MULTICLASS U-NET FOR LIVER AND TUMOR SEGMENTATION IN ABDOMEN CT SCANS

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ABSTRACT

Liver tumor segmentation in CT(Computed Tomography) scan images plays a critical role in diagnosis, treatment planning and monitoring of liver diseases. In recent years, deep learning techniques, particularly the U-Net architecture, have shown remarkable success in medical image segmentation tasks. However, segmenting both liver and tumor regions accurately in CT scans presents unique challenges due to variations in shape,size and intensity levels of lesions.This paper presents a novel multiclass U-Net architecture designed specifically for liver tumor segmentation in CT scan images. The proposed model integrates both liver and tumor classes into a unified segmentation framework, enabling simultaneous extraction of relevant anatomical structures and pathological regions. The U-Net architecture is well-suited for this task, as it effectively captures spatial dependencies and hierarchical features within the input images.Key components of the proposed multiclass U-Net include an encoder-decoder structure with skip connections for feature fusion, convolutional layers with batch normalization and non-linear activations, and a final softmax layer for pixel-wise classification into liver and tumor classes. The model is trained using a large dataset of annotated CT scans, leveraging techniques such as data augmentation and transfer learning to improve generalization performance.The proposed multiclass U-Net achieves state-of-the-art performance in liver tumor segmentation tasks, accurately delineating both liver and tumor regions across different patient cohorts.The experiments demonstrated that this method can accurately segment liver tumors.We achieved True value Accuracy of up to 98.4%.

Keywords: - *Multiclass U-Net,Accuracy , Encoder, Decoder,Segmentation*

1. INTRODUCTION

The primary objective of this project is to develop a multiclass U-Net architecture tailored specifically for liver tumor segmentation in original CT scan images. By leveraging the hierarchical features learned by the U-Net model, we aim to achieve precise and efficient segmentation of both liver and tumor regions.
The proposed approach encompasses several key components:
Data Preprocessing: We perform preprocessing steps on the original CT scan images to enhance contrast and normalize intensity levels. These preprocessing techniques help improve the quality of input images and facilitate more accurate segmentation results.Multiclass U-Net Architecture: Our model extends the traditional U-Net framework to accommodate multiclass segmentation, enabling simultaneous extraction of liver and tumor regions. The encoding-decoding architecture of the U-Net model allows for the capture of both local and global features essential for accurate segmentation.Training Strategy: To address challenges such as class imbalance and limited annotated data, we employ data augmentation techniques during model training. By augmenting the dataset with variations of the original images, we aim to enhance the model's robustness and generalization capability.

Evaluation Metrics: We evaluate the performance of our proposed method using standard evaluation metrics such as the Dice coefficient (DC), accuracy, loss. These metrics provide quantitative measures of segmentation accuracy and enable comparison with existing techniques.By developing an automated system for liver tumor segmentation, we aim to assist clinicians in accurate diagnosis, treatment planning, and monitoring of liver diseases. The proposed method has the potential to streamline medical workflows, reduce human error, and improve patient outcomes in liver tumor management.work Introduction related your research work Introduction related your research work Introduction related your research work Introduction related your research work Introduction related your research work.

2. LITERATURE REVIEW

Liver tumor segmentation in CT scans has garnered significant attention in medical imaging due to its critical role in diagnosis, treatment planning, and monitoring of liver diseases. The utilization of deep learning techniques, particularly U-Net architectures, has shown promising results in automating liver tumor segmentation tasks. This literature review aims to summarize key findings and methodologies from relevant studies in this field.

Amir Zaghloul El-Sayed Gharib(2019)[1] proposed an improved U-Net architecture for liver and liver tumor segmentation with reduced false positives. Their work focused on enhancing the U-Net model's performance by addressing the challenge of false positives in liver tumor segmentation. By implementing novel features and modifications to the standard U-Net architecture, they achieved more accurate segmentation results which we considered as our existing model.

Alom et al. (2021)[2] conducted a comprehensive survey, offering insights into various deep learning-based approaches for liver tumor segmentation. Their review highlights the progress made in this field, discussing different methodologies and their effectiveness in segmenting liver tumors from medical images.

Yan et al. (2018)[3] presented a study focusing on liver tumor segmentation specifically in CT images, employing deep learning methods. Their work demonstrates the applicability of CNNs in accurately delineating liver tumors, showcasing the potential of these techniques in clinical settings.

Zhu et al. (2018)[4] proposed a deep learning-based framework tailored for liver tumor segmentation in CT images. Their approach leverages CNNs to achieve precise segmentation results, offering a robust solution for automatic tumor delineation, which is crucial for various medical applications.

Christ et al. (2017)[5] introduced a cascaded fully convolutional neural network architecture for automatic liver and tumor segmentation in both CT and MRI volumes. Their method demonstrates promising results in accurately segmenting liver tumors from complex medical images, showcasing the effectiveness of deep learning-based approaches in handling diverse imaging modalities.

Litjens et al. (2017)[6] conducted a survey focusing on deep learning techniques for liver tumor segmentation on CT scans. Their review provides valuable insights into the state-of-the-art methodologies, discussing the strengths and limitations of different approaches, and highlighting potential avenues for future research in this domain.

In conclusion, the studies collectively contribute to the advancement of liver tumor segmentation in CT scans through the utilization of deep learning techniques, particularly U-Net architectures. By addressing various challenges and exploring innovative methodologies, these works have paved the way for more accurate and efficient automated segmentation approaches, thereby facilitating improved clinical decision-making and patient care in the field of hepatology and oncology.

3. DATASET

The researchers worked with medical professionals to generate masks for segmentation of liver and tumor for each CT scan slice in the dataset, they made this dataset available in LITS challenge2017 competetion.We obtained the dataset from the Kaggle datasets.This dataset contains 130 CT Scan volumes and each volume contains 400 image slices in every angle of view.The dataset also contains mask foe each slice named to each corresponding image slice.Thus,it contains 52000 image slices among which 85 percent are used for training purpose and 15 percent are used for testing purpose.Below is an example of CT scan and its corresponding mask.

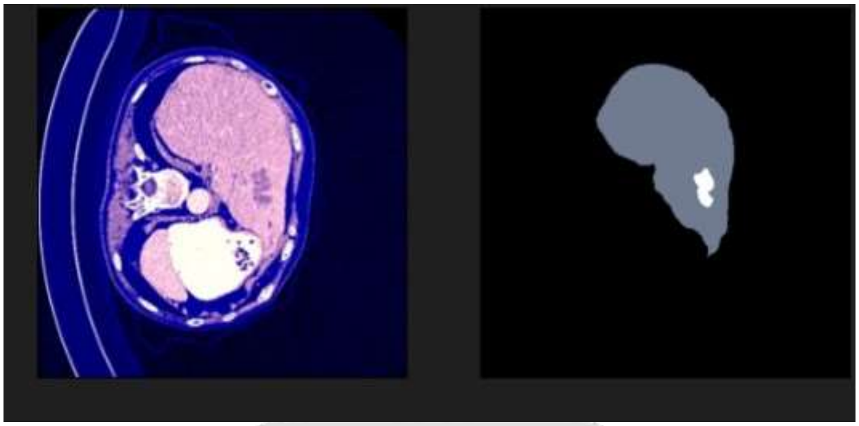

Fig.1: Abdomen CT Scan Slice and its corresponding segmentation mask for liver and tumor

4. PREPROCESSING AND AUGUMENTATION

Preprocessing of image data is made easier by utilizing the Keras Image Data Generator. Each pixel value in the training set is normalized because the generator is configured with the rescale parameter set to 1/255, which results in the range [0, 1]. To provide consistent input data for both the training and assessment phases, the testing set also goes through the same rescaling process. The generated normalized images are used as the basis for abdomen CT scan dataset analysis and efficient model training.

Keras Image Data Generator facilitates augmentation in the training set. at improve dataset variety, it adds shear and zoom transformations, with training parameters set at 0.2. We lower the possibility that the model may focus too much on particular details by improving its adaptability to various types of input data. As the model's flexibility increases through modifications, so does its capacity to analyze images.

5. PROPOSED WORK

The U-Net architecture was originally designed for biomedical image segmentation, particularly for tasks like segmenting cells or organs within medical images. It's a convolutional neural network (CNN) architecture that consists of a contracting path to capture context and a symmetric expanding path that enables precise localization. The original U-Net typically ends with a single-channel output layer using a sigmoid activation function, where each pixel is classified as either part of the object of interest or not.For multiclass segmentation, the output layer needs to be adjusted to accommodate multiple classes. You can use a softmax activation function with multiple channels.Below is the proposed flow chart of our proposed model.

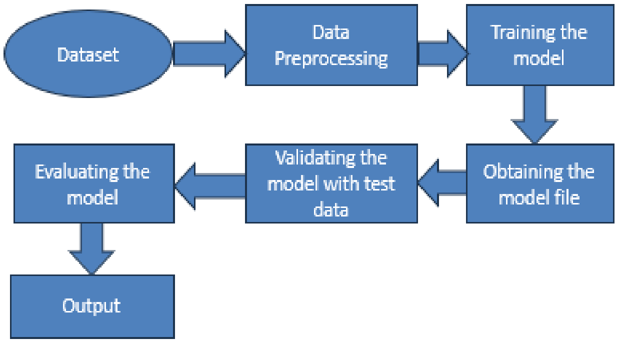

Fig.2: Flow chart of the proposed model.

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5.1 Multiclass U-Net Architecture:

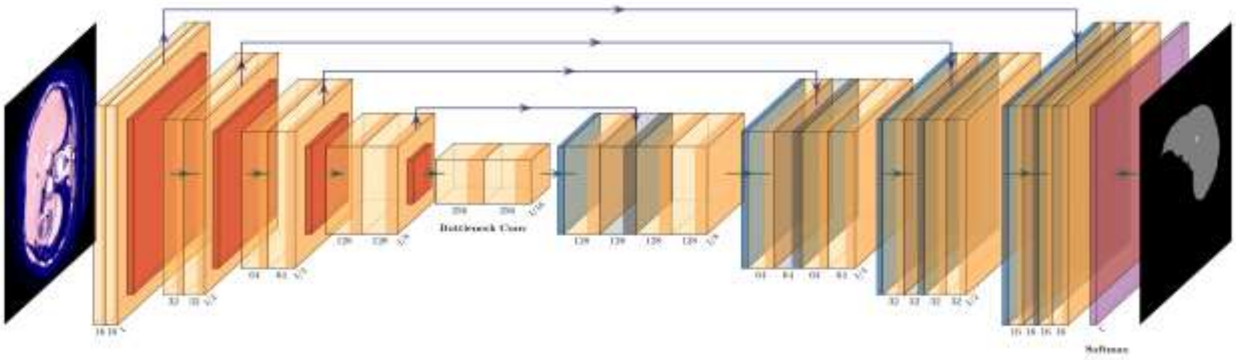


Fig-3: Multiclass U-Net Architecture

In our proposed methodology,we are using multiclass U-net architecture in Convolutional Neural Networks(CNN) which is used when we have multiple classes to segment.The architecture of U-Net is characterized by its U-shaped structure, which consists of a contracting path followed by an expanding path. The U-shape is formed by downsampling layers, known as the contracting path, which progressively reduces the spatial dimensions of the input image, followed by upsampling layers, known as the expanding path, which gradually restores the spatial dimensions to generate the final segmentation output.

5.1.1 Layers in Architecture:

- **Convolution Layer**: Convolutional layers are fundamental components of CNN architectures used in liver and tumor segmentation projects, as they enable the network to effectively extract relevant features from medical images and accurately delineate the boundaries of liver tissue and tumors**.**
- **Maxpooling Layer**: MaxPooling layers play a vital role in liver tumor segmentation projects by downsampling feature maps, introducing translation invariance, reducing computational complexity, and aiding in learning hierarchical features, ultimately leading to accurate segmentation results**.**In our model, our images arereduced to a size from 512 to 32 while passing through maxpooling layers.
- **Dropout Layer**: Dropout layers are an essential component in liver tumor segmentation projects as they aid in preventing overfitting, improving generalization, handling noisy data, and making the network more robust and reliable for accurate segmentation results.
- **Concatenate Layer**: Concatenate layers play a crucial role in liver tumor segmentation projects by enabling feature fusion, multi-scale analysis, skip connections, model flexibility, and semantic information integration, ultimately leading to more accurate and robust segmentation results.
- **Batch Normalisation Layer**: Batch normalization layers in the network architecture for liver and tumor segmentation projects can lead to more stable training, faster convergence, and improved segmentation accuracy, ultimately enhancing the overall performance of the deep learning model.

In this project,we are acquisisting a dataset which contains CT scan slices and corresponding segmentation masks.In that mask, we have 3 classes of segmentation, they are :
i.Background
ii.Liver
iii.Tumor

In the output layer of the architecture, we use softmax as activation layer instead of sigmoid.Softmax is used in the output layer of multiclass classification models where the goal is to predict probabilities across multiple classes.By this, instead of number of masks,we can segment bothe the liver and tumor with the help of single mask for both liver and tumor.

Libraries used in the above proposed model:

- Tensorflow
- Keras
- Albumentations
- Numpy
- OpenCV
- Matplotlib

Below table shows aa brief introduction of libraries used for this model.

Software Package	Purpose
Keras	Entails building, training, and evaluating convolutional neural networks with ease and flexibility, facilitating efficient development in medical image segmentation.
TensorFlow	Backend used by Keras ,provides a lower-level interface allowing fine-grained control over CNN architectures.
NumPy	Facilitates efficient manipulation and processing of multidimensional arrays, crucial for handling medical image data in tasks like liver and tumor segmentation within TensorFlow and Keras frameworks
Albumentations	Accelerates liver and tumor segmentation projects by offering an efficient pipeline for data augmentation, enhancing the robustness and generalization of convolutional neural networks trained on medical image datasets
matplotlib	Plots graphs over metrics like accuracy,dice coefficient.

Table-1: List of Libraries

We have used python coding language and VS Code and Google Colab platforms to do this project.

6. EXPERIMENT AND RESULT

This model was trained and validated for 5 consecutive epochs as part of the experimental work.According to the obtained csv file ,the proposed approach has a training accuracy of 98.5% and validation accuracy of 98%. For the loss metric,in training we have obtained a loss of 0.03 % and in testing we obtained a loss of 0.33%.We have also calculated dice coefficent metric.

DICE-COEFFICIENT: The Dice coefficient is a measure of the overlap between two sets, A and B. In the context of image segmentation, A represents the ground truth segmentation mask and B represents the segmentation produced by the algorithm being evaluated.
In liver tumor segmentation project, a high Dice coefficient indicates that the algorithm's segmentation closely matches the manually annotated ground truth, which suggests that the algorithm is accurately identifying and delineating liver tumors in medical images. Therefore, researchers and developers often strive to achieve higher Dice coefficients as a measure of the algorithm's performance and accuracy in medical image segmentation tasks and its valueranges from 0 to 1.

Epochs vs Accuracy:
The below graph shows the relation between the epochs and the accuracy.if the number of epochs is increased then the accuracy may increase.But, increasing of accuracy stops if it is overfitted, to reduce overfitting we used earlystopping which stops the increase of epochs if there is no increase in accuracy.

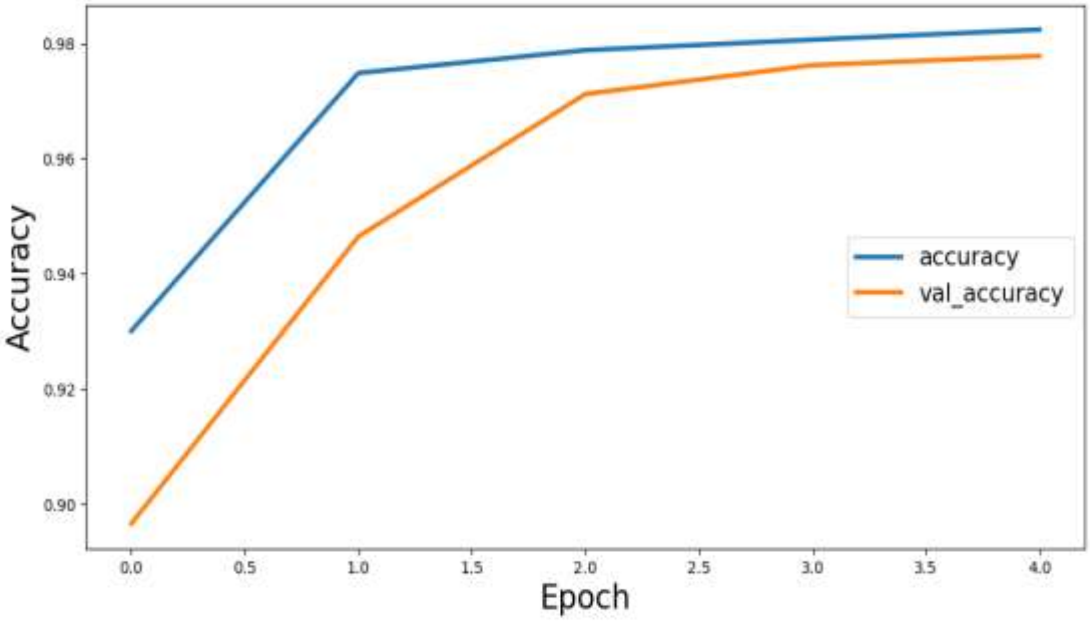


Fig.4. Epoch vs Accuracy Graph

Epoch vs Dice Coefficient Graph:

The below graph shows the relation between the epochs and the dice coefficient.If the number of epochs is increased then the dice coefficient value may increase.This dice coefficient metric gives us the overlap of predicted or generated segmentation mask with the ground truth mask.

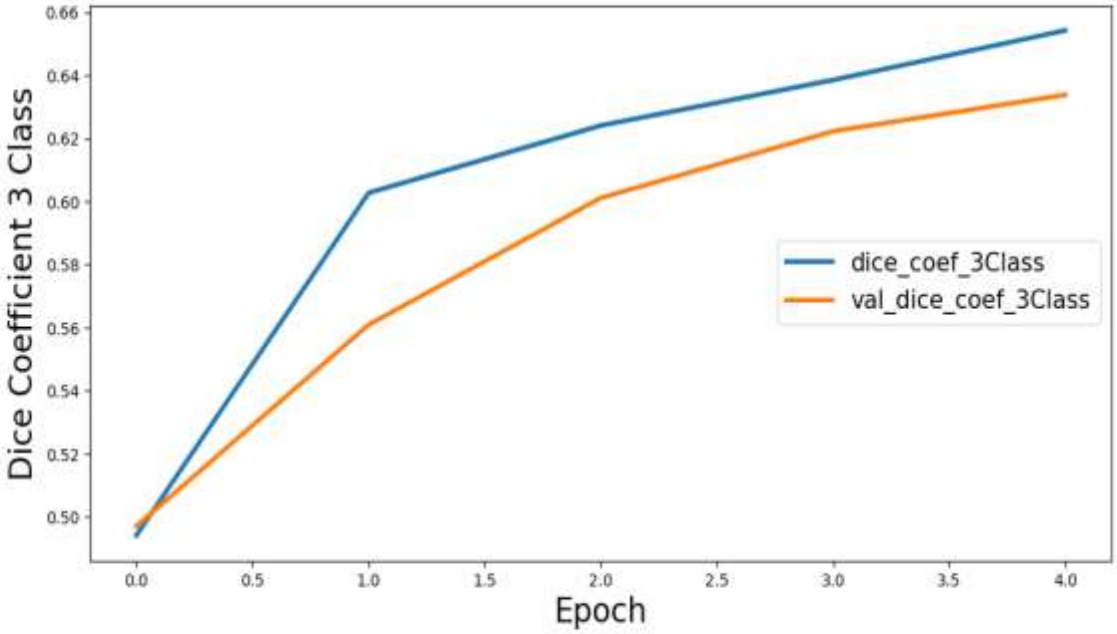
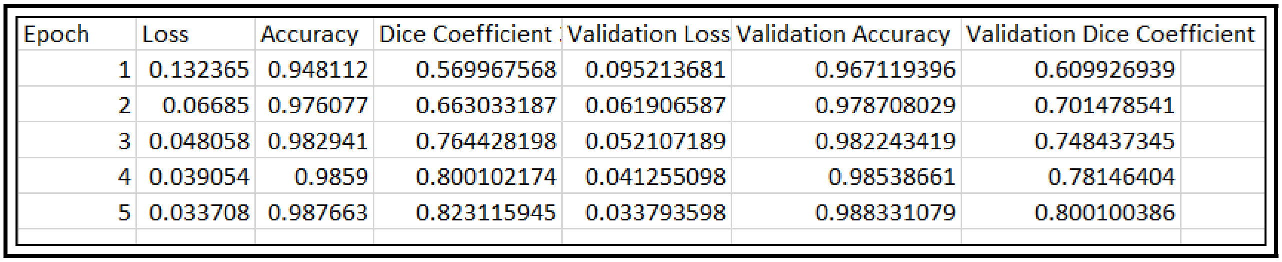


Fig.5. Epoch vs Dice Coefficient Graph

6.1**Performance Evaluation Metrics:** The below is metrics table that contains training accuracy,validation accuracy,training loss ,validation loss, training dice coefficient and validation dice coefficient which helps us to know how well our model is trained and performed.These metrics are taken for every epoch.



Epoch	Loss	Accuracy	Dice Coefficient	Validation Loss	Validation Accuracy	Validation Dice Coefficient
1	0.132365	0.948112	0.569967568	0.095213681	0.967119396	0.609926939
2	0.06685	0.976077	0.663033187	0.061906587	0.978708029	0.701478541
3	0.048058	0.982941	0.764428198	0.052107189	0.982243419	0.748437345
4	0.039054	0.9859	0.800102174	0.041255098	0.98538661	0.78146404
5	0.033708	0.987663	0.823115945	0.033793598	0.988331079	0.800100386

Table-2: Evaluation Metrics of Each Epoch

6.2Results:

In our testing results we obtain both our ground truth mask which is present in the dataset and as well as the generated mask which is produced by our trained model.Both the masks should be similar and equal, then only we can say our model is trined perfectly. Below are the images after testing.

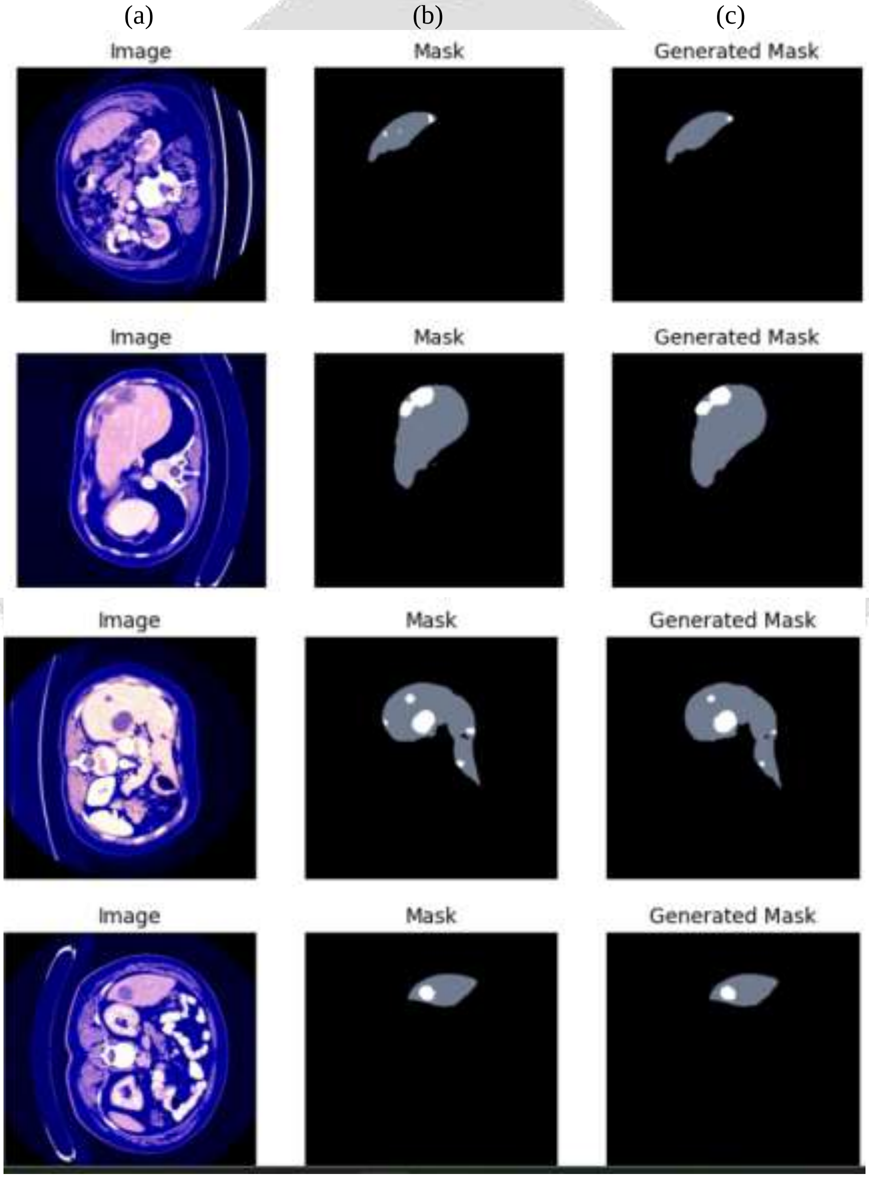


Fig. (a) Original CT Scan Slice,(b) Ground Truth Mask,(c) Generated Mask

In the above figure (a),(b) are the original CT scan image slices and their corresponding masks which are provided in the dataset,(c) is the mask which we generated using the trained model.We can see that both the masks are very much similar and equal.

7.CONCLUSION

Our proposed methodology demonstrates the effectiveness of employing Convolutional Neural Networks, specifically a multi-class U-Net architecture, for liver tumor segmentation in CT scan images. Through rigorous Evaluation using metrics such as Dice coefficient and Accuracy, we have shown that our approach achieves accurate and robust segmentation results, providing valuable assistance to radiologists in diagnostics, treatment planning and monitoring for liver tumors.Our method exhibits promising computational efficiency and generalization capability across diverse datasets,laying the groundwork for its potential clinical adoption. While further research is warranted to address challenges and enhance the model’s performance, our findings underscore the significant contribution of deep learning techniques to advancing medical image analysis and improving patient care in oncology.

8.REFERENCES

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