Team : Code Blue

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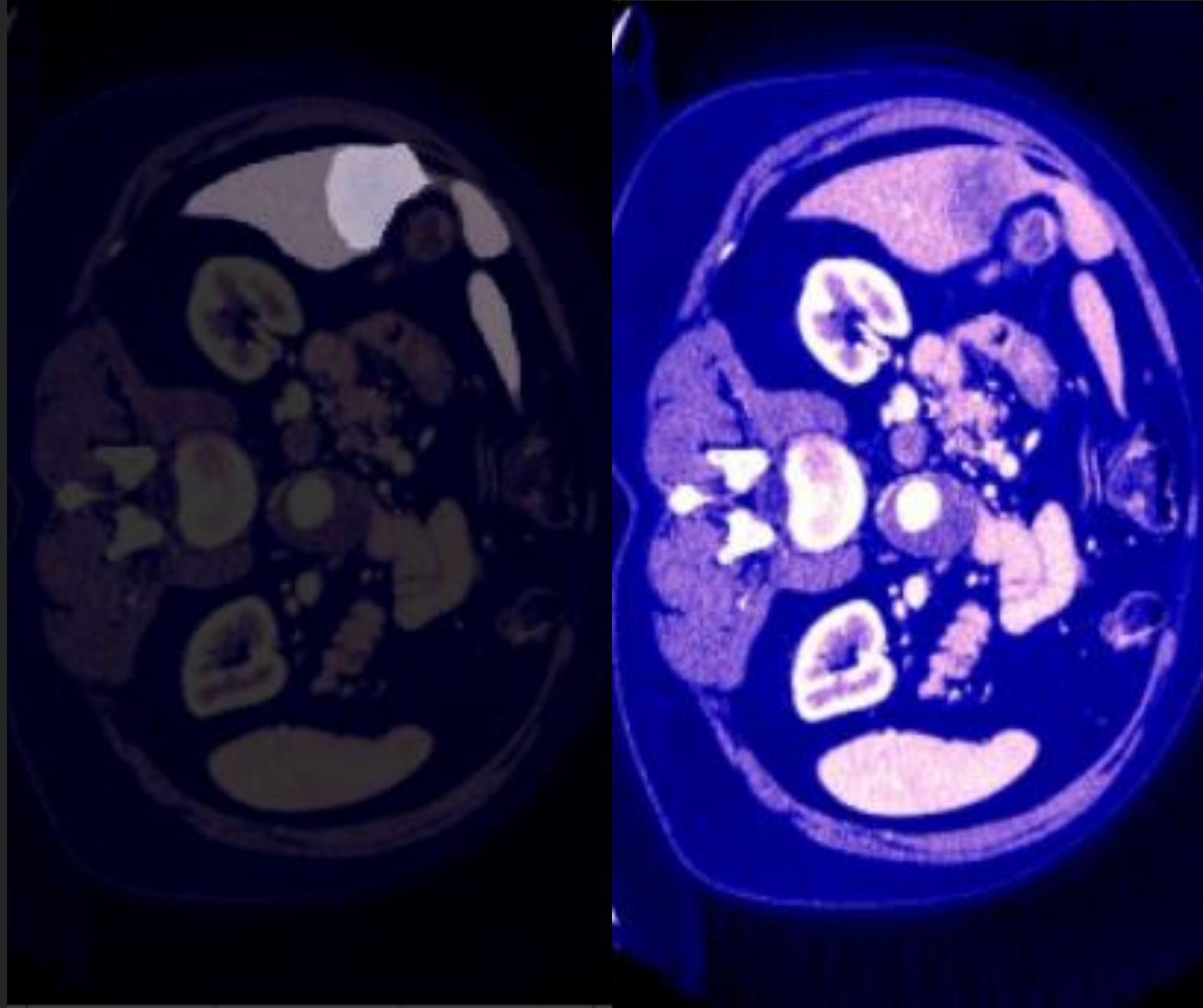


Problem Statement

To create a framework for the segmentation of the liver and liver tumors from abdominal CT scans that can be used as a clinical reference and to implement the same as an application.

Proposed Solution

Liver tumor segmentation is regarded as one of the most difficult semantic segmentation tasks in medical imaging. The manual segmentation of CT scans is a taxing and error-prone process that is known to have a low inter-professional agreement because of the quantity of CT scans that are currently being generated in clinics and the high variability in the location, size, and appearance of liver tumors as a result computer-assisted tumor segmentation has become an increasingly sought-after solution to this problem. We have proposed a unique preprocessing scheme that extracts 2D slices from the CT volumes and enhances the contrast between liver and non-liver tissue and liver-tumor and liver tissue respectively. Unlike traditional 3D liver-tumor segmentation models ours is based on a 2D framework which greatly reduces the computational cost. The proposed model has a novel architecture that uses two encoders- one with pre-trained weights and the other without, giving it a W shape. The proposed method achieved one of the highest ever recorded dice scores on the LiTS-17 dataset making it a clinical benchmark. We further aim to deploy the proposed scheme on a web-based platform so that it can be used as a tool in clinical settings for referential diagnosis.

Model Architecture

- **Fig 1(a)** : Schematic of the W-Net architecture.
- The W-Net is a novel architecture designed to combine the strengths of a model which undergoes residual learning from scratch and on that uses pre-trained weights (transfer-learning)
- Encoder 1 and the decoder do not have any pretrained weights. Their design is roughly based on the Residual U-Net but with a multitude of architectural enhancements to cater specifically to the task of liver and liver tumor segmentation.
- Squeeze and Excite blocks have been added to both encoder and decoder to allow channel wise weighting of feature maps. The squeeze-and-excitation (SE) network developed by Hu et al. adds a content-aware mechanism to weigh each channel adaptively. The SE block first estimates the importance of each channel (feature map) and then weights each channel according to its importance. This ensures that the channel with more relevant spatial information gets a higher contribution in the output feature map compared to the other channels.
- Res-blocks have been integrated into the backbones of both encoder 1 as well as the decoder. This helps the model to converge faster by mitigating the problems of exploding and vanishing gradients and propagation loss.
- ASPP has been implemented at the bottlenecks of both the encoders. The abdominal CT slices not only have plenty of local specifics but also have an almost limitless macro target expansion. As a result, in order to extract multiscale features for liver and liver tumor extraction, ASPP is required.
- A Resnet-50 model pretrained on the imagenet dataset serves as the second encoder. The very last FC layers have been taken off. The main intuition behind using the second encoder is to ease the training of the model. Due to the pretrained model's ability to extract global specifics with ease the first encoder and the decoder can then use these features to extract local specifics that are relevant to the task

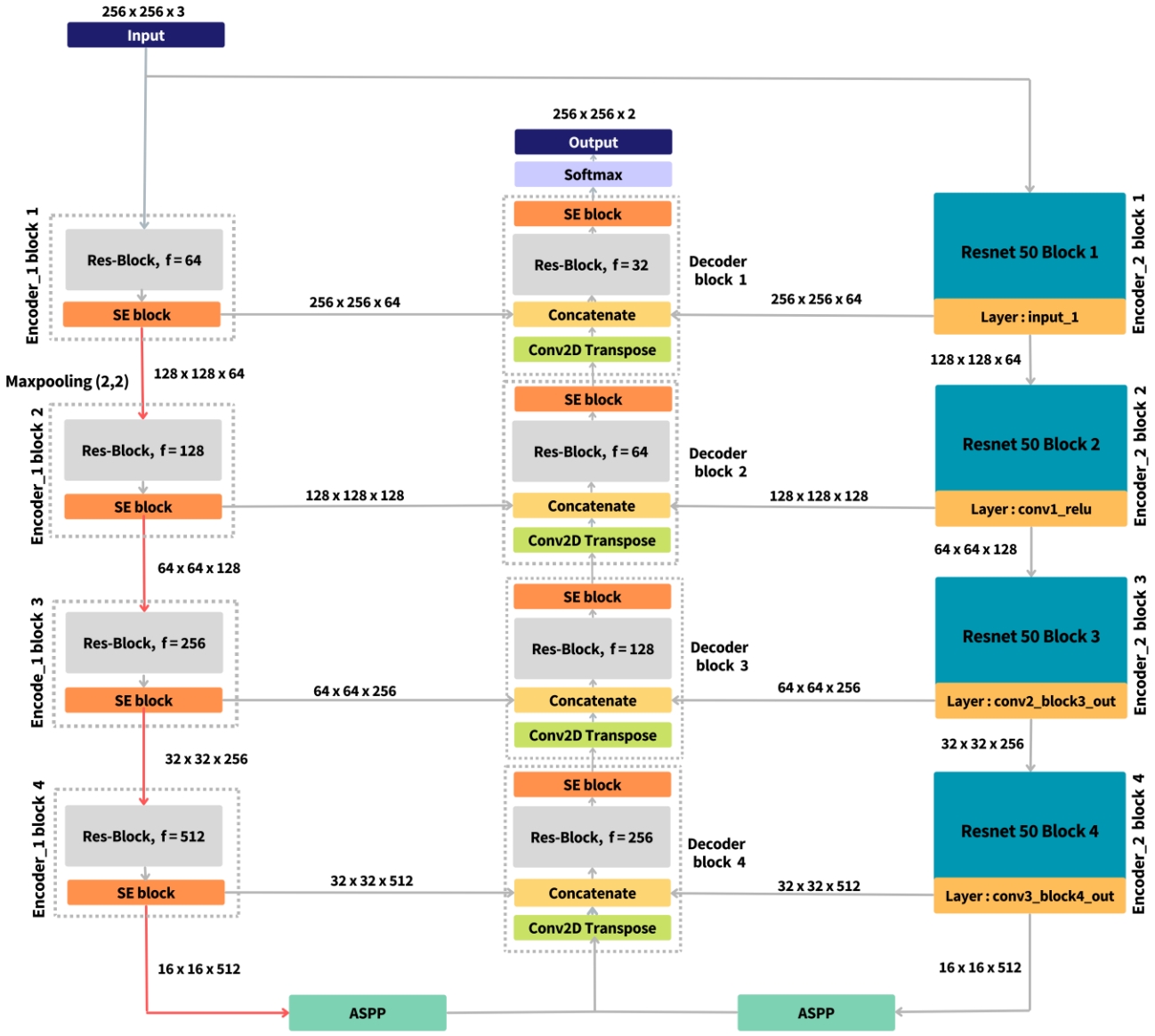


Fig : 1(a)

Model Architecture

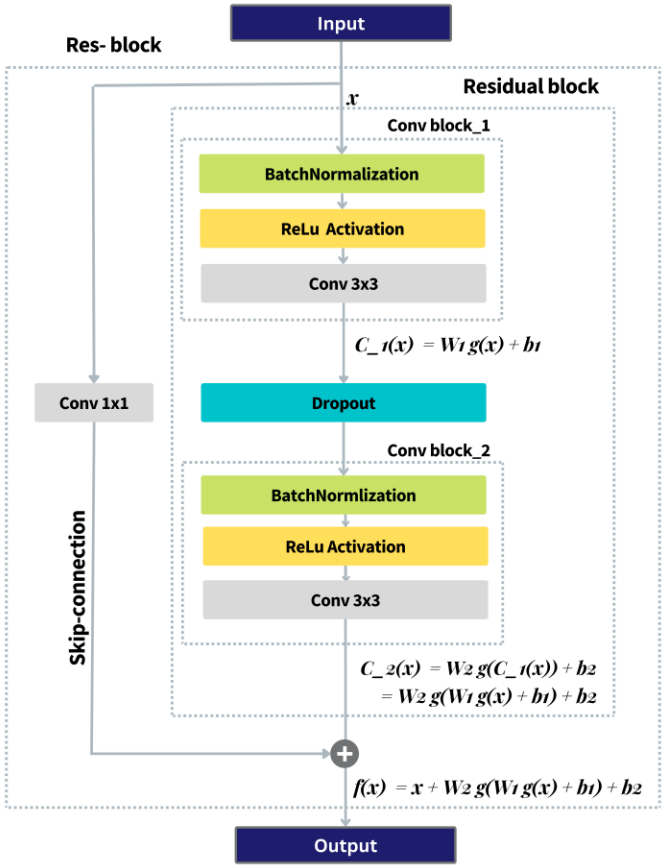


Fig : 1(b)

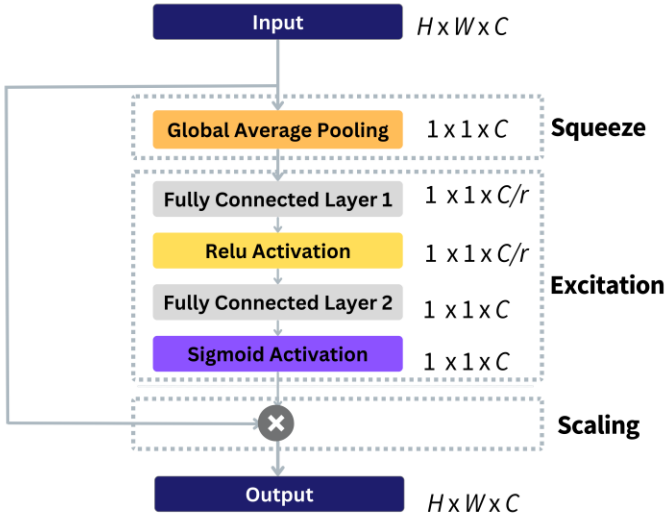


Fig : 1(c)

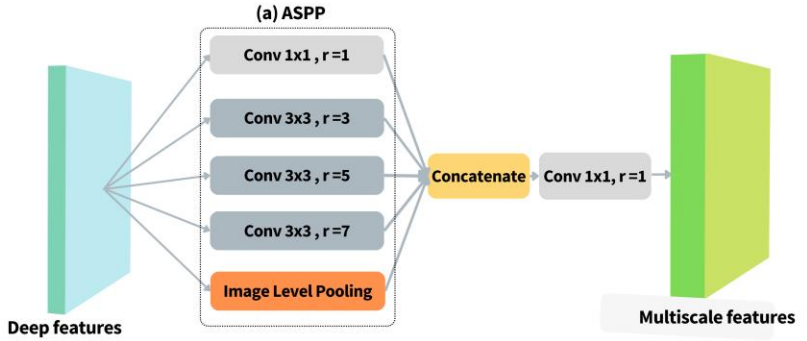


Fig : 1(d)

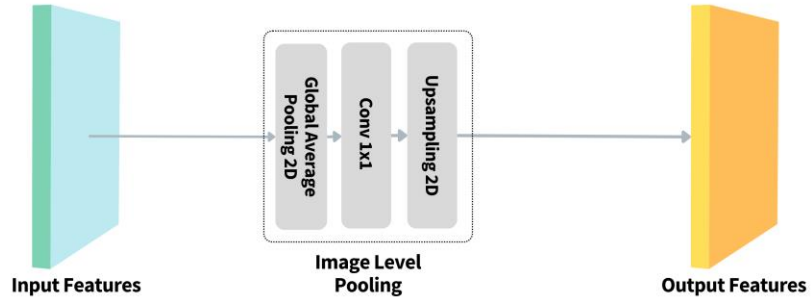


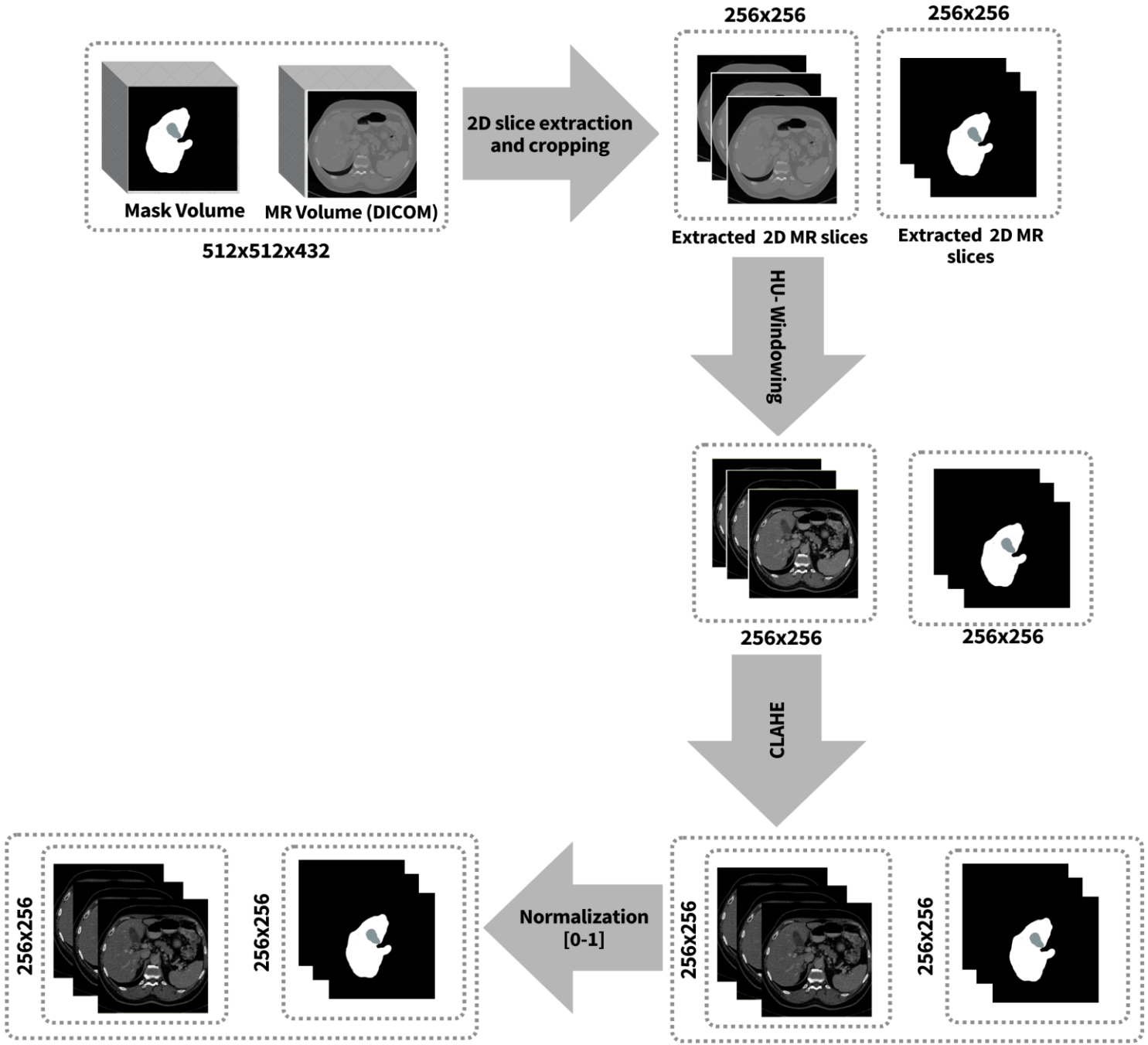
Fig : 1(e)

Fig 1(b): Layer sequence in Res-block, **Fig 1(c)**: Layer sequence in SE block, **Fig 1(d)**: Layer sequence in ASPP (r represents the dialation rate), **Fig 1(e)**: Layer sequence in image level pooling.
These are some of the basic blocks used in the W-Net architecture.

Pre-Processing Methodology

Steps involved :

- Extraction of 2D MR slices and corresponding masks from the patient MR volumes and cropping them to 256 x 256
- Application of HU-Windowing [0-200] to the extracted MR slices to enhance the representation of liver and soft organ tissue.
- Application of Contrast Limited Adaptive Histogram Equalization (CLAHE) to enhance the contrast between healthy liver and liver tumor tissue.
- Normalization of the MR and mask slices [0-1]
- Finally the processed MR slices and their corresponding masks are fed to the training algorithm.



RESULTS :

- Figures on the right show the training-validation curves for W-Net on preprocessed slices from the LiTS-17 dataset for the evaluation metrics – Dice + Focal Loss, Dice-coefficient and IoU (Intersection over union).

- A total of 58,348 slices were extracted from the patient volumes.

- Slices with no positive pixels in the corresponding masks were discarded

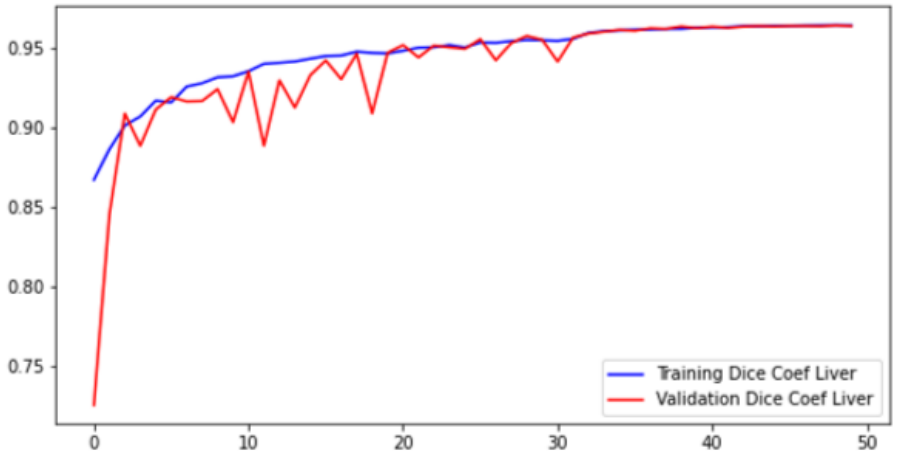
- Of these 75% were used for training 15% for validation and 10% for testing.

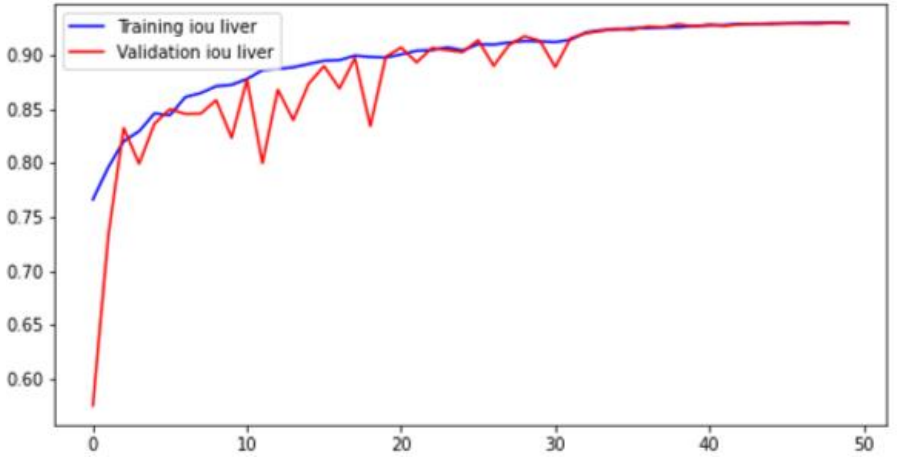
- Image data-generator was used to introduce image augmentations such as random contrast, random rotate, random flip, elastic deformations, etc. during training.

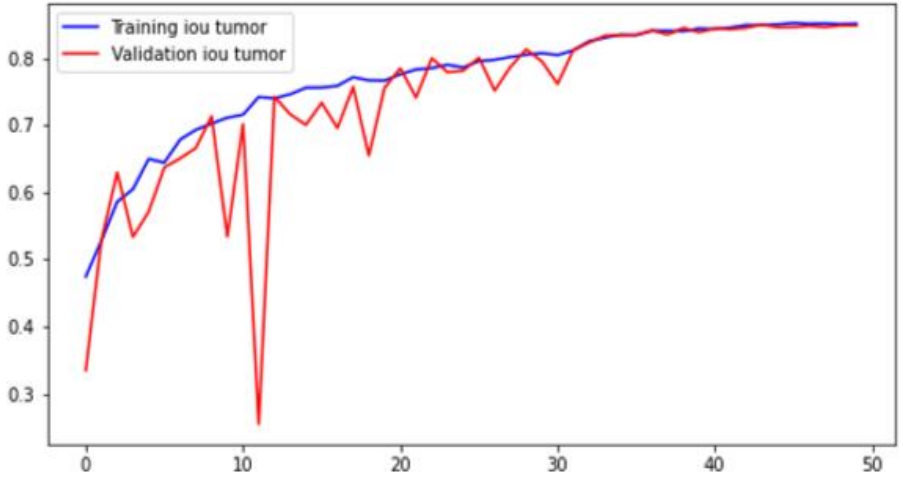
- A combination of Focal and Dice loss was used as the loss function while training.

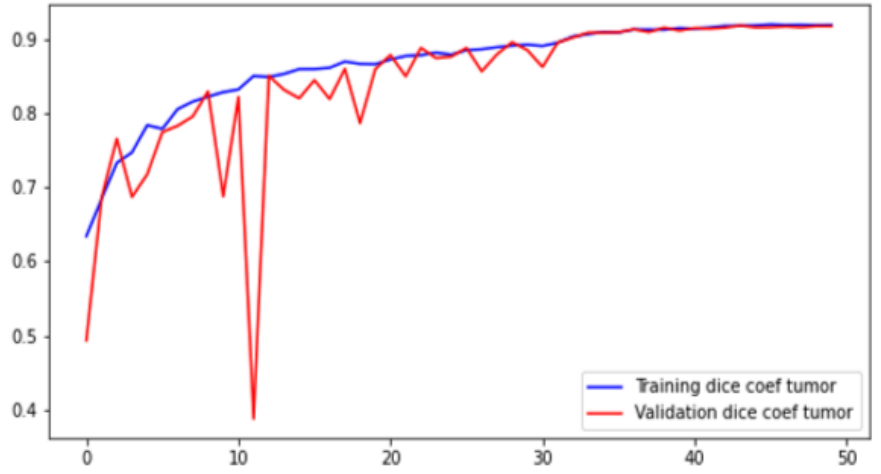
- The nearly absolute and smooth convergence of the training and validation curves indicate that there is negligible overfitting implying high reliability of the segmentation results.

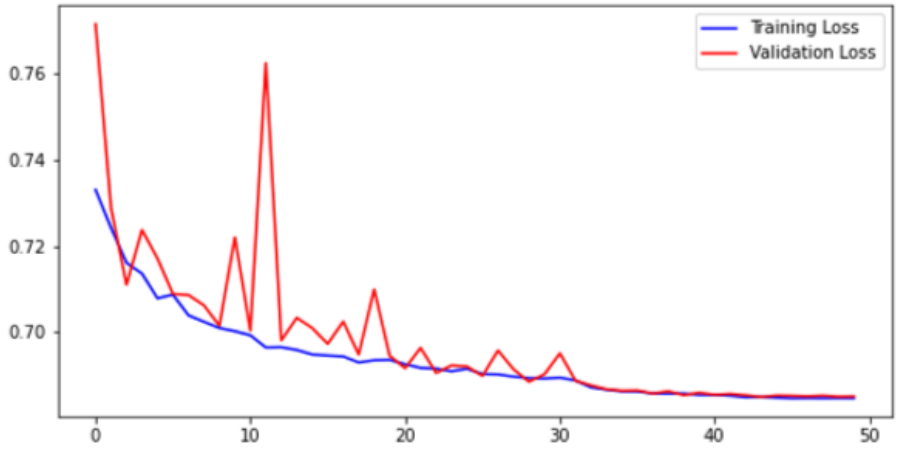
- The final results on the test set are enlisted in **Table 1**









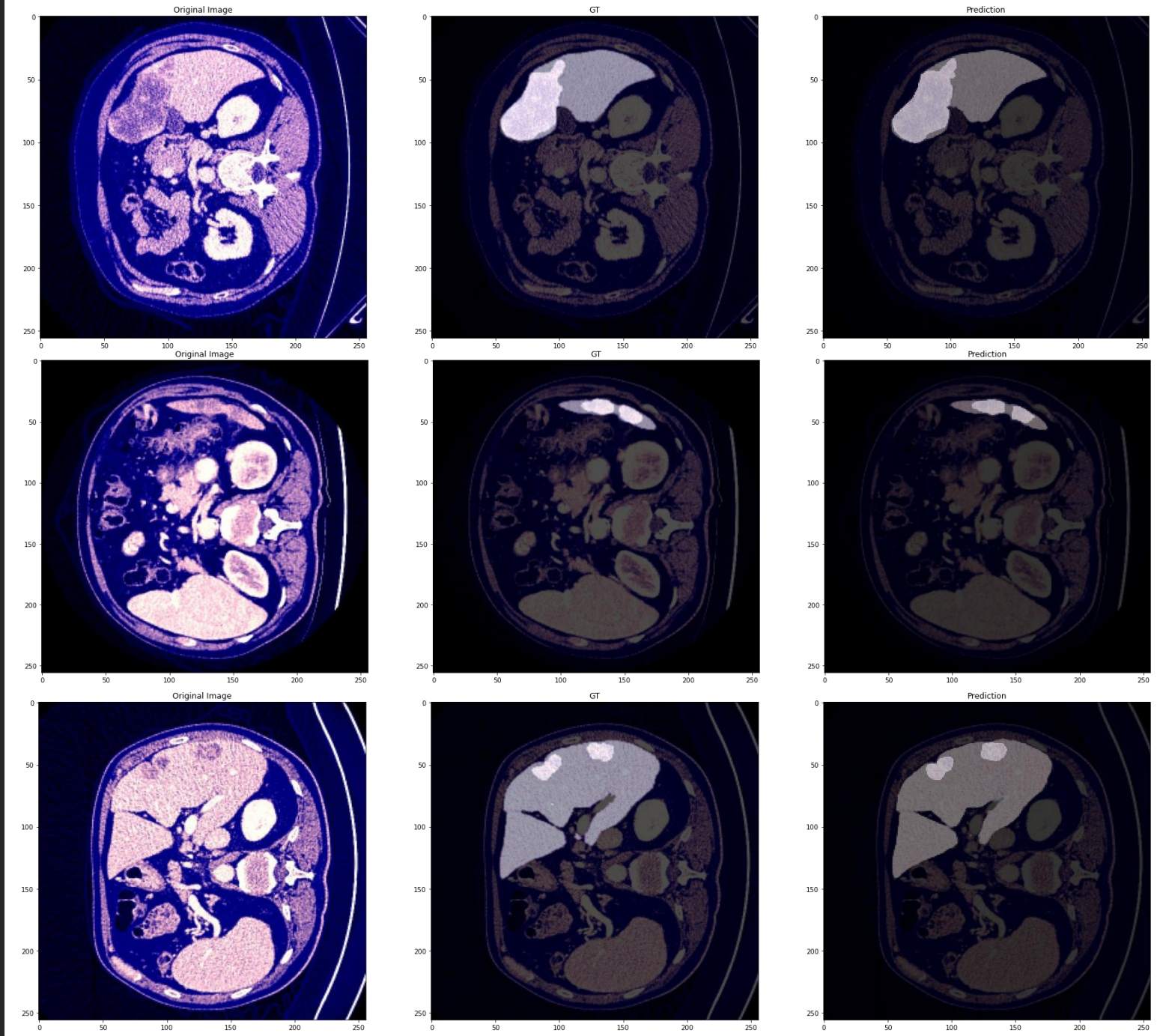


RESULTS :

Figure on the right shows a comparative analysis between the predicted masks and the ground truths for some of the randomly selected 2D CT slices from the test set.

Observations :

- The predicted masks show a high degree of correlation with the ground-truths.
- Predicted gross organ boundaries are found to be nearly exact.
- Hardly any false positives are seen in the segmentation outputs indicating high specificity.



Comparative Analysis

Method	Dice_Liver	Dice_Tumor	IoU_Liver	IoU_Tumor	Sensitivity_Liver	Sensitivity_Tumor	Specificity_Liver	Specificity_Tumor
W-Net	**0.97**	**0.92**	**0.94**	**0.86**	**0.97**	**0.93**	**0.99**	**0.99**
HFRU-Net [1]	0.96	0.77	**0.94**	0.74	-	-	-	-
Eres-UNet++ [2]	0.96	0.91	0.92	0.84	-	-	-	-
RDCTrans-UNet [3]	0.93	0.90	-	-	0.88	0.86	0.98	0.94
RMS-UNet [4]	**0.97**	0.86	-	-	-	-	-	-
Res-UNet [5]	**0.97**	0.89	-	-	-	-	0.96	0.95
X-Net 3D [6]	0.96	0.76	0.88	0.67	-	-	0.95	0.93

Table 1

- **Table 1** presents a comparative analysis on the liver and liver-tumor segmentation performance of the proposed architecture with some of the state of the art methods based on the evaluation metrics – Dice score, IoU, Sensitivity, and Specificity.

- It is clear from the study that the liver segmentation performance of the W-Net has minor increments over some of the state of the art methods. However when it comes to liver-tumor segmentation the W-Net outperforms the competition by a very high margin.

$$IoU = \frac{|X \cap Y|}{|X \cup Y|} = \frac{TP}{TP + FP + FN} \qquad where,\ IoU \in [0, 1]$$

$$DC = \frac{2 \times TP}{2TP + FP + FN} \qquad where,\ DC \in [0, 1]$$

$$Sensitivity = \frac{TP}{TP + FN}$$

$$Specificity = \frac{TN}{TN + FP}$$

*All data presented in **Table 1** is based on the results of the test set.

References: [1], [2], [3], [4], [5], [6]

Thank You

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