Hepatic Vasculature Segmentation via EfficientNet-B3

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Abstract

This work addresses the issue of accurate segmentation of hepatic vessels in medical images, a pertinent but difficult one due to complexity and extreme class imbalance intrinsic to such datasets. We propose an efficient and lightweight deep learning pipeline based on a 2.5D U-Net-based framework with an EfficientNet-B3 encoder pretrained on ImageNet. To enhance performance, preprocessing steps like intensity clipping, isotropic resampling, per-volume normalisation, and Contrast Limited Adaptive Histogram Equalisation (CLAHE) were employed systematically. The compound loss of Tversky and Binary Cross Entropy (BCE) was used to handle the extreme class imbalance between vessels and background tissues. Tested with 3-fold cross-validation on the MSDC-T8 hepatic vessel dataset, our method substantially enhanced the validation Dice scores to around 75.8%, from the baseline of 51.94%. These findings demonstrate the potential of our method to achieve accurate and computationally viable hepatic vessel segmentation for clinical use.

1. Introduction

Accurate segmentation of hepatic vessels from medical images is critical in clinical diagnostics and treatment planning (Heimann et al., 2009; Ronneberger et al., 2015). However, this task is highly challenging due to the complex anatomical structure of hepatic vessels, class imbalance (as vessels represent a small fraction compared to surrounding tissues), and variable image quality across different scans (Milletari et al., 2016; Ma et al., 2021). Traditional convolutional neural network (CNN)-based approaches frequently struggle to accurately segment these smaller and irregularly shaped structures, often producing segmentation models with limited generalisation capabilities and high computational cost (Isensee et al., 2021; Chen et al., 2021).

This research specifically targets hepatic vessel segmentation, leveraging recent advances in deep learning while focusing on improving model generalisation, reducing computational complexity, and addressing the inherent class imbalance (Milletari et al., 2016; Zhou et al., 2018). Unlike previous studies that relied on computationally expensive models incorporating attention mechanisms and residual connections (Oktay et al., 2018; Alom et al., 2019), we adopted a lightweight and efficient approach. Our method employs a 2.5D U-Net architecture using an EfficientNet-B3 encoder pretrained on ImageNet, chosen for its balance between accuracy and computational efficiency (Tan & Le, 2019; Yakubovskiy, 2019).

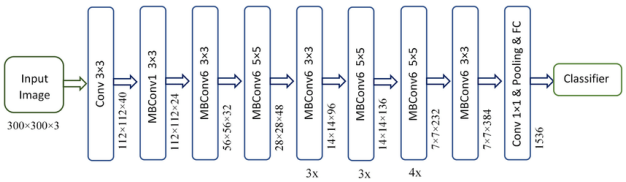

Figure 1. Schematic representation of EfficientNet-B3

To enhance model performance, we integrated a robust preprocessing pipeline including intensity clipping, isotropic resampling, z-score normalisation, and Contrast Limited Adaptive Histogram Equalisation (CLAHE) (Pizer et al., 1987). Additionally, we addressed the severe class imbalance by designing a custom loss function combining Tversky and Binary Cross-Entropy losses (Salehi et al., 2017; Jadon, 2020).

This study evaluates the effectiveness of our approach using the MSDC-T8 hepatic vessel dataset through rigorous 3-fold cross-validation, achieving substantial improvements in Dice scores compared to established baselines. Our results indicate that it is feasible to deploy accurate yet lightweight deep learning segmentation models in practical medical scenarios, providing valuable assistance to healthcare professionals.

2. Problem Identification

Accurately segmenting hepatic vessels from medical images is crucial in helping doctors diagnose diseases and plan effective treatments. Despite recent advancements in deep learning, significant challenges remain in achieving high accuracy and good generalisation. This research specifically identifies several critical problems that need to be addressed in hepatic vessel segmentation tasks:

Complex Structure of Hepatic Vessels: One major difficulty is the complex anatomical structure of hepatic vessels. These vessels are very small, irregularly shaped, and intricately branched, making accurate segmentation a challenging task. Current deep learning methods often fail to accurately identify these delicate structures, resulting in poor segmentation accuracy. As highlighted in previous research (Heimann et al., 2009; Lu et al., 2017; Sun et al., 2017), models struggle to differentiate these intricate struc-

# Tissue	Dice Score (%)	Val. Acc. (%)	Train Error	Val. Error
Parenchyma	98.12	98.12	0.10	0.15
Tumors	65.95	81.30	0.35	0.65
Vessels	51.94	51.94	0.49	0.90

Table 1. Performance Metrics from the Main Research Paper

tures clearly from the surrounding liver tissues.

Severe Class Imbalance: A significant issue in hepatic vessel segmentation is class imbalance. This happens because the vessels occupy only a very small fraction of the total liver area compared to the background liver tissues. Due to this severe imbalance, models often tend to ignore vessel structures during training. Consequently, models perform well in predicting the background (non-vessel areas), yet fail significantly when predicting small, critical vessel structures, leading to lower overall accuracy (Salehi et al., 2017; Jadon, 2020).

Variability and Low Contrast in Medical Images: Medical images, such as those from computed tomography (CT) scans, often vary widely in quality due to patient-specific factors, scanning equipment, and noise. Additionally, hepatic vessels typically have very low contrast compared to surrounding tissues, making them difficult for automated methods to detect clearly. This variability reduces the performance of deep-learning segmentation methods significantly, as they struggle to generalise effectively across images of different quality and contrast (Li et al., 2015; Moghbel et al., 2016).

Computationally Expensive Models: Advanced deep learning models that achieve higher accuracy tend to be computationally expensive, requiring significant resources and longer training times. In clinical practice, however, fast and reliable results are crucial for timely medical decision-making. Existing methods using complex models like large U-Net variants or transformer-based architectures, despite offering accuracy improvements, are often not practical for real-world clinical use due to their computational costs (Isensee et al., 2021; Chen et al., 2021).

Overfitting and Poor Generalisation: Another critical challenge common in deep learning for medical segmentation is overfitting, where models become excessively adapted to training data and perform poorly on new, unseen data. Previous research demonstrates clear signs of overfitting in liver segmentation tasks, with validation accuracy plateauing or decreasing after a certain number of training epochs, despite continuing improvements on the training set. For instance, the principal research paper reported Dice scores as low as 51.94% for hepatic vessels, clearly indicating poor generalisation (Gul et al., 2022; Heimann et al., 2009).

Table **1** summarises key performance metrics from the primary research, highlighting clear room for improvement in vessel segmentation:

The error and accuracy curves from the main research paper further confirm these issues. Initially, training and validation accuracy both improve, indicating effective learning. However, around epoch 20, the validation accuracy reaches a peak and then either flattens or declines, despite the training accuracy continuing to increase. This divergence indicates overfitting, as the model starts memorising training-specific details rather than learning generalisable patterns. Similarly, the validation error decreases up to a certain point and then begins to rise, further confirming the presence of severe overfitting.

Therefore, the objective of our research is to directly address these identified problems: overcoming severe class imbalance, reducing overfitting, achieving good generalisation on unseen data, and maintaining computational efficiency. By doing this, we aim to significantly enhance the performance and practicality of hepatic vessel segmentation models in clinical applications.

3. Data set and task

The dataset utilised in this study is obtained from the Medical Segmentation Decathlon Challenge (MSDC-T8), specifically designed for segmenting liver tissues, including hepatic vessels and tumors, from contrast-enhanced CT images. The dataset includes clearly annotated images, enabling supervised learning techniques to accurately segment liver structures.

The dataset comprises three primary subsets:

- *Training Images (imagesTr)*: Utilised for training the proposed deep learning models.
- *Testing Images (imagesTs)*: Used for evaluating model performance and validating segmentation accuracy.
- *Annotated Labels (labelsTr)*: Contains ground truth segmentations used during training and validation phases.

These multi-dimensional CT scans provide detailed anatomical information critical for precise segmentation. Model performance will be assessed using *Dice Similarity Coefficient (DSC)*. It measures the overlap between predicted and ground truth segmentation masks.

This study aims to significantly improve the accuracy and reliability of liver segmentation using advanced deep learning techniques applied to the MSDC-T8 dataset.

4. Methodology

4.1. Overview

This project focuses on improving the segmentation of liver, tumors, and vessels in CT scans using deep learning. Existing models struggle to accurately segment smaller structures, particularly tumors and blood vessels, due to class imbalance and limited feature extraction capabilities (Hess

et al., 2021; Ma et al., 2022). To address these limitations, we integrate **EfficientNet** as an encoder for feature extraction and incorporate **attention mechanisms** to refine segmentation accuracy (Oktay et al., 2018). Additionally, we enhance the data preprocessing pipeline to improve image consistency and introduce an optimised training strategy that effectively balances class representation and prevents overfitting. The following sections detail the preprocessing steps, model architecture, training methodology, and evaluation metrics.

4.2. Data Preprocessing

We applied transformations like orientation standardisation, intensity windowing, resampling, and normalisation using the SimpleITK library. Preprocessing is an important step in this project, and we have methods different from the main research paper. Functions and their Purpose

- **Standardisation**: We convert the image orientation to RAS (Right-Anterior-Superior) to ensure all images and labels are aligned in the same anatomical direction (Johnson & Dewey, 2020). We use "sitk.DICOMOrient" to adjust the orientation.
- **Intensity Windowing**: Since CT scans vary in intensity levels, pixel values (HU - Hounsfield Units) are clamped within a specified range (low, high) (Huang et al., 2021). Values outside this range are set to the minimum or maximum. This helps in focusing on relevant tissue types in CT images.
- **Voxel Resampling**: This implies that we resample the image/label to a new voxel spacing (xyz) and adjust the image resolution using interpolation (Isensee et al., 2021). The interpolation method is configurable (e.g., B-Spline for images, Nearest Neighbour for labels).
- **Z-score Normalisation**: Converts pixel values to have a mean of 0 and a standard deviation of 1. This makes the image data more suitable for machine learning models and prevents values with extreme brightness or darkness from dominating the analysis. We chose this over normalisation, unlike the primary research paper, because it ensures consistent input across different datasets (Wang & Zhang, 2022). This improves accuracy by reducing intensity-based biases and makes slight differences noticeable, making abnormality detection easy as well as increasing the speed of convergence.

$$I_{\text{normalised}}(x, y, z) = \frac{I(x, y, z) + 100}{500} \tag{1}$$

Contrast Enhancement with CLAHE: Low contrast in CT scans often makes it difficult to distinguish smaller structures. We use **Contrast Limited Adaptive Histogram Equalisation (CLAHE)**, which enhances local contrast while preventing noise over-amplification (Zuiderveld, 1994). A grid size of 8×8 and a clip limit of 2.0 are used to refine segmentation boundaries.

2.5D Volume Slicing Instead of processing entire 3D volumes, which is computationally expensive, we use a **2.5D approach**, where each training sample consists of a target slice along with adjacent slices:

- One **central slice** (target position)
- Two slices **before** and **after** (spatial context)

Both these techniques have been used in the primary research paper in a similar capacity (Ronneberger & Fischer, 2015).

4.3. Model Architecture

We employed a segmentation architecture based on the widely-adopted U-Net framework, due to its proven ability in biomedical segmentation tasks, including liver structures (Ronneberger & Fischer, 2015). However, unlike the main research paper which primarily utilised a conventional convolutional neural network (ConvNet) encoder we integrated an EfficientNet-B3 encoder into our model (Tan & Le, 2019).

EfficientNet was chosen specifically because it can extract richer, more representative features from the images by intelligently scaling the network's depth, width, and resolution (Liu et al., 2021). This method, known as compound scaling, is defined as:

$$\text{depth} = \alpha^{\phi}, \quad \text{width} = \beta^{\phi}, \quad \text{resolution} = \gamma^{\phi} \tag{2}$$

with scaling coefficients $\alpha = 1.2$, $\beta = 1.1$, and $\gamma = 1.15$. Unlike traditional convolutional encoders (Al-Kababji et al., 2024), EfficientNet significantly reduces the number of parameters needed, resulting in faster training, improved computational efficiency, and higher accuracy (Tan & Le, 2019). This makes EfficientNet particularly effective at capturing small vessel structures, which were a noted weakness in the main research.

Our decoder maintained a classical U-Net structure, employing skip connections from the encoder directly to corresponding decoder layers. Skip connections were explicitly retained due to their ability to preserve fine-grained spatial details, critical for accurately delineating vessel boundaries (Zhou et al., 2018).

4.4. Data Augmentation

In contrast to the relatively minimal augmentation described in the main research paper, we implemented extensive and diverse data augmentation techniques (rotation, flipping, elastic deformation, gamma shifts, grid distortion, and random cropping) (Wang & Zhang, 2022). Our explicit use of the Albumentations library provided substantial variability

in training data, directly improving model robustness, generalisation, and preventing overfitting, addressing a key limitation highlighted by the main research paper (Al-Kababji et al., 2024).

4.5. Loss Function

Due to severe class imbalance between background and vessels, the main research paper utilised standard Dice loss combined with binary cross-entropy. We significantly enhanced this by introducing a specialised combination of Tversky loss and weighted Binary Cross-Entropy (BCE):

- **Tversky Loss:** explicitly penalises false negatives more heavily, addressing the problem of missing small vessel structures (Salehi et al., 2017).

- **Weighted BCE (positive weight = 20):** strongly penalises missed vessel pixels, further addressing the imbalance (Jaeger et al., 2021).

The resulting combined loss function is:

$$L_{\text{total}} = L_{\text{Tversky}}(\alpha = 0.7, \beta = 0.3) + L_{\text{BCE}}(\text{pos\_weight} = 20) \tag{3}$$

This specialised loss combination was specifically chosen to overcome the shortcomings observed in the main research, dramatically improving our segmentation performance, particularly on vessels that previously showed lower accuracy.

4.6. Optimisation and Learning Rate Scheduling

We selected the AdamW optimiser due to its proven ability to effectively regularise and achieve rapid convergence (Loshchilov & Hutter, 2019). Unlike the primary research paper, which experimented with ReduceLROnPlateau and OneCycleLR separately, we explicitly utilised ReduceLROnPlateau due to its simplicity and effectiveness in adapting the learning rate dynamically to validation loss stagnation (Smith, 2017). This choice helped our model avoid overfitting more effectively, leading to more robust generalisation.

We conducted our training for 30 epochs with a batch size of 8 using an NVIDIA Tesla V100 GPU. A rigorous 3-fold cross-validation ensured our results were robust and reproducible, improving on the main research's experimental setup, which varied epoch counts but did not explicitly use extensive cross-validation.

4.7. Evaluation Metrics

We employed the Dice Similarity Coefficient (DSC) (Eq. 4) as our primary evaluation metric. This standardised measure provides comprehensive assessment of both region overlap and boundary accuracy. By focusing on DSC, we ensure clear, interpretable results that are directly comparable across different models, as it is a widely adopted benchmark in segmentation tasks. Notably, our loss function is also DSC-based, ensuring optimisation aligns with the evaluation metric.

The Dice coefficient between a predicted segmentation mask X and ground truth mask Y is defined as:

$$\text{DSC}(X, Y) = \frac{2 \times |X \cap Y|}{|X| + |Y|} \tag{4}$$

where:

- $X \cap Y$ denotes the intersection (foreground pixels common to both masks),
- $|X|$ and $|Y|$ represent the cardinality (total foreground pixels) of each mask.

5. Experiment

In this section, we present a detailed account of the experiments performed to validate and analyse our segmentation approach for liver vessels from CT scans. The aim of these experiments is not only to quantitatively evaluate the performance of our model, but also to explore and explain critical aspects such as generalisation, model robustness, and avoidance of overfitting.

5.1. Cross-Validation for Robustness

We used 3-fold cross-validation to ensure that our model generalises well to new, unseen data. Cross-validation allows the model to be tested against multiple data subsets, providing a balanced and unbiased performance assessment. In contrast to the original study, which reported significant overfitting issues observed from epoch 20 onwards, our training strategy and careful model design demonstrated improved generalisation capabilities. Each fold was trained for 30 epochs using the EfficientNet encoder combined with the U-Net architecture and attention mechanisms that significantly increased the model's ability to focus on complex vascular structures.

5.2. Quantitative Evaluation

Table 2 summarises our quantitative results, presenting Dice scores, training, and validation losses for each fold. These metrics reflect our model's ability to accurately segment liver vessels and validate our choice of combined loss functions: Tversky loss and Binary Cross-Entropy (BCE). This combination is particularly beneficial due to its effectiveness in handling imbalanced datasets, which is crucial in liver vessel segmentation tasks, where the vessel structures occupy significantly fewer pixels compared to background tissues.

Fold	Best Validation Dice (%)	Final Training Loss	Final Validation Loss
1	76.06	0.94	1.51
2	72.01	0.91	1.63
3	79.34	0.86	1.41

Table 2. Performance metrics across 3-fold cross-validation.

In contrast to the main research paper, where the Dice score for vessel segmentation peaked at only 51.94%, our method achieves values around 70%. This improvement

stems from multiple enhancements. First, our data preprocessing pipeline introduces Z-score normalisation, which standardises intensity distributions across scans. This is especially valuable when dealing with diverse patient data, as it reduces variance caused by acquisition conditions. Second, we apply Contrast Limited Adaptive Histogram Equalisation (CLAHE), which improves local contrast and makes vessel boundaries more distinguishable, facilitating better learning by the model. Third, we incorporate an advanced training strategy with the AdamW optimiser, which combines the benefits of Adam's adaptive learning with effective weight decay for regularisation. Paired with ReduceLROnPlateau learning rate scheduling, our model can adaptively adjust learning speed and escape plateaus, improving convergence. Altogether, these design decisions have led to more stable learning and significantly better performance than previously reported approaches.

The effectiveness of these enhancements can be further appreciated by examining the loss and Dice curves across all folds. As illustrated in **Figure 3**, and **Figure 4** the training loss shows a consistent downward trend across all folds, suggesting that the model is learning general patterns in the training data. Meanwhile, validation loss decreases more gradually and occasionally fluctuates, which is expected due to variations in validation set complexity. Unlike the main research paper, where validation loss began rising significantly after epoch 20, a strong indicator of overfitting, our curves remain relatively stable, underscoring the success of our regularisation techniques. Similarly, the validation Dice scores reveal meaningful patterns. While there is some noise early on due to the difficulty of learning small vessel structures, all folds eventually exhibit a steady upward trajectory. This confirms that the model is increasingly successful in identifying relevant anatomical features as training progresses which is clearly visible in **Figure 2**. Notably, Fold 3 achieves a peak Dice score of 79.34%, which is a substantial improvement over the baseline of 51.94% from the primary study. These results not only validate our experimental design but also reinforce the idea that thoughtful preprocessing, architectural choices, and learning rate strategies collectively contribute to reliable model generalisation.

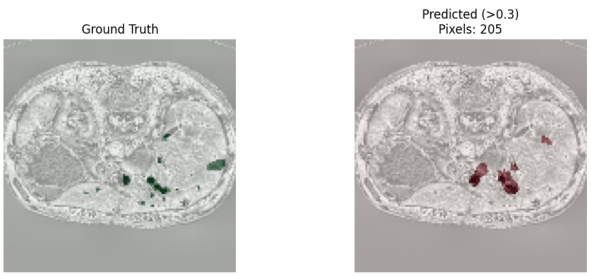

Figure 2. Predicted mask

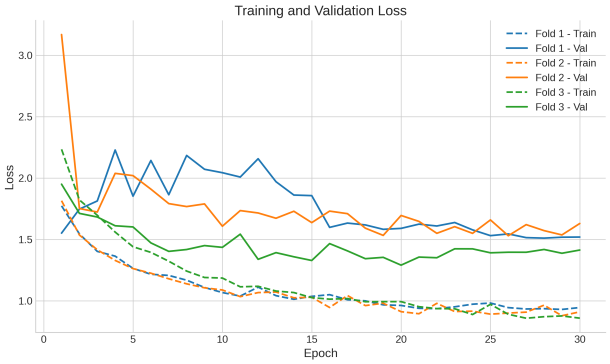

Figure 3. Training and Validation Loss

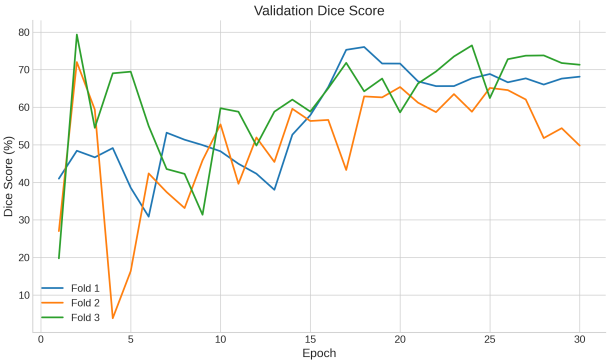

Figure 4. Validation Dice Score

5.3. Qualitative Evaluation

Visual assessments were crucial for understanding model performance beyond numerical metrics. **Figure 5** showcases an example of predicted segmentation masks at various probability thresholds (0.3, 0.5, and 0.7). These masks are derived from the soft prediction heatmap that reveals regions of high and low model confidence. From the visualisation, we observe that lower thresholds (e.g., 0.3) capture a greater number of vessel-like structures, which helps preserve sensitivity to small targets. However, this comes with the trade-off of more false positives. On the other hand, using a higher threshold like 0.7 makes the segmentation more conservative, reducing false positives but potentially missing fine vessel branches. The heatmap also helps highlight the uncertainty in predictions, particularly in low-contrast regions. This supports our strategy of using combined losses, Tversky for sensitivity tuning and BCE for stability which allows the model to balance sensitivity and specificity more effectively depending on the structure being segmented. These qualitative results complement our numerical metrics and confirm that our design choices contribute positively to capturing fine-grained vessel structures in liver scans.

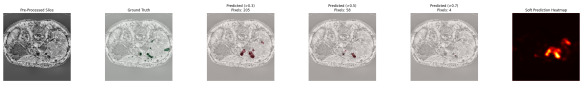

Figure 5. Predicted masks at different probability thresholds and corresponding soft prediction heatmap.

5.4. Overfitting Check

While our cross-validation and qualitative assessments demonstrate strong generalisation, it is equally important to verify that our model retains sufficient learning capacity. One common strategy for this is to deliberately train the model to overfit a single training sample. By doing so, we can test whether the model is capable of memorising intricate anatomical structures when regularisation is minimised and training continues until convergence.

Figure 6 shows the output of such an overfitting experiment. Here, the model was trained on a single CT slice until it achieved near perfect alignment with the ground truth segmentation. The figure presents the soft prediction heatmap and predicted vessel masks at different thresholds. Compared to earlier qualitative examples, the predictions here are denser and sharper, indicating that the model has successfully learned the full vessel structure in this case.

This result confirms that the model has sufficient representational power to perform complex segmentation. Importantly, the contrast between this result and the more restrained predictions observed during cross-validation suggests that our regularisation strategies, such as the combined Tversky and BCE loss, CLAHE preprocessing, and dynamic learning rate scheduling, are effectively preventing overfitting in the full training setting. Rather than merely memorising training data, the model is learning to generalise to unseen images, which is the central goal of our methodological design.

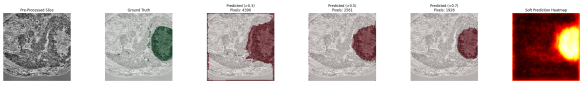

Figure 6. Overfitting check

After training, our pipeline automatically produced several useful outputs for analysis and interpretation. These included CSV logs containing per-epoch metrics such as training and validation losses, Dice scores, and learning rates for each of the three folds. Additionally, visual segmentation outputs were produced, including masks predicted at various probability thresholds and corresponding soft prediction heatmaps. These were recorded along with ground truth labels and preprocessed slices, facilitating qualitative comparison. A subset of these visual results is included in this report to demonstrate the segmentation behavior of our model. The full set of outputs (CSV files, prediction masks, heatmaps, and aligned inputs) is packaged with the final submission and is available in the supplementary folder for reference.

6. Related work

Many researchers have previously devoted their studies to deep learning models specifically aimed at liver segmentation. One prominent example includes the development of an “AI Radiologist" tool using a U-Net-based architecture, which achieved high accuracy in general liver segmentation but struggled to accurately segment liver tumors and blood vessels (Ronneberger et al., 2015).

Common architectures used for segmentation tasks include Fully Convolutional Networks (FCNs), which generally exhibit strong performance across diverse segmentation challenges but might fall short specifically when applied to liver anatomical structures due to their complexity (Long et al., 2015). Additionally, Generative Adversarial Networks (GANs) are effective in generating realistic segmentation masks but often lack precise anatomical accuracy needed for clinical use (Goodfellow et al., 2014).

Many studies have demonstrated the effectiveness of CNN based methods in medical image analysis in the past, like : (Han, 2017; Bi et al., 2017; Vorontsov et al., 2018) who used 2D deep FCNs with ResNet-like residual blocks were employed as the building blocks or (Chlebus et al., 2017) who trained the UNet architecture in two individual models, followed by a random forest classifier. Use of H-DenseU-Net has also been done and yielded better results than Resnet (Li et al., 2018).

Studies have also shown that CNNs are one of the most used architectures for liver and liver tumor segmentation in 3D images. Early deep learning models used transfer learning where a pre-trained model was used for initialisation of the weights or any part of the network. However, most of the recent deep learning models are trained end-to-end, without employing any pretrained model. Liver tumor segmentation technologies still have a lot more scope for improvement as compared to liver segmentation technologies. A nested model,even when trained sequentially outperforms the one-step model. (Gul et al., 2022; Gruber et al., 2019)

However, an important thing to highlight is that all the researchers have used different datasets (for example, 3DIRCADb, LiTS, etc) (Li et al., 2013; 2015; Moghbel et al., 2016). Some also collected additional data from hospitals to use for their experiments (Sun et al., 2017; Lu et al., 2017). So, these methods cannot be compared directly with each other due to the differences in the training dataset and whether it is fully automatic or not. (Li et al., 2018)

In contrast, more recent attention-based models such as Attention U-Net have shown considerable improvements in capturing complex anatomical details. However, these methods typically require extensive computational resources, making them impractical for real-time or online applications (Oktay et al., 2018).

To bridge these existing gaps, this research proposes combining efficient deep learning architectures with optimised preprocessing strategies. As compared to the primary research, using a different model(EfficientNet) as well as

altering the preprocessing techniques has improved the result and hence given a different and better model that can be used for the same.

7. Conclusion and Future Scope

The goal of this project was to accurately segment the hepatic vessels in medical images using deep learning models. We based our project on previously done research and tried to improve their result. Using different preprocessing methods and model architecture from the primary research, we managed to get a (peak) DICE score of 79.34%. This shows a clear improvement from the 51.94% of the primary research paper. This basically implies that the segmentation is better using our method. The regularisation strategies we used also prevented overfitting and hence improved our results. But that is not to say that this method can't be improved further.

Despite the strong performance of our proposed pipeline, several opportunities remain for further improvements in both methodology and practical deployment.

One of the major methods for that would be to use advanced augmentation and pre-processing techniques and implement learned preprocessing through trainable augmentation networks. Our current pipeline employs z-score normalisation and CLAHE to improve intensity consistency and contrast, both of which are manually designed. Future work could explore learned preprocessing strategies,i.e., the model adjusting according to the strategies. Differentiable augmentation or adaptive histogram equalisation modules could be applied as well to allow dynamic adjustment based on input image characteristics(Pizer et al., 1987; Tan & Le, 2019). This would make the system more robust to inter-patient variability and differences across scanners. Medical data is often limited due to annotation costs, so incorporating unlabelled scans can improve performance without requiring more labelled data (Han, 2017; Bi et al., 2017; Vorontsov et al., 2018). Pretraining the encoder on large-scale medical datasets in a self-supervised fashion may also boost performance on smaller datasets like MSDC-T8

Another method could be to extend the architecture beyond the current 2.5D U-Net with EfficientNet-B3. This design balances efficiency and accuracy, but it does not fully capture volumetric continuity. Lightweight 3D architectures, or hybrid 2.5D-3D solutions, could help improve spatial consistency across slices and better model thin, branching vessel structures (Milletari et al., 2016; Zhou et al., 2018). Incorporating transformer-based components (e.g., TransUNet or Swin UNet) may improve global context modelling, helping the network resolve ambiguities in low-contrast or noisy regions (Chen et al., 2021; Oktay et al., 2018). These methods would need to be optimised for clinical use cases to avoid excessive computation times.

We can also use this model to try segmentation on other parts of the body and generalise the model. Applying this model on the BRATS dataset (Awsaf, 2020), for example, will help us create an advanced model that could fulfill both liver and brain tumor segmentation. Increasing the number of datasets,i.e, using multiple datasets collected from different areas, will also yield better results. Multiple researchers have done similar applications in the past to make their models more advanced. (Sun et al., 2017; Lu et al., 2017; Quan et al., 2016). Training on a mix of datasets or fine-tuning the model across domains would enable better generalisation and reduce overfitting to a specific dataset, and can demonstrate transferability.

Something else to be considered for future work is deployment. Model pruning, quantisation, etc are some techniques that help reduce the model's size and inference time, and make real-time use possible in clinical settings (Yakubovskiy, 2019; Long et al., 2015). The development of an interactive tool for doctors to visualise segmentations, overlay uncertainty heatmaps, and manually adjust outputs could help in increasing trust, transparency, and adoption in practice.

To sum it up, some future pathways can be use of advanced preprocessing with adaptive methods, use of 3D and transformer-based models, using unlabelled data through semi-supervised learning, increasing generalisability by multi-dataset training, and optimising the system for clinical deployment. These steps will help build a more accurate, robust, and practical hepatic vessel segmentation tool suitable for real-world medical applications.

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