

Original Article

DR-UNET: A Hybrid Model For Classification of Glioma using Transfer Learning on MR Images

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Abstract –In medical imaging, one of the tough tasks is the classification of tumors present in the human brain. The work concentrates on the detection of the exact infected location in the human brain that consists of tumor and provide suitable techniques to administer treatment for the same. To achieve this objective, although there are various deep learning techniques employed by different researchers, an attempt has been made in this work to diagnose the existence of tumors using transfer learning. The experimentation has been carried out on the standard benchmark dataset-BraTs 2018. A hybrid model has been developed in this work for classifying the tumor as benign or malignant. The hybrid model is developed using depth-wise convolutions instead of the traditional approach in combination with the residual block being introduced in the final layer into the modified U-Net model deployed using a pre-trained VGG-16 model for classification. This hybrid model was then fine-tuned by varying certain vital hyperparameters to obtain an accuracy of about 92.30%.

Keywords - Transfer Learning, Deptwise-CNN, VGG-16, Semantic Segmentation, Residual U-Net, Fine Tuning.

I. INTRODUCTION

Glioma is one of the primitive forms of tumor that occurs more commonly in the human brain. They are the resultant of gluey cells that are a part of the human nervous system. There are different types and grades of Glioma [1]. As indicated by the World Health Organization, major genetic variations have lead to the rise of using computer-aided diagnosis tools for treatment [2] of the same in humans. Biomedical Imaging provides a platform for researchers to contribute to the diagnosis of tumors in the human brain by developing various applications[3]. Tremendous work has been carried out in the classification of tumors on medical resonate images. MR Imaging is one of the most preferred techniques for the analysis of tumors as it upholds the vital characteristics of the image chosen for

Architecture for semantic segmentation. It is observed from the literature that U-Net can yield promising results in the extraction of tumors in the field of biomedical imaging[20].

experimentation. Since the most common type of tumor occurring in the human brain irrespective of the age of the person is glioma, a hybrid model has been developed in accordance with the same to classify the image sample as benign or malignant. Many transfer learning [4] approaches exist, of which the standard VGG-16 model has been chosen here for experimentation. The survey carried out previously in [5] upholds that the CNN's[6] are the best suitable deep learning architectures for image classification and other tasks. However, research, on the other hand, claims that U-net model architecture [7] is most sought for analysis of biomedical images. Thus this paper concentrates on bridging the hybrid preprocess technique developed by Dheeraj and et al. with the modified U-Net model and use the weights obtained from the pretrained VGG-16 model to rightly classify the tumor as benign or malignant. This work in comparison to the work carried out using cascading

II. RELATED WORK

In the comparative work [8] carried out, it is observed that deep learning architectures have a better persay over the machine learning architectures for classification in medical imaging since the amount of data available for experimentation is very limited. From literature, it is evident that CNN is one of the most sought architecture for the classification of images. U-Net architecture is one of the recent advancements chosen for semantic segmentation of tumors, which uses the techniques like pruning, quantization [9-12] in selecting the optimal weights against competent models from scratch for factorizing depth-wise convolution models [13-15]. In [16], traditional machine learning techniques are used for classification. However, the results from work carried out in [17] show that CNNs produce better performance considering spatial distance techniques on the pixels. In [18,19] patch-wise segmentation technique using CNN was developed, which is used in the proposed work here with the modified variant of U-Net

III. PROPOSED METHODOLOGY

As a matter of fact, it is observed from the literature that machine learning architectures suffered from the generic problem of extraction of dominant features due to the limited access to these handcrafted techniques. To overcome this



problem, deep learning techniques have emerged to add a new dimension to biomedical applications [21-23].

It is evident from the previous work that is training the network using the transfer learning approach is efficient and faster than the traditional way of training the model using random weights[24-26].

In the proposed work, the U-Net model variant with connections of 128 to 1024 up-sampling and 1024 to 128 down-sampling blocks as against the standard architecture of 64 to 1024 and 1024 to 64 sampling filter is designed. This model is then intercepted with a residual block containing a branched series of filters is developed to accept the preprocessed image obtained by applying a hybrid technique

of LDA and PCA. Then this image is subjected to training by using the standard pre-trained weights that are obtained from the VGG-16 deep learning model. In the proposed model, padding of 1*1 pixel is added with padding of 1-pixel being appended after every convolutional layer to prevent the loss of any kind of spatial characteristic of the segmented image. Finally, this VGG-16 model is subjected to fine-tuning using the block-wise batch normalization technique to perform the prediction. The residual block

The proposed architecture is as shown in fig 1

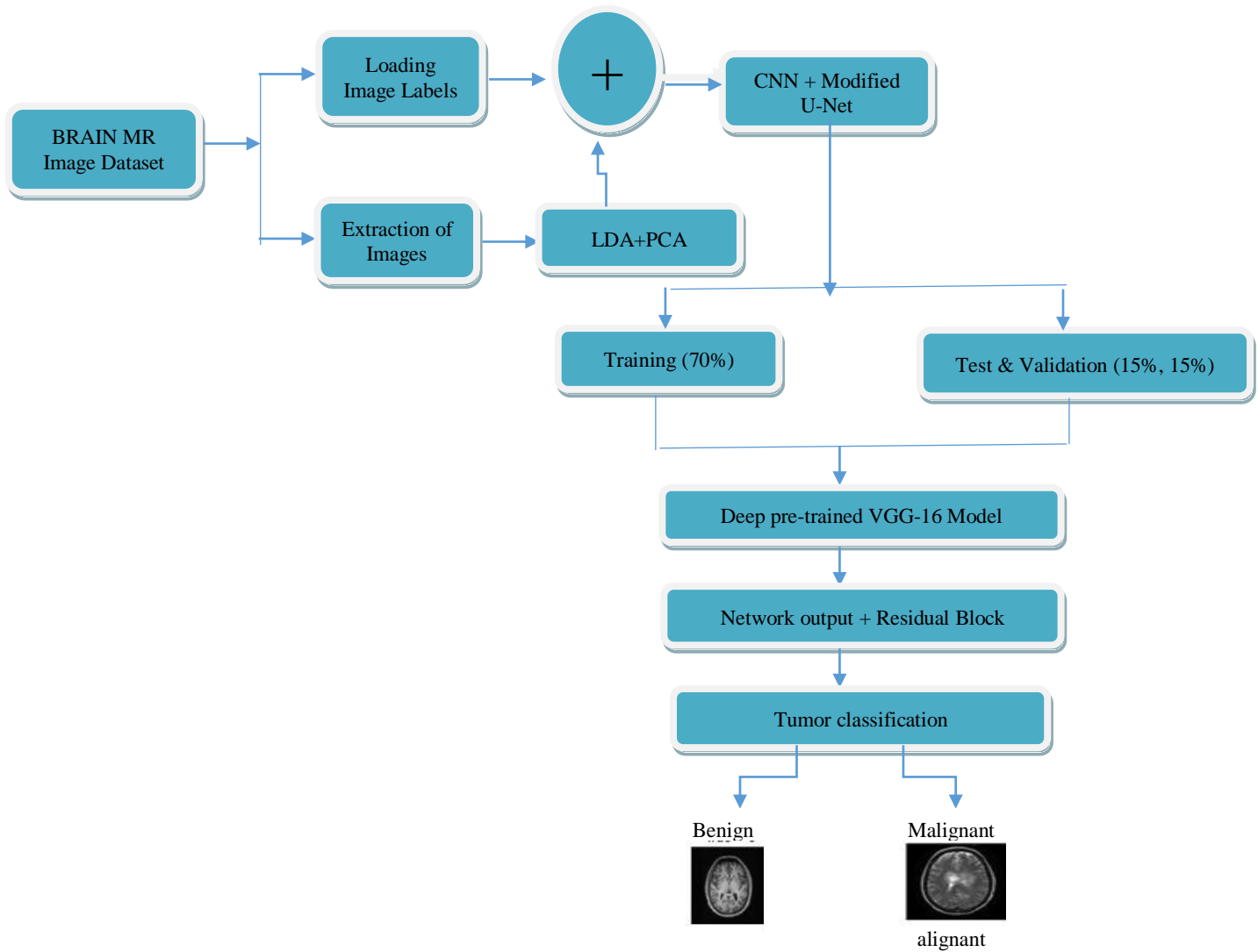


Fig 1: Proposed Architecture of DR-UNET Model

The proposed architecture interfacing the residual block with the model is as shown in fig 2.

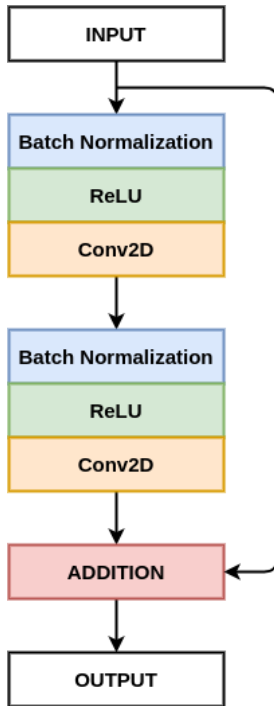


Fig 2: Residual Block Architecture

IV. RESULTS AND DISCUSSIONS

In the proposed work, an attempt has been made initially to differentiate between the normal brain and tumorous brain in the dataset chosen for experimentation. BraTs 2018 data set has been chosen for benchmarking. The pretrained VGG-16 model is used with an image dimension of 224X224, generating a feature map of (7,7,512). Further this output is flattened to reduce it to the one-hot vector of size 1,25088 features. ReLU activation function is applied to reduce the problem of vanishing gradient.

The training parameters were chosen for tuning the model-1 by varying the epochs, learning rate, and batch size are shown below:

Model 1 Parameters:

- Epochs : 25
- Learning Rate : 0.0002
- Batch Size: 4

The accuracy score obtained for the above model during the prediction is around 86.53%.

The training parameters were chosen for tuning the model-2 by varying the epochs, learning rate, and batch size are shown below:

Model 2 Parameters:

- Epochs : 50

- Learning Rate : 0.0005
- Batch Size: 8

The accuracy score obtained for the above model during the prediction is around 90.38%.

Evaluation Metrics:

From the experimentation carried out, it is very clear that the performance of model-2 is better than model-1 and hence the F-measure was obtained for model-2 to measure it.

The Accuracy score and the report of the classification are as shown below table for Model-2.

Table 1: F-1 Measure of Model-2

	Precision	Recall	F1-score	Support
Normal	0.90	0.90	0.90	21
Tumor	0.94	0.94	0.94	31
Accuracy			0.92	52
Macro Avg	0.92	0.92	0.92	52
Weighted Avg	0.92	0.92	0.92	52

The specificity and sensitivity for the model were also calculated and are as recorded in fig 4 by generating the confusion matrix.

Confusion Matrix: [[19 2] [29 2]] ----- Specificity: 0.9355 Sensitivity: 0.9048
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Fig 4: Confusion Matrix for Model-2

The graphs for training versus validation accuracy of the classifier are plotted in fig 5.

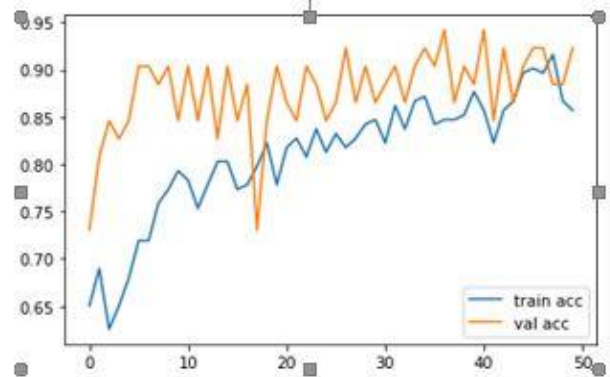


Fig 5: Plot for Training vs Validation accuracy

The graphs for training versus validation loss of the classifier is plotted in fig 6.

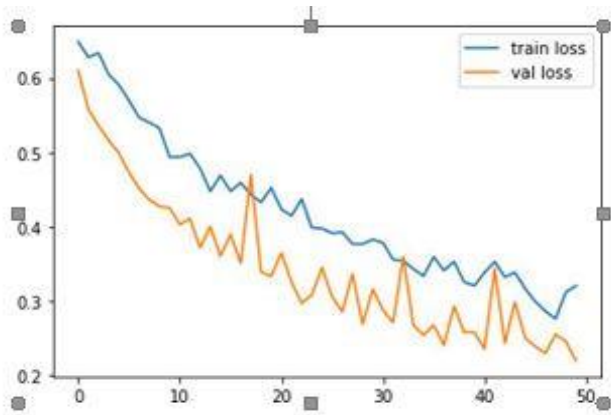


Fig 6: Plot for Training vs Validation loss

From this work it can also be claimed that the hybrid technique of LDA and PCA which is used for preprocessing along with the modified U-Net model used for segmentation and classification of tumor as cancerous or non cancerous by using the pretrained VGG-16 model has been successfully able to rightly diagonise the test image based on the ground truth data as shown in fig 7.

About 30 test samples were randomly selected for validation.

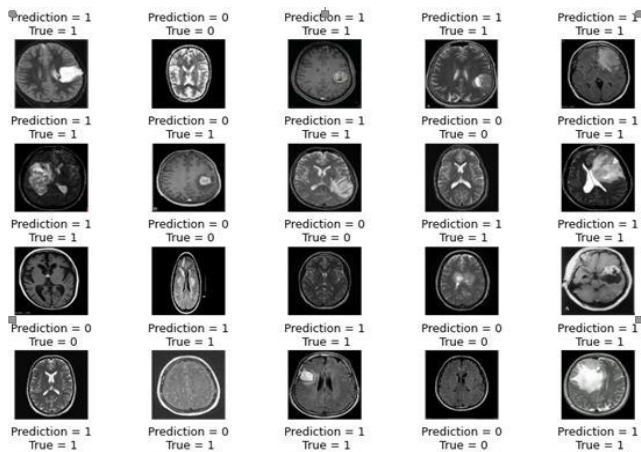


Fig 7: 30 samples for random validation test compared with their ground truth values

V. CONCLUSIONS

It can be observed from the results and graphs that the model-2 parameters can be fixed for the classification model to rightly classify the image as benign or malignant. Also, it can be observed that from the accuracy graph as shown in the fig 5 that, there is a sudden drop in the validation accuracy which has been fixed and controlled by varying over the number of epochs. Also, from the loss graph as shown in fig 6, it can be noticed that there is a sudden rise seen in the validation loss which has been controlled.

Thus the experimentation carried out on the BraTs dataset hereby signifies that this hybrid technique is found to

produce an accuracy measure of about 92.30% for the model-2 and further fine tuning leads to downfall in the performance measure. Hence the model tested here can be used for any further analysis in near future for developing applications.

REFERENCES

- [1] Weller M, Wick W, Aldape K, Brada M, Berger M, Pfister SM, Nishikawa R, Rosenthal M, Wen PY, Stupp R, Reifenberger G. Glioma. Nat Rev Dis Primers. (2015) Jul 16;1:15017. doi: 10.1038/nrdp.2015.17. PMID: 27188790.
- [2] Louis, D.N.; Holland, E.C.; Cairncross, J.G. Glioma classification: A molecular reappraisal. Am. J. Pathol. (2001), 159, 779. [CrossRef].
- [3] Louis DN, Perry A, Reifenberger G, von Deimling A, Figarella-Branger D, Cavenee WK, Ohgaki H, Wiestler OD, Kleihues P, Ellison DW. The 2016 World Health Organization Classification of Tumors of the Central Nervous System: a summary. ActaNeuropathol. 131(6) (2016) 803-20. doi: 10.1007/s00401-016-1545-1. Epub 2016 May 9. PMID: 27157931.
- [4] Valverde JM, Imani V, Abdollahzadeh A, De Feo R, Prakash M, Ciszek R, Tohka J. Transfer Learning in Magnetic Resonance Brain Imaging: A Systematic Review. Journal of Imaging. 7(4) (2021) 66. https://doi.org/10.3390/jimaging7040066.
- [5] Dheeraj D, Prasantha H S, Analysis Of Performance Of Ensemble Based Machine Learning Algorithms For Classification Of Glioma Using MR Images, Turkish Journal of Computer and Mathematics Education, 12(12) (2021) 4101-4108.
- [6] Anil Kumar B , Dr.P Rajesh Kumar, Tumor Classification using Block wise fine tuning and Transfer learning of Deep Neural Network and KNN classifier on MR Brain Images, International Journal of Emerging Trends in Engineering Research, 8(2) (2020) 574-583.
- [7] Ronneberger, O.; Fischer, P.; Brox, T. U-Net: Convolutional Networks for Biomedical Image Segmentation. Form. Asp. Compon. Softw, 9351 (2015) 234–241.
- [8] Dheeraj D., Prasantha H.S., Study of Machine Learning vs Deep Learning Algorithms for Detection of Tumor in Human Brain,International Journal of Computer Sciences and Engineering, 8(1) 57-63.
- [9] LeCun, Y.; Denker, J.S.; Solla, S.A. Optimal Brain Damage. Adv. Neural Inf. Process. Syst., 2 (1990) 598–605.
- [10] Hassibi, B.; Stork, D.G. Second Order Derivatives for Network Pruning: Optimal Brain Surgeon. Available online:https://authors.library.caltech.edu/54983/3/647-second-order-derivatives-for-networkpruning- optimal-brain-surgeon.pdf.
- [11] Alvarez, J.M.; Salzmann, M. Compression-aware Training of Deep networks 2017. Available online: http://papers.nips.cc/paper/6687-compression-aware-training-of-deep-networks
- [12] Han, S.; Mao, H.; Dally,W.J. Deep Compression: Compressing Deep Neural Networks with Pruning, Trained Quantization, and Human Coding. Available online: https://arxiv.org/abs/1510.00149
- [13] Howard, A.G.; Zhu, M.; Chen, B.; Kalenichenko, D.; Wang, W.; Weyand, T.; Andreetto, M.; Adam, H. MobileNets: E cient Convolutional Neural Networks for Mobile Vision Applications. Available online: https://arxiv.org/abs/1704.04861
- [14] Zhang, X.; Zhou, X.; Lin, M.; Sun, J. ShueNet: An Extremely Efficient Convolutional Neural Network for Mobile Devices. In Proceedings of the 2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition 2018, Salt Lake City, AL, USA, 18–22 June (2018) 6848–6856
- [15] Qin, Z.; Zhang, Z.; Chen, X.; Peng, Y. FD-MobileNet: Improved MobileNet with a Fast Downsampling Strategy. 2018. Available online: https://ieeexplore.ieee.org/abstract/document/8451355
- [16] Zhang W. et al., Deep convolutional neural networks for multi-modality isointense infant brain image segmentation, Neuroimage.
- [17] D. Nie, L. Wang, Y. Gao, and D. Sken, Fully convolutional networks for multi-modality isointense infant brain image segmentation, in Proceedings—International Symposium on Biomedical Imaging.
- [18] A. De Brébisson and G. Montana, Deep neural networks for

- anatomical brain segmentation, in IEEE Computer Society Conference on Computer Vision and Pattern Recognition Workshops.
- [19] Moeskops P., Viergever M. A., Mendrik A. M., De Vries L. S., Benders M. J. N. L., and Isgum I., Automatic Segmentation of MR Brain Images with a Convolutional Neural Network, *IEEE Trans Med. Imaging*.
- [20] Ronneberger O., Fischer P., and Brox T., U-net: Convolutional networks for biomedical image segmentation, in *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*
- [21] Deepak S, Ameer PM. Brain tumor classification using deep CNN features via transfer learning. *Comput. Biol. Med.* 2019;111:103345. doi: 10.1016/j.combiomed.2019.103345.
- [22] Ioffe, S., Szegedy, C.: Batch Normalization: Accelerating Deep Network Training by Reducing Internal Covariate Shift, arXiv:1502.03167 [cs].
- [23] He, K., Zhang, X., Ren, S., Sun, J.: Deep Residual Learning for Image Recognition, arXiv:1512.03385 [cs].
- [24] Toğaçar M, Ergen B, Cömert Z. BrainMRNet: brain tumor detection using magnetic resonance images with a novel convolutional neural network model. *Med. Hypotheses.* (2020) 134:109531. doi: 10.1016/j.mehy.2019.109531.
- [25] Sharif MI, Li JP, Khan MA, Saleem MA. Active deep neural network features selection for segmentation and recognition of brain tumors using MRI images. *Pattern Recogn. Lett.* 129 (2020) 181–189. doi: 10.1016/j.patrec.2019.11.019.
- [26] Bernal J, et al. Deep convolutional neural networks for brain image analysis on magnetic resonance imaging: a review. *Artif. Intell. Med.*, 95 (2019) 64–81. doi: 10.1016/j.artmed.2018.08.008.
- [27] Swati ZNK, et al. Brain tumor classification for MR images using transfer learning and fine-tuning. *Comput. Med. Graph.*, 75(2019) 34–46. doi: 10.1016/j.compmedimag.2019.05.001.
- [28] Talo, Muhammed, Ulas Baran Baloglu, Özal Yıldırım, and U. Rajendra Acharya. Application of deep transfer learning for automated brain abnormality classification using MR images. *Cognitive Systems Research* 54 (2019) 176-188.
- [29] Yao, W.; Zeng, Z.; Lian, C.; Tang, H. Pixel-wise regression using U-Net and its application on pansharpening. *Neurocomputing*, 312 (2018) 364–371.
- [30] Hesamian, M.H.; Jia, W.; He, X.; Kennedy, P. Deep Learning Techniques for Medical Image Segmentation: Achievements and Challenges. *J. Digit. Imaging*, 32 (2019) 582-596.
- [31] Y. Fu, T. M. Hospedales, T. Xiang, and S. Gong, Transductive multiview zero-shot learning, *IEEE Trans. Pattern Anal. Mach. Intell.*, 37(11) 2332–2345.
- [32] Ö. Çiçek, A. Abdulkadir, S. S. Lienkamp, T. Brox, and O. Ronneberger, 3D U-net: Learning dense volumetric segmentation from sparse annotation, in *Proc. MICCAI*, (2016) 424–432.
- [33] N. Tajbakhsh et al., Convolutional neural networks for medical image analysis: Full training or fine tuning? *IEEE Trans. Med. Imag.*, 35(5) (2016) 1299–1312.
- [34] Brain tumor dataset. https://figshare.com/articles/brain_tumor_dataset/1512427. Accessed 17 Feb 2020
- [35] N. Tajbakhsh et al., Convolutional neural networks for medical image analysis: Full training or fine tuning?, *IEEE Trans. Med. Imag.*, 35(5)(2016) 1299–1312.
- [36] L.-C. Chen, G. Papandreou, I. Kokkinos, K. Murphy, and A. L. Yuille, DeepLab: Semantic image segmentation with deep convolutional nets, atrous convolution, and fully connected CRFs, *IEEE Trans. Pattern Anal. Mach. Intell.*, 40(4) 834–848.