

BRAIN TUMOR CLASSIFICATION

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Declaration

We declare that the Submitted Report is our original work and no values and context of it have been copy-pasted from anywhere else. We take full responsibility, that if in the future, the report is found invalid or copied, the last decision will be of the Faculty concerned. Any form of plagiarism will lead to the disqualification of the report.

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Abstract

In this documentation, we will see how we can detect a tumor in the brain from an MRI image using the Singular-Value Decomposition (SVD) concepts which is an optimal matrices decomposition in the least square sense. Singular-Value Decomposition (SVD) is an effective way to split the system into independent components, where each of them has its own set of contributions. After we decompose the image using SVD, with the help of these singular values, we calculate the threshold value which plays an important role in determining the tumor.

Here, we classify an image as abnormal or normal brain based on the value of the threshold calculated.

Introduction

This project aims to be beneficial in identifying brain tumors using a simple but efficient way algorithm. Traditionally the brain tumor was identified by the medical practitioner using the MRI scans and only through experiential knowledge. To make the process of identification much faster, easier and efficient, we developed an algorithm to automate this procedure.

The algorithm is mainly based on SVD decomposition and further focuses on the singular value matrix. The data with large numbers can be reduced into a smaller subset with all the features of the actual data, so can be used to predict the pattern or a problem using the SVD decomposition.

So to differentiate between the normal brain and the abnormal brain we apply this SVD decomposition to obtain the singular values of the image. Using the singular value obtained we compute whether or the there is a tumor present in the MRI of the brain image uploaded.

Role of SVD

SVD is one of the best techniques to convert some Matrix A into different components, making a diagonal matrix with all the important value of it stored in that matrix. It's often used as a data reduction tool that reduces the dimensions of a matrix keeping in mind the important values of that matrix which we call sigma in our expression.

Let's see the mathematical expression

$$A = U \sigma V^T$$

Let's see this in detail

$$= \left(\begin{array}{c|c} \begin{array}{c} u_1 \\ \vdots \\ u_r \end{array} & \begin{array}{c} u_{r+1} \\ \vdots \\ u_m \end{array} \\ \hline \begin{array}{c} \vdots \\ \vdots \end{array} & \begin{array}{c} \vdots \\ \vdots \end{array} \end{array} \right) \left(\begin{array}{ccc} \sigma_1 & & \\ & \ddots & \\ & & \sigma_r \\ & & & 0 & \\ & & & & \ddots \\ & & & & & 0 \end{array} \right) \left(\begin{array}{c} \text{---} \\ \text{---} \\ \text{---} \\ \text{---} \end{array} \right) \begin{array}{c} v_1^T \\ v_r^T \\ v_{r+1}^T \\ v_n^T \end{array} \left. \begin{array}{l} \text{---} \\ \text{---} \\ \text{---} \\ \text{---} \end{array} \right\} \begin{array}{l} \text{row}(A) \\ \text{null}(A) \end{array}$$

col(A) null(A)

U = Left Singular Vector (Orthogonal)

σ = Singular Matrix

V = Right Singular Vector (Orthogonal)

Here, if A contains only r important values, then σ also contains the same number of singular values. Also in U and V , the columns and rows specified as $\text{null}(A)$ become 0, after multiplying it with σ since, other than the diagonal elements (only r elements), all the remaining are zeros.

In this topic, we use SVD to obtain the singular values which play a major in the decision criterion of classification of brain tumor.

Proposed Algorithm

We actually start our algorithm by training it with a unique data set. We give a set of images to the algorithm to train it. In the proposed algorithm, we have two stages to proceed with.

The first one being the algorithm training part while the second one is classifying the given images as normal or abnormal based on whether the brain image has a tumor or not.

In the first stage, after we take the image, we convert it to the grey level eliminating a dimension of colour from it. Then using the concept of SVD, we decompose the matrix of the image and focus on the singular values (σ matrix from the above explanation), which are the most important values for that image.

After picking the singular values of the matrix, which reside in the principle diagonal of the σ matrix, we take the norm of all the singular values followed by taking the mean of it, and fixing it as our Base value (which we called BaseV in the code).

Now, preceding further to the next stage, we now take an input image and classify it as normal or abnormal based on whether the image has tumor or not.

To classify the image, we need to take it first, and we again convert the image to the grey level image, followed by computing the singular values of it and taking the norm of it.

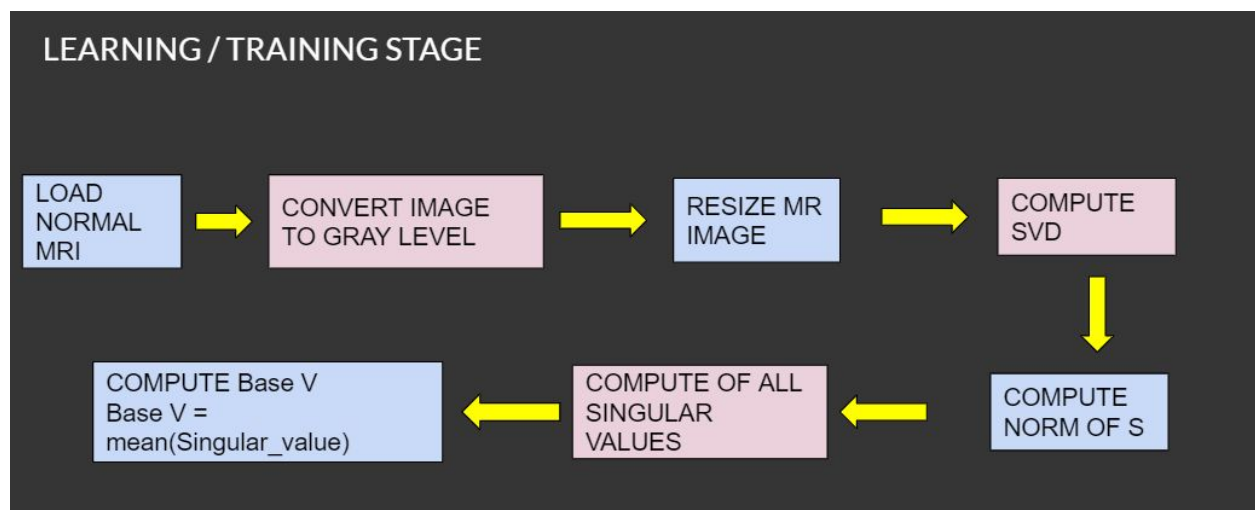
We stored this norm as NewV in our code.

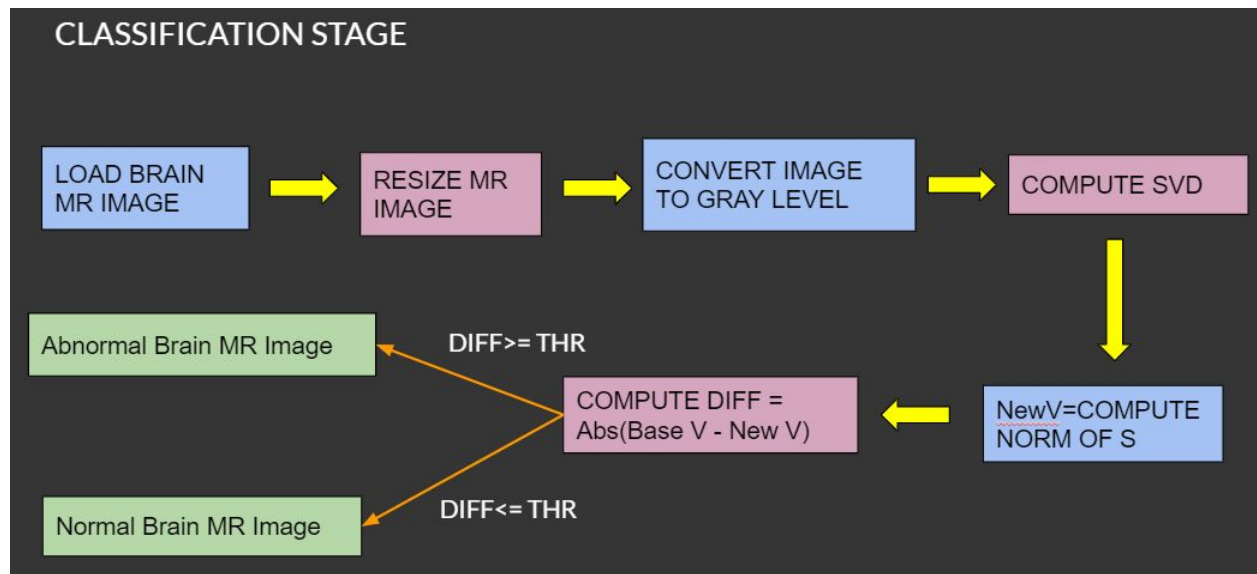
Coming to an end, we now classify the image based on the threshold value which is computed accurately only by experiments and observations.

Let us see the step by step procedure of the proposed algorithm

We first start with the

Training stage:



Classification stage:

Code

Training Model:

```
clc;
clear all;
close all;
%Collecting the svd decomposition with positive result
k = 25; % k is the number images we train
n=zeros(1,k); % array to store the norm values
for i=1:k
    imagepath=strcat('path',num2str(i),'.jpg');
    imdata = imread(imagepath);
    fig=im2double(imdata);
    fig=rgb2gray(imdata);
    fig=imresize(fig,[100 100]);
    fig=im2double(fig);
    [U,S,V]=svd(fig);
    Singular_Value=diag(S);
    a=norm(Singular_Value);
    n(i)=a;
end
BaseV = mean(n)
```

Classification model:

Image load function:

```
global img

[path , nofile] = imgetfile();
if nofile
    errordlg('No image Loaded','Error');
end
[~,name,~] = fileparts(path);
assignin('base','name',name);
img=imread(path);
img=im2double(img);

axes(handles.axes1);
imshow(img)
set( handles.img,'String', evalin('base','name') )
title ( '\fontsize{20}\color{rgb}{0.996,0.592,0.0} Brain MRI ')
```

Prediction Function:

```

% --- Executes on button press in predict.
function predict_Callback(hObject, eventdata, handles)
% hObject    handle to predict (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global img
THR =5;
BaseV=22.005;
bwimg=im2gray(img);
bwimg=imresize(bwimg,[100 100]);
[~, S , ~]=svd(bwimg);
Singular_Value=diag(S);
NewV=norm(Singular_Value);
diff = abs(BaseV-NewV);
if diff<=THR
    prediction='Normal';
else
    prediction='Abnormal';
end
set( handles.newv, 'String', num2str(NewV,3) )
set( handles.diff, 'String', num2str(diff,3) )
set( handles.pre, 'String', prediction )
if prediction == "Abnormal"
    set( handles.pre, 'ForegroundColor', [1,0,0] )
else
    set( handles.pre, 'ForegroundColor', [0,1,0] )
end

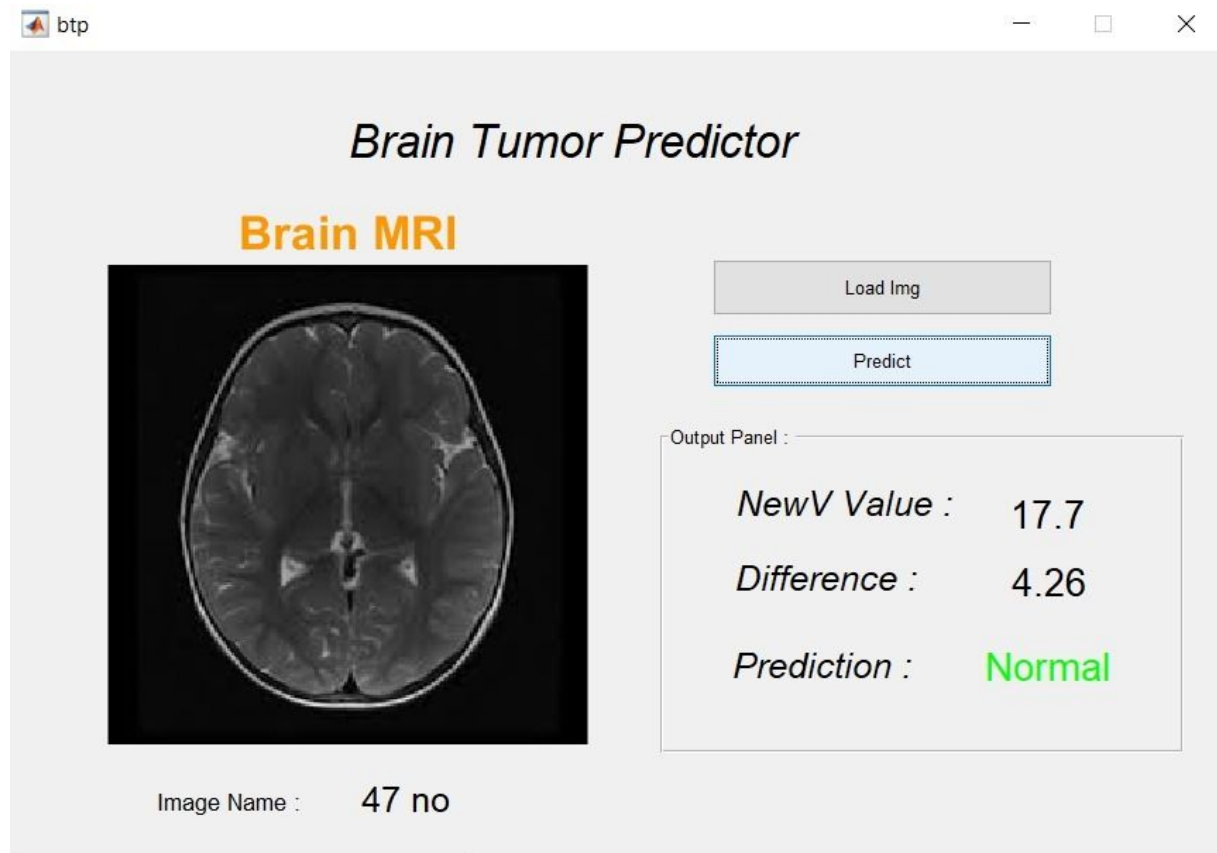
```

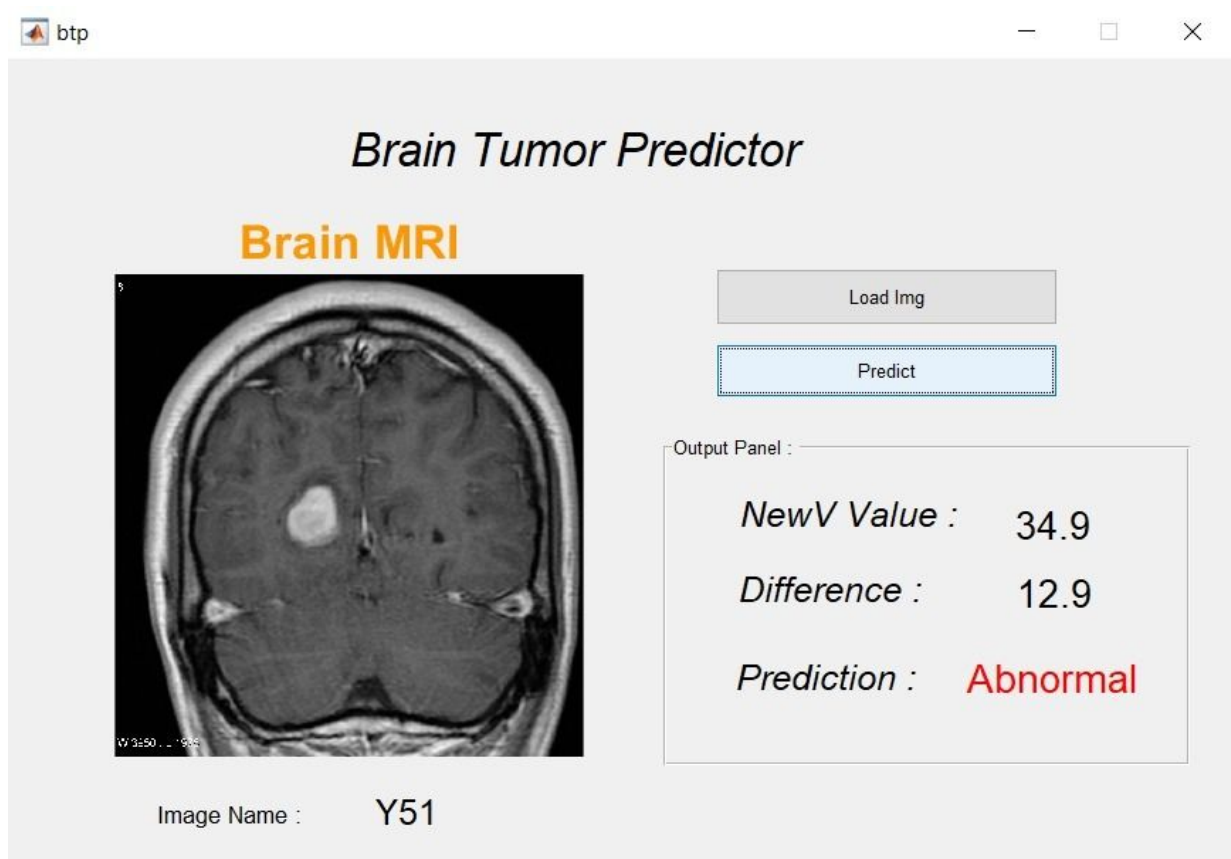
Results

We successfully classified the images as abnormal and normal brains after training the algorithm with a data set.

The following are the screenshots of some images which after passing in the predictor predicted the accurate output.

Normal Brain



Abnormal Brain (with tumor)**References**

Some youtube content and Wikipedia