Received: 8 July 2020 | Revised: 7 March 2021 | Accepted: 24 March 2021

IET Image Processing

DOI: 10.1049/ipr2.12219

The Institution of Engineering and Technology WILEY

ORIGINAL RESEARCH PAPER

Brain tumour cell segmentation and detection using deep learning networks

Sanjeevirayar Bagyaraj[1] | **Rajendran Tamilselvi**[2] | **Parisa Beham Mohamed Gani**[2] | **Devanathan Sabarinathan**[3]

[1] Department of Biomedical Engineering, Sri Sivasubramaniya Nadar College of Engineering, Kalavakkam, Chennai, Tamil Nadu, India

[2] Department of Electronics and Communication Engineering, Sethu Institute of Technology, Kariapatti, Chennai, Tamil Nadu, India

[3] Couger Inc, Tokyo, Japan

Correspondence
S. Bagyaraj, Department of Biomedical Engineering, Sri Sivasubramaniya Nadar College of Engineering, Kalavakkam 603110, India.
Email: bagyarajs@ssn.edu.in

Abstract

Medical science is a challenging area for various problems associated with health care and there always exists scope for continuous medical research. The major challenges in medical imaging are in the region of lesion, segmentation and classification of tumours in the brain. Several technical challenge exists in the classification due to the variation in the tumour size, shape, texture information and location. There is a need for automatic identification of high-grade glioma (HGG) and lower-grade glioma (LGG). The management and grade of brain tumour depend on the depth of the tumour. Due to its irregular features, manual segmentation involves longer time and also increases the misclassification rate. Inspired by these issues, this paper introduces two automatic deep learning networks called U-Net-based deep convolution network and U-Net with dense network. The proposed method is evaluated in our own brain tumour image database consisting of 300 high-grade brain tumour cases and 200 normal cases. To improve the overall efficiency of the network, data augmentation is applied in both training and validation. The proposed U-Net-based Dense Convolutional Network (DenseNet) architecture is compared with the performance of U-Net architecture and concluded that the proposed DenseNet produces a higher dice value. The validation results have revealed that our proposed method can have better segmentation efficiency. Also, the performance of the proposed DenseNet achieved better results compared with the state-of-the-art algorithms. Validation of the test images proves that segmented output classification of tumour risk and the normal region produces a sensitivity of 88.7%, Jaccard index of 0.839, dice score value of 0.911, F1 score of 0.906 and specificity of 100% using U-Net-based DenseNet architecture.

1 | INTRODUCTION

Several types of cancer have been detected and exist in this world, including cancerous brain tumours. Brain tumours can be potentially life threatening, affecting all domains of the patient's life, making life a tragedy. Brain Tumour is identified through the pathological cells in the nucleus of the brain and an intracranial solid neoplasm. Therefore, there is a need for early detection of the brain tumour along with vigorous treatment. Malignant (hard) brain tumour turns into brain cancer [1, 2].

Tumours arising from the brain are called primary brain tumours and based on the depth of the aggressiveness tumours are normally classified from grade 1 to 4. Among the four grades, grades 1 and 2 are semi-malignant tumours that are not very vigorous. Grade 3 and 4 tumours, known as malignant tumours, are very harmful and may cause death. Magnetic resonance imaging (MRI) focuses or screens the brain glimos in an efficient way. These tumours are visible with T2-FLAIR and the advanced lesions are visible with the help of contrast-enhanced T1 scans.

Soft tissue is highly enhanced in the MRI scan which is a non-invasive technique. Also, the relevant details of the tumour are derived from MRI along with other imaging modalities such as computed tomography (CT), positron emission tomography (PET), and magnetic resonance spectroscopy (MRS). But the most effective method for tumour localisation is the

MRI method. The manual segmentation involves huge data for identification of brain tumor and also misleading in the classification results when compared with the expert opinion. If the physician's knowledge of a particular disease is not sufficient enough to take the right decision, manual segmentation may lead to misclassification. When a large amount of data is needed to be processed at the same time, it could lead to some human error. Hence, automated detection and segmentation methods are preferred for reducing human error and misclassification. As medical diagnosis becomes digitised, development of an accurate detection method is greatly expected. The proposed method yields more accurate results on segmentation. This proposed automated system can be practically used in scan centres, research centres and laboratories.

In today's improved medical industry, advancement in computer vision and image processing is a priority as it plays a major role in tumour identification and classification of tumours at a higher accuracy rate. Brain tumour diagnosis and treatment are well nurtured through a computer-aided diagnosis (CAD). The three-fold steps in the CAD system are (i) Identification of tumour region of interest (ROI) (ii) Extraction of necessary features and (ii) Classification.

The major critical issues that arise in the tumour segmentation are:

(i) Invisible or inadequate contrast enhancement of the tumour in the scanned image
(ii) Due to the large contrast agent, poor tumour segmentation
(iii) Diverse types of tumour; with different tumour subregions and spatial resolutions
(iv) A lot of artefacts present due to the coverage of larger slices in the image sequence.

Many advanced machine learning and deep learning methods are available for tumour detection and classification based on the automatic feature extraction method. Some proposed architectures in machine learning provide good performance accuracy, but automatic methods are not used in clinical analysis. This paves the way for finding a better solution to automatic methods in machine learning techniques. Artificial intelligence is predominant in machine learning research using mathematical analysis for data classification. Various techniques are used today in place of conventional methods to attain better accuracy in diagnosis. Some of the prominent approaches are: support vector machines (SVM), random forests (RF) and artificial neural networks (ANN) in machine learning [2].

The deep convolutional networks have been greatly aided by advanced computer vision. Among various deep convolutional networks, U-Net and DenseNet architecture can be used for medical applications. A type of fully convolutional network is the U-Net architecture used for better segmentation in medical imaging. U-Net has a symmetrical architecture and consists of the downsampling path and the upsampling path. A large amount of feature maps are located in the upsampling path due to their symmetrical nature. Additional feature sets are collected from each foregoing layer in DenseNet and derives their feature parameters to all consequent layers. This information is concatenated with the prior information; thus arriving at a collective knowledge from all the consequent layers. The additional number of channels defines the growth rate k. The network can be thin as the number of channels are less. Due to this structure, the computational and memory efficiency increases. Both these architectures are used for tumour segmentation and classification.

The organisation of the paper is as follows: Section 1 deals with the introduction and Section 2 deals with the related literature survey of tumour detection in the brain. Section 3 deals with U-Net architecture and DenseNet proposed for the segmentation and classification Section 4 deals with results and discussion. Section 5 concludes the proposed work.

2 | RELATED WORK

In the last few decades, various research challenges have emerged in brain tumour localisation and classification of grades. In this literature review, papers related to deep learning in brain tumour is reviewed and the major contributions are discussed.

The author in [1] describes model-based learning for multimodal MRI images for brain tumour segmentation. U-net architecture is used for feature extraction for the training phase for better segmentation. For classification, the author used extremely randomised trees to classify normal and malignant tumours. Brain Tumour Segmentation Challenge database (BRATS) 2013 is used with the results of dice metric of 0.85 for an entire tumour, 0.81 for tumour core and 0.72 for enhancing tumour core. The author in [2] proposes multi kernel-based probabilistic clustering and deep learning classifier. MRI modality is used for the clinical study. The major three-fold process is segmentation, feature extraction and classification. The median filter is used for pre-processing and better denoising performance. The classification of the normal or pathological condition is validated through a deep learning classifier. The author compares the proposed work with the Feed-Forward Back Propagation Network (FFBN). The average sensitivity, specificity and accuracy of the proposed method are 0.88, 0.80 and 0.83 with the highest values of about 1, 0.85 and 0.94. The authors in [3] propose an efficient, fully automatic brain tumour segmentation method for measuring the depth of the tumour. The U-net deep convolutional architecture is used for segmentation and the results are validated in BRATS 2015 dataset. BRATS 2015 database consists of 220 high-grade brain tumours and 54 low-grade tumour cases. The author is able to show better accuracy and high efficiency with the proposed method.

In [4], the authors present an all-embracing literature look at various deep learning techniques for MRI analysis. The various architectures, their normalisation methods, feature map details and the classification methods are explained in detail. In [5], UNet++, a dominant technique is presented for image segmentation. The necessary encoder and decoder are connected to the skip connections between the subsequent layers. The proposed pathways reduce the semantic gap between the feature maps in the preceding layers.

The UNet++ is compared with U-Net architecture. The experimental results indicate that UNet++ with deep control attain an IoU gain of 3.9 and 3.4 over U-Net.

In [6], the author discusses the risk validation in prostate cancer. Histological images are used to identify small consistent cancer portions. Due to the invariability of the image texture in histological images, the semi-supervised method is not up to the mark for this scenario. The author proposes a multi-scale U-Net model to catalogue images. The method gives better results in output Jaccard index of 65.8% across 4 classes (stroma, Gleason 3, Gleason 4 and benign glands), and 75.5% for three classes (stroma, benign glands, prostate cancer). The author in [7] makes another study to afford a wide-ranging overview of various tumours and other imaging details. The paper mainly focuses on segmentation methods, registration information and designing a model in tumour localisation and classification. The validation parameters are also analysed for conventional imaging modalities. The present scenario and the requirements for the future are all discussed as a standard for physicians in tumour assessment in the paper. In [8], the authors propose a new innovative method for tumour classification based on sparse coding and dictionary learning. The dictionary is constructed through combined topological and texture features. The experimental results reveal that the sparse coding-based classification is superior to other state-of-the-art methods.

In [9], a fully automatic method is proposed for brain tumour segmentation which involves both support vector machine and conditional random fields (CRF) using different intensity levels and textures, respectively. The proposed method is swift and depends on certain strategies. In [10], the author discusses the importance of feature extraction for tumour segmentation. The author favours the intracranial feature extraction for better accuracy. The deformation dataset is used for classification purposes. The author in [11] proposes a 3D CNN architecture for lesion segmentation using skip connections. The results are validated in BRATS 2015 and 2016 challenges. The experimental results show very good accuracy when compared with other methods. In [12], the authors directly perform the multiple clustering algorithms with the presence of incomplete kernel matrices. In [13], the authors propose a method to segment all categories of tumour. First, the brain is segmented using a new approach, robust to the presence of tumours. Tumour detection is carried out with unsymmetrical region selection and using the fuzzy method. The segmentation method is based on spatial relation which gives rise to better segmentation of the tumours. The results are validated by relating with manual segmentations. In [14], the challenge in the automatic method is viewed by the authors in a detailed way and propose an alternate method. A better solution providing good quantification of tumour and oedema volume provides better pre-planning and diagnosis. An efficient texture features extraction is involved for classification accuracy. Asymmetric texture and intensity level improve the accuracy for all tissue classes. Long-range feature selection is provided from 100 mm to a full 200 mm. The proposed method gives better accuracy and high speed. The authors in [15] propose a convolutional neural networks (CNN with small 3×3 kernels for automatic segmentation of tumours. The depth and overfitting depend on the kernel architecture. Data augmentation and normalisation are carried out for pre-processing of the images. BRATS 2013 is used for validation of the results. The dice similarity coefficient (DSC) metric is obtained as 0.78, 0.65 and 0.75 for the complete, core and enhancing regions.

In [16], the author presents a convolutional neural network for the automatic segmentation of brain tumours in MRI images based on a U-net architecture and DenseNet architecture. The results are validated on the BRATS 2018 segmentation challenge and the dice scores are 0.79, 0.90, 0.85 with 95% accuracy. In [17], a better segmentation and feature extraction is proposed using dense convolutional neural networks. The features in the spatial domain are fed into a recurrent neural network for classification. The results provide better effectiveness and efficiency. In [18], the authors propose a U-Net architecture for different medical image segmentation. Also, NAS-Unet is proposed to consist of DownSC and UpSC on a U-like backbone network. The architecture is evaluated on the various image datasets.

In [19], the author discusses convolutional neural networks (CNNs), which are used for medical image analysis over the past few years. The U-Net architecture is designed with standard convolution layers, pooling layers and upsampling layers. A novel CNN architecture, called Dense-Res-Inception Net (DRINet) is proposed for providing a solution to the challenging issue of tumour segmentation. In [20], the author's objective is to segment a three month old's paediatric brain tumour tissue MRI. The white matter and grey matter present in the brain show analogous T1 and T2 relaxation times, and exact intensity values on both T1- and T2-weighted MRI scans. The author proposes a loss function for segmentation. Fast image segmentation is proposed with a better architecture. The proposed method reduces complexity and has better accuracy. In [21], the author introduces the DenseNet which has an interconnection in the forward region connecting all the preceding layers. The feature maps are given as input to the other subsequent layers. DenseNet has less computation time to achieve high performance. From the above literature survey, it is inferred that still now, a method with comprising results is not proposed for the segmentation of tumour from the MRI scan images.

The major contributions of our work are:

1. A new dataset of 300 high-grade gliomas (HGG) and 200 normal MRI scan images are collected and a new dataset named 'SITBMRI' is created.
2. U-Net architecture and U-Net-based DenseNet architecture with auto-encoder for feature mining are proposed for brain tumour segmentation and classification process.
3. Better accuracy is achieved compared to the state-of-the-art methods.

3 | PROPOSED METHODOLOGY

The proposed methodology involves two phases as Phase I- Pre-processing and augmentation, Phase II- Segmentation and classification based on U-Net architecture and U-Net-based DenseNet architecture. The block diagram of the proposed

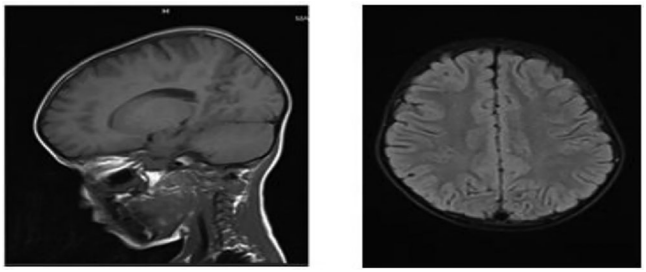

FIGURE 1 Different views of brain image

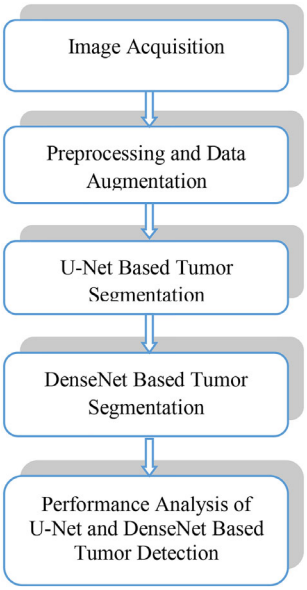

FIGURE 2 Block diagram of the proposed method

work is shown in Figure 2. In the proposed flow, first the input brain images are processed for their intensity enhancement to produce better segmentation results. It is necessary to train the architecture with huge image data to improve the accuracy of the system, thus proving the necessity of data augmentation in this work. Two different U-Net architectures are used for brain tumour segmentation and the results are experimented with and validated using our internally collected brain MRI images.

3.1 | Pre-processing and augmentation

Pre-processing is executed to enhance the contrast of the brain MRI images in all sequences. Intensity normalisation is carried out to have uniform contrast across all the images. The input images are normalised and the augmentation process is applied to create a huge dataset. As the collected annotated samples are very few, data augmentation is very essential in training the deep convolutional network. The data augmentation produces better network performance by increasing more supplementary training data from the internally collected dataset. The type of transformations applied during the augmentation process is listed in Table 1. Flipping is done in both horizontal and vertical directions of the MRI images.

TABLE 1 Data augmentation

Methods	Choice
Shear range	0.5
Horizontal flip	True
Vertical flip	True

3.2 | U-Net architecture for segmentation

A standard U-Net architecture is used for the brain tumour segmentation process. The U-Net architecture is composed of three main parts:

- The shrinking /compression path
- Bottleneck
- The elaboration/decompression path

Relevant or essential information is depicted in the decompression path and the localisation information is illustrated in the compression path. Both the appropriate and location information is combined in the U-Net to have to combine localisation and context, which is necessary to predict a high-quality segmentation map. There is no presence of dense layers, only kernel is depicted.

3.2.1 | Shrinking /compression path

The shrinking path is composed of

- 3 × 3 Convolution Layer + activation function (with batch normalisation)
- 3 × 3 Convolution Layer + activation function (with batch normalisation)
- 2 × 2 Max Pooling

The rationale behind the compression path is to identify the prospective region of the image and it is the basis for the segmentation. This information is relocated to the decompression path through skip connections. The feature maps are doubled at the pooling layer, for example, if it is 64 in the first block, it will be doubled to 128 in the next block.

3.2.2 | Bottleneck

The transitional path between the shrinking and elaboration path is the bottleneck. Two convolutional layers assemble the bottleneck.

3.2.3 | Elaboration/decompression path

The elaboration path is patterned with

- Deconvolution layer
- Concatenation with the relevant feature map from the contracting path

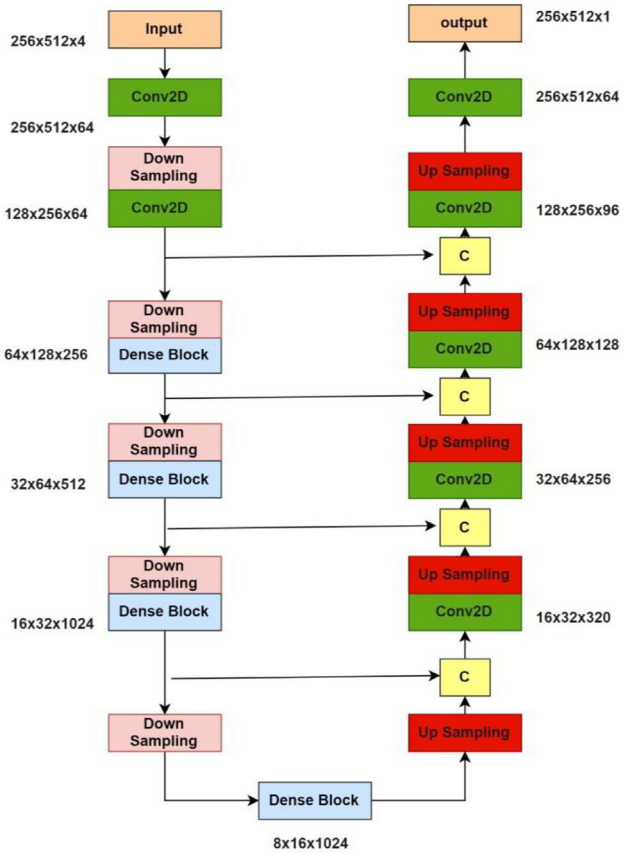

FIGURE 3 Detailed layers architecture in DenseNet

- 3 × 3 Convolution layer + activation function (with batch normalisation)
- 3 × 3 Convolution layer + activation function (with batch normalisation)

The principle behind this elaboration path is to activate specific localisation pooled with contextual information from the contracting path. To avoid overfitting, the training is carried out on augmented data, thus increasing the number of training examples. The dataset with 500 images is considered for analysis. Out of the 500 images, 400 images in the dataset are set aside for augmentation and training. Considering synchronisation, the remaining 100 images are used in validation. Loss function from the softmax layer is used to minimise the error function.

3.3 | DenseNet-based segmentation

The DenseNet architecture is shown in Figure 3. The input images are normalised and augmented as explained in section 3.1. To enhance the information flow between the layers a well-established connectivity pattern is established. The connection between the preceding layers presents better information flow.

Feature maps of the preceding layers Z_1, Z_2.....$Z_{k\text{-}1}$ representing the final layer as:

$$Z_k = H_k(Z_1, Z_2, \ldots .Z_{k-1}) \quad (1)$$

TABLE 2 Parameters used in DenseNet

Stage	Parameters	Value
Initialisation	Bias	0
ReLU	Leaky	0.1
Training	Epochs	1000
	Batch	4

where Z1, Z2 are the feature maps in the adjacent layers which are concatenated and densely connected. The model input size is 256 × 512 × 4 with lab channel and the output of the model is 256 × 512 ×1. Pre-trained DenseNet with 121 blocks in the encoder and decoder with upsampling convolutional blocks have been used. In Equation (1), a composite function H (.) is defined for mapping. In DenseNet, multiple inputs are concatenated into a single tensor. Compound, densely connected dense blocks are utilised to smoothen the process of downsampling. The transition layers between the blocks consist of a layer and a pooling layer. The transition layers used in our experiments consist of a batch normalisation layer and a 1 × 1 convolutional layer followed by a 2 × 2 average pooling layer.

3.3.1 | Activation function

The conversion of the data is executed in such a way that the output data does not change concerning the input data. The definition of Rectifier linear units (ReLU), is:

$$f(x) = \max(0, x) \quad (2)$$

This function produces better output when compared with the conventional activation function. But the injection of constant 0 spoils the flow of gradient and in turn affects the adjustment in the weight value. A variable using a leaky parameter is used called a Leaky Rectifier linear unit (LReLU).

The slope of this function introduces a small variation in the negative portion and is represented as:

$$f(x) = \max(0, x) + \alpha \min(0, x) \quad (3)$$

where α is the leakiness parameter. The parameters used for the DenseNet are tabulated in Table 2.

4 | EXPERIMENTAL RESULTS

4.1 | SITBMRI dataset creation

The proposed method involves the collection of MRI databases from the radiologists and scan centres. A new database 'SITBMRI' consists of 500 images. The images are grouped as 'normal' and 'abnormal' images based on the physician's opinion. All the image sequences consist of T1, T1c, T2 and FLAIR.

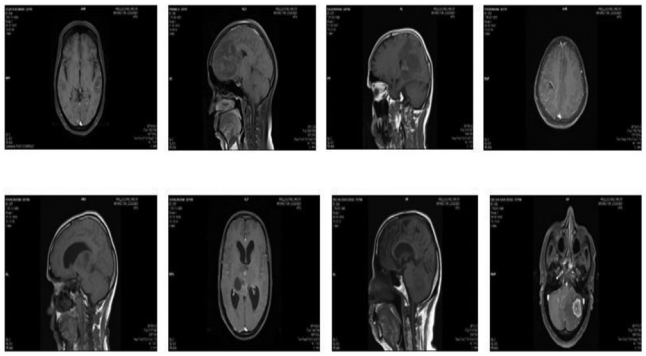

FIGURE 4 An example images from SITBMRI dataset

The volume of MRI images for the created database is 240 × 240.

All the images in the dataset are manually ground truth images are created based on the expert opinion or radiologists. An example of brain MRI images from our internally collected dataset is shown in Figure 4.

4.2 | Evaluation parameters

The evaluation of the proposed architecture is done using the standard parameters such as DSC, Jaccard Index Specificity, Sensitivity and F1 score. The DSC informs the convolved value between the manual demarcate tumour regions and the automatically segmented region. It defines the true positive, false positive and false negative measurements, respectively where TP, FP, TN and FN are the true positive, false positive, true negative and false-negative rates, respectively. The parameters are defined as:

$$\text{JaccardIndex} = \text{TP}/(\text{TP} + \text{FN} + \text{FP}) \tag{4}$$

$$\text{Specificity} = (\text{TN})/(\text{TN} + \text{FP}) \tag{5}$$

$$\text{Sensitivity} = \text{TP}/(\text{TP} + \text{FN}) \tag{6}$$

$$\text{F1score} = 2\text{TP}/(2\text{TP} + \text{FN} + \text{FP}) \tag{7}$$

4.3 | Training and optimisation

The dice coefficient is used as a metric for evaluation during the training process. For training, a stochastic gradient-based optimisation is used to inhibit the cost function. An adaptive moment estimator (Adam) is used in our net to approximately calculate the parameters. In this Adam optimiser, the updation of parameters is invariant to a rescaling of the gradient. Also, it does not require stationary objectives and naturally performs the step annealing. This Adam optimiser algorithm can be used instead of the classical stochastic gradient descent procedure to update network weights iterative based on training data. For each network weight, the learning rate is maintained and it is separately adapted as learning unfolds. It combined the advantages of the adaptive gradient algorithm (AdaGrad) and root mean square propagation (RMSProp). In general, the first and second moments of gradients are utilised to revise and adjust the exact moving average of the present gradients. The bound of our Adam optimiser chosen are learning rate = 0.0001 and a maximum number of epochs = 100. The weight function is initialised with the mean of zero, the standard deviation of 0.01 and all biases are initialised to 0. Overfitting is reduced by utilising the increased number of images using data augmentation. The number of images used for training and testing is 500. A batch size of four is used for training and a kernel size is 3 × 3.

TABLE 3 Comparison of parameter values using U-Net architecture for the proposed dataset

Dataset	Sample count	Sensitivity	Specificity
Training	400	0.778	0.895
Validation	100	0.872	0.92
	Jaccard value	**Dice value**	**F1 score**
Training	0.809	0.834	0.817
Validation	0.832	0.732	0.797

TABLE 4 Comparison of parameter values using U-Net with DenseNet architectures for the proposed dataset

Dataset	Sample count	Sensitivity	Specificity
Training	400	0.882	1.0
Validation	100	0.887	1.0
	Jaccard value	**Dice value**	**F1 score**
Training	0.823	0.879	0.887
Validation	0.839	0.911	0.906

4.4 | Discussion

Two kinds of benchmark 2D convolutional networks, U-Net and DenseNet architecture are proposed for segmentation of the tumour part in the brain images. In the experimentation, the performance of the architectures is improved by normalising the brain MRI images. Various parameters such as sensitivity, specificity, Jaccard value, dice score and F1 scores are computed and validated. Segmentation is carried out to classify normal and abnormal cancer cells. The augmentation method is applied to carry out accurate segmentation in terms of dice value. LReLU is used in the architecture for better augmentation results.

Table 3 narrates the DSC results and sensitivity values for both the architectures. From Table 3, it is observed that the U-Net architecture achieved a 0.834 DSC value. Table 4 shows the quantitative results of our proposed architecture compared to the results of U-Net. Here we tabularise the DSC and the numbers dyed the results of the best method.

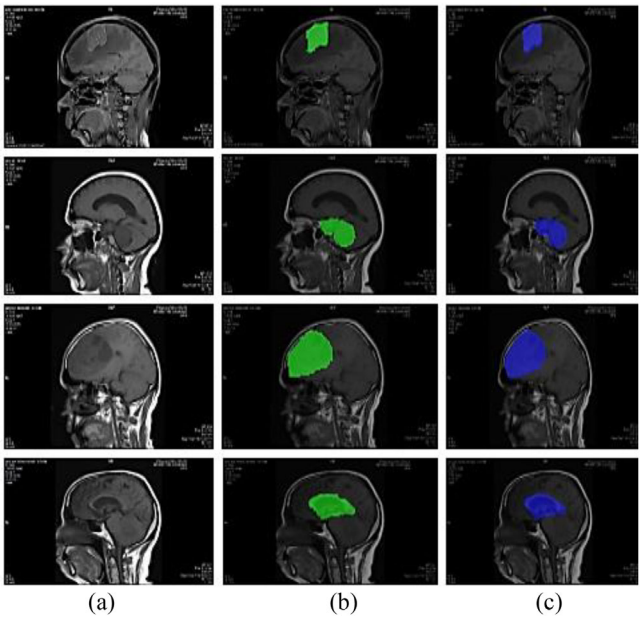

FIGURE 5 (a) Input images (sagittal, transaxial and coronal view) (b) Ground truth images (c) Segmented image

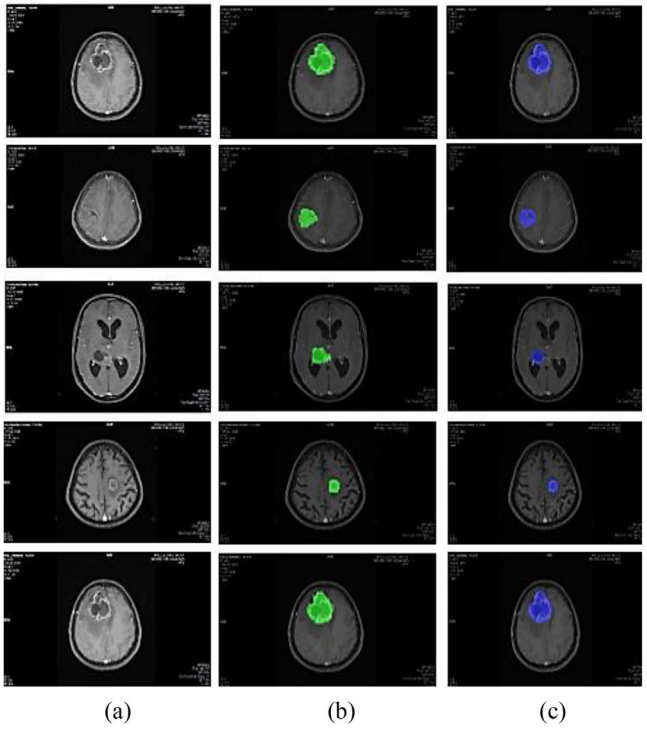

FIGURE 6 (a) Input images (transaxial, coronal and sagittal view) (b) Ground truth images (c) Segmented image

The U-Net DenseNet architecture with a batch size of four produces results of a better dice value of 0.879 and 0.911 when compared with a dice value of 0.834 and 0.732 using U-net architecture. The segmentation accuracy is improved by using various convolutional layers in U net architecture. Also, in DenseNet architecture, DenseNet is added to improve the performance of the architecture. The addition of dense blocks improved the feature map extraction and improved the segmentation accuracy. Also, the overfitting problem is avoided and improved the density population in DenseNet architecture utilising better augmentation procedure. The accuracy of the deep convolutional networks in the DenseNet depends on the surveillance from the loss function. Deep supervision is the extraordinary feature of the DenseNet. Only a single layer classifier will be noticed at the top of the network which identifies the required feature to the preceding layers through two or three transition layers. As the loss function is used throughout the structure, no complexity is noticed. The qualitative results of the tumour-detected brain images are shown in Figure 5, 6 and 7. Figure 5a shows the sagittal, transaxial and coronal view of brain images. Figure 5b, and 5c show their respective ground truth and tumour segmented images respectively.

Similarly, Figure 6a shows the transaxial, coronal and sagittal view of another sample image and its ground truth in 6b and segmented image in 6c. Similarly, Figure 7a shows the transaxial, coronal and sagittal view of a sample image and its ground truth in 7b and segmented image in 7c.

The proposed dataset using U net did not produce a better result in terms of dice value and F1 score. Our proposed DenseNet produced better segmentation and classification results as shown in Tables 3 and 4. The efficiency of our proposed net has also been compared with the

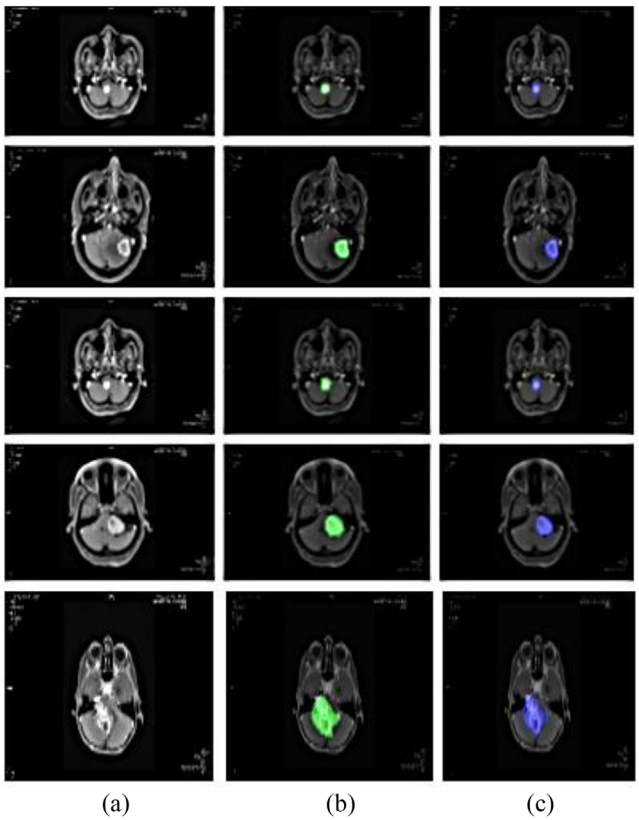

FIGURE 7 (a) Input images (transaxial, coronal and sagittal view) (b) Ground truth images (c) Segmented image

TABLE 5 Comparative result analysis with state-of-the-art algorithms

Method	Sensitivity	Specificity	Jaccard value	Dice value	F1 score
HaiThanh Le et al. [1]	0.82	–	–	0.72	–
Gladis et al. [2]	0.667	0.75	–	–	–
Hao Dong et al. [3]	–	–	–	0.81	–
Sérgio Pereira, et al. [14]	0.68	–	–	0.62	–
Sen Liang et al. [19]	43.2	80.2	–	–	
Wei Chen et al. [22]	–	–	–	0.83893	–
Tchoketch Kebir et al. [23]	0.73	0.66	–	–	–
U-Net [our dataset]	0.872	0.92	0.832	0.732	0.797
Proposed (Dense Net)	**0.887**	**1.0**	**0.839**	**0.911**	**0.906**

state-of-the-art algorithms. The comparative results analysis was listed in Table 5. From the table it is inferred that the proposed DenseNet achieved better results in terms of dice score and sensitivity when compared to the other methods in the literature.

5 | CONCLUSION

Two different architectures are used for the segmentation of tumours known as U-Net and DenseNet. The proposed architecture uses the best feature maps for segmentation. Direct connections between the layers exist in the DenseNet. Accuracy is improved with the parameters without degradation of the images. The proposed data set is compared with both the architectures. Only fewer parameters are required for the design of DenseNet and very little computation is archived to accomplish better accuracy results. The connection between the layers is very simple and includes good mappings. Using the concept of features reuse, the DenseNet model is compact and active. The processing time for testing 100 images for segmentation is about nine seconds for our proposed DenseNet architecture. In the future, sensitivity and dice score can be improved by increasing the number of training and testing images.

REFERENCES

1. Le, H.T., Pham, H.T.: Brain tumour segmentation using U-Net based fully convolutional networks and extremely randomized trees. Vietnam J. Sci. Tech. Eng. 60(3), 19–25 (2018)
2. Rathi, V.G.P., Palani, S.: Brain tumor detection and classification using deep learning classifier on MRI images. Res. J. App. Sci. Eng. Tech. 10(2), 177–187 (2015)
3. Dong, H., Yang, G., Liu, F., et al.: Automatic brain tumor detection and segmentation using U-Net based fully convolutional networks. In: Annual Conference on Medical Image Understanding and Analysis, Oxford, 15–17 July 2017
4. Bernal, J., et al.: Deep convolutional neural networks for brain image analysis on magnetic resonance imaging: A review. Artif. Intell. med. 95, 64–81 (2019)
5. Zhou, Z., et al.: UNet++: A Nested U-Net Architecture for Medical Image Segmentation. In: Stoyanov, D. et al. (Ed.) Deep Learning in Medical Image Analysis and Multimodal Learning for Clinical Decision Support, Lecture Notes in Computer Science, pp. 3–11,Springer (2018)
6. Li, J., et al.: A multi-scale u-net for semantic segmentation of histological images from radical prostatectomies. In: Proceeding AMIA Annual Symposium, American Medical Informatics Association, Apr 16 2017,
7. Bauer, S., et al.: A survey of MRI-based medical image analysis for brain tumor studies. Phys. Med. Biol. 58(13), 97–129 (2013)
8. Al-Shaikhli, S.D.S., Brain tumor classification using sparse coding and dictionary learning. In:Proceeding IEEE International Conference on Image Processing, Paris, France, 27—30 Oct (2014)
9. Bauer, S., : Fully automatic segmentation of brain tumor images using support vector machine classification in combination with hierarchical conditional random field regularization. In: Proceeding of the International Conference on Medical Image Computing and Computer-assisted Intervention, Berlin, Heidelberg: Springer, pp. 354–361 (2011)
10. Jui, S.L., et al.: Brain MRI tumor segmentation with 3D intracranial structure deformation features. IEEE Intell. Syst. 31(2), 66–76 (2015)
11. Kamnitsas, K., et al.: DeepMedic for brain tumor segmentation. In: Proc. International workshop on Brainlesion: Glioma, multiple sclerosis, stroke and traumatic brain injuries, pp. 138–149, Springer, Cham (2016)
12. Liu, X., et al.: Multiple kernel $ k $ k-means with incomplete kernels. IEEE Trans. Pattern Anal. Mach. Intell. 42(5), 1191–1204 (2019)
13. Khotanlou, H., et al.: 3D brain tumor segmentation in MRI using fuzzy classification, symmetry analysis and spatially constrained deformable models. Fuzzy Sets Syst. 160(10), 1457–1473 (2009)
14. Bianchi, A., et al.: Brain tumor segmentation with symmetric texture and symmetric intensity-based decision forests. Proc. IEEE 10th IntSymp Biomed Imaging, San Francisco, California, USA, pp. 748–751 (2013)
15. Pereira, S., et al.: Brain tumor segmentation using convolutional neural networks in MRI images. IEEE Trans. Med. Imaging 35(5), 1240–1251 (2016)
16. Stawiaski, J.: A pretrained densenet encoder for brain tumor segmentation. In: International MICCAI Brain Lesion Workshop, Cham: Springer, pp. 105–115 (2018)
17. Zhou, Y., et al.: Holistic brain tumor screening and classification based on densenet and recurrent neural network. In: International MICCAI Brain Lesion Workshop, Cham: Springer, pp. 208–217 (2018)
18. Weng, Y., et al.: NAS-Unet: Neural architecture search for medical image segmentation. IEEE Access 7, 44247–44257 (2019)
19. Chen, L., et al.: DRINet for Medical Image Segmentation. IEEE Trans. Med. Imaging 37(11), 2453–2462 (2018)
20. Liang, S., Zhang, R., Liang, D., et al.: Multimodal 3D DenseNet for IDH Genotype Prediction in Gliomas. Genes 9(8), 382 (2018)
21. Hashemi, S.R., Prabhu, S.P., Warfield, S.K., et al.: Exclusive independent probability estimation using deep 3D fully convolutional DenseNets: Application to IsoIntense infant brain MRI segmentation. In:Proc. International Conference on Medical Imaging with Deep Learning, London, 8–10 July (2019)

22. Chen, W., et al.: S3D-UNet: Separable 3D U-Net for brain tumor segmentation. Proc. International MICCAI Brain Lesion Workshop, pp. 358–368, Springer, Cham (2018)
23. Tchoketch Kebir, S., Mekaoui, S., Bouhedda, M.: A fully automatic methodology for MRI brain tumour detection and segmentation. Imaging Sci. J. 67(1), 42–62 (2019)

How to cite this article: Bagyaraj, S., et al.: Brain tumour cell segmentation and detection using deep learning networks. IET Image Process. 15, 2363–2371 (2021). https://doi.org/10.1049/ipr2.12219