B.Tech Minor Project Report

COT-415

on

BRAIN TUMOR DETECTION AND CLASSIFICATION

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CERTIFICATE

I here by certify that the work which is being presented in this B.Tech Minor Project (COT-415) report entitled "**Brain Tumor Detection and Classification**", in partial fulfillment of the requirements for the award of the **Bachelor of Technology in Computer Engineering** is an authentic record of my own work carried out during a period from July 2019 to December 2019 under the supervision of Dr. Ritu Garg, Asst. Professor, Computer Engineering Department.

The matter presented in this project report has not been submitted for the award of any other degree else where.

Signature of Candidate

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This is to certify that the above statement made by the candidates is correct to the best of my knowledge.

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Abstract

To improve patient's health, early diagnosis of brain tumor plays very important role. As we are moving towards modern era, people are facing severe diseases, one of which is Brain Tumor. There are various types of brain tumors, one of which is Gliomas, which is our area of interest in present research work to classify between benign and malignant brain tumor. We are using T1-weighted MRI brain tumor images. There are various steps in our proposed methodology, Image acquisition is first step, followed by image segmentation based on Otsu's methods, followed by feature extraction using Gray-Level-Color-Co-Occurrence Matrix (GLCM), Stationary Wavelet Transform (SWT), and Principal Component Analysis (PCA), followed by classification using fusion of classifiers including K-Nearest Neighbors(KNN), Decision Tree (DT) and Random Forest (RF), based on Majority Voting Method. Overall, proposed work works on various parameters such as precision, accuracy, sensitivity, specificity, Youden-Index, F1-score. Most challenging part is brain tumor segmentation, which is carried out by choosing proper threshold value in Otsu's method. Another challenging task is proper brain tumor classification, for which there is need of good classifier which is our proposed work for present work. Image processing has a vital role in bio-medical field as it automates disease detection, whether it is breast cancer, brain-tumor, liver-cancer and so on. MRI images are used in proposed work, which is best source to work with brain tumor segmentation and classification. SWT serves the purpose for image enhancement, PCA is used to reduce the dimensions of image, which helps in reducing the time and space complexity, GLCM is used for extracting features such as Contrast, Entropy, Correlation, Energy, Homogeneity and so on. In the proposed work, hybrid classifier based on RF, DT and KNN is used because they performed best on various parameters as compare to other classifiers such as Naïve Bayes (NB),Support Vector Machine (SVM), Artificial Neural Network (ANN), RF, DT, and KNN.In present time, we are moving to automate disease detection and classification, which saves human efforts, money and time. Overall, proposed work gives good accuracy of 97.305%, sensitivity of 97.04%, specificity, precision of 97.73%, F1-score of 97.50%, Youden-Index of 97.36%.

Introduction

A lot of work has been done in this bio-medical field since last decade, one of which is brain tumor segmentation and classification. There are numerous techniques to solve above problem based on both machine learning and deep learning. In machine learning, we are working with Random Forest, K-Nearest Neighbor, Naïve Bayes, Decision Tree, Artificial Neural Network, and so on. In deep learning, we are working with Convolutional Neural Network (CNN), Generative Automative Network (GAN), Rescue-Net, Capsule Network and so on.Over the past several decades, significant work has been conducted in this field. There are many methods which are already proposed for the brain tumor segmentation and classification.

The simplicity of computation and degree of user supervision can decide the clinical acknowledgement of diagnosis techniques. However, on large scale work has been performed in this field but still clinicians depend on manual determination of tumor, due to lack of link between researchers and clinicians. Several classifiers are already used for classification and detection of brain tumors which include – artificial neural network (ANN), support vector machine (SVM), sequential minimal optimization (SMO), convolutional neural network (CNN), FCM, learning vector quantization (LVQ), probabilistic neural network-radial basis function (PNN-RBF), backpropagation neural network (BPNN), hybrid of genetic algorithm and support vector machine (GA-SVM). Many of these techniques give good accuracy, however, the best accuracies are calculated using deep learning algorithms. Moreover, they have disadvantage over traditional methods as they need large dataset for training, have high time complexity, are less accurate for applications where we have availability of small dataset and require expensive GPUs which ultimately increases cost to the users, also selecting the right deep learning tools is also a challenging task as it need knowledge regarding various parameters, training method and topology. The challenging task in Brain Tumor is due to high variability and inherent MRI data characteristics, e.g., in tumor sizes or shapes, tumor detection, area calculation, segmentation, classification and finding uncertainty in segmented region. The most significant task in image understanding is image segmentation, because it helps in feature extraction, area calculation and significance in many real life applications. It can be used for example estimation of tumor volume, tissue classification, blood cells delineation, localization of tumors, matching of atlas, surgical planning and image registration. For monitoring of oncologic therapy, the accurate and

morphology quantification of tumors are very important task. Clinicians plan are highly expensive because they depend on various imaging techniques such as PET, MRI and CT. The clinical methods provide extract pertinent information and comprehensive analysis from images. Computational techniques help to investigate the details present in medical images. Imaging methods can be used to find position of brain tumors. MRI provides more significant information in contrast to other imaging modalities like CT. It is envisaged that the private multinational companies like, Siemens, Becton Dickinson, Medtronic, Accenture, GE Medical Systems, Atlantic Biomedical P. Ltd, Bicon, Serum Institute of India, Panacea Biotec Limited, Wockhardt, Bharat Serums and Vaccines Limited and others, will definitely be interested with the proposed methodology, as they are already working in the bio-technology field. However, the good accuracies are obtained by deep learning algorithms.This proposed work will be aimed at improving the performance by traditional classifiers instead of going to deep learning. As traditional classifiers have advantage over deep learning algorithms as they require small dataset for training and have low computational time complexity.

Motivation

This proposed work will be aimed at improving the performance by traditional classifiers instead of going to deep learning. As traditional classifiers have advantage over deep learning algorithms as they require small dataset for training and have low computational time complexity. It can add further research work in the field of brain tumor identification. As it is fact that brain tumors are one of the most life threatening all forms of cancer. This project will be implementing huge task because of inherent MR data features and huge variations, e.g., in tumor shapes or sizes, tumor detection, segmentation, and classification. Moreover, NITI Aayog is also working to bring AI based medical treatments for early detection and classification of diseases. Overall it will have good utilization in Biomedical Technology.In the above proposed methodology, there will be many steps which we will have to implement. The Discrete wavelet transform (DWT) is inferior then Stationary wavelet transform (SWT) as it has the problem of the lack of translation – invariance. In order to reduce complexity, we will also use PCA as it will reduce number of features and GLCM for Texture features -13 Features. In order to improve the classification accuracy as Benign or Malignant Brain Tumor, we have proposed a new hybrid classifier – RF+KNN+DT based on Majority Voting Method. In this project we will also do comparative studies of various classifiers – SVM, KNN, DT, RF, NB, ANN, Hybrid Classifier (Proposed).In this project we will also calculate area of Complete Tumor region, a user friendly GUI will also be developed for the ease of access to above implemented model.

Literature Review

Both theoretical and experimental work of International arena are available in the research papers. Some of work done by good researchers is described below:

Xuan and Liao et al [1].: In this work they proposed a method for tumor detection. Feature consist of 3-types texture-based, intensity-based, symmetry-based. Then, 40 features are selected, 13 intensity-based, 26 texture-based and 1 symmetry-based. Feature extraction is done from different image type such as FLAIR, T1 and T2 images. The dataset has 10 patients with 3 volumes each with 24 slices of MRI images. The database is distributed halfly into testing and training sets.

Othman et al. [2]: In this work feature extraction is done by using Daubechies wavelets with DWT from MRI images. Each image consists of 17,689 feature vectors. Finally, classification is done using SVM kernel function RBF.

Sindhumol S. et al. [3]: In this paper, they presented a technique spectral clustering (SC) for brain tumor classification. MRI images are segregated into different clusters using the spectral distance. Feature reduction is done by using ICA and classification by using SVM. The database is composed of 40 normal and 20 abnormal MRI images.

Abd-Ellah et al. [4]: In this paper, they proposed a novel method for brain tumor cancer. Preprocessing of MRI images is done with help of Median filters. Feature extraction is done by DWT and PCA is used for feature reduction. Finally, classification is done by SVM classifier using RBF kernel function. The database consists 80 image. SVM is trained using 43 abnormal and 5 normal images, and testing is done by using 27 abnormal images and 5 normal images.

Yang et al.: In this work they proposed a new algorithm for brain tumor. Haar wavelets and 2D-DWT is used for feature extraction based on 3-layers. SVM is used for classification with kernel RBF. The dataset consists of 256*256 pixels and 90 T2 MRI images, including 85 abnormal images and 5 normal. Feature reduction is done from 65536 to only 10 by using 3-level waveletenergy process.

H. Kalbkhani et al. [5]: In this work they proposed the subband of the detail coefficients and 2D DWT using (GARCH), Feature reduction is done from 61440 to 24 features. Feature extraction is done by Linear discriminant analysis (LDA), which are further reduced using PCA. Finally,

detection is done by using SVM and KNN identifier. The database consist of normal and abnormal MRI images in ratio 10 to 70. The testing set comprises of 7 normal and 49 abnormal images, while training set contains 3 normal and 21 abnormal images.

Chandra et al.[6]: In this project, they proposed a new clustering algorithm based on PSO optimisation with help of MRI images. The clusters and corresponding centroids are being find out by algorithm, among them global best is considered. The dataset consist of 62 normal and 110 abnormal MRI images.

Deep and Devi et al.[7]: In this project, they proposed a system in which statistical method are used for texture feature extraction, Neural network and BPNN are used in segmentation and uncovering stages. The database consist of 42 images, which are further divided into training and testing as 30 and 12 respectively.

Saritha et al.[8]: In this research work, they proposed a method for normal or abnormal classification of brain tumor images. Three features are extracted using spider web plots based on wavelet entropy-based. Classification is done by using PNN. The database contains 75 images: 60 abnormal and 15 normal. A total 23 images are used for testing and 50 for training.

P. Dhanalakshmi et al.[9]: In this research work, they used k-means clustering for segmentation and then area is calculated using formula sqrt(P)*.264, where P is the no. of pixel with value 1. The proposed algorithm shows the reproducibility and good performance.

Divya Kaushik et al.[10]: In this work, segmentation is done using genetic algorithm. The corners of the brain tumor region are also extracted based on proposed algorithm.

G. Vishnuvarthanan et al. 2015[11]: In this work, tumor segmentation and identification is done by using unsupervised learning methods. The result shows the various types of tumors at various locations.

Mohan J et al. 2015[12]: In this research work, neutrosophic sets are used for automatic brain tumor segmentation. The result shows 99.52% high specificity and 98.37% accuracy.

Proposed Work

The proposed method has carried out Hybridization of Traditional Classifiers to compete in accuracy with deep learning approach. Moreover, the proposed project innovates from other research work mainly in accuracy, precision, area calculation and reducing time and space complexity, reducing cost to the users and can be easily adopted by the less skilled people.Overall it aimed at improving the performance by traditional classifiers instead of going to deep learning Fig.1.

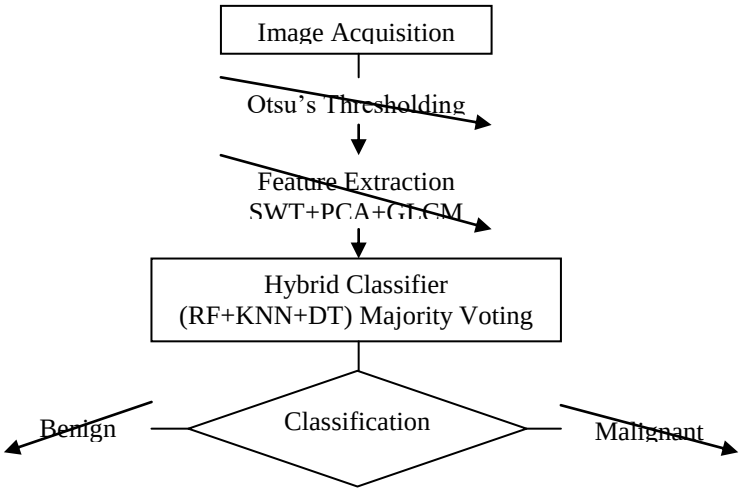


Fig 1. Flow diagram for Proposed Work.

Image Acquisition

In this step, we collect data from a justified source or collect it ourselves. The authenticity of the source is very important as that ensures the validity and accuracy of data. Only with valid data, we can get valid results and test the efficiency of the presented work. The images collected are completely unprocessed. Image are composed into training and testing in 85:15.

Otsu's Thresholding

Otsu's Thresholding is a technique used for automatic image thresholding. It calculates the threshold value which separates the background and the foreground by calculating the measure of spread for the pixel level on both sides of the threshold. It selects the value for which the intra-class intensity variance is minimized. The intra-class variance is calculated as the weighted sum of variance of both classes.

SWT

This algorithm is used for image enhancement. Earlier DWT was used, but due to the lack of translation invariance of DWT, SWT is used for image de-noising.As far as signal is a concern, there are slow changes that can be captured with the help of Fourier Transform, whereas images undergo abrupt changes which can be captured with the concept of wavelets. Wavelet is a small oscillation whose frequency inversely varies with scaling.

PCA

It is an algorithm used for dimension reduction from a large set of features to a smaller set without much information loss. It helps in reducing both the time and space complexity. PCA is an orthogonal transformation of dependent variables to linearly independent variables known as principal components. The first principal component has the highest variances; successive components contain the most significant possible variance such that it remains orthogonal to previous components.

GLCM

This algorithm is used for feature extraction from a binary image. Features that are extracted using this algorithm are Energy, Contrast, Correlation, Homogeneity, and so on.GLCM calculates the texture of the image by calculating the frequency of corresponding pixels and their spatial relationships.

RF

It is a supervised learning classification algorithm that comprises of many decision trees. Random Forest is ensemble classifier forms on a fusion of many decision trees. It calculates the result on the bases of the majority voting method. Random forest is more superior then the decision tree as it overcomes the problem of over-fitting.

KNN

It is used for both classification and regression. It uses Euclidean distance for classify the given input test data. K is number of nearest neighbors from which Euclidean distance is calculated for classification of desired data. It is very fast method as time computation is Euclidean distance between points.

DT

This method is used for classification. It has tree like hierarchical structure, where each internal node represents a feature and leaf node represents type of classification. It has limitation that it undergoes over-fitting. To reduce the over-fitting, depth of the tree can be restricted.

Hybrid (RF+KNN+DT)

This is our proposed classifier for brain tumor classification and segmentation. This hybrid classifier consists of RF+KNN+DT based on Majority Voting Method. It outperforms all the existing machine learning classifier, when compared on various parameters like accuracy, precision, specificity, recall, F1-score, Youden-Index and so on. Fig.2.

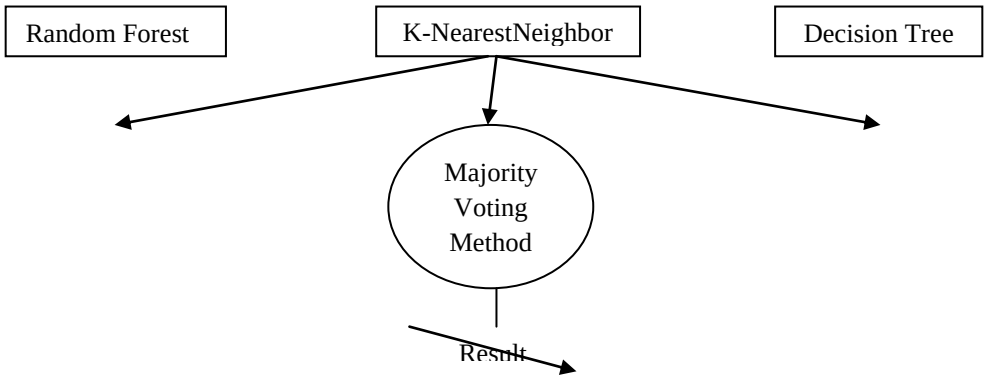


Fig.2. Represents the proposed hybrid classifier

Pseudo code for Hybrid Classifier

```
1.  procedure Hclassifier() {
2.  Mdl1 = Model of Random Forest with 100 Trees;
3.  Mdl2 = Model of KNN with K=1;
4.  Mdl3 = Model of Decision Tree;
5.  p1 = predict from Mdl1;
6.  p2 = predict from Mdl2;
7.  p3 = predict from Mdl3;
8.  var ryt = 0; var lft = 0;
9.  if p1 is "Malignant" then
10.         ryt=ryt+1;
11. else
12.         lft=lft+1;
13. end
14. if p2 is "Malignant" then
15.         ryt=ryt+1;
16. else
17.         lft=lft+1;
18. end
19. if p3 is "Malignant" then
20.         ryt=ryt+1;
21. else
22.         lft=lft+1;
23. end
24. if ryt is greater then lft then
25.         species = "Malignant";
26. else
27.         species = "Benign";
28. end
29. }
```

DFD

Level 0 DFD

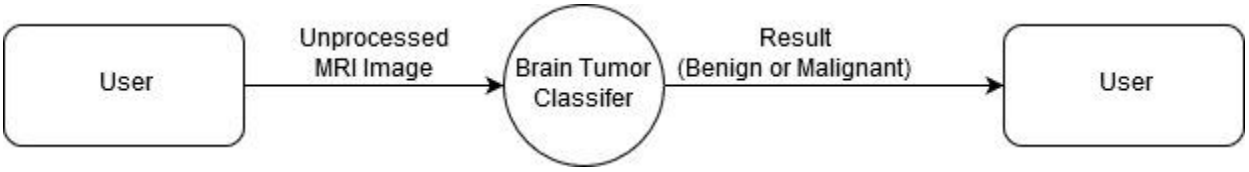


Fig. 3. Represents Level-0 DFD

Level 1 DFD

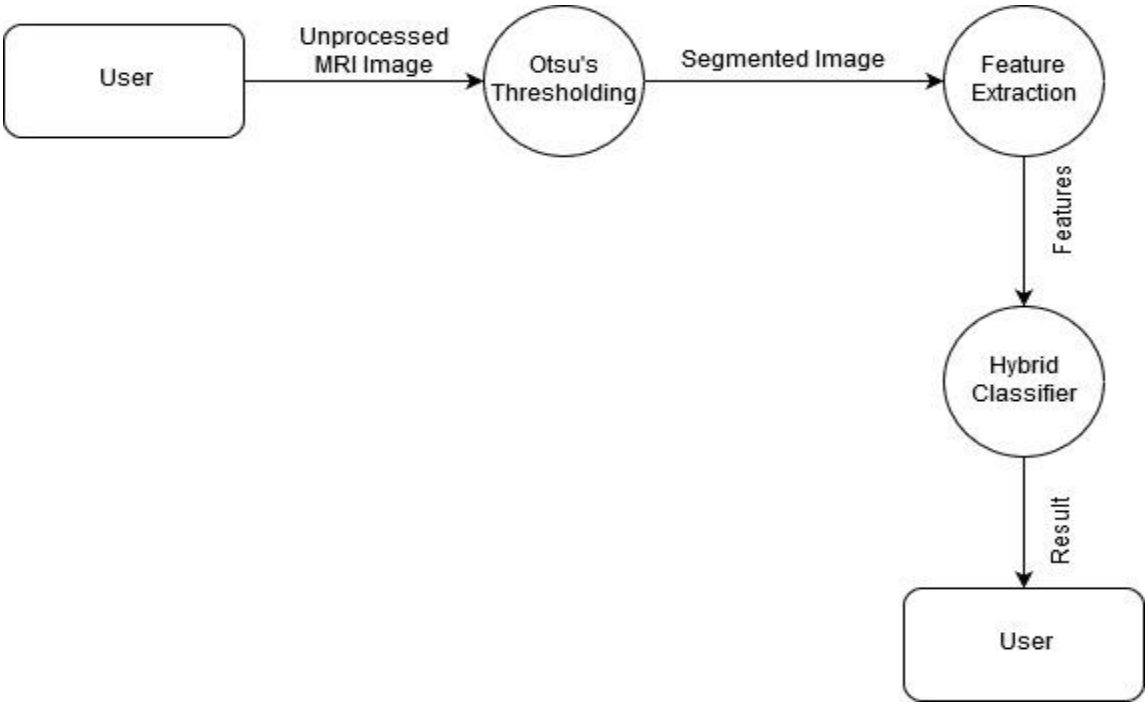


Fig. 4. Represents Level-1 DFD

Level 2 DFD

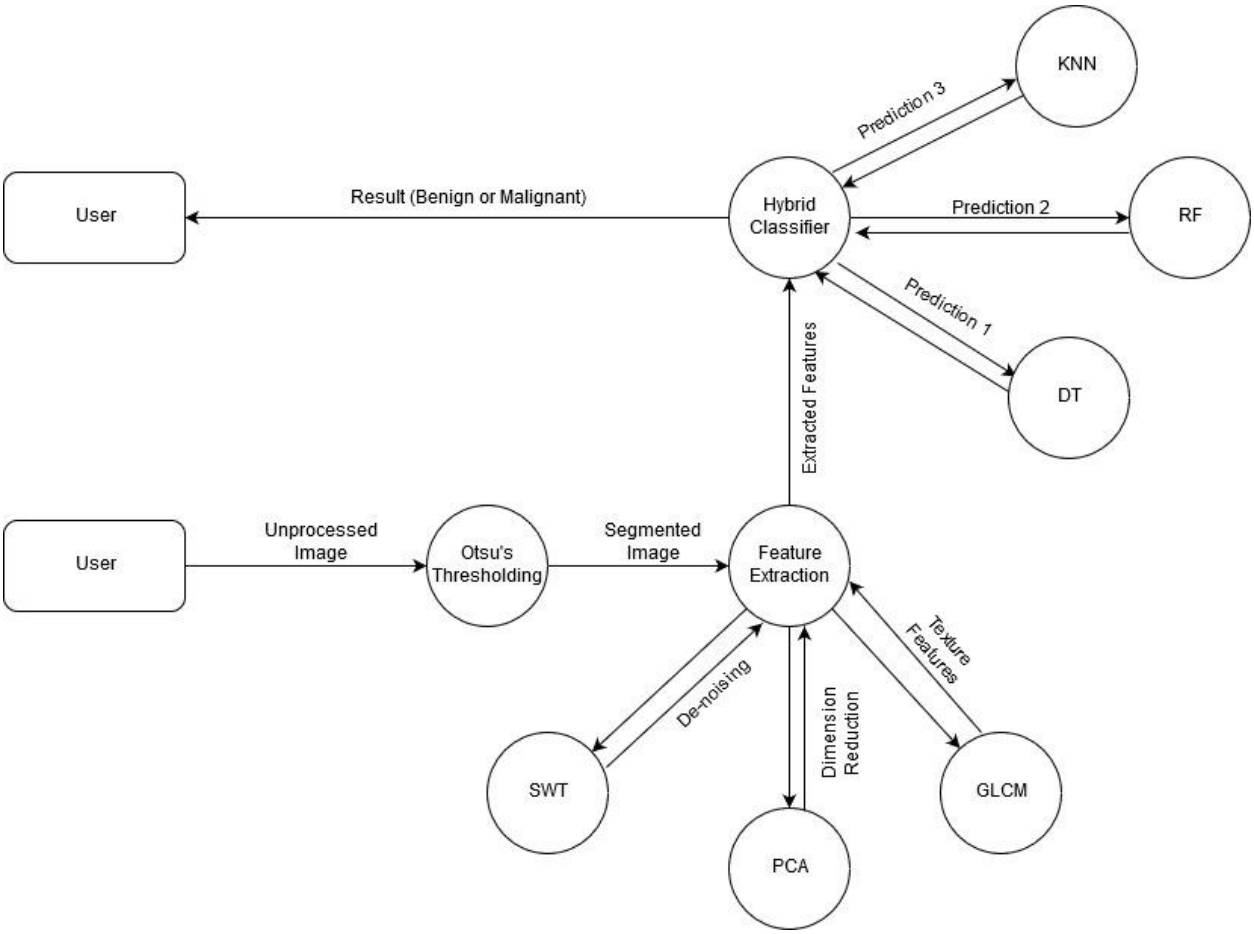


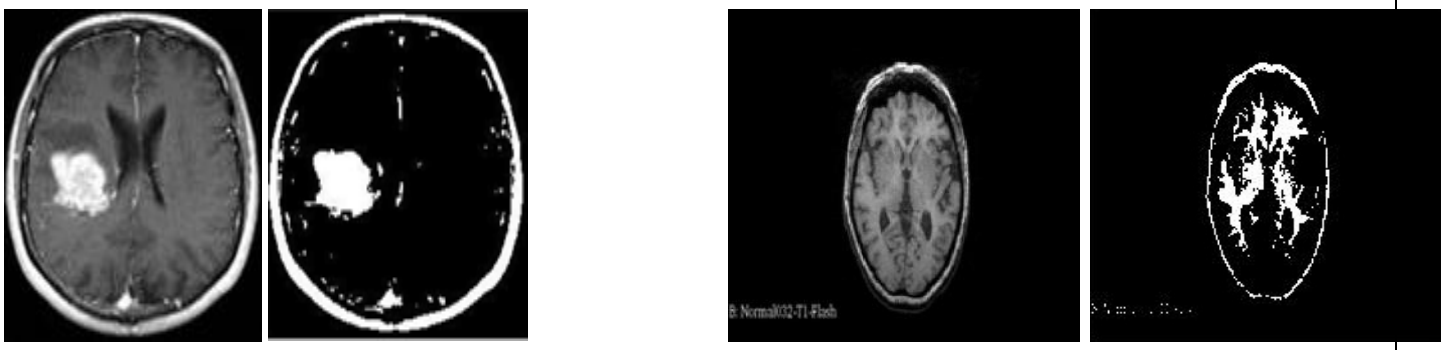
Fig. 5. Represents Level-2 DFD

Implementation and Results

In this step, we collect data from a justified source or collect it ourselves. The authenticity of the source is very important as that ensures the validity and accuracy of data. Only with valid data, we can get valid results and test the efficiency of the proposed work. The images collected are completely unprocessed. Dataset is divided into training and testing as 85:15. Table 1.

Table.1. Database for Benign and Malignant classification

Database	Training Dataset	Testing Dataset
Benign	1086	192
Malignant	1086	192



(a) (b)(c)(d)

Fig.6. Represents (a), (c) Brain Tumor T2-wieghted Image and (b), (d) Segmented Images

The following parameters are used for measuring robustness of the proposed work, which are shown below

$$\text{Accuracy} = \frac{(TP+TN)}{(\text{TP}+\text{TN}+\text{FP}+\text{FN})} \quad (1)$$

$$\text{Sensitivity} = \frac{TP}{(\text{TP}+\text{FN})} \quad (2)$$

$$\text{Specificity} = \frac{TN}{(\text{TN}+\text{FP})} \quad (3)$$

$$\text{Youden Index} = \text{Sensitivity} + \text{Specificity} - 1 \quad (4)$$

$$\text{Precision} = \frac{TP}{(\text{TP}+\text{FP})} \quad (5)$$

$$\text{F1-Score} = \frac{2 * Precision * Recall}{\text{Precision} + \text{Recall}} \quad (6)$$

Table.2. Classification parameters of the proposed scheme

Classifier	Accuracy%	Precision%	Sensitivity%	F1-score%	Youden Index%	Specificity %
Proposed Method (KNN+RF+DT)	**97.305**	**97.73**	**97.04**	**97.50**	**97.36**	**97.60**
SVM (Kernel) RBF	93.038	92.38	93.82	94.79	89.50	92.26
Linear	85.56	85.20	86.07	85.41	70.72	85.05
Polynomial	89.39	88.79	90.22	90.25	80.39	88.58
Naïve Bayes	81.33	81.68	80.83	81.62	63.54	81.85
Decision Tree	93.157	93.58	92.80	95.45	90.98	93.51
Neural Network	93	92.57	93.27	95.30	90.61	92.76
KNN	94.765	94.92	94.30	94.35	95.20	95.23

Table 2. describes the comparison of various machine learning based classifiers and our proposed method, which outperforms on all other classifiers. Sensitivity represents the robustness of the benign brain tumor, which is quite good. Specificity represents the robustness of the malignant brain tumor classification, which is quite high and good for proper classification. F1-score represents the overall relationship between precision and recall. Youden-Index represents the maximum difference between True positive and false positive. High value of Youden-Index is desirable, which we get through our proposed methodology. High value of precision is also achieved through our proposed method. Overall, our proposed method outperforms all existing machine learning methods. The above results are shown graphically below:

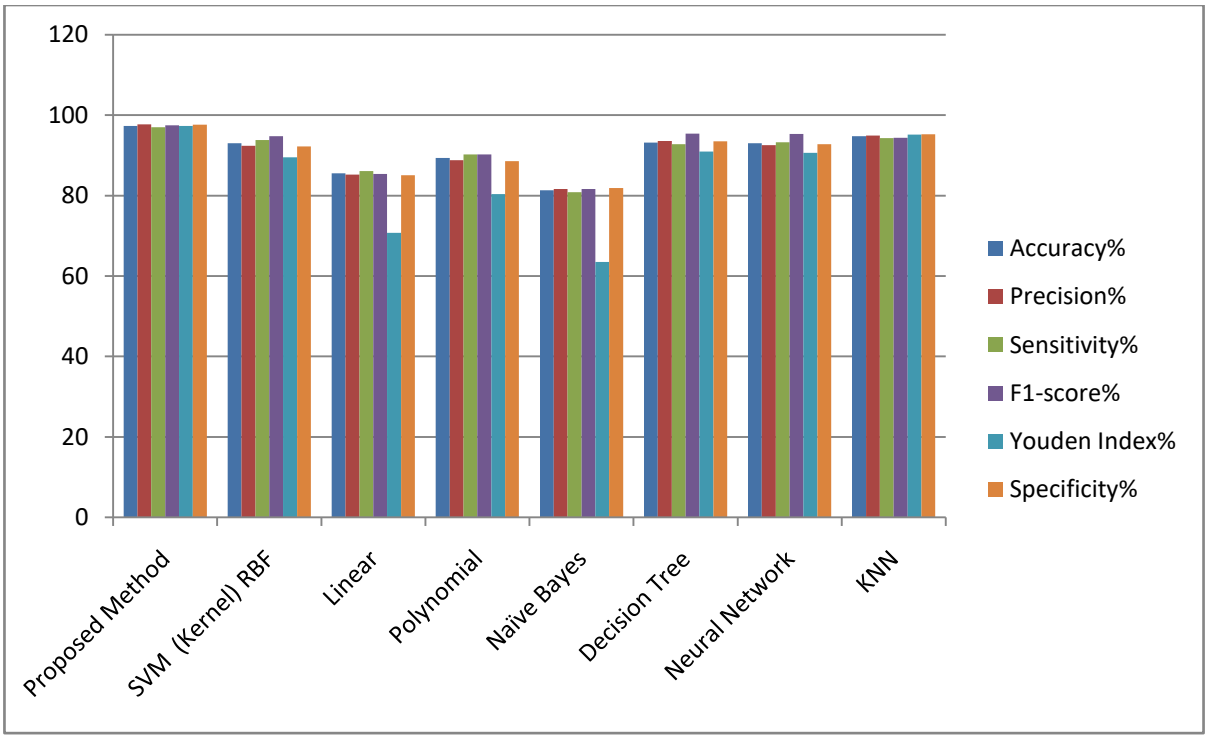


Fig.7. Represents the bar graph of all the above calculated parameters.

Conclusion

The proposed work aimed to improve the accuracy using traditional classifiers. Hybrid classifier outperforms all existing machine learning classifiers. Otsu's method is used for segmentation. Feature extraction is done using SWT+PCA+GLCM, which is quite good method to get proper de-noising, low computation complexity features. Brain Tumor segmentation is most challenging work, which is done using the proper choice of threshold value in Otsu's method. This proposed work can definitely give some input to the brain tumor segmentation and classification. Experiments are conducted with software MATLAB 2017a with a personal computer of 4 GB memory, Windows 10 64-bit operating system, and Intel (R) Core (TM) i3-6006U CPU @ 2.00 GHz. Overall, proposed method is good and novel, which outperforms on various parameters such as accuracy 97.305%, precision 97.73%, specificity 97.60%, sensitivity 97.04%,Youden-index 97.36%, and F1-score 97.50%. In future, work related to classification can be done using deep learning techniques such as CNN, Rescue-Net, GAN and so on. We can also use more techniques for segmentation such as watershed method, k-means, Genetic Algorithms and so on.

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List of Publications

1. Ginni Garg and Mantosh Biswas.: "Improved Neural Network based Plant diseases Identification", The First International Conference on "Advanced Communication & Computational Technology (***ICACCT-2019***)", Springer, Scopus-Index, LNEE format.

2. Ginni Garg, Shubham and Ashish.: "Brain Tumor classification based on hybrid classifier", Submitted in Science Direct Journal – "Measurement", Elsevier.

Appendix

Source Code:

```
%code for calculating the accuracy.

load train_input1;

load train_sout1;


X = train_input1;

Y = train_sout1;

hWaitBar = waitbar(0,'Evaluating Maximum Accuracy');

count = 0; ZP =0; ZN =0; YP = 0; YN = 0;

NumTrees = 100;

  Mdl1 = TreeBagger(NumTrees, X, Y, 'OOBPrediction', 'on');

    k = 1;

    Mdl2 = fitcknn(X, Y, 'NumNeighbors', k);

      Mdl3 = fitctree(X, Y)

for i=1:2172

    p1 = predict(Mdl1, X(i,:));

    p2 = predict(Mdl2, X(i,:));

    p3 = predict(Mdl3, X(i,:));

    ryt = 0; lft = 0;

    if(p1 == string(Y(i)))
```

```
    ryt=ryt+1;
else
    lft=lft+1;
end
if(p2 == string(Y(i)))
    ryt=ryt+1;
else
    lft=lft+1;
end
if(p3 == string(Y(i)))
    ryt=ryt+1;
else
    lft=lft+1;
end
if(lft<ryt)
    count=count+1;
     if(Y(i)=="Benign")
        ZP = ZP+1;
    elseif(Y(i)=="Malignant")
        ZN = ZN+1;
    end
```

```
    elseif(Y(i)=="Benign")
        YP = YP+1;
    elseif(Y(i)=="Malignant")
        YN = YN+1;
    end
    waitbar(i/2172);
end
spfy = ZN/ (ZN+YP);
prcn = ZP/(ZP+YP);
rcll = ZP/(ZP+YN);
F1 = 2*prcn*rcll / (prcn+rcll);
YI = rcll + spfy -1;
delete(hWaitBar);
accr = count/2172*100;
load train_input2;
load train_sout2;
X = train_input2;
Y = train_sout2;
TP1 = ZP;
TN1 = ZN;
FN1 = YN;
```

```
FP1 = YP;
hWaitBar = waitbar(0,'Evaluating Maximum Accuracy');
count = 0; ZP =0; ZN =0; YP = 0; YN = 0;
for i=1:384
    % Predict the output of an identified model
    p1 = predict(Mdl1, X(i,:));
    p2 = predict(Mdl2, X(i,:));
    p3 = predict(Mdl3, X(i,:));
    ryt = 0; lft = 0;
    if(p1 == string(Y(i)))
        ryt=ryt+1;
    else
        lft=lft+1;
    end
    if(p2 == string(Y(i)))
        ryt=ryt+1;
    else
        lft=lft+1;
    end
    if(p3 == string(Y(i)))
        ryt=ryt+1;
```

```
    else
        lft=lft+1;
    end
    if(lft<ryt)
        count=count+1;
         if(Y(i)=="Benign")
            ZP = ZP+1;
        elseif(Y(i)=="Malignant")
            ZN = ZN+1;
        end
    elseif(Y(i)=="Benign")
        YP = YP+1;
    elseif(Y(i)=="Malignant")
        YN = YN+1;
    end
    waitbar(i/384);
end
delete(hWaitBar);
spfy2 = ZN/ (ZN+YP);
prcn2 = ZP/(ZP+YP);
rcll2 = ZP/(ZP+YN);
```

```
F12 = 2*prcn2*rcll2 / (prcn2+rcll2)

YI2 = rcll2 + spfy2 -1;

accr2 = count/384*100;

TP1 = TP1+ZP

TN1 = TN1+ZN

FP1 = FP1+YP

FN1 = FN1+YN

Proposed = 0

spfy = spfy*.85 + spfy2*.15

prcn = prcn*.85 + prcn2*.15

rcll = rcll*.85 + rcll2*.15

F1 = F1*.85 + F12*.15

YI = YI*.85 + YI2*.15

accr = accr*.85 + accr2*.15

sprintf('Accuracy of Fusion Classifier is: %g%%', accr);


%code for the user input and then identification
[Fnme,Pnme] = uigetfile('*.jpg;*.png;*.bmp','Pick an MRI Image');
if isequal(Fnme,0)||isequal(Pnme,0)
   warndlg('User Press Cancel');
else
   P = imread([Pnme,Fnme]);
   P = imresize(P,[200,200]);
```

```
  imshow(P);

end

    I = P;
    img = im2bw(I,.6);
    img = bwareaopen(img,80);

    imshow(img);

img = double(img);
[A1,H1,V1,D1] = swt2(img,1,'db4');
DWT_feat = [A1,H1,V1,D1]; %%imp
G = pca(DWT_feat);
g = graycomatrix(G);
stats = graycoprops(g,'Contrast Correlation Energy Homogeneity');
Cnst = stats.Contrast;
Crr = stats.Correlation;
Engy = stats.Energy;
Hnty = stats.Homogeneity;
Mn = mean2(G);
Sd = std2(G);
Ery = entropy(G);
RMS = mean2(rms(G));
Vre = mean2(var(double(G)));
a = sum(double(G(:)));
Smth = 1-(1/(1+a));
Kts= kurtosis(double(G(:)));
Skns = skewness(double(G(:)));
```

```
m = size(G,1);
n = size(G,2);
in_diff = 0;
for i = 1:m
   for j = 1:n
      temp = G(i,j)./(1+(i-j).^2);
      in_diff = in_diff+temp;
   end
end
IDM = double(in_diff);

feat = [Cnst,Crr,Engy,Hnty, Mn, Sd, Ery, RMS, Vre, Smth, Kts, Skns, IDM];

load feat_input;
load feat_output;
load string_output;

X = feat_input;
Y = string_output;

NumTrees = 100;
  Mdl1 = TreeBagger(NumTrees, X, Y, 'OOBPrediction', 'on');
k = 1;
   Mdl2 = fitcknn(X, Y, 'NumNeighbors', k);
 Mdl3 = fitctree(X, Y);
 p1 = predict(Mdl1, feat);
 p2 = predict(Mdl2, feat);
 p3 = predict(Mdl3, feat);
 rht = 0; lft = 0;
 if(p1 == string("Malignant"))
       rht=rht+1;
```

```
else
   lft=lft+1;
end
if(p2 == string("Malignant"))
   rht=rht+1;
else
   lft=lft+1;
end
if(p3 == string("Malignant"))
   rht=rht+1;
else
   lft=lft+1;
end
if(rht>lft)
   species = "Malignant"
else
   species = "Benign"
end
```