MR BRAIN TUMOR TREATMENT USING SUPPORT VECTOR MACHINE AND DECISION TREE CLASSIFIERS

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ABSTRACT

Brain tumor detection and classification are crucial tasks in medical imaging and play a vital role in the treatment planning process. This abstract presents a method for brain tumor treatment using Convolutional Neural Networks (CNNs). CNNs are deep learning models that have shown remarkable success in various computer vision tasks, including medical image analysis. The proposed approach leverages the power of CNNs to automatically learn discriminative features from Magnetic Resonance (MR) brain images. The dataset used in this study consists of pre-processed MR images of patients with different types of brain tumors. These images are labeled with ground truth information indicating the presence and type of tumor. The CNN model is trained using a large set of labeled MR images, allowing it to learn complex patterns and features that distinguish healthy brain tissue from tumor regions. The training process involves iterative optimization of the network's parameters, guided by a loss function that measures the dissimilarity between predicted and actual tumor labels. Once trained, the CNN model can be used for tumor detection and classification on new, unseen MR brain images. Given an input image, the model analyzes its features and outputs a prediction indicating the presence of a tumor and its type if detected. This information can assist medical professionals in diagnosing and planning appropriate treatment strategies. To evaluate the effectiveness of the proposed approach, extensive experiments are conducted on a diverse set of MR brain images. The experimental results demonstrate the potential of CNNs in achieving high accuracy and robustness in brain tumor detection and classification tasks.

Keywords: Brain tumor, Deep learning, CNN.

1. INTRODUCTION

Machine learning algorithms have the potential to be invested deeply in all fields of medicine, from drug discovery to clinical decision making, significantly altering the way medicine is practiced. The success of machine learning algorithms at computer vision tasks in recent years comes at an opportune time when medical records are increasingly digitalized. The use of electronic health records (EHR) quadrupled from 11.8% to 39.6% amongst office-based physicians in the US from 2007 to 2012 [1]. Medical images are an integral part of a patient's EHR and are currently analyzed by human radiologists, who are limited by speed, fatigue, and experience. It takes years and great financial cost to train a qualified radiologist, and some health-care systems outsource radiology reporting to lower-cost countries such as India via tele-radiology. A delayed or erroneous diagnosis causes harm to the patient. Therefore, it is ideal for medical image analysis to be carried out by an automated, accurate and efficient machine learning algorithm. Medical image analysis is an active field of research for machine learning, partly because the data is relatively structured and labelled, and it is likely that this will be the area where patients first interact with functioning, practical artificial intelligence systems. This is significant for two reasons. Firstly, in terms of actual patient metrics, medical image analysis is a litmus test as to whether artificial intelligence systems will actually improve patient outcomes and survival. Secondly, it provides a testbed for human-AI interaction, of how receptive patients will be towards health altering choices being made, or assisted by a non-human actor.

TYPES OF MEDICAL IMAGING

There is a myriad of imaging modalities, and the frequency of their use is increasing. Smith-Bindman et al. [2] looked at imaging use from 1996 to 2010 across six large integrated healthcare systems in the United States, involving 30.9 million imaging examinations. The authors found that over the study period, CT, MRI and PET usage increased 7.8%, 10% and 57% respectively. Modalities of digital medical images include ultrasound (US), X-ray, computed tomography (CT) scans and magnetic-resonance imaging (MRI) scans, positron emission tomography (PET) scans, retinal photography, histology slides, and dermoscopy images. Fig. 1. shows some example medical images. Some of these modalities examine multiple organs (such as CT, MRI) while others are organ specific (retinal photography, dermoscopy). The amount of data generated from each study also varies. A histology slide is an image file of a few megabytes while a single MRI may be a few hundred megabytes. This has technical implications on the way the data is pre-processed, and on the design of an algorithm's architecture, in the context of processor and memory limitations.
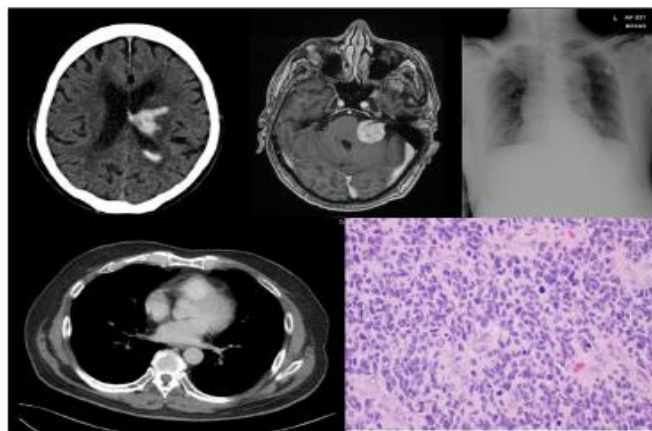

Fig. 1: A collage of images depicting medical images, from left to right, top to bottom: an axial CT brain scan with a left-sided hemorrhagic stroke, an axial MRI brain scan with a left-sided brain tumor, a normal chest X-ray, a normal axial CT lung scan, and a histology slide with high grade glioma (a brain tumor).

2. LITERATURE SURVEY

Idanis Diaz introduced automatic brain tumour segmentation (ABTS) method for segmenting different constituents of the tumour in the brain. The approach was applied on four magnetic resonance image modalities to find the edema and gross tumour volume (GTV). The ABTS segmentation algorithm uses a histogram multi-thresholding technique and morphological operations like geodesic transformations. The registered images containing the standard MR sequence was applied as input. The first step was thresholding, followed by Skull, Edema and gross tumour volume (GTV) segmentation. The method is fast and accurate for images produced from different scanners as it automatically identifies thresholds based on the histograms.

Meiyan Huang derived a novel classification framework. In this paper, the local independent projection was introduced into the classical classification model. Calculations of the local independent projections for LIPC (independent projection-based classification) method are carried out where Locality is an important parameter. LIPC technique also takes into consideration the data distribution of different classes by learning a model called soft max regression. This can further improve classification performance. The proposed method consists of four major stages, i.e., pre-processing, tumour segmentation using the LIPC method, feature extraction, and post-processing with spatial constraints. A multi-resolution framework was embedded to reduce the costs of computation.

Experimental results were obtained for Synthetic Data as well as Image data. The challenges of tumour segmentation methods which arise due to the complex characteristics exhibited by the brain tumour MRI images, such as high diversity in the appearance of tumour and the ambiguous boundaries of the tumour, were addressed by this method.

Jin Liu provided a comprehensive overview for MRI-based tumour segmentation methods and described the different imaging modalities. The pre-processing operations and the state of the art methods of MRI-based brain tumour segmentation were explained in details. Then, the results of the MRI-based tumour segmentation were evaluated and validated. Finally, an objective assessment was presented to address the future developments and trends of the brain tumour segmentation methods using MR Images. Many segmentation techniques have greatly aided in finding a solution to the various challenges posed by the semiautomatic and fully automatic systems.

Dr Mohd Fauzi Bin Othman proposed an overview of MRI brain tumour classification using Field Programmable Gate Array (FPGA) implementation. Field Programmable Gate Arrays are the most suitable option for real time analysis of algorithms used in image processing, as they can be customized and are flexible. They save time and money for implementation of new segmentation techniques on hardware. In this approach, an advanced kernel-based technique such as Support Vector Machine (SVM) is used for classifying the MRI data images as normal (without a brain tumour) and abnormal (with a brain tumour). Wavelet transform is used to eliminate noise and then inverse wavelet transform is applied to obtain the output image which is free from noise. Thus, a wavelet-based feature extraction is performed. However, SVM is not very precise with large data sets as it is dependent on the size of the input data. Hence, it is suggested that the SVM could be collaborated with clustering method to obtain better evaluation results.

Deepthi Murthy T.S. suggest that efficient segmentation can be performed by using the thresholding technique followed by application of morphological operations. In this paper, features of the brain tumour like centroid, perimeter and area, are calculated and evaluated from the segmented tumour image. Pre-processing was done using sobel operator which was followed by the process of histogram equalization (to equalize the intensities/pixels of the image) for the enhancement of the image. Then, the process of segmentation using morphological operations was performed in order to acquire the region of interest. Thus, the tumour was detected. In future work, it is suggested to determine more features in order to classify the different types of tumour.

Hongzhe Yang presented a comprehensive survey on brain tumour detection methods and also the technologies using MR images. Some segmentation techniques discussed were based on Classification and Clustering Technology, Continuous Deformable Models, Spatially Discrete Approaches, Hybrid Methods with Feature Information and Atlas–based Segmentation. The experimental results gave measurements of Overlap, Hausdorff Distance, Dice Coefficient (and False Ratio), Sensitivity and Specificity.

Heena Hooda have discussed the performance efficiency of various techniques used in segmentation of MR images. The evaluation and performance parameters were obtained on the basis of percentage calculation of the amount of error which was later compared to the ground truth.

The radiologists in clinics spend about 10-15 minutes to diagnose one report. Manual detection is not only time consuming but also prone to human errors. Automatic systems can accurately detect tumours, saving time and yielding reliable results. In this paper, an approach to detect brain tumours automatically, without initial estimates, is illustrated. The average dice coefficient gives a reliable and accurate value for the database used. The segmentation algorithm is simple which is followed by labelling. Fuzzy C-Means clustering technique which uses the fuzzy

logic to establish a degree of belonging to each pixel is used. This technique is also known as soft clustering and gives accurate results.

The author in [3] presented a segmentation algorithm that was based on improved watershed approach. This approach provided some better enhancements over manual segmentation algorithms, but it was suffering from few restrictions like over segmentation and sensitive to false edges. In [4], a fuzzy implementation has been presented by the author named fazel. Fuzzy is a set of rules and regulations, in which the segmentation depends on the membership values. However, fuzzy wasn't without drawbacks, it suffers from computational complexity due to its dependency on membership function. Later, many researchers tried to implement hybrid combos with the integration of FCM algorithm. Author in [5] presented an effective segmentation of tissue in brain images by utilizing the combo of spatial information and FCM, this resolved the issue found in [4], but it was also taking more computational time to segment an image and also suffer from false edges. To overcome the limitations of above-mentioned segmentation algorithms, the author in [6] proposed an efficient segmentation algorithm which utilized k-means clustering for segmenting MR brain image. This approach was an extended version for the watershed, manual segmentation and FCM based algorithms. Segmented output of k-means is quite better than those algorithms and this takes very less time to compute the segmented images. From then many researchers tried to implement integrated algorithms with the combination of k-means clustering to get the enhanced performances in [7-10]. However, this K-means depends on the selected centroids initially. It needs new centroids to be updated by calculating the mean of obtained clustered points in the first iteration. The mean of these values provides the floating values which were not favorable for replacing as a new centroid. Therefore, K-means must optimize for the integer or scalar centroid to be replaced with the existing centroid. In [11], the author has proposed a pillar- based approach to optimize the K-means clustering, in which the maximum value is selected instead of calculating the mean value to replace the initial centroid. Authors in [19-21] presented a hybrid algorithm for tumor detection and extraction from brain images, but they failed to detect the tumor with higher accuracy. Correspondingly, there has been a dramatic increase in the number of research papers published on CNN architecture and applications, such that CNNs have become the dominant architecture in medical image analysis.

3. PROPOSED SYSTEM

CONVOLUTIONAL NEURAL NETWORKS

Currently, CNNs are the most researched machine learning algorithms in medical image analysis [4]. The reason for this is that CNNs preserve spatial relationships when filtering input images. As mentioned, spatial relationships are of crucial importance in radiology, for example, in how the edge of a bone joins with muscle, or where normal lung tissue interfaces with cancerous tissue. As shown in Fig. 2., a CNN takes an input image of raw pixels, and transforms it via Convolutional Layers, Rectified Linear Unit (RELU) Layers and Pooling Layers. This feeds into a final Fully Connected Layer which assigns class scores or probabilities, thus classifying the input into the class with the highest probability.

CONVOLUTION LAYER

A convolution is defined as an operation on two functions. In image analysis, one function consists of input values (e.g. pixel values) at a position in the image, and the second function is a filter (or kernel); each can be represented as array of numbers. Computing the dot product between the two functions gives an output. The filter is then shifted to the next position in the image as defined by the stride length. The computation is repeated until the entire image is covered, producing a feature (or activation) map. This is a map of where the filter is strongly activated and 'sees' a feature such as a

straight line, a dot, or a curved edge. If a photograph of a face was fed into a CNN, initially low-level features such as lines and edges are discovered by the filters. These build up to progressively higher features in subsequent layers, such as a nose, eye or ear, as the feature maps become inputs for the next layer in the CNN architecture.

Convolution exploits three ideas intrinsic to perform computationally efficient machine learning: sparse connections, parameter sharing (or weights sharing) and equivariant (or invariant) representation [22]. Unlike some neural networks where every input neuron is connected to every output neuron in the subsequent layer, CNN neurons have sparse connections, meaning that only some inputs are connected to the next layer. By having a small, local receptive field (i.e., the area covered by the filter per stride), meaningful features can be gradually learnt, and the number of weights to be calculated can be drastically reduced, increasing the algorithm's efficiency. In using each filter with its fixed weights across different positions of the entire image, CNNs reduce memory storage requirements. This is known as parameter sharing. This is in contrast to a fully connected neural network where the weights between layers are more numerous, used once and then discarded. Parameter sharing results in the quality of equivariant representation to arise. This means that input translations result in a corresponding feature map translation. The convolution operation is defined by the $*$ symbol.
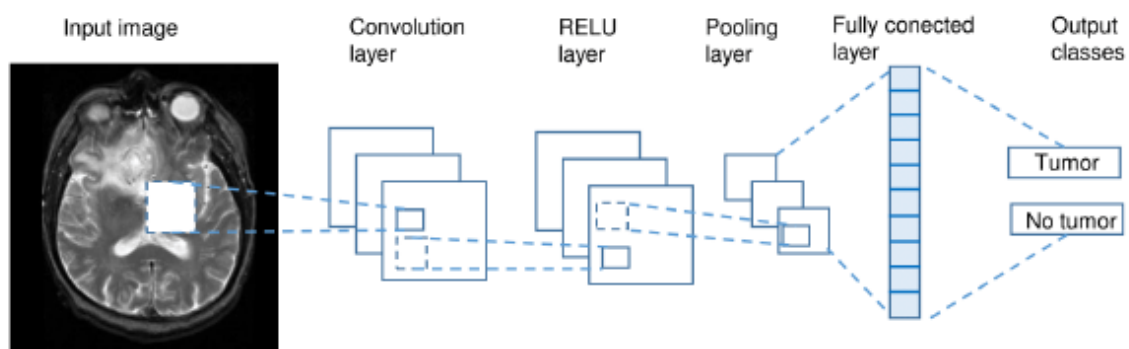

Fig. 2. In this example disease classification task, an input image of an abnormal axial slice of a T2-weighted MRI brain is run through a schematic depiction of a CNN. Feature extraction of the input image is performed via the Convolution, RELU and pooling layers, before classification by the fully connected layer.

RECTIFIED LINEAR UNIT (RELU) LAYER

The RELU layer is an activation function that sets negative input values to zero. This simplifies and accelerates calculations and training, and helps to avoid the vanishing gradient problem. Mathematically it is defined as: $f(x)=\max(0,x)$. (6) where x is the input to the neuron. Other activation functions include the sigmoid, tanh, leaky RELUs, Randomized RELUs and parametric RELUs.

POOLING LAYER

The Pooling layer is inserted between the Convolution and RELU layers to reduce the number of parameters to be calculated, as well as the size of the image (width and height, but not depth). Max-pooling is most commonly used; other poolinglayersincludeAveragepoolingandL2-normalization pooling. Max-pooling simply takes the largest input value within a filter and discards the other values; effectively it summarizes the strongest activations over a neighborhood. The rationale is that the relative location of a strongly activated feature to another is more important than its exact location.

FULLY CONNECTED LAYER

The final layer in a CNN is the Fully Connected Layer, meaning that every neuron in the preceding layer is connected to every neuron in the Fully Connected Layer. Like the convolution, RELU and pooling layers, there can be 1 or more fully connected layers depending on the level of feature abstraction desired. This layer takes the output from the preceding layer (Convolutional, RELU or Pooling) as its input, and computes a probability score for classification into the different available classes. In essence, this layer looks at the combination of the most strongly activated features that would indicate the image belongs to a particular class. For example, on histology glass slides, cancer cells have a high DNA to cytoplasm ratio compared to normal cells. If features of DNA were strongly detected from the preceding layer, the CNN would be more likely to predict the presence of cancer cells. Standard neural network training methods with backpropagation [10] and stochastic gradient descent help the CNN learn important associations from training images.

TRANSFER LEARNING WITH CNNs

Unlike general natural image recognition tasks, medical image analysis lacks large labelled training datasets. As a comparison, the Kaggle 2017 Data Science Bowl to detect tumors in CT lung scans had a dataset of approximately 2000 patient scans, while ILSVRC 2017 had over 1 million images across 1000 object classes [23]. Transfer learning involves training a machine learning algorithm on a partially related or un-related dataset, as well as a labelled training dataset, to circumvent the obstacle of insufficient training data. Essentially the weights learned or pre-trained during the training of a CNN on one (partially related or un-related) dataset are transferred to a second CNN, which is then trained on labelled medical data using these weights. The weights can be applied to some or all layers of the CNN, except the last fully connected layer. Although transfer learning techniques are commonly used in medical image analysis in conjunctions with CNNs, it is worth noting that they can be applied to other general machine learning algorithms as well.

4. RESULTS AND DISCUSSION

```
Model: "sequential_1"
_____
Layer (type)                 Output Shape              Param #
=================================================================
conv2d_1 (Conv2D)            (None, 62, 62, 32)        896

max_pooling2d_1 (MaxPooling2 (None, 31, 31, 32)        0

conv2d_2 (Conv2D)            (None, 29, 29, 32)        9248

max_pooling2d_2 (MaxPooling2 (None, 14, 14, 32)        0

flatten_1 (Flatten)          (None, 6272)              0

dense_1 (Dense)              (None, 128)               802944

dense_2 (Dense)              (None, 1)                 129
=================================================================
Total params: 813,217
Trainable params: 813,217
Non-trainable params: 0
_____
```
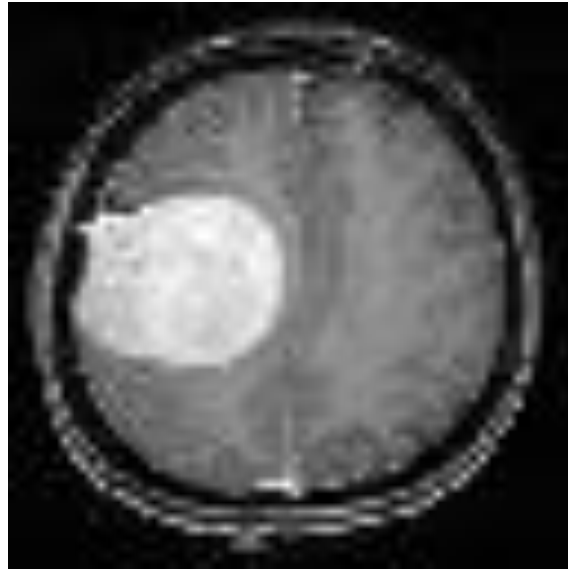
```
In [13]: if result[0][0] == 0:
             prediction = 'Benign'
         else:
             prediction = 'Malignent'
         print("Detected tumor type is %s"%prediction)

         Detected tumor type is Benign
```

5. CONCLUSION AND FUTURE SCOPE

The application of Convolutional Neural Networks (CNNs) in the treatment of brain tumors through Magnetic Resonance Imaging (MRI) has shown promising results. CNNs have proven to be effective in accurately detecting and segmenting brain tumors from MRI scans. This technology has the potential to revolutionize the diagnosis and treatment of brain tumors by providing faster and more accurate results compared to traditional methods. The use of CNNs in MR brain tumor treatment offers several advantages. Firstly, CNNs can analyze large amounts of MRI data quickly, allowing for faster diagnosis and treatment planning. Additionally, CNNs can automatically extract meaningful features from MRI scans, reducing the reliance on manual interpretation by radiologists and minimizing human error. The high accuracy and reliability of CNN-based tumor detection and segmentation also contribute to improved treatment outcomes.

Future Scope

The future of MR brain tumor treatment using CNN holds several exciting possibilities. Here are a few potential areas of future research and development:

— Improved segmentation techniques: Although CNNs have achieved impressive results in tumor segmentation, further advancements can be made to enhance the accuracy and precision. Research can focus on developing more sophisticated CNN architectures or incorporating other deep learning techniques to improve segmentation performance.

— Multi-modal fusion: Currently, CNNs primarily rely on single-modal MRI data for tumor detection. Future research can explore the fusion of multiple MRI modalities, such as T1-

weighted, T2-weighted, and diffusion-weighted images, to provide a more comprehensive and detailed analysis of brain tumors.

— Real-time tumor monitoring: CNNs can potentially be integrated into real-time MRI systems to monitor tumor growth and response to treatment over time. This would enable clinicians to make informed decisions regarding treatment adjustments based on up-to-date information.

— Integration with treatment planning systems: CNN-based tumor detection and segmentation can be integrated with treatment planning systems to assist in radiation therapy or surgical interventions. This integration could improve precision and help optimize treatment strategies for individual patients.

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