



SEGMENTATION OF MULTI-MODAL BRAIN TUMOUR USING DEEP LEARNING ALGORITHM

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Abstract

A proper diagnosis and effective treatment of a brain tumour require trustworthy segmentation. Automated solutions for brain tumour segmentation are often welcomed due to the high cost, long duration, and inherent subjectivity of the traditional process. However, developing automatic segmentation algorithms for these tumours has been a difficult task for the past few decades due to the location-, shape-, and size-specific heterogeneity of brain tumors. In this paper, we develop a multi-model deep learning segmentation of brain tumor images. The model is developed in such a way that it segments well the regions of tumour regions. The simulation is conducted to find the model efficacy. The results of simulation shows that the proposed method achieves higher grade of segmentation accuracy than the other existing methods.

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Keywords: brain tumour, segmentation, multi-model segmentation, deep learning

DOI Number:10.14704/nq.2022.20.8.NQ44534

NeuroQuantology 2022; 20(8): 5073-5083

1. Introduction

A brain tumour develops when brain cells multiply uncontrollably [1,2]. Malignant and benign tumours of the brain are the two categories that can be found. Dangerous brain tumours can grow more quickly due to the influence of gravity within the skull. Brain injury is a life-threatening emergency that can occur at any time. Twenty-one thousand eight hundred and twenty adults will lose their lives to primary CNS malignancies in 2020 [3].

Depending on the kind and stage of the disease, MRIs of the brain might show quite different characteristics [4,5]. Therefore, MRI examinations have replaced all previous methods of diagnosing and categorising brain tumors. The MRI aids the medical team in evaluating tumours for the purpose of treatment planning. The specifics of the patient cancer will be taken into account while designing a treatment plan, including the cancer size, type, and grade, as well as its



exact location. A wide range of variation is possible for these parameters, depending on the specifics of the patient situation. Therefore, proper diagnosis and categorization of brain tumours are prerequisites for effective therapy [6].

Existing manual procedures for identifying brain tumours and tracking their progression over time [7] need to be replaced with automated solutions because to their high cost in terms of time and error. In the past ten years, deep neural networks (DNNs) have proven to be highly effective, as evidenced by their success in recent multimodal BraTS tasks [8]. Convolutional neural networks are another widely used deep learning method. These networks perform exceptionally well with both two- and three-dimensional medical images [9,10].

Similar to this, transfer learning is used when there is not enough data or processing power to train a model from scratch [11]. Applying what is learned in one endeavour to another is what this strategy is all about [12]. Feature fusion is used to boost detection precision by identifying and merging a set of critical features that are highly intertwined with one another. In addition, smart feature selection is often crucial for reducing the time and space complexity [13,14].

Automated systems confront a variety of difficulties that degrade their performance while attempting to classify multimodal data relating to brain tumors. Feature extraction and classifier-based classification are the two most common approaches taken during the classification process. Extraction of features is crucial to pattern recognition as it allows for the drawing of conclusions about an item based on its most salient qualities.

The efficiency of the classifier, however, focuses on the accuracy of the features used to make the classification. Scientists studying computer vision have taken note of deep learning recent achievements in the medical field. However, not all deep learning features aid in precise categorization, and some of them may greatly slow down the execution process. Moreover, the precision of the classification may be impacted by some of these characteristics. It because certain

tumours share DNA. Accurate feature extraction is difficult with the poor contrast nature existing between T1 tumours and T1 tumours with contrast enhancement.

In this research paper, we develop a deep learning segmentation model to find the imaging modalities. In order to reduce the problem of low contrast nature, the study creates a technique based on linear contrast enhancement and optimised it using histogram equalization. The goal of sparse Convolutional Neural Network (CNN) models was to provide a more informative feature vector.

2. Related works

The identification of changed features within the MRI imaging, such as shape and texture, was essential for classifying multimodal brain tumours. The adoption of a CAD system by computer vision specialists as a means of detecting these cancers is on the rise. The first step in a CAD system is to locate and organise relevant data for tumour classification, while the second is to actually detect and label tumors. This study aimed to isolate the difficulty of diagnosing multimodal brain tumours as a distinct research topic. Because of the small number of truly remarkable researches, we settled on the BRATS series as our primary classification system.

In [15], the authors reported a convolutional neural network-based technique for classifying brain tumors. To develop a solution, they thought about the tumor structural heterogeneity in relation to the surrounding areas. They were successful in doing so by manually building a small number of kernels, which allowed the neural structures to keep their relatively light weights. Using these weights, they were able to improve accuracy to 97.5%.

The deep learning system built by Sharif et al. [16] actively detects and classifies brain tumours for the purposes of diagnosis and treatment. After the image had been contrast-enhanced, it was sent to the deep learning model named Saliency-based Deep Learning method so that a saliency map could be built. This helped them focus on the most important parts of the image. We next applied thresholding to the resulting images and used



those to fine-tune the Inception V3 CNN model that we had previously trained. They also combined information from a convolutional neural network with that from a dominating rotating local binary pattern to produce an improved classification method. The best vector was then identified using the PSO algorithm, and a choice was made using the Softmax classifier. After applying their method to the BRATS datasets from 2015, 2017, and 2018, they found that it enhanced classification accuracy.

A new CNN-based technique for classifying multimodal tumours was presented by Sajjad et al. [17]. At first, they used convolutional neural networks to identify and isolate tumour regions in the MRI data. After gathering their initial data, the team supplemented it with extra information in order to properly train a CNN model. The augmented brain data was then used to fine-tune the CNN. Using enriched data yielded superior results when applied to the selected datasets, hence that layer was incorporated into the recommended approach for cancer classification. The development in the network [22][23] and computation[25] offers lot of improvements in this field.

Amin et al. [18] developed a CNN to distinguish between various cancers of the brain. The proposed method begins with the DWT fusion operation, which enhances the quality of the original MRI scan, and continues with the application of a partial diffusion filter, which eliminates noise. The cancers were first isolated using a global thresholding

technique, and then the researchers classified them using a convolutional neural network (CNN) model.

Toacar et al. [19] successfully classified brain tumours utilising a CNN and feature selection hybrid approach. The improvement in precision was over 90%. The amount of computer time required to complete the aforementioned steps was not provided. In today world, however, the most crucial aspect of any automated systems is the availability of computational time.

Vijh et al. [20] created a particle swarm optimization (PSO) algorithm that uses Otsu approach to classify the images. After they used anisotropic diffusion (AD) filtering to eliminate noise from brain MRI scans. Features extracted from the images are utilised to train a CNN to improve the process of classification.

A detailed examination of the multi-grade brain tumour classification system was published by Muhammad et al. [21]. They detailed the various steps required for brain tumour classification (BTC), including tumour preprocessing, feature extraction, and the classification step itself. They talked at length on the potential of current deep learning algorithms for Bitcoin and the limitations of those techniques.

3. Proposed Method

In this section, we develop a model for segmentation using sparse CNN model that aims at proper segmentation of tumour regions in the brain. The illustration of which are given in Figure 1.

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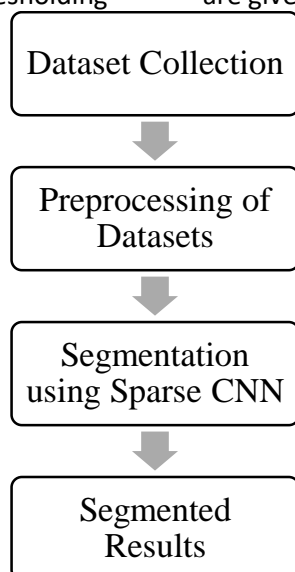


Figure 1: Proposed Model

3.1. Pre-processing

While the vast majority of brain tumour segmentation have focused on segmentation process alone, however the pre- and/or post-processing are not much focussed to improve performance. Each image in the BraTS dataset has a isotropic resolution on a skull-stripped one, which is a MRI imaging and this is preprocessing extensively to obtain good sample set.

The preprocessing allowed for this to happen. Segmentation outcomes may be influenced by the presence of intensity non-uniformities in MR data. It possible that slight patient movement or inhomogeneity in the magnetic field are to blame for these discrepancies. To get rid of these artefacts, several of the models entered into the BraTS contests used bias correction. A vast majority of individuals use the N4 bias field correction algorithm found within the N4ITK instrument.

All of the magnetic resonance images in the BraTS dataset have irregular intensity distributions due to the vast variety of scanners and clinical procedures that were used to capture them. For this reason, the normalisation preprocessing step is crucial to the automatic brain tumour segmentation task on the BraTS dataset.

The employment of histogram matching techniques is one such method of non-parametric normalisation. Data augmentation is an important part of the preprocessing procedure that should not be missed when working with a small dataset. Taking this extra measure can assist broaden the applicability of the findings. The obtained data set is modified in such a way that it is inverted,

mirrored, and rotated to gain more observations. There was a decrease in the number of erroneous positive predictions after some people reduced the size of their brains by eliminating the irrelevant background voxels.

3.2. Post-Processing

Using a simple post-processing technique, the precision of the segmentation can be improved. The idea behind this method is to get rid of the potentially deceptive clusters of tiny tumours that emerged throughout the prediction process. In most cases, the overall size of the clusters that are to be removed is compared to a predetermined threshold value to determine which ones can be safely removed.

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3.2.1. Deep Learning Segmentation

Assuming that data samples $x = \{x_1, x_2, x_3, x_4, x_5\}$, the study uses CNN auto-encoders to learn the x feature subset. The study refers to Input Layer (Layer 1), Hidden Layer (Layer 2), and Output Layer (Layer 3). The training aims to reduce the gap between the input and output layers by fine-tuning the reconstruction layer. Considering that the hidden layer can be mined for the data main features, it feasible that this distinct data representation should be considered a separate data representation.

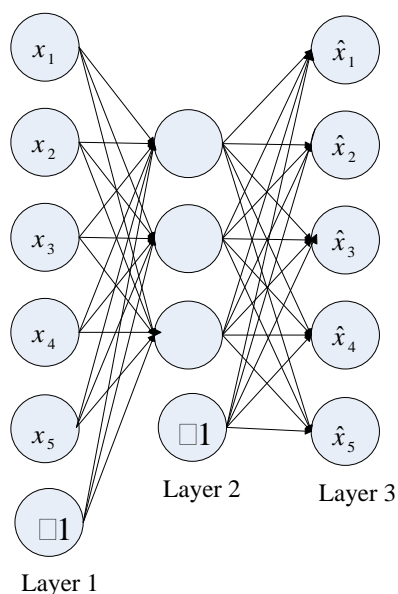


Figure 2: Sparse CNN

The auto-encoder network, in fact, was designed to perform very well in a certain task $h_{w,b}(x) \gg x$. Since this architecture limits the number of neurons in the hidden layer, it may be able to extract the latent properties of the data. In order to process a 32×32 pixel image, a network of 1024 neurons is required. A small, dense representation of the image can be trained using an auto-encoding with a 50 hidden neurons. The goal of analyses like principal component analysis, linear least

squares, and similar techniques is the same. As opposed to the exposed layer, the buried layer has few connections between neurons. In fact, we may also discover the underlying features of the data by applying the sparse limitations when the hidden neurons is significant. This holds true regardless of how many neurons are present in the epidermal layer. Since the activation of j^{th} hidden neuron is assumed to be a_j the network may be made sparse in this way. Because of this, we can now create a sparse network.

$$r_j = \frac{1}{m} \mathring{\mathbf{a}} \begin{matrix} m \\ i=1 \end{matrix} a_j x_i \quad (1)$$

m - neurons in input layer.

r_j - sparse parameter.

The study can rule out the possibility of a significant variation in this constant

parameter by noting that it is expected to be very near to the sparse constant ($r_j \approx 0.05$). Using the KL distance function guarantees optimal r_j outcomes when solving the hidden layer.



$$KL(r||r_j)=r \log \frac{r}{r_j} + (1- r) \log \frac{1- r}{1- r_j} \quad (2)$$

For an STCNN convolution layer to do its job, all that required is for the spatio-temporal convolution kernel to accurately describe the input of each feature map. Unfortunately, the method reliance on a human-controlled context limits the network capacity for autonomous learning and, hence, its ability to gain insight into the world. Because of this, the network ability to understand the world is hindered.

The feature maps of the output layer of l^{th} sampling layer can be computed with just the bias term b_j^ℓ and kernel W_{ij}^ℓ , if the l^{th} layer is receiving N_{in} feature maps as input. To ensure that the input feature maps X_j^ℓ are all taken into account while making the final feature map X_j^ℓ selection, we employ a constrained sparse parameter α_{ij} . The resulting formula for the j^{th} feature map X_j^ℓ can be written as follows.

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$$X_j^\ell = f \left(\sum_{i=1}^{N_{in}} \alpha_{ij} (X_i^{\ell-1} * W_{ij}^\ell) + b_j^\ell \right) \quad (3)$$

Furthermore, it must meet the requirements:

$$\sum_i \alpha_{ij} = 1, \text{ and } 0 \leq \alpha_{ij} \leq 1 \quad (4)$$

The study aims at finding the relationship between the l^{th} subsampling layer and its consecutive convolution layer that will be employed in the back-propagation approach. This underlying relationship between connections will be utilised during the process. Once that happens, the leftover residual $d^{\ell+1}$ from the subsequent layer could

be sent in the other direction. The j^{th} feature map residual δ_j^ℓ can be calculated using the gradient descent technique. Let assume the output a is a derivative $f'(z_j^\ell)$ variable of an activation function f input z_j^1 at the last layer. The following formula exemplifies the method of computation:

$$\delta_j^\ell = f'(z_j^\ell) \bullet conv2(\delta_j^{\ell+1}, rot180(W_j^{\ell+1})) \quad (5)$$

Rotating the convolution kernel is necessary for performing cross-correlation computations on the convolution function $conv2(\bullet)$.

As a result of this limitation, the sparse CNN is predicted to provide sparse output. These two forms of operation look very different from one another, but they both accomplish the same goals. The sparse auto-encoder neural network is useful for extracting coarse



features from raw data. The output layer neurons are only partially activated so as to make use of sparse constraints.

Here the study talks about how to train a network to find the simplest representation of data by restricting the inputs that can activate a output layer neuron. When training a network, it is necessary to set a maximum number of inputs per neuron. This will allow the network to derive input data features.

Each of the feature maps produced by this framework uses the feature maps produced by the layer below as inputs during the spatial-temporal convolution. This is the key contribution of this framework. However, the sparse limitations place severe limits on the number of feature maps applied to final feature map.

4. Results and Discussions

We display the recommended ELM classifier classification results using BraTS 2015, 2017, and 2018. For each dataset, we performed ten rounds of cross-validation with a 60:40 split ratio.

Also, we have included the results of three popular classifiers so that you can compare our own accuracy with that of the competition. Several examples are the CNN, AlexNet and DenseNet classifiers. Effectiveness of each classifier was measured by a variety of metrics including accuracy, precision, recall and f-measure.

Prior to any testing, the proposed technique was extensively simulated in MATLAB 2019b. The study was conducted on a machine with 16 GB of RAM on an intel i5 CPU. A considerable time efficient is realised when feature extraction and segmentation were performed using a graphics processing unit (GPU). For the purpose of the test, we also timed how long it took to do certain operations. However, the duration of each task varied greatly and was determined solely by the circumstances in which it was performed.

Results for the BraTS 2015 Dataset

The proposed segmentation was shown to be competitive with industry standards like CNN, AlexNet and DenseNets. It should be noted that separate sets of results were presented for the two experimental pipeline processes

described above. The results included the classification time in seconds in addition to the accuracy and FNR used for validation. The most significant results are highlighted here. Using the proposed method, the DenseNet classifier accuracy was increased to 98% (FNR = 1.74%).

With the proposed strategy, Softmax categorization might be accomplished in as little as a few seconds (81.02). Though it is not a quickest segmentation model (87.41 seconds), the proposed sparse CNN was nonetheless very near to Softmax and much quicker than the others.

Results for the BraTS 2017 Dataset

The results of section displays the outcomes of the classification work performed on the BraTS 2017 dataset. Results of a comparison between the recommended approach and some other classifiers, such as CNN, AlexNet and DenseNets. It should be noted that separate sets of results were presented for the two experimental pipeline processes described above. Results included not only accuracy and FNR as validation criteria, but also the amount of time in seconds needed to complete the classification.

The test findings show that the proposed selection method significantly reduces the time spent classifying test taker responses. As an indicator of the classifier improved efficacy, the proposed technique resulted in the shortest time possible for DenseNet classification (90 seconds).

Results of the BraTS 2018 Dataset

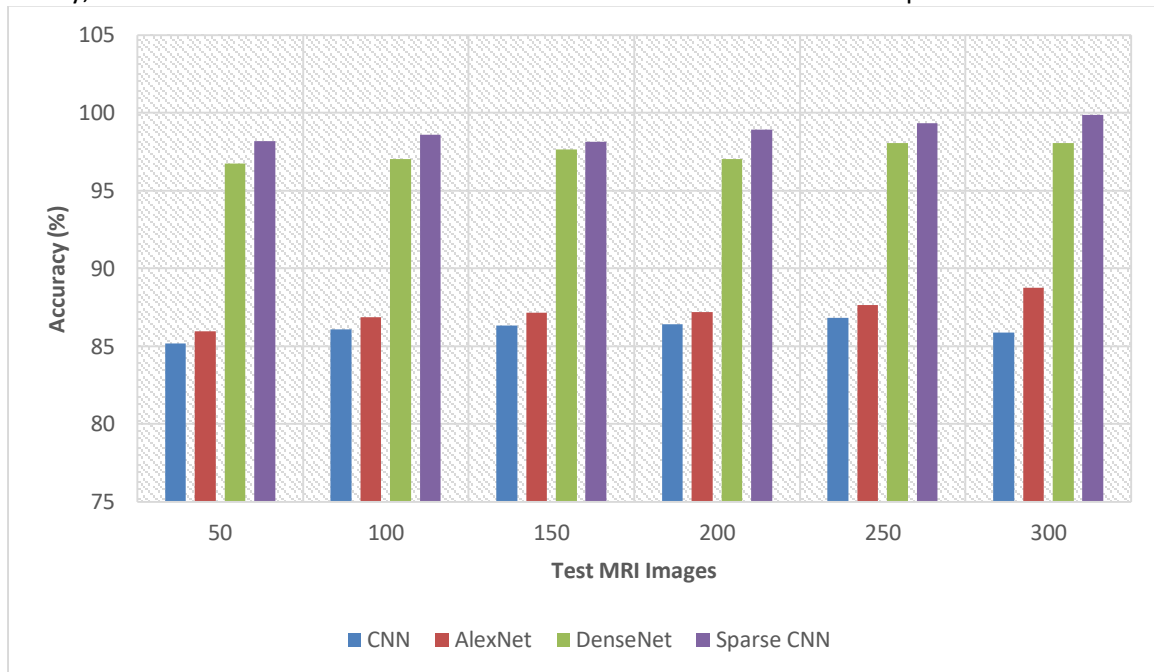
The figure displays the outcomes of classifying the data from the BraTS 2018 dataset. The proposed method outcomes were compared to those of various other common classifiers, including CNN, AlexNet and DenseNets. To show that the proposed method works, we created an ELM classifier with a maximum accuracy of 94%, as shown in the table below. The supposed FNR rate was 6.7%. By implementing the proposed method, the Naive Bayes classifier improved its accuracy to at least 89%.

To further analyse the provided data, we additionally calculated the classification accuracy for sparse CNN. An optimal 92% accuracy was reached by the classifier as in



Figure 3. It was found that the DenseNet classifier could be run most efficiently in 64 seconds using the proposed method. This time around, however, performance was tied to specifics of the hardware, such as the graphics processing unit (GPU), total system memory, and so on. The test results and

accuracy data presented show that the proposed method for segmenting brain tumours is both reliable and time-efficient. The results of Figure 4 shows that the precision of the BraTS datasets drops by almost 8% overall if the contrast enhancement is not implemented.



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Figure 3: Results of Segmentation Accuracy

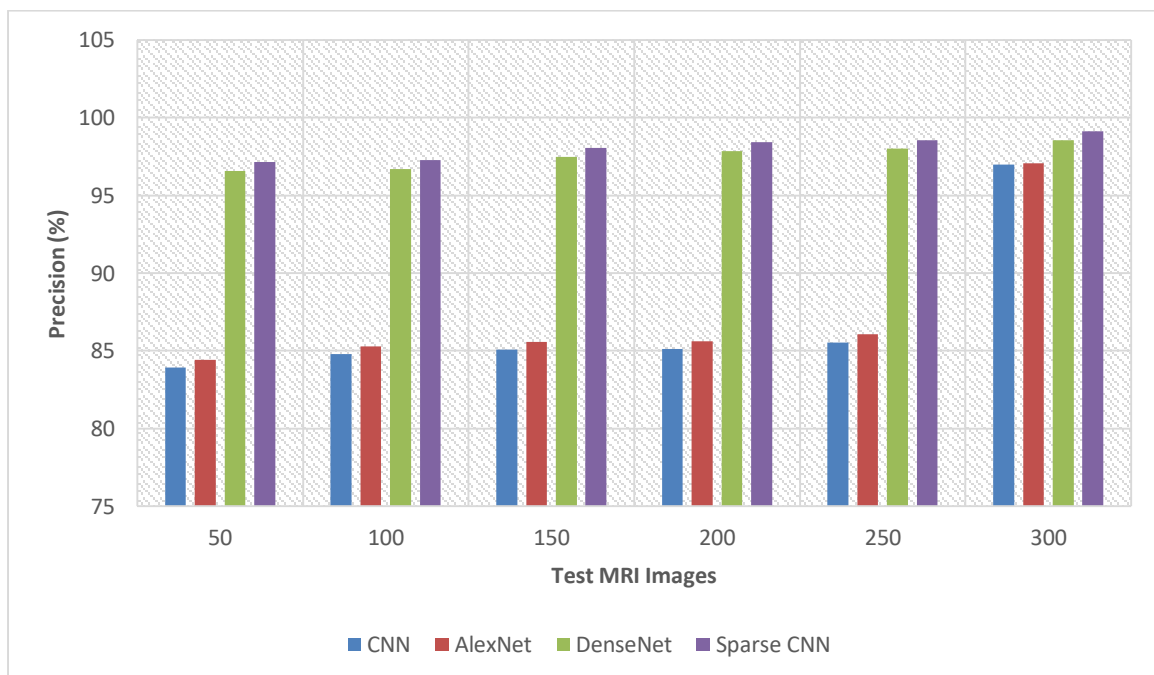


Figure 4: Results of Precision



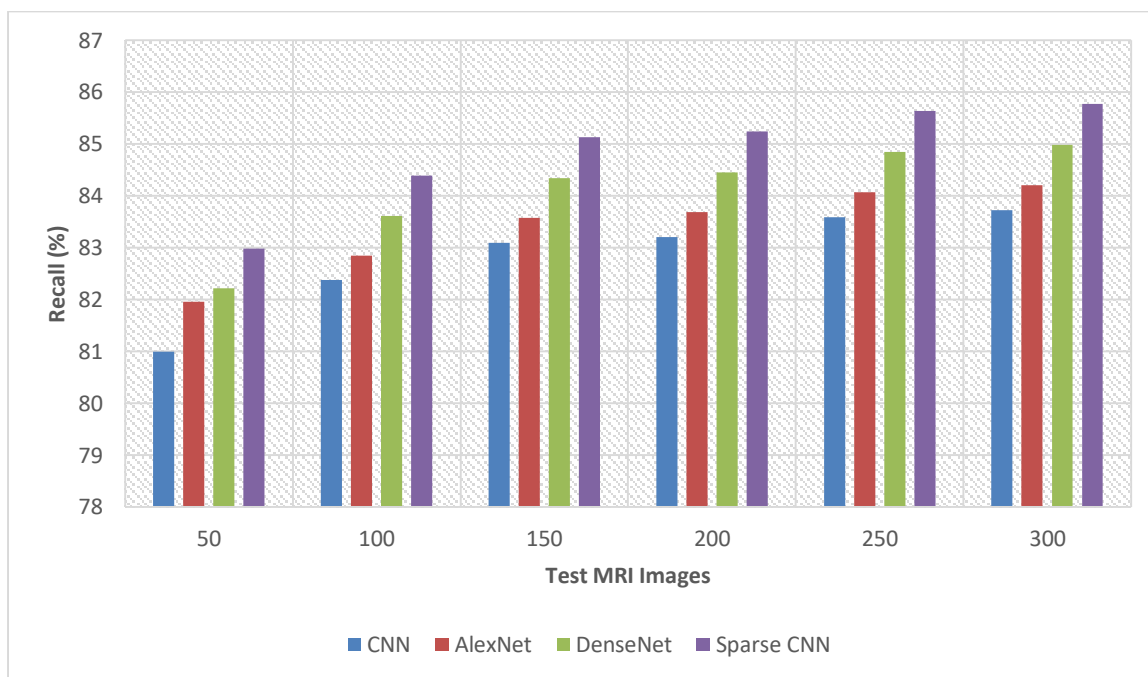


Figure 5: Results of Recall

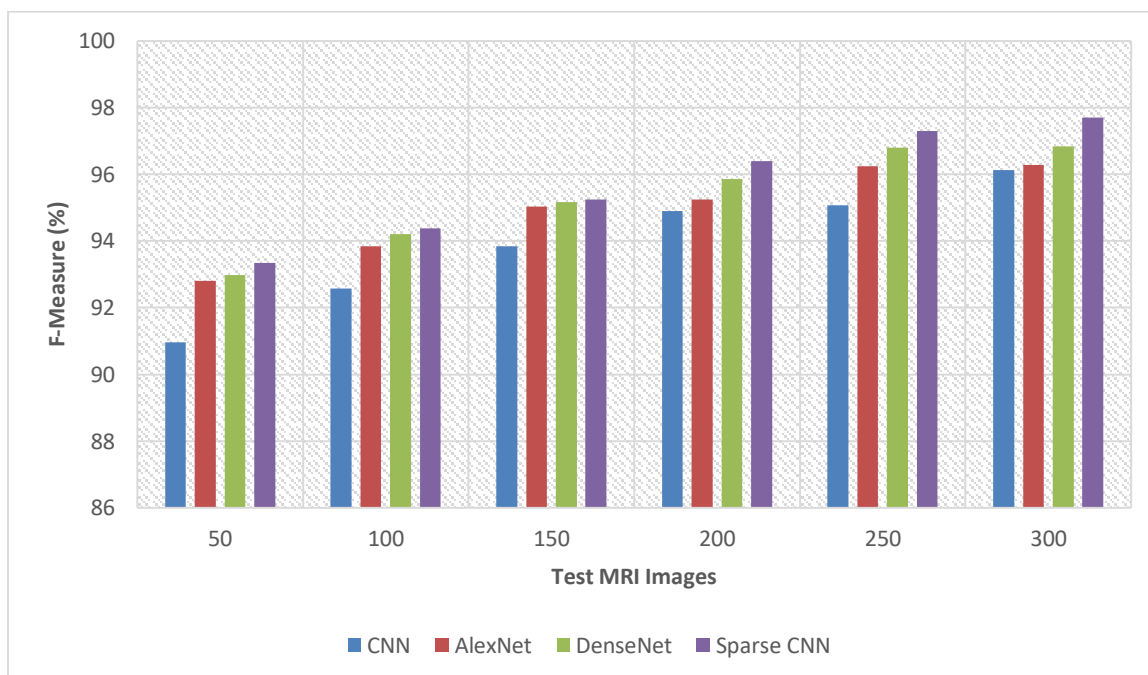


Figure 6: Results of F-Measure

Adding more attributes has the most negative impact on the categorization accuracy. Due to the fact that AlexNet architecture necessitated a feature length of 4096 on Sparse CNN but only 1000 on DenseNet, the target MSER could not be reached during the selection process as in Figure 5 and 6. In addition, Sparse CNN time was noticeably

greater than the described method because of the additional features it included.

5. Conclusions

In this paper, we develop a multi-model deep learning segmentation of brain tumor images. The model is developed in such a way that it segments well the regions of tumour regions. The simulation is conducted to find the model



efficacy. The results of simulation shows that the proposed method achieves higher grade of segmentation accuracy than the other existing methods. The results of the proposed method were statistically analysed in depth to determine how trustworthy they were. In future, the study may use deeper models on the data using measures like standard error of the mean and variance.

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