies the rigidity in the contour by combining with the second derivative term.

γ (gamma): Specifies the step size

κ (kappa): Acts as the scaling factor for the energy term.

W (Eline): Weighing factor for the intensity-based potential term.

W (Eedge): Weighing factor for the edge-based potential term.

W (Eterm): Weighing factor for termination potential term.

Iterations: Number of iterations for which contour’s position will be computed.

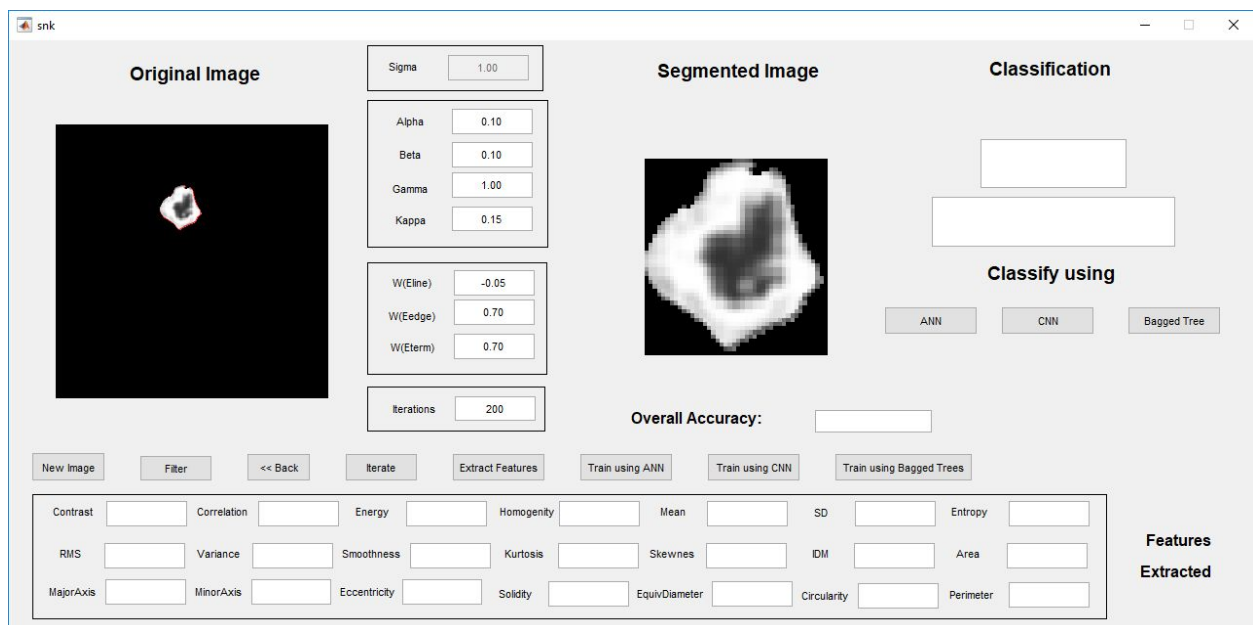


Figure 7: Segmented image

- 9) Now, click on “Extract features” to extract the shape, texture, and intensity based features from the segmented image. The values of the features extracted will be displayed below in the “Features Extracted” section.

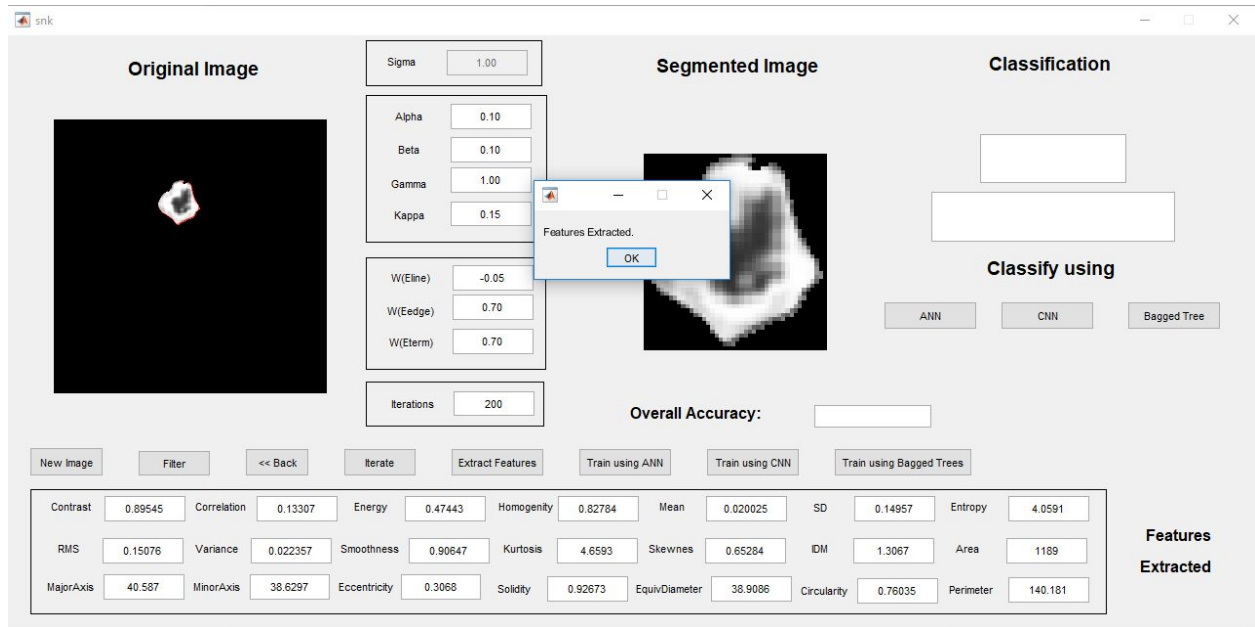
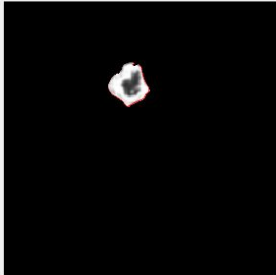


Figure 8: Features Extracted

- 10) The user has 2 options once he has extracted all the features.
 - a) Use the pre-trained model to classify our input into their respective classes.
 - b) Train the model right now and then classify our input into their respective classes.
- 11) If you want to train the model right now, click on any of the three options of “Train using ANN” or “Train using CNN” or “Train using Bagged trees”. The model will be trained and the overall accuracy will be displayed on the dialog box above. If you want to use the pre-trained model, directly go to the next step.
- 12) You can classify your input using ANN, CNN or Bagged Trees. Click on your choice. The output class and subclass will be displayed in the dialog box above. The accuracy of the pre-trained model will also be displayed.

Original Image



Sigma

1.00

Alpha

0.10

Beta

0.10

Gamma

1.00

Kappa

0.15

W(Elne)

-0.05

W(Edge)

0.70

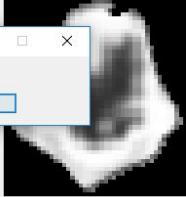
W(Eterm)

0.70

Iterations

200

Segmented Image



Classification

Malignant

High Grade Glioma

Classify using

ANN

CNN

Bagged Tree

Tumor classified.

OK

Overall Accuracy:

84.6154

New Image

Filter

<< Back

Iterate

Extract Features

Train using ANN

Train using CNN

Train using Bagged Trees

Contrast	0.89545	Correlation	0.13307	Energy	0.47443	Homogeneity	0.82784	Mean	0.020025	SD	0.14957	Entropy	4.0591
RMS	0.15076	Variance	0.022357	Smoothness	0.90647	Kurtosis	4.6593	Skewnes	0.65284	IDM	1.3067	Area	1189
MajorAxis	40.587	MinorAxis	38.6297	Eccentricity	0.3068	Solidity	0.92673	EquivDiameter	38.9086	Circularity	0.76035	Perimeter	140.181

Features
Extracted