

MRI Image Analysis Application

Amit Bhujbal¹ S. T. Patil²

¹Student, Vishwakarma Institute of Technology, Pune, amit.bhujbal15@vit.edu

²Professor, Vishwakarma Institute of Technology, Pune, patil.st@gmail.com

Abstract : The advances in medical imaging have led to new multi-dimensional imaging modalities that have become important clinical tools in diagnostic radiology. The two modalities capable of producing multidimensional images for radiological applications are Computed Tomography (CT) and Magnetic Resonance Imaging (MRI). Normally the first radiologic examination in suspicion of stroke is brain CT imaging. But MRI provides high resolution images with excellent soft tissue characterization capabilities. A comparative analysis for the diagnosis of stroke on CT and MRI images is presented in this paper. The algorithm proposes the use of Digital Image processing tools for the identification of infarct and Hemorrhage in human brain. Preprocessing of medical images is done by median filtering. Segmentation is done by Gabor filtering and seeded region growing algorithm. The method is demonstrated on the CT and MRI brain images having different types of infarcts. The results of the method are evaluated visually. The proposed method is promising for detection of stroke and also establishes that MRI imaging is superior to CT imaging in stroke detection.

IndexTerms— MRI analysis, Scan, detect, Core ML, swift, Xcode.

I. INTRODUCTION

The advances in medical imaging have led to new multi-dimensional imaging modalities that have become important clinical tools. MRI provides high resolution images with excellent soft tissue characterization capabilities. MRI images is presented in this paper. The algorithm proposes the use of Digital Image processing tools

In brain MRI analysis, image segmentation is commonly used for measuring. This diversity of image processing applications has led to development of features and introducing MRI intensity distributions of the brain tissue. Ease of use

1. Quick image processing
2. To detect correct diagnosis
3. Easy print or softcopy

II. APP DETAILS

The various sections of the application are as follows:

1. Scan Image: Import from photos
2. Result: Image Processing diagnosis by machine learning.
3. Details: Brain tumor which stages information
4. Print: Add fill patient details Forms and print out or soft copy

III. SAMPLE IMAGE:

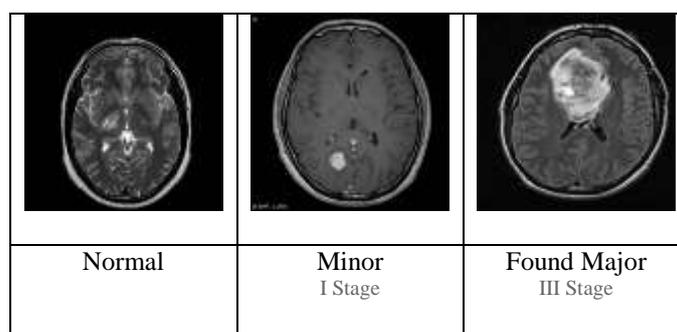


FIGURE 1: SAMPLE MRI IMAGE

IV. FLOW DIAGRAM

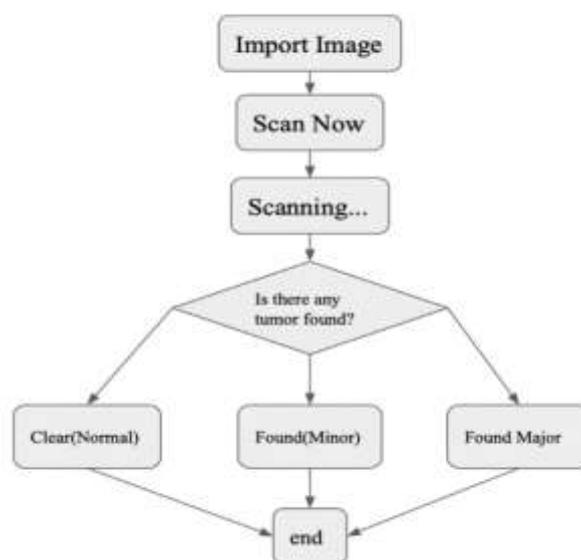


FIGURE 2: FLOW CHART

V. SUPPORT VECTOR MACHINE

In machine learning, support-vector machines (SVMs, also support-vector networks) are supervised learning models with associated learning algorithms that analyze data used for classification and regression analysis. Given a set of training examples, each marked as belonging to one or the other of two categories, an SVM training algorithm builds a model that assigns new examples to one category or the other, making it a non-probabilistic binary linear classifier (although methods such as Platt scaling exist to use SVM in a probabilistic classification setting). An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on the side of the gap on which they fall.

In addition to performing linear classification, SVMs can efficiently perform a non-linear classification using what is called the kernel trick, implicitly mapping their inputs into high-dimensional feature spaces.

When data are unlabelled, supervised learning is not possible, and an unsupervised learning approach is required, which attempts to find natural clustering of the data to groups, and then map new data to these formed groups. The support-vector clustering algorithm, created by Hava Siegelmann and Vladimir Vapnik, applies the statistics of support vectors, developed in the support vector machines algorithm, to categorize unlabeled data, and is one of the most widely used clustering algorithms in industrial applications.

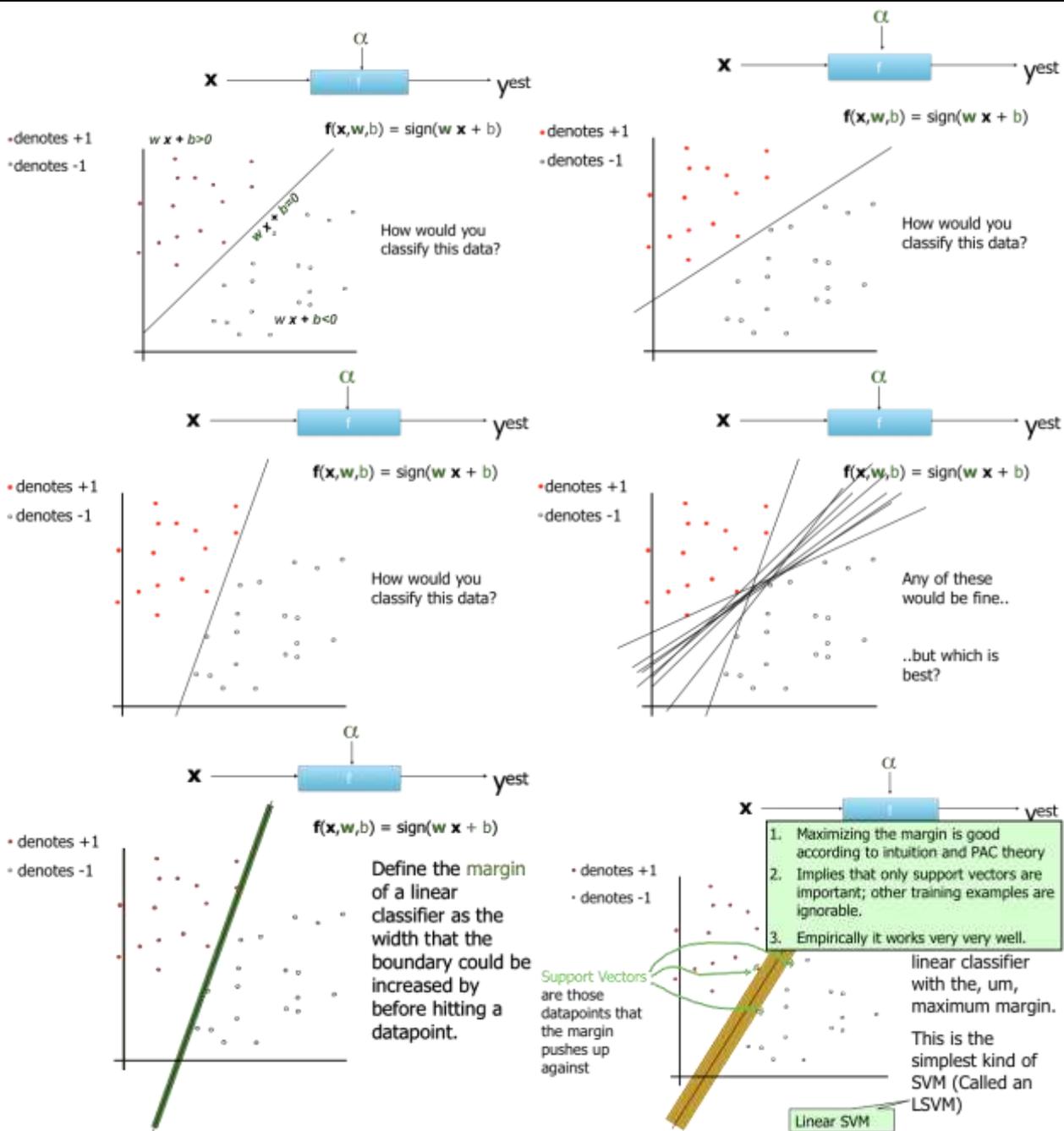
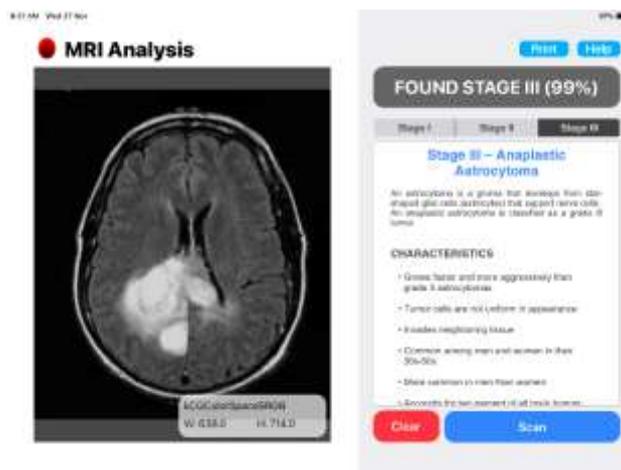


FIGURE 3: SUPPORT VECTOR MACHINE

VI. SCREENSHOT



MRI ANALYSIS on iPad

FIGURE 4: SCREENSHOT

VII. RESULT

The experimental results achieved 96.51% accuracy, 94.2% specificity, and 97.72 sensitivity, demonstrating the effectiveness of the proposed technique for identifying normal and abnormal tissues from brain MR Images

VIII. CONCLUSION

In this study, using MR images of the brain, we segmented brain tissues into normal tissues such as white matter, gray matter, cerebrospinal fluid (background), and tumor-infected tissues. Fifteen patients infected with a glial tumor, in benign and malignant stages, assisted in this study. We used preprocessing to improve the signal-to-noise ratio and to eliminate the effect of unwanted noise. We used an algorithm based on threshold technique to improve the performance. Furthermore, we used transform to segment the images and support vector machine to classify the tumor stage by analyzing feature vectors and area of the tumor. In this study, we investigated texture based and histogram-based features with a commonly recognized classifier for the classification of brain tumor from MR brain images. From the experimental results performed on the different images, it is clear that the analysis for the brain tumor detection is fast and accurate when compared with the manual detection performed by radiologists or clinical experts. The various performance factors also indicate that the proposed algorithm provides better result by improving certain parameters such as mean, MSE, PSNR, accuracy, sensitivity, specificity, and dice coefficient. Our experimental results show that the proposed approach can aid in the accurate and timely detection of brain tumor along with the identification of its exact location. Thus, the proposed approach is significant for brain tumor detection from MR images.

REFERENCES

- 1]. Xcode Documentation - <https://developer.apple.com/documentation/xcode>
- 2]. Swift Documentation - <https://developer.apple.com/documentation/swift>
- 3]. Core ML Documentation - <https://developer.apple.com/documentation/coreml>
- 4]. YouTube - <https://www.youtube.com/>
- 5]. Liu J, Aoki M, Illa I, et al. Dysferlin, a novel skeletal muscle gene, is mutated in Miyoshi myopathy and limb girdle muscular dystrophy. *Nat Genet* 1998;20:31–6. 10.1038/1682
- 6]. Bashir R, Britton S, Strachan T, et al. A gene related to *Caenorhabditis elegans* spermatogenesis factor fer-1 is mutated in limb-girdle muscular dystrophy type 2B. *Nat Genet* 1998;20:37–42. 10.1038/1689
- 7]. Nguyen K, Bassez G, Krahn M, et al. Phenotypic study in 40 patients with dysferlin gene mutations: high frequency of atypical phenotypes. *Arch Neurol* 2007;64:1176–82. 10.1001/archneur.64.8.1176
- 8]. Illa I, Serrano-Munuera C, Gallardo E, et al. Distal anterior compartment myopathy: a dysferlin mutation causing a new muscular dystrophy phenotype. *Ann Neurol* 2001;49:130–4. 10.1002/1531-8249(200101)49:1<130::AID-ANA22>3.0.CO;2-0
- 9]. Amato AA, Brown RH. Dysferlinopathies. *Handb Clin Neurol* 2011;101:111–8. 10.1016/B978-0-08-045031-5.00007-4