Software Design Document

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1. Introduction

1.1Purpose

The purpose of the Software Design document is to provide a full description of the proposed system "BRAINYOLOGY" and how it is expected to be built based on the use cases shown previously in the Software Requirement Sheet document. Information such as sequence diagram and class diagram are deeply explained. Also, this document defines the functional requirements and their impact on the system architecture and design. Moreover, it shows the functionality of each subsystem and component. On the other hand, how components interact with each other.

1.2Scope

"BRAINYOPLY" is a system that aims to target the adult male and female brain tumor patients. Our research scope is MRI images and Detect brain tumor only. We will be working on detecting the volume of the tumor. We will integrate this system with many hospitals. The main objective of the proposed system is helping doctors to give accurate diagnose to the brain tumor patient. Calculation of the tumor volume enables the doctors to predict the degree of the tumor will affect which part of the patient body. It will be accurate with low cost and high processing speed.

1.3Overview

The Software Design document is divided into 7 sections with different subsections. First section is an introduction that provides a brief

description of the project including its purpose, scope, objectives. The second section includes the System overview which includes a comprehensive description of what is we are building, including options and features. The third section is the system Architecture; it includes "BRAINYOLOY" Architecture Design including a high level overview of the system, class diagram and sequence diagram. Fourth section is mainly the Data Design, describing how the data is processed, stored and handled in the system. Fifth section consists of Component Design; a closer look is taken of each component giving it a description and a pseudo code. The user interface is briefly shown the six sections. Finally, the seventh section provides the requirement matrix.

2. System Overview

BRAINYOLY" is a simple solution for doctors for brain tumor volume calculation. Since tumor volume calculation is a trivial task for the doctors to do from the MIR images the proposed system is aiming to make this task a lot easier by using MRI slices, which will be the input to our system. We will calculate the volume of the tumor, and construct a 3D model for the whole brain and for the tumor using 2D input slices, and then the doctor will be able to interact with controller device for intuitive fast mapped to a real brain model. The system will be implemented to help doctors to give accurate diagnose to the brain tumor patient. Calculation of the tumor volume enables the doctors to predict the degree of the tumor will affect which part of the patient body. It will be accurate with low cost and high processing speed. The importance of the system that according to Cancer Index Organization (1), People newly diagnosed with brain cancer are 108,600 and those who died in the year 2015 as a result of brain cancer were 72,300. Consequently, doctors will have an application for the first time in Egypt that will calculate the volume of the brain tumor and convert the 2D MRI images to 3D model and the most important it will not be expensive.

3- System Architecture

- **Images processing technics layered in more detailed**

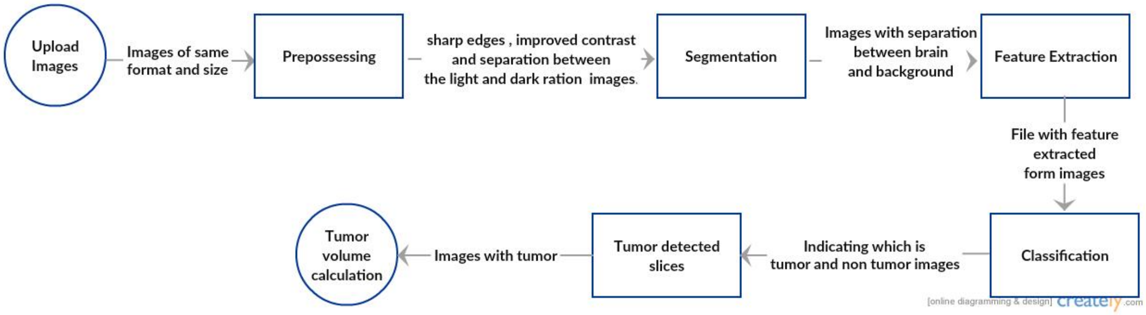
Upload Images
Images of same format and size
Prepossessing
sharp edges , improved contrast and separation between the light and dark ration images.
Segmentation
Images with separation between brain and background
Feature Extraction
File with feature extracted form images
Classification
Indicating which is tumor and non tumor images
Tumor detected slices
Images with tumor
Tumor volume calculation
[online diagramming & design] creately.com

Figure 3.1.1: Image processing layer using pipe filter.

- **Tumor detection and 3D reconstruction layers in more details.**

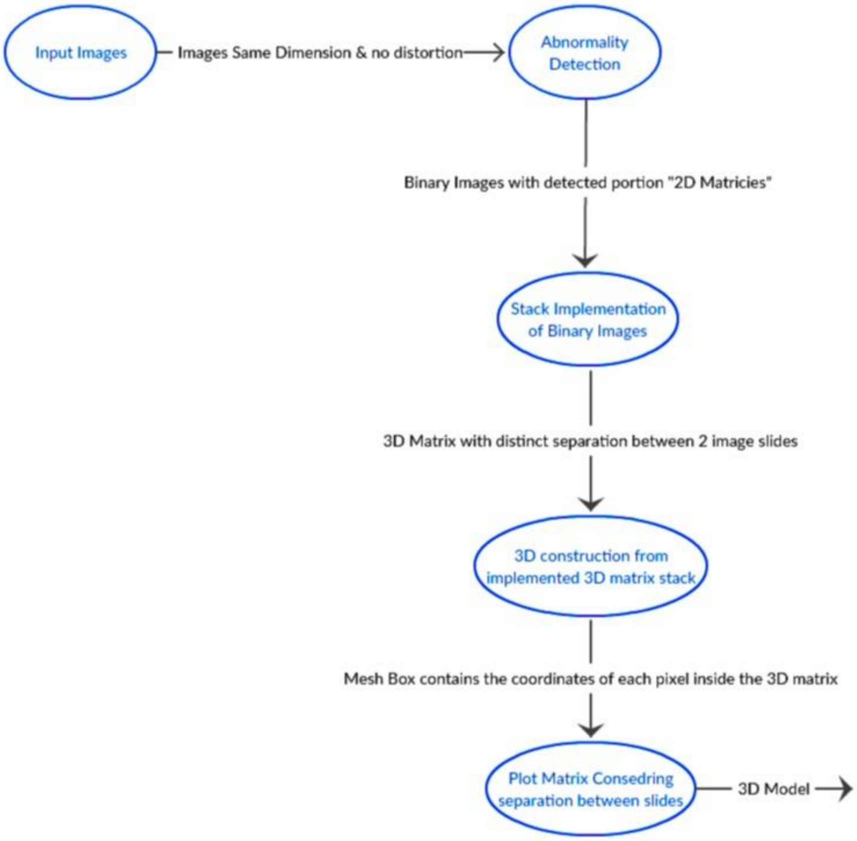
Input Images
Images Same Dimension & no distortion
Abnormality Detection
Binary Images with detected portion "2D Matricies"
Stack Implementation of Binary Images
3D Matrix with distinct separation between 2 image slides
3D construction from implemented 3D matrix stack
Mesh Box contains the coordinates of each pixel inside the 3D matrix
Plot Matrix Consedring separation between slides
3D Model

Figure 3.1.2: Tumor detection and 3D reconstruction layer.

- **Hardware architecture diagram**

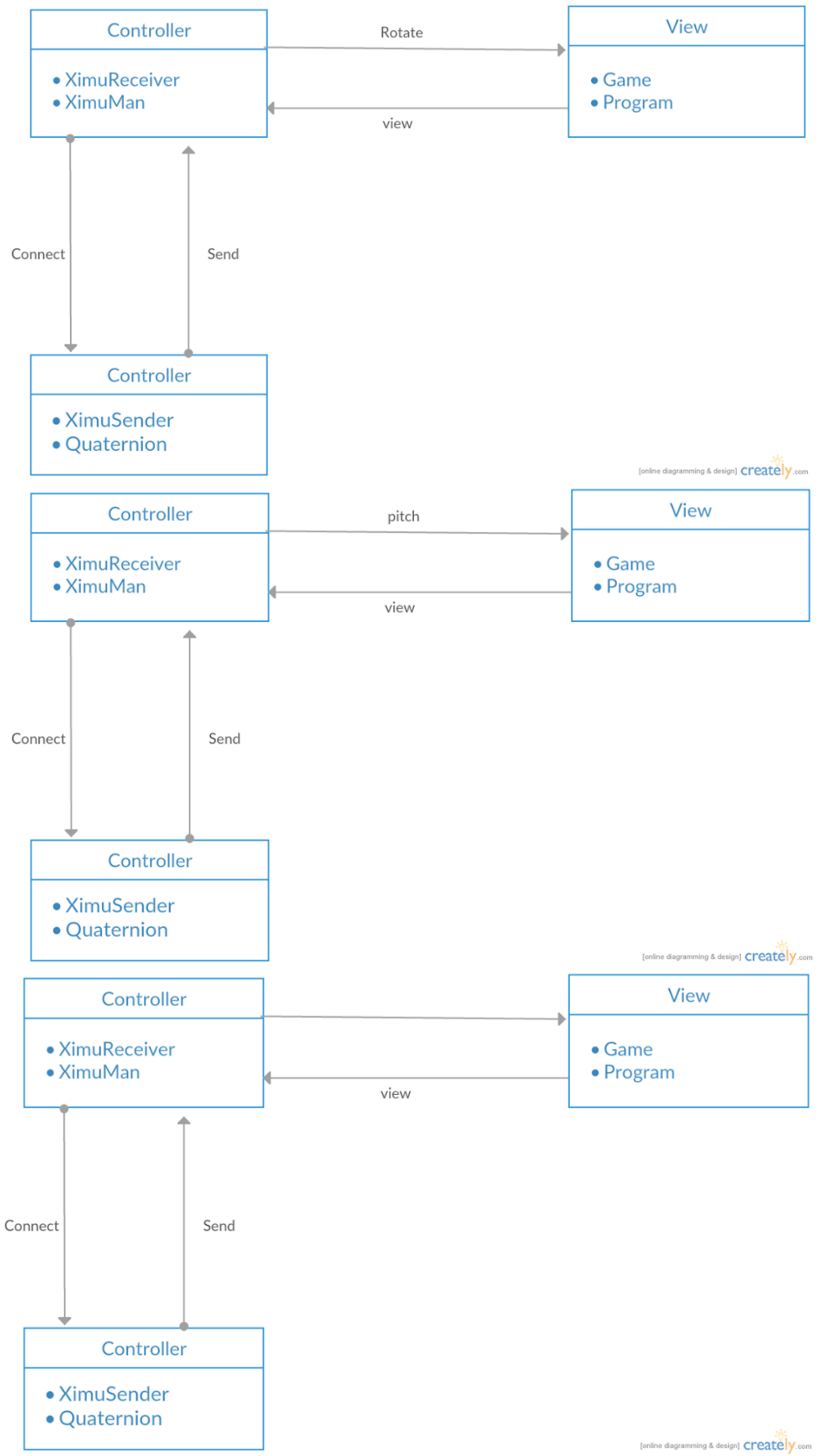

Figure 3.1.3: Hardware architecture diagram using MVC.

3.2 Sequence Diagram

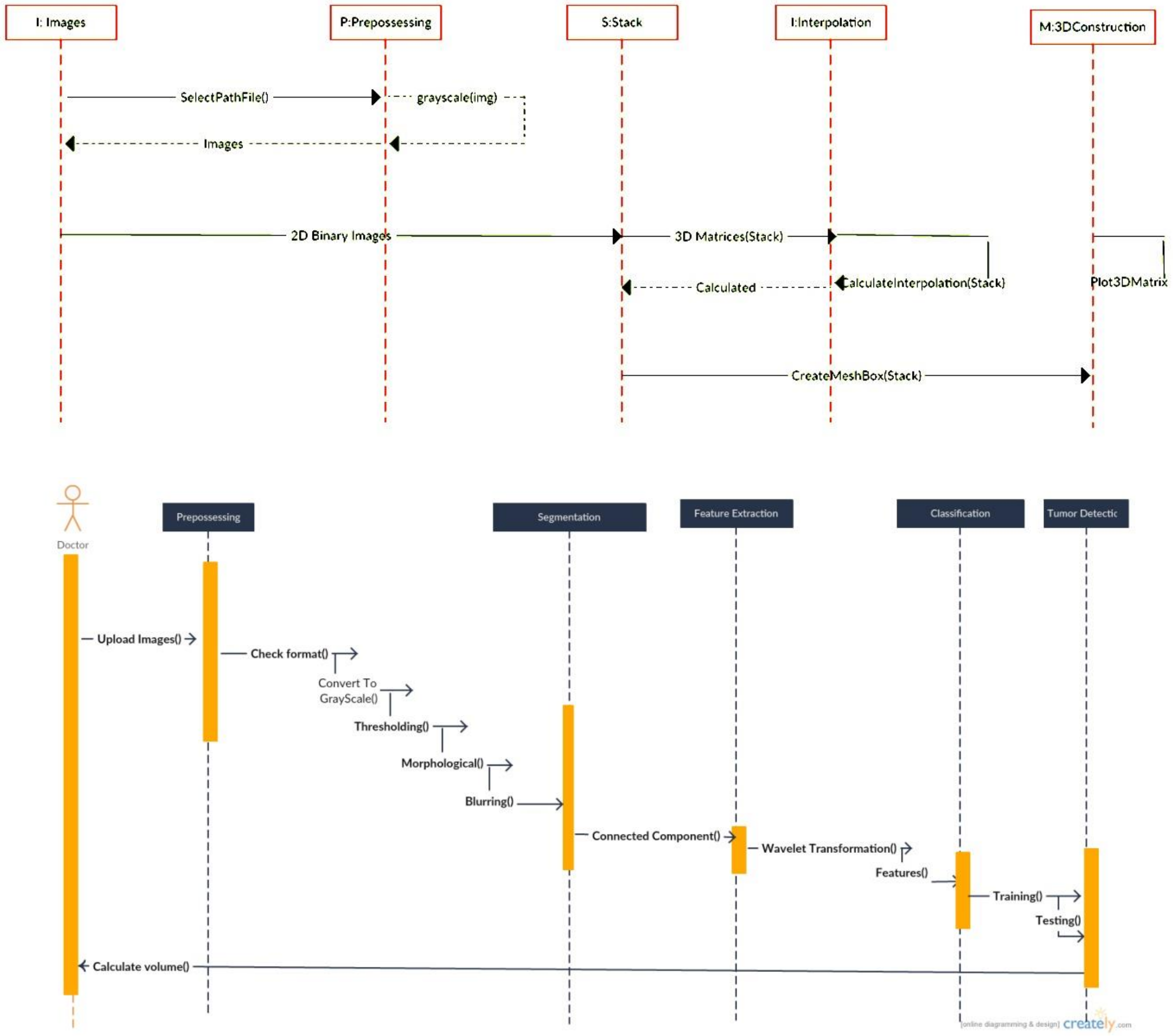

Figure 3.2.2: The sequence diagram from 3D reconstruction.

3.3 Design rational

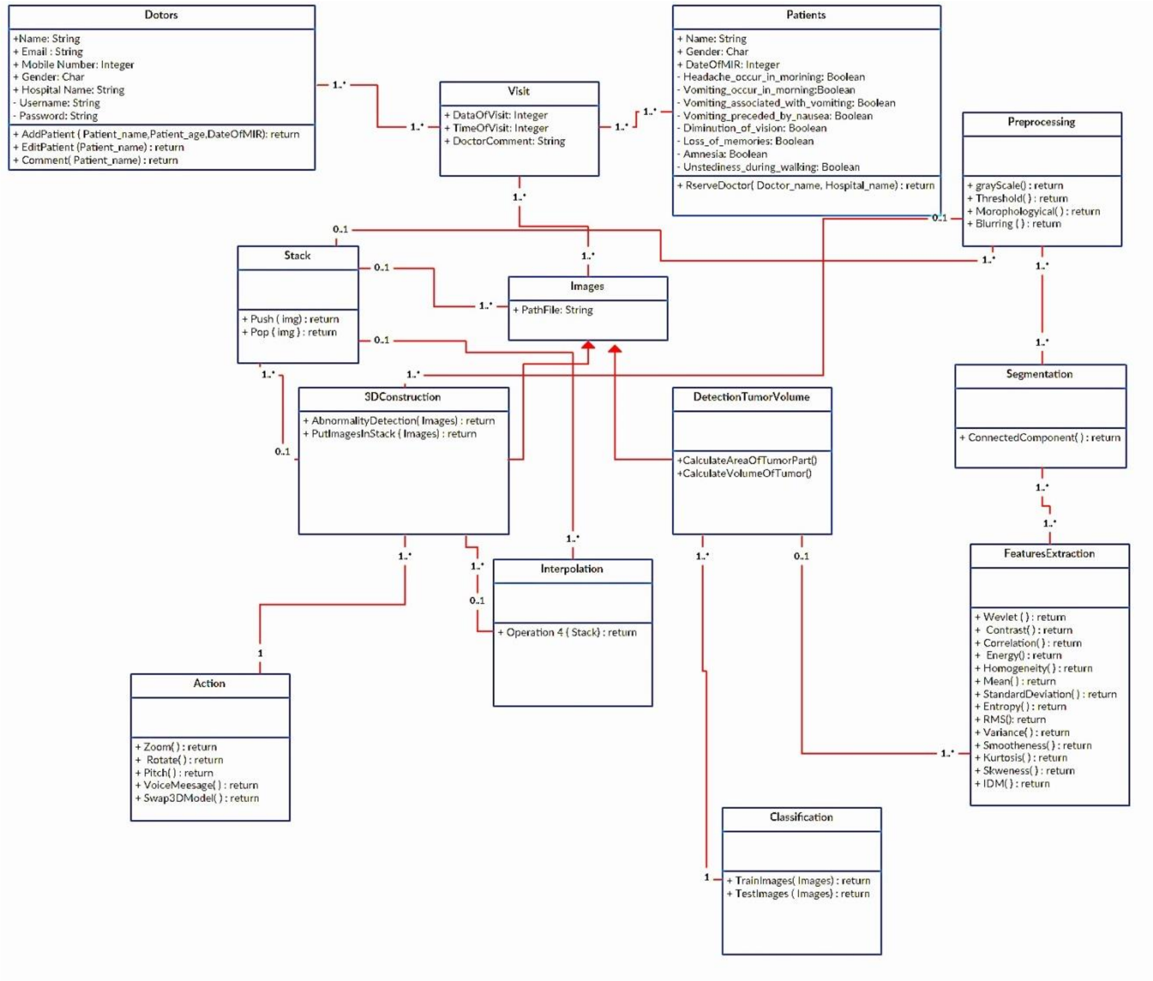

Figure 3.3.1: The system class diagram.

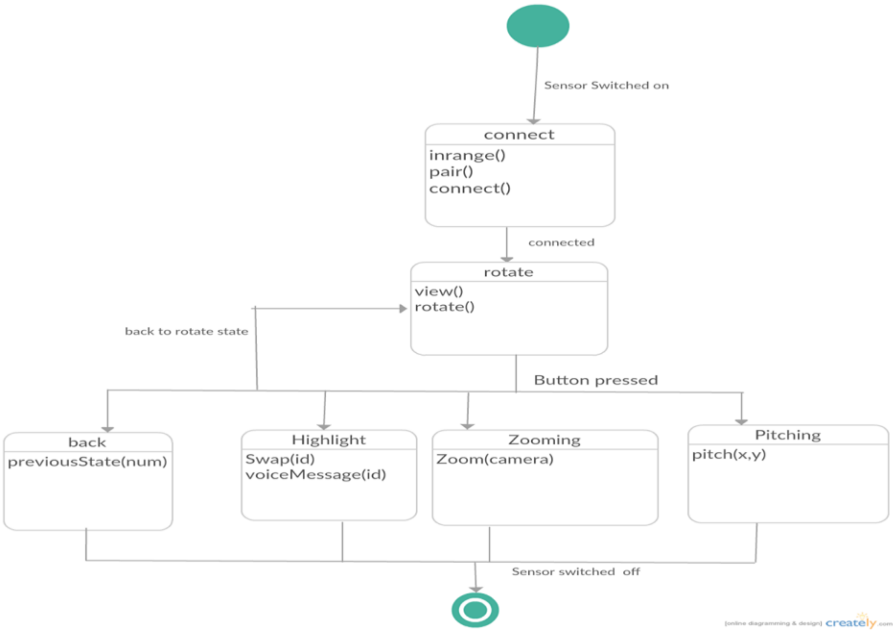

Figure 3.3.2: State diagram for TUI.

States	definition
Connect	The sensor will connect to the device using fastConnect() function
Rotate	The current shown 3d model will rotate exactly as the sensor current orientation using all of the functions rotateX(),rotateY(),RotateZ()
Zoom	When the button zoom pressed on the dummy head the current 3d model will zoom in or out using function zoom()
Pitch	When any of the arrow buttons pressed on the dummy head the current shown 3d model will pitch from it’s current location to the arrow direction.
Back	The system will go back to the rotating state
Highlight	When the anatomy buttons pressed the system will swap the current 3d model to another 3d model using swap() function

4- Data Design

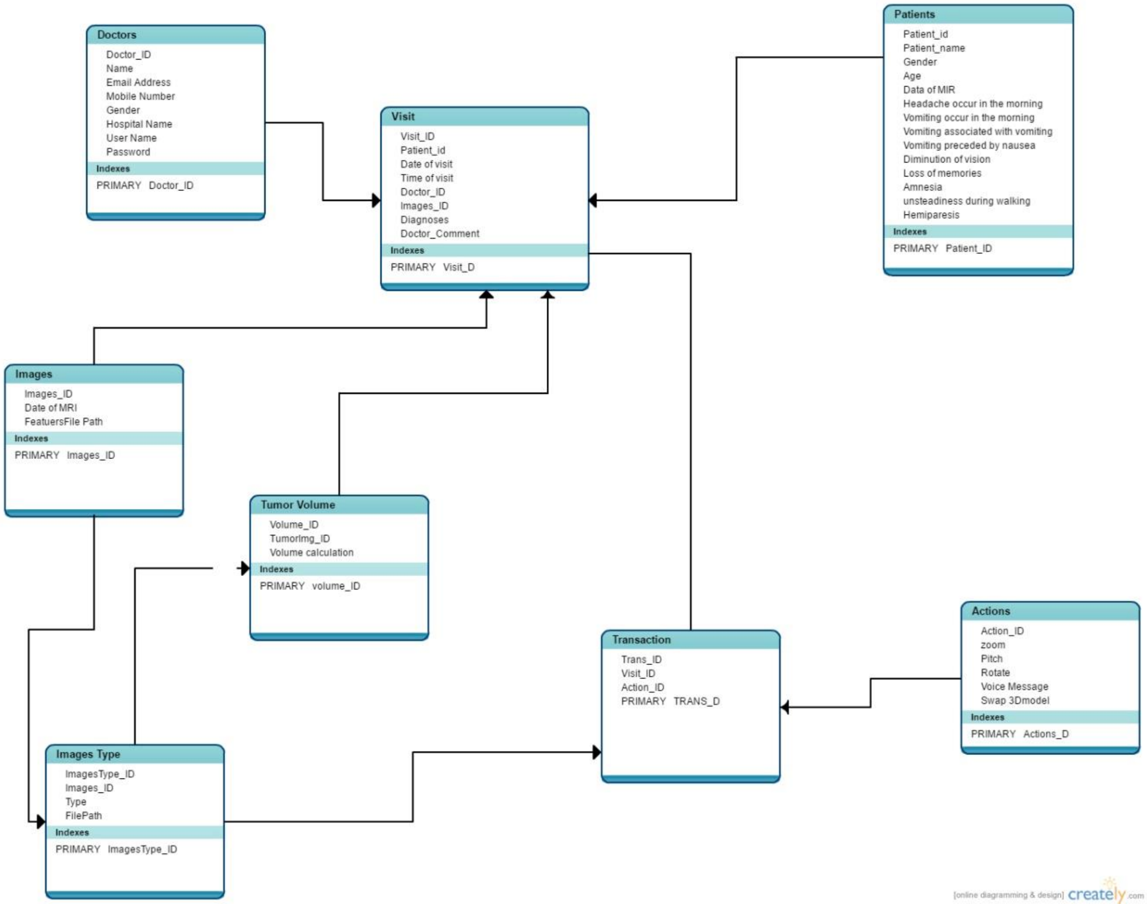

Figure 4.1 Database Tables

4.1Data Description

BRAINYOLOY is a desktop application which needs a database to save the doctors information along with their patient's information, the form that the patient will fill it. For each patient there will be a visit or more where the doctor can save the patient the date and time of the visit the patient's MRI images, the tumor images and the tumor volume calculation, the doctor will be able to add a comment in each visit. Doctors will be able to add or edit patient's information along with MRI images. For the 3D construction part it will be save in a file that which it's path will be added to patient' visit. For the Interaction part there will be a table which saves the action taken by the hardware device as rotate, zoom and pitch.

Table 4.1.1: Structure of table Doctor

Column	Type	NULL	Default
Doctor_ID	Int(11)	NO	
Name	Varchar(25)	NO	
EmailAddress	Varchar(75)	NO	
MobileNumber	Int(11)	NO	
Gendenr	Varchar(25)	NO	
Hospital	Varchar(25)	NO	
UserName	Varchar(25)	NO	
Password	Varchar(25)	NO	

Table 4.1.2 Structure of table Patient

Column	Type	NULL	Default
Doctor_ID	Int(11)	NO	
Name	Varchar(25)	NO	
Gender	Varchar(75)	NO	
Age	Int(11)	NO	
Date ofMRI	Int(11)	NO	
Mobile Number	Int(11)	NO	
Headache occur in the morning	BOOLEAN (3)	NO	
Vomiting occur in the morning	BOOLEAN (3)	NO	
Vomiting associated with vomiting	BOOLEAN (3)	NO	

Vomiting preceded by nausea	BOOLEAN (3)	NO	
Diminution of vision	BOOLEAN (3)	NO	
Loss of memories	BOOLEAN (3)	NO	
unsteadiness during walking	BOOLEAN (3)	NO	
Hemiparesis	BOOLEAN (3)	NO	

Table 4.1.3 Structure of table Visit

Column	Type	NULL	Default
Visit_ID	INT(11)	NO	
Patient_ID	INT(11)	NO	
Doctor_ID	INT(11)	NO	
DateOfVisit	Varchar(25)	NO	
TimeOfVisit	Varchar(25)	NO	
Diagnoses	Varchar(25)	NO	
Images_ID	INT(25)	NO	
Volume_ID	Int(11)	NO	
Comment	TEXT(25)	NO	

Table 4.1.4 Structure of table Images

Column	Type	NULL	Default
Image_ID	Int(11)	NO	
Date	Varchar(25)	NO	
Images	Varchar(75)	NO	
FeaturesFilePath	Text(25)	NO	

Table 4.1.5 Structure of table Image_Type

Column	Type	NULL	Default
Image_Type_ID	Int(11)	NO	
Image_ID	Int(25)	NO	
Type	Varchar(75)	NO	

Table 4.1.6 Structure of table tumor volume

Column	Type	NULL	Default
Volume_ID	Int(11)	NO	
Image_Type_ID	Int(25)	NO	
Image_ID	Int(75)	NO	
Volume cal	Int(25)	NO	

Table 4.1.7 Structure of table Actions

Column	Type	NULL	Default
Action_ID	Int(11)	NO	
Zoom	Text(25)	NO	
Pitch	Text(75)	NO	
Rotate	Text(25)	NO	
Voice Message	Text(50)	NO	
Swap 3D model	Text(50)	NO	

Table 4.1.8 Structure of table Transaction

Column	Type	NULL	Default
Trans_ID	Int(11)	NO	
Image_Type_ID	Int(25)	NO	
Visit_ID	Int(75)	NO	
Action_ID	Int(25)	NO	
DataFile	Text(50)	NO	

5- Component Design

Our proposed system is divided into three important parts here will be the explanation of each component used in those three parts provided with the most important algorithms, equation, pseudo code and sources of information

5.1 First part Tumor detection:

a. Data input and refining of image

In this algorithm we enter a series of magnetic resonance imaging (MRI) which might contain tumor regions in them. Now all images will go through a series of process. First the images will be checked for dimension. If it is not of the same dimension they are made into same dimension by resizing them into a standard size. The final obtained images will be checked for its type. If it is other than gray scale image it

is converted into gray scale image which will be our input for the next part of the process.

b. Preprocessing

After the images has been resized and converted in to gray scale. A thresholing equation [1] will be applied to separate between dark and light regions. We will use morphological and erosion algorithms [2]. That sharps the edges of the image and then removes all the noisy parts. Using Gaussian algorithm [1] for blurring to smooth the images will be the final out of the preprocessing process and the input to the next process. Figure 5.1 shows an example of the input images. and the results of preprocessing phase after applying Threshold and morphological algorithms.

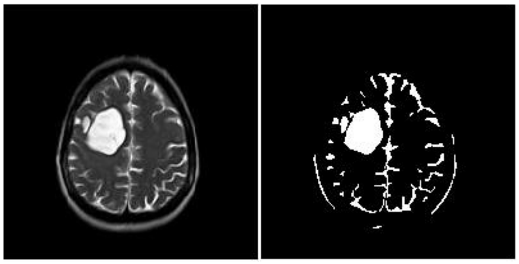

Figure 5.1.1: Input and output of preprocessing.

c. Segmentation

The preprocessed images will be the input to the next phase. The Segmentation process produces a binary image with detected portion as the white region and rest of the part is blackened region. The algorithm to apply this phase is connected component algorithm [2] .It's grouping together all pixels with the same class that are touching each other. Each set of pixels representing a segment is often referred to as a connected component Figure 5.2 shows an example of the input images to the segmentation phase and the results of the segmentation phase after applying connected component algorithm.

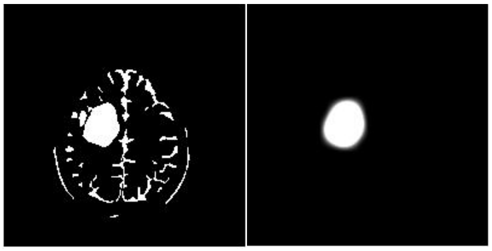

Figure 5.1.2: Input and output segmentation.

d. **Feature Extraction**

The segmented objects obtained from the last process will used to extract some algorithm used for feature extortion is Single-level discrete 2-D [1]. This algorithm is the Inverse of Direct wavelet Transformation (IDWT). It is defined as:

$$W\varphi(j0,k)=\frac{1}{\sqrt{M}}\sum_{z} f(x)\varphi j0k(x) \qquad (1) W\varphi(j,k)$$

$$=\frac{1}{\sqrt{M}}\sum_{z} f(x)\varphi jk(x) \qquad (2)$$

$$f(x)=\frac{1}{\sqrt{M}}\sum\nolimits_{K} W\varphi(j0,k)\varphi jok(x)+\frac{1}{\sqrt{M}} \qquad \textbf{(3)}$$

Discrete variable *x* = 0,1,2,…,*M*−1. Normally we let *j* $_0$ = 0 and select *M* to be a *M* = 2 ^{J}) so that the summations in Equations (1), (2) and (3) are performed over *x* = 0,1,2,…,*M*−1, *j* = 0,1,2,…, *J*−1, and *k* = 0,1,2,…,2 ^{j} − 1. The coefficients defined in Equations (1) and (2) are usually called *approximation* and *detail coefficients*, respectively. The features which are extracted from the images defined as he following equations.

Contrast (4)

$$\sum_{i,j} |i-j|\ p(i,j)\text{^}2$$

P= pixels.

Correlation (5)

$$\sum_{i.j}\frac{(i-\mu i)(j-\mu j)p(ij)}{\sigma i\ \sigma j}$$

μ = mu

σ = Sigma

Energy (6)

$$\sum\nolimits_{i,j} p(i,j)\text{^}2$$

P= pixels.

Homogeneity (7)

$$\sum\nolimits_{i,j}\frac{p(i,j)}{1+|i-j|}$$

P= pixels.

Mean **(8)**

$\underline{\mu = (\Sigma X_i) / N}$

μ = mu

Standard deviation **(9)**

$$\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(xi - \mu)^{\wedge}2}$$

Variance **(10)**

$\underline{\sigma^2 = \Sigma (X_i - \mu)^2 / N}$

Root Mean Square (RMS) **(11)**

$$\sqrt{\sum_{i=1}^{n} \alpha i^{\wedge}2}$$

Smoothness

1-(1/(1+Sum{k})) **(12)**

Kurstosis

kurtosis(double(G(:))) **(13)**

Skewness

skewness(double(G(:)) **(14)**

Inverse Difference Movement

G(i,j)./(1+(i-j).^2) **(15)**

e. Classification

After obtaining the segmented object features. System will process to the next process in image processing technics which is classification. The classification is divided into two phase. The training phase and then the test phase. In the training phase the system will use the computed features to differentiate between tumor features and non-tumor features. In the testing phase the system should recognize the images with the tumor and the images that don't have the tumor. The algorithm used in the classification phase is support victor machine (SVM) [3]. This algorithm plots each data item as a point in n-dimensional space where n is number of features you have with the value of each feature being the value of a particular coordinate. Then,

we perform classification by finding the hyper-plane that differentiates the two classes very well. Figure 3 shows an example of hyper-plane .Support Vectors are simply the co-ordinates of individual observation. Support Vector Machine is a frontier which best segregates the two classes (hyper-plane/ line).

5.2 Second Volume Calculation.

a. **Cross section Area of the tumor.**
   After obtaining the slides which contain tumor from image processing techniques, we will apply "Sobel" algorithm to sharp the edges of the tumor in each slice. After applying sobel, the last step is applying "chain code" algorithm which is used to select the points on the boundaries of tumor part and transmit its coordinates. These coordinates help us to get the cross section area of the tumor in all slices [4].

b. **Calculation of area of slides in between two given consecutive slides.**
   We convert 1mm to 3.77952 pixels which is multiplied to the distance between two consecutive slides to get the number of pixel between two slides. Now we consider each pixel as an individual slide we can get the volume by adding areas of the slides. But if there is a missing area of some slides, so we can use method called"interpolation". In this method we plot the obtained value in are vs sliding number graph to get the area of missing slices [4].

c. **Volume estimation using area from each slice**
   From the above obtained area we use the concept of stack to calculate the volume of the tumor content in the slices.Each slice is given by: I[1:M,1:N] and the total height is "x", then the volume is "V", M → Number of rows , N → Number of columns [5].

$$V = \sum_{m=1}^{M}\sum_{n=1}^{N} I_1[m,n] + \sum_{m=1}^{M}\sum_{n=1}^{N} I_2[m,n] + \sum_{m=1}^{M}\sum_{n=1}^{N} I_3[m,n] + \ldots + \sum_{m=1}^{M}\sum_{n=1}^{N} I_x[m,n] \qquad (16)$$

$$V = \sum_{K=1}^{x}\sum_{m=1}^{M}\sum_{n=1}^{N} I_K[m,n] \qquad (17)$$

$$V = \sum_{K=1}^{x} X[K] \qquad (18)$$

Where

$$\sum_{m=1}^{M}\sum_{n=1}^{N} I_{K}[m,n] = X[K] \qquad (19)$$

5.3 Experiments and discussion

We used deferent datasets from deferent places. First we visited “Farid Habib hospital” [6] hospital. We took five cases on CDs. Each CD had just one case. Then we visited “El salam international hospital” [7]. We took five more cases on CDs. And finally we visited “Ain Shams University Specialized Hospital” [8] and we took five more cases on CDs. We are working on a dataset of 15 cases. Each CD contains exactly 501 images. Actually we don’t need all those images. The MRI scan takes images from three different plans Axial, Sagittal and coronal [9]. Each plan takes (15-20) images. So the total important images are in range of (50-60) images. Table 1 will show the experiments we applied to the system using 50 images as a training data and 35 images as a testing data. In Table 1 the experiments shows the accuracy of the system after using different type of segmentation which are kmnean and connected components.

Table 1: The applied segmentation experiments.

	Segmentation type	Accuracy
Experiment(1)	Connected components	95%
Experiment(2)	Kmnean	85%

As shown in the previous table that the connected component segmentation gave the system “95” accuracy as mentioned in paper [2]. But kmeans segmentation gave the system “85%” accuracy as mentioned in paper [1]. Table 2 show the experiments we applied with the different type of kernel function in SVM classification which are linear, polynomial, quadratic and Radial Basis Function along with the two types of wavelet transformation which are Single-level discrete 2-D and Discrete wavelet transformation. We applied normalization and log transformation function to the numbers of the feature extraction.

Table 2: Table of experiments.

	Features	Classification	Wavelet	Normalization	Log transformati	Accuracy

					on	
Experiment 1	All	SVM Kernel Fun. “Linear”	Single-level discrete 2-D	✓	✓	95%
Experiment 2	All	SVM Kernel Fun. “Linear”	Single-level discrete 2-D	✘	✘	50%
Experiment 3	Contrast-correlation-Energy-Homogeneity	SVM Kernel Fun. “Linear”	Single-level discrete 2-D	✓	✓	66%
Experiment 4	All	SVM Kernel Fun. “Linear”	Single-level discrete 2-D	✘	✘	75%
Experiment 5	All	SVM Kernel Fun. “Linear”	Discrete Wavelet Transform	✓	✓	88%
Experiment 6	All	SVM Kernel Fun. “polynomial” with order 1	Single-level discrete 2-D	✓	✓	72%
Experiment 7	All	SVM Kernel Fun. “polynomial” with order 1	Single-level discrete 2-D	✓	✘	70%
Experiment 8	Contrast-correlation-Energy-Homogeneity	SVM Kernel Fun. “polynomial” with order 1	Single-level discrete 2-D	✘	✘	66%

Experiment 9	All	SVM Kernel Fun. “quadratic”	Discrete Wavelet Transform	✓	✓	70%
Experiment 10	All	SVM Kernel Fun. “quadratic”	Single-level discrete 2-D	✓	✓	80%
Experiment 11	Contrast-correlation-Energy-Homogeneity	SVM Kernel Fun. “quadratic”	Single-level discrete 2-D	✓	✓	66%
Experiment 12	All	SVM Kernel Fun. “rbf” Sigma 1	Single-level discrete 2-D	✓	✓	92.3%
Experiment 13	All	SVM Kernel Fun. “rbf” Sigma 1	Single-level discrete 2-D	✓	✗	70%
Experiment 14	All	SVM Kernel Fun. “rbf” Sigma 1	Single-level discrete 2-D	✗	✗	68%
Experiment 15	Contrast-correlation-Energy-Homogeneity	SVM Kernel Fun. “rbf” Sigma 1	Single-level discrete 2-D	✓	✓	66%
Experiment 16	All	SVM Kernel Fun. “rbf ”	Discrete Wavelet Transform	✓	✓	80%

6. Requirements Matrix

Function Requirements	Statues	Technical specification
Register	On progress	
Login	On progress	
Add/Edit patient	On progress	
Preprocessing	Completed	2D gray scale images all the images are of the same size and format, with sharpen edges, and improved contrast and separation between the light and dark ration
Segmentation	Completed	Images with is divided in to multiple segments the brain is separated from the back ground.
Feature extraction	Completed	File with feature extracted from images
Classification	Completed	Images with tumor
Tumor volume calculation	Completed	Volume calculation
Create Voxel Images	On progress	
Construct Meta	On progress	
Calculate Interpolation Between Brain's Slices.	On progress	
Plot 3D brain	On progress	
Rotating	Completed	Rotating the 3D model
Zooming	On progress	
Pitching	On progress	
Highlighting	On progress	

9 References

[1] M.Fathima Zahira1 and M.Mohamed Sathik “AN EFFECTIVE ANALYSIS OF MRI BRAIN IMAGES AND 3D RECONSTRUCTION”, in International Journal of Advanced Research in Biology, Ecology, Science and Technology (IJARBEST), February 2016, pp1- 16.

[2] R. Naveenkumar, S. Sanjay “Morphological Image Processing Approach for 2D to 3D Reconstruction of MRI Brain Tumor from MRI Images”, in The International Journal Of Science & Technoledge, May 2014, pp1-5

[4] Kavita A.Ugale, Prof. Dr. S.T. Patil “3D Reconstruction of Brain MRI using Support Vector Machine ”,in International Journal of Advanced Research in Computer Science and Software Engineering, 7, July 2015, pp 1-5

[5] Walid Shahab, Hazem Al-Otum and Farouq Al-Ghoul “A Modified 2D Chain Code Algorithm for Object Segmentation and Contour Tracing”, 3, July 2009

[6] Farid Habib hospital ,5th District Center Plot 5, Block 16081, , 5th District Obour City, Kaliobeya.

[7] El salam International hospital, Corniche El Nile ،Athar an Nabi, Misr Al Qadimah, Cairo Governorate

[8] Ain shams university specialized hospital, El-Khalifa El-Maamoun, El-Qobba Bridge, Al Waili, Cairo Governorate