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Tumor size estimation and 3D model viewing using Deep Learning

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ABSTRACT
Cancer is the most deadly and dreaded disease ever encountered by mankind and tumor size plays a crucial role in determining the severity and treatment for the same. Therefore, it becomes imperative to estimate the dimensions of the associated tumor with paramount accu-racy and precision so as to enable radiologists and doctors, in general, to effectively pre-scribe a treatment post-diagnosis. Current estimation approaches of tumor size involve the manual click and drag measurements by radiologists which are functional but prone to a lot of manual errors and redundancies. To improve the overall accuracy and efficiency of the process, the authors propose a Deep learning solution that uses DICOM scan images to de-termine the dimensions of the tumor. Furthermore, this solution provides a 3D representation of the tumor for clear perception and comprehension and also provides treatment suggestions that aid doctors throughout the treatment. The pipeline consists of two models namely, CNN model for detection performs with an accuracy of 97.6% and a ResUNet model to segment tumor out of the brain image with accuracy of 91.54%.

KEYWORDS: DICOM, Medical Image Processing, ResNet50, ResUNet, Transfer Learning, Brain Tumor.
Citation:

INTRODUCTION
Cancer is a leading cause of death worldwide, accounting for nearly 10 million deaths in 2020. Cancer arises from the transformation of normal cells into tumour cells in a multi-stage process that generally progresses from a precancerous lesion to a malignant tumour. The cancer burden can also be reduced through early detection of cancer and appropriate treatment and care of patients who develop cancer. Many cancers have a high chance of cure if diagnosed early and treated appropriately. A correct cancer diagnosis is essential for appropriate and effective treatment because every cancer type requires a specific treatment regimen. Treatment usually includes radiotherapy, chemotherapy and/or surgery. Tumor size helps in better understanding the severity of the disease. The conventional method for finding the tumor size is by finding the dimensions of the tumor manually by the radiologists for each frame of a single scan. This method might result in erroneous estimations of tumor size. There is a risk of wrong treatment given to the patient using these conventional methods if the estimated size is incorrect. This method is also very tedious and time consuming for the radiologists to analyse the scan frame by frame to determine the dimensions. The authors have used two dataset consisting of MRI scan images of brain pertaining to over 700 test subjects in total. The first dataset is TCGA-LGG (The Cancer Genome Atlas Low Grade Glioma) which was used for training the segmentation model, and the second dataset RSNA-MICCAI (Radiological Society of North America - Medical Image Computing and Computer Assisted Intervention Society) is used for validation and testing the overall performance of the model. Using two completely different datasets enables, the model to adapt to various inputs and reduces overfitting and promotes generalisation. The authors have come up with a deep learning model pipeline where the user inputs the MRI scans for estimating the size of the tumor. The proposed solution will first check for any tumors present in the scan, which will be done by the ResNet-50 classifier model. If any tumor is detect by the classifier, the corresponding tumor is fed into the segmentation model where the model looks for pixels containing the tumor and carves it out. The authors have used RSNA-MICCAI (Radiological Society of North America - Medical Image Computing and Computer Assisted Intervention Society) for segmentation. After separating the tumor pixels from the scan, the size of the tumor is estimated using information present in the

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DICOM and pixel scaling factor. The authors also provide 3D visualization of the tumor so that the doctor and the patient can have a better understanding of the tumor in terms of size, spatial position, integrity, texture, shape etc. Using the 3D visualization it will enable an accurate craniotomy, ensure the maximum level of safety during resection, and minimize neurological deficits caused by surgery, thus, a safe surgery can be performed within the appropriate range and time. This will eventually result in a lower infection rate, rapid recovery, and a decrease in the incidence of neurological deficits in patients. All in all, this solution aims to automate the estimation process using Deep Learning models to reduce any risk of inadvertent determination of tumor size. The proposed method will be a time saver for the doctors and radiologists.

MRI SCANS

Magnetic Resonance imaging (MRI) is a medical imaging technique which has seen leaps and bounds of development over the years. It is used to create detailed intricate images slices of tissues and organs of a body which can later be used for various medical diagnosis, followed by treatment. MRI scans are used to detect brain tumor and estimate its dimensions, but they can be utilized for various other ailments such as brain injury, Stroke, dementia, infections and in general body aches. But air and hard bone do not emit MRI signal, hence these areas appear black in the scan. Blood, soft tissues, and bone marrow vary in their depth and intensity from black to white, based on the amount of fat and water content present in each tissue. Clinicians and radiologists compare the dimensions and distribution of these bright and dark areas to determine if a given tissue is healthy or deteriorating.

LITERATURE SURVEY

Zhimin Zhu et. al. [4] used FT-IR spectroscopy combined with chemometrics to predict the size of tumor size in breast cancer. Three models were evaluated based on the pathological tumor size measured after surgery and included grid search support vector machine regression (GS-SVR), back propagation neural network optimized by genetic algorithm (GA-BP-ANN), and back propagation neural network optimized by particle swarm optimization (PSO-BP-ANN).

Faleh H. Mahmood et. al. [7] used image segmentation techniques to estimate the lung tumor size in CT images. Linear filtration, background clipping, and image normalization have been adopted to perform the pre-processing operations on the CT images. The resulted segmented CT images, and then used to extract the tumor region from lung's image by introducing the seeded region growing algorithm [15,16].

Ravikumar M Sinojiya et. al. [11] used Image segmentation to detect and measure the size of tumor from MR image. An input image is converted into fixed size then pre-processed by a Gaussian low pass filter which improves the quality of an image. Then the image is segmented using the thresholding method in which by selecting the threshold value an image is segmented. Then using the region of interest the segmented image is cropped and then after measuring the size of the segmented image using pixels for the treatment planning.

Rippel, Oliver et. al. [12] have used a 3D convolutional encoder-decoder architecture based on 3D U-Net for heart and prostate segmentation tasks with good performance scores but couldn't reproduce the same results when used for other small organs such as liver, pancreas and lungs. The low scores might be due to false positives and label imbalance.

Hatamizadeh, Ali et. al. [13] proposed a modern transformer model, an AutoML model, for lesion segmentation which not only searches for the best neural architecture but also finds the best combination of hyper parameters and data augmentation strategies.The AutoML model was validated on several large-scale public lesion segmentation datasets.

Radzi SFM et. al. [14] presented a tree-based pipeline optimization tool (TPOT) as a method for determining ML models with significant performance and less complex breast cancer diagnostic pipelines.

Joanna Jaworek-Korjakowska et. al. [3] predicted the thick-ness of Melanoma, popular skin cancer type based

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on Convolu¬tional Neural Network with VGG-19 Model Transfer Learning. Benjamin Ribba et. al [6] reviewed the studies on the use of Model-Based Tumor-Size Metrics to Predict Survival. Other studies [1, 2, 5, 8, 9, 10] focussed on detecting the presence of a tumor, classifying the type of tumor, growth rate of the tumor and survival rate of the patient.

Ezhilarasi R et. al. [19] have used AlexNet model to detect and classify different types of tumors that are present in the brain MRI images. Along with AlexNet model as a base, they have also implemented Region Proposal Network (RPN) by Faster R-CNN algorithm. They have also made use of Transfer learning in their system pipeline which helped them reduce their training time and improved their accuracy in classifying the different types of brain tumors. The authors have implemented transfer learning where they have trained out model with first dataset and tested and validated the model performance using second dataset, as the authors were inspired by the drastic improvement in their metrics due to transfer learning.

Diakogiannis et. al. [20] have proposed a novel segementation model, ResUNet-a, that utilizes a UNet encoder/decoder backbone, coupled with residual connections, atrous convolutions, pyramid scene parsing pooling and multi-tasking inference. Even though their actual intended application for their proposed system is scene understanding of high resolution aerial images, its usage in medical image analysis has proven to be highly efficient with commendable performance. ResUNet-a tried to determine sequentially the boundary of the tumors present in the scan, the distance transform of the segmentation mask, the segmentation mask and a coloured reconstruction of the input with differentiation between the tumor and rest of the scan. Each step depends on the output and performance of the previous step, hence they are conditioned based on each other. Zhou, Z. et. al. [22] have used a modified UNet architecture, UNet++, which performs better on medical images than normal UNet models that perform with natural scenic im-ages. They were able to achieve this huge performance jump in segmentation of lesions in medical images through their modification in the architecture [17,18]. The modification was done to the skip connections where under normal conditions in UNet models, the feature map from encoder blocks will be directly fed into the corresponding decoder block, thus resulting in dissimilar feature set. Whereas in the modification that they introduced, UNet++ uses nested skip connections which enriches the feature map from encoder block before it is fused with the feature map of the corresponding decoder block, which reduces the dissimilarity between the two feature maps. They believe this reduction in the dissimilarity is responsible for the increase in their model's performance.

Olaf Ronneberger et.al. [23] have used Fully convoluted network model to perform segmentation. what's more interesting about their work is that they have managed to get performance and accuracy of the model at par with other highly efficient models with far less dataset. They were able to achieve this using data augmentation and a few modifications in their Fully connected Convolution network. Their modification consists of using a unsampling layer at the end of every convolution layer to transfer context information to higher resolution layers. As a result of which, the expansive path is almost symmetric to the contracting path and yields a u-shaped architecture.

Su Run et. al. [24] have aimed at overcoming the limitations of convolution kernel with a fixed receptive field and unknown prior to optimal network width in U-Net by coming up with two novel modifications to their model, MSU-Net. First modification in their model is that they have used multiple convolution sequence extract more semantic features from the images. The limitation of unknown network width is overcome by efficient coupling of convolution kernel with different receptive fields.

A. Mostayed et. al. [25] have proposed a modified architecture of UNet++ model [21, 26], context-adaptive UNet model, where it overcomes the downsides to using UNet++, namely over consumption of space and memory and the necessity to learn from a higher order of parameters. They overcame the need for more power by eliminating the concatenation operations in U-Net architecture which resulted in the reduction of the number of parameters in the network. In order to locally adapt the convolutions in the decoder layers, they have replaced the concatenations of the encoder features in the decoding layers by using them as guiding features. This modified connection helps the network to learn the object boundaries more accurately with a

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smaller number of parameters to learn. Dominik Mu'ller et. al. [27] have developed an open-source python library, MIScnn, to ease the process of creating a deep learning pipeline, especially for image segmentation and medical image analysis. The framework also provides modular utilities to preform data augmentation, data processing, validation of the model (K4 validation). they also provide high configurability and multiple open interfaces that allow full pipeline customization.

DATASET AND DATA PREPROCESSING

The proposed work utilizes two datasets from Kaggle data repository namely: TCGA-LGG (The Cancer Genome Atlas Low Grade Glioma) dataset and RSNA-MICCAI (Radiological Society of North America - Medical Image Computing and Computer Assisted Intervention Soci¬ety) Brain Tumor Radio genomic Classification. The TCGA dataset contains 2556 scan images of tumor present in the brain and 1373 scan images of brain with no tumor. The RSNA-MICCAI dataset contains over 575 subjects with each subject having MRI brain images ranging from 50 to 300 images per subject. Each subject in this dataset has 4 types of scan images that are: FLAIR (Fluid attenuated inversion recovery), T1W (T1 weighted), T2W (T2 weighted) and T1WCE (Tubercular abscess). The ratio of T1W and T2W is the measure of white matter integrity.

The authors have particularly used FLAIR as it contains scans from lateral view which gives us the whole picture of the tumor and its surroundings.

In the TCGA-LGG dataset, both the tumor, the ground truth mask image and the ground truth mask super¬imposed on the tumor image are available. It has 2556 scan images of tumor present in the brain and 1373 scan images of brain with no tumor. Even though there might seem to be a slight data imbalance, the effect of it is counteracted by sampling and data augmentation. The figure ?? clearly shows the disparity in the number of scans that contains tumor in it and those that doesn't have tumor in it. The TCGA-LGG dataset also comes with a .CSV file which acts as ground truth file containing the patient ID and other associated parameters such as RNASe-qCluster, MethylationCluster, RPPACluster, OncosignCluster, COCCluster, neoplasmhistologic grade.

A. Data PreProcessing

One of the first few hurdles authors faced during the inception of their work is the conversion of DICOM format images to a suitable format for further processing and usage as input to the models. The authors tried converting the DICOM image to bitmap array, JPEG, PNG format but all those formats resulted in loss of quality and loss of significant data.

After spending substantial amount of time in trying out all possible formats, the authors chose the TIFF (Tag Image File format) format. In TIFF format, both the image and the data information associated with the image is stored in the file. After converting the DICOM scans to TIFF format, normalization was performed to normalize the pixel array to 256 cross 256 images as every image pertaining to each subject varies across subjects and locations. After Normalizing the image, Conversion of color image from RGB format to grayscale format was performed as it reduces the computational requirement. Processing RGB format images requires way more GPU computational power and resources than processing grayscale. Along with normalisation and grayscale conversion, the authors have also tried to reduce the noise in the scans to facilitate smoother processing and to prevent code complexity. Another advantage of converting scans to grayscale is that developers have to only keep track of either 0 or 1(black and white) whereas for RGB the range goes from 0 to 255.

SYSTEM ARCHITECTURE

The proposed system consists of a Deep Learning model which detects the tumor and estimates the exact dimensions of the same. Deep learning method is used for Image segmen¬tation. This estimation is done to hundreds of frames for a single subject using which a superimpose all the layers into a single object can be performed to form a 3D model of the tumor. System architecture for the same is shown in Figure 1. The

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processed image is sent to a CNN model to detect the presence of a tumor. A Convolutional Neural Network (ConvNet/CNN) is a Deep Learning algorithm which can take in an input image, assign importance (learnable weights and biases) to various aspects/objects in the image and be able to differentiate one from the other. The pre-processing required in a ConvNet is much lower as compared to other classification algorithms. While in primitive methods filters are hand-engineered, with enough training, ConvNets could learn these filters/characteristics.

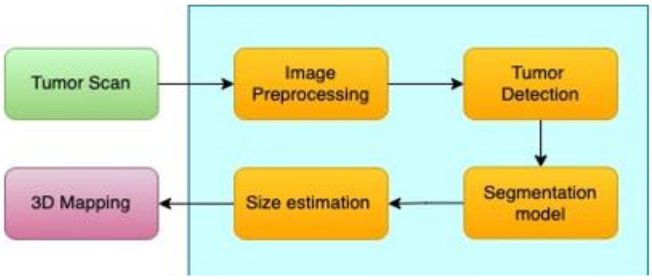

Fig. 1. System Architecture

The architecture of a ConvNet is analogous to that of the connectivity pattern of Neurons in the Human Brain and was inspired by the organization of the Visual Cortex. Individual neurons respond to stimuli only in a restricted region of the visual field known as the Receptive Field. A collection of such fields overlap to cover the entire visual area.

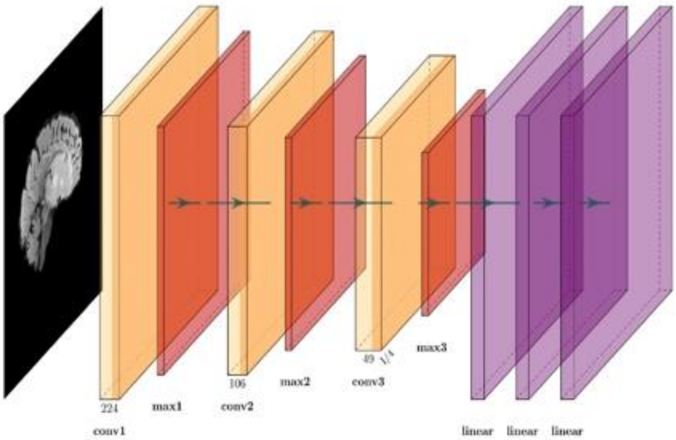

Fig. 2. CNN Architecture

Once the tumor is detected, it is fed into modified U-Net model,ResU-Net, the exact tumor found in the scan. Using this clustering data, the exact size of that tumor on that specific scan can be extracted.

U-net model has gained huge popularity in recent times when it found profound applications in medical imaging field. The model that was employed to segment the tumor is ResU-Net. It is essentially a U-Net with Encoder-Decoder backbone and Residual blocks. The model also makes use of skip connections which result in improved efficiency of the model and prevents overfitting.

Another novel point in this work is that the authors have made use of transfer Learning. Transfer learning as a new machine learning paradigm has gained increasing attention lately. In situations where the training data in a target domain are not sufficient to learn predictive models effectively, transfer learning leverages auxiliary source data from other related source domains for learning. The authors have implemented transfer learning in the sense where they have trained the segmentation model using “TCGA-LGG” dataset of TIFF format and tested the same model using “RSNA-MICCAI Brain Tumor Radiogenomic” dataset. Transfer Learning promotes modularity and generalisation where model trained through one particular type of dataset is able to perform with general datasets as well with commendable performance and accuracy.

A. Size Estimation

After tumor segmentation, the region of interest is obtained. The obtained tumor section size is estimated using the scan size proportion to the pixels in the clustered data. Estimating the exact area of that tumor and its dimension using this method is possible. The authors used Island algorithm to cluster all the non-zero values (pixel corresponds to tumor) and find the total count of the pixels which give us the pixel area. The authors then find all such scan images with tumor and sort them in the order of the area. After determining the slice width and then count the total number of such slices per tumor per subject, it will help in will determining the depth. As seen in fig 4, The authors choose the slice with the largest cross-sectional area and then extract the corresponding length and width as that particular tumor slice will give an accurate idea about the 2D dimension.

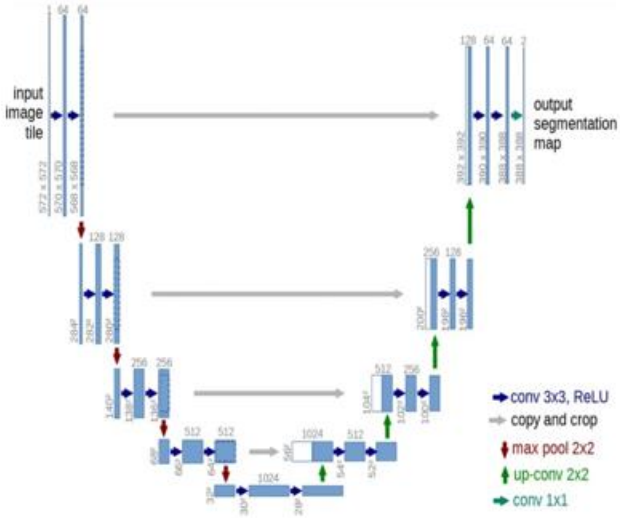

Fig. 3. U-Net Architecture

The authors have employed Island Search Algorithm to find the total number of grouped non-zero pixels and in turn adding them up gives the total pixel area of that tumor slice of that series of images. Given a Boolean 2D matrix, finding the number of islands is essentially connecting 1s that forms an island. The backbone of this algorithm is DFS search algorithm where as soon as a 1 is found in the matrix, the algorithm checks for any other 1 present in the nearest neighbours. So, using this algorithm, the number of tumors in a particular given slice of the scan can be found. As a result of this potential multiple tumors in a slice of image could also be detected.

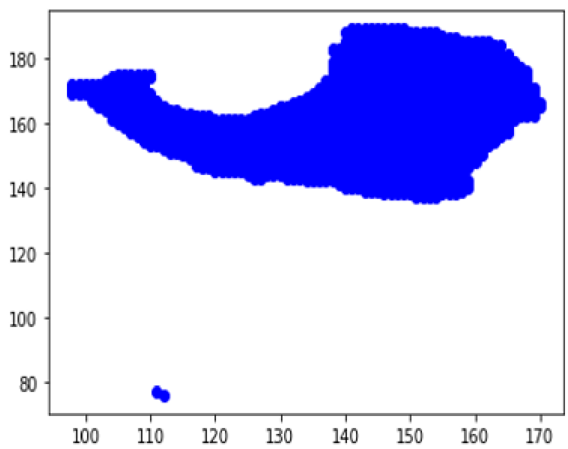

Fig. 4. 2D View of a tumor slice

B. 3D Mapping

After estimating the tumor length, width, depth, area in each individual MRI scan of the cross section of the brain, all the sections of the tumor data are superimposed to form an accurate 3D representation of the tumor.

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This 3D model provides a better visualization of the tumor. It will also provide the user with some sense of dimension, spatial arrangement, tumor's position and overall shape. This will be much more useful for doctors and patient to see the tumor in real world situation rather in a 2-Dimensional view such as X-RAY scans. Doctors can obtain insights into the stereoscopic location of the tumor, appropriate surgical corridor or approach to the tumor, effective craniotomy design, and goal of the surgery using the 3D-brain tumor model. It will enable an accurate craniotomy, ensure the maximum level of safety during resection, and minimize neurological deficits caused by surgery, thus, a safe surgery can be performed within the appropriate range and time. This will eventually result in a lower infection rate, rapid recovery, and a decrease in the incidence of neurological deficits in patients. First segregate all the scan images with tumors and their predicted masks and kept them aside for further use. Those same masks were used to predict the length, width, depth and area to plot the pixels in 3D spatial format using Plotly python package. Figure 5 shows a view perspective of the 3D mapping.

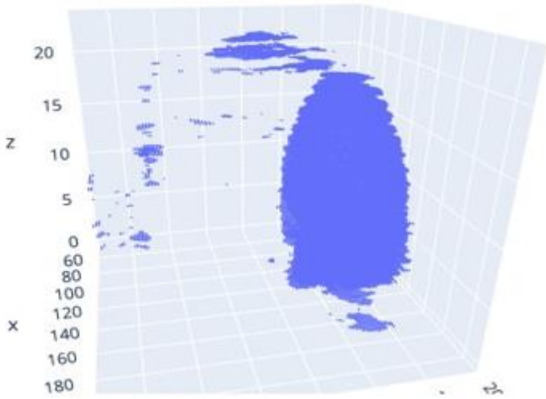

Fig. 5. 3D View of a tumor for a random subject

EXPERIMENT AND RESULTS

A. CNN MODEL SPECIFICATION

The CNN model was employed for detection of tumor in slices of MRI images has the following model specification.

The authors have used ResNet50 weights to train CNN model to perform classification whether the given scan has tumor or not. After 30 epochs, it is clearly visible in figure 6 that loss function is decreasing as the number of epochs kept increasing. It is noticed that there are a few plateau regions where the loss function stopped decreasing and it started increasing even though number of epochs increased. Such situations call for early stopping where the model has reached the saturation point.

TABLE I. CNN MODEL SPECIFICATION

Parameter	Value
Batch Size	187
Number of Sample	3929
Optimizer	Adam optimizer
Loss Function	Categorical Cross Entropy
Learning Rate	0.2
Epoch	30

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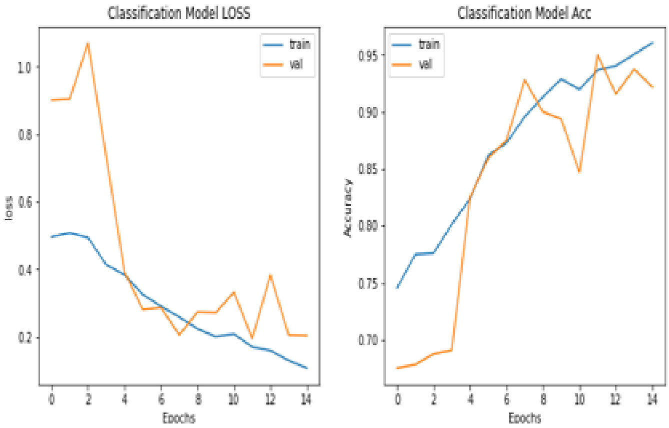

Fig. 6. Loss and Accuracy graph for Classification model

	precision	recall	f1-score	support
0	0.93	0.98	0.96	402
1	0.95	0.85	0.90	188
accuracy			0.94	590
macro avg	0.94	0.91	0.93	590
weighted avg	0.94	0.94	0.94	590

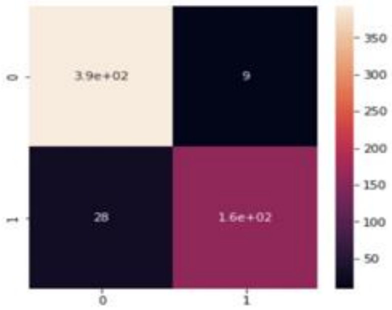

Fig. 7. Confusion matrix and Heatmap for CNN model

TABLE II UNET SPECIFICATION

Parameter	Value
Batch Size	72
Number of Sample	1373
Optimizer	Adam optimizer
Loss Function	Focal Tversky
Learning Rate	0.05
Epsilon	0.1
Epoch	20

In stark contrast to the loss function, classification model accuracy has increased as the number of epochs increased. But similar to the loss function, accuracy also experiences such deviation from the given pattern where accuracy reaches a peak value at around 10 epochs and then the accuracy starts dropping and then it stabilizes at 97.46% accuracy.

B. UNET MODEL SPECIFICATION

As similar to CNN model, in figure 8 UNetUNet model also shows a similar pattern where as the number of

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total epochs increase, the loss function also decreases steadily. But there is no significant plateau or saturation point in the case of the segmentation model. Similarly, As the total number of epochs increase, the Unet's tversky score also increases which shows that the model performs better as the number of epochs increase. It is noticed that there is a steep drastic increase in the tversky score after 3 epochs and then it gradually increases.

Fig. 8. Tversky Loss and Accuracy UNET segmentation model

Figure 9 which depicts the Receiver Operating Curve (ROC) which shows the performance of the UNet segmentation model. This plot has considered two parameter variables, they are True Positive Rate and False Positive rate.

True Positive rate means that the input brain image has tumor present in it and the predicted value also indicates the presence of a tumor. False Positive rate means that the input brain image doesn't have tumor present in it but the predicted value depicts the presence of tumor in the brain.
To validate the performance of the segmentation model, Intersection Over Union (IOU) metric was measured. An impressive benchmark score of IOU, 0.92 was achieved.

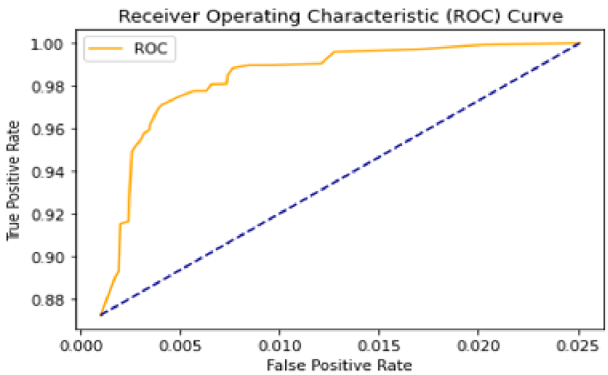

Fig. 9. ROC of the predicted and segmented tumor

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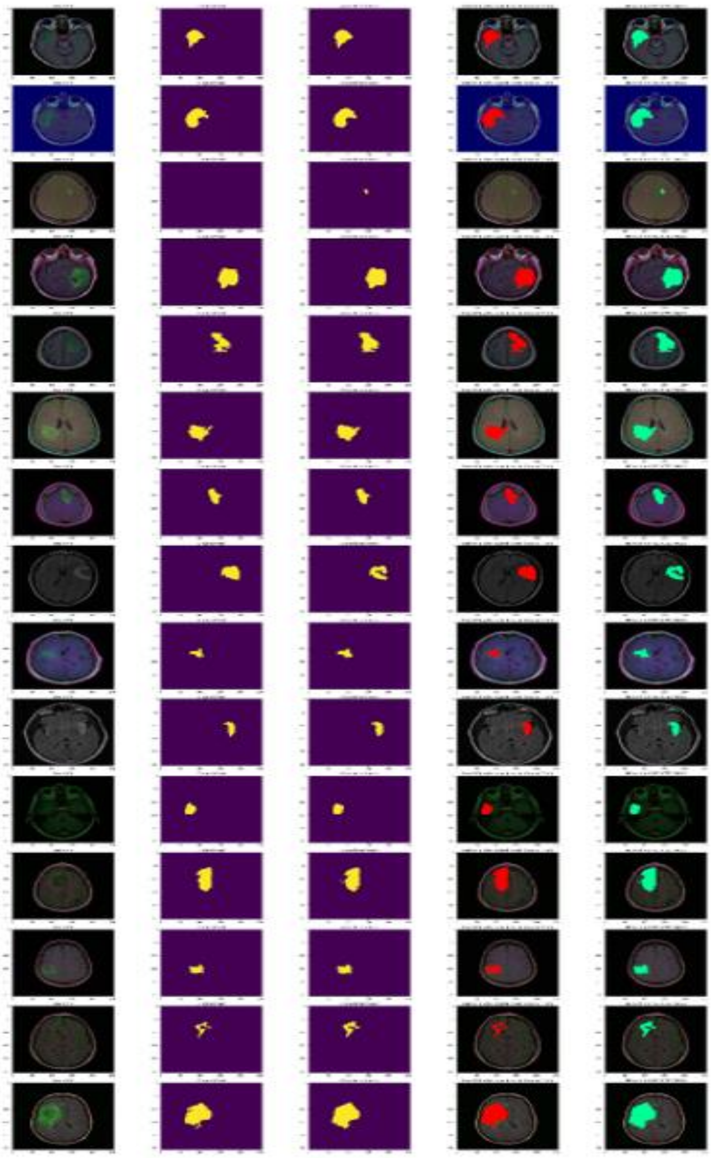

Fig. 10. Results of the Segmentation model

As shown in figure 10, the brain image with the tumor present in it in the first column, the second column comprises of the ground truth values of the segmentation mask, the third column consists of the segmenta¬tion masks predicted by ResUNet model, the fourth column consists of the ground truth values of the brain tumor scans superimposed with the ground truth masks, the last column consists of the predicted mask superimposed on the brain image with tumor present in it.

CONCLUSION

Cancer is the deadliest disease where some of the body cells grow uncontrollably and spread to various parts of the body. body. In the current work, the authors have identified the importance of determining the tumor size accurately for the treatment of the disease. Authors also understood the need of a 3D view of the tumor for the industry experts to get a better understanding of the subject under examination. To conclude, the authors have discussed, the detailed design and related algorithms for a project to determine the size of the tumor and the 3D model of the tumor.

Initially data cleansing was done which was in dicom format to tiff, the presence or absence of a tumor was predicted using ResNet architecture of Convolution neural network. This is model helped us to identify the existence of a tumor and later to segment the same from the scan image.

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Secondly the tumor area of interest is segmented using ResUNet on a different dataset where ground truth for mask of the tumor was given. Transfer learning was applied and trained the segmentation model on a different dataset and integrated the model results on a different dataset to get the required results. The segmented area is mapped to exact dimensions of the tumor. Finally, the segmented tumor from each slice of the scan is mapped to a 3D dimensional space that gives an overall tumor view to the industrial experts.

Declaration

The manuscript consists of sub sections such as Abstract, Introduction, Materials & Methods, Results, Discussion and Conclusion. The manuscript complies with the format as mentioned in the instructions to the authors. The compliance of Ethical Standards was mentioned below.

Ethical Responsibilities of Authors

The manuscript is not submitted to more than one journal for simultaneous consideration.

Compliance with Ethical Standards

Conflict of Interest: All Authors and co-authors declare that they have no conflict of interest.

Ethical Approval: This article does not contain any studies of human participants or animals performed by any of the authors.

Informed Consent: Informed consent is not necessary as this article does not involve human or animal participants.

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