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Advanced machine learning for enhanced abdominal organ segmentation

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ABSTRACT

This research evaluates the ResUnet model's performance in using computed tomography (CT) images to segment various abdominal organs. Weak boundaries, computing efficiency, and anatomical diversity are the current obstacles in abdominal multi-organ segmentation. By merging residual networks with U-Net, ResUnet overcomes obstacles by increasing precision and effectiveness, which qualifies it for use in medicine. The model's effectiveness was assessed on a number of organs, and the segmentation accuracy was measured using the dice similarity coefficient (DSC). The ResUnet model's ability to precisely segment organs with distinct borders was proved by its exceptional accuracy in segmenting important organs, such as the liver (mean DSC: 0.880) and spleen (mean DSC: 0.830). However, the model struggled to separate the esophagus correctly (mean DSC: 0.000) and struggled with smaller and more complex organs like the pancreas (mean DSC: 0.429) and gallbladder (mean DSC: 0.143). These results highlight the method's limitations when handling organs with asymmetrical shapes or hazy borders.

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1. INTRODUCTION

Over the last several decades, there have major breakthroughs within the domain of medical imaging, especially in the development of tools for visualizing the human body's interior architecture. Among these methods, abdominal imaging is essential for the detection and management of a variety of illnesses, such as malignancies, liver problems, and gastrointestinal issues. However, manually separating abdominal organs from medical images-like computed tomography (CT) or magnetic resonance imaging (MRI) scans-remains a time-consuming and labour-intensive process. Because radiologists' range in their skill levels and interpretations, this technique is likewise prone to fluctuation. An increasing number of people are interested in using machine learning (ML) approaches, especially deep learning (DL), to automate and increase the accuracy of abdominal segmentation as a solution to these problems [1].

The area of medical imaging has seen a revolutionary change because to ML, particularly DL, which provides robust tools for autonomous image processing. Convolutional neural networks (CNNs) have shown especially good results in tasks including segmentation, object detection, and picture categorization. In the context of abdominal imaging, these models can learn to identify and delineate multiple organs simultaneously, with a level of precision that often surpasses traditional methods. For instance, the development of fully automated segmentation techniques, such as the ALAMO model, has demonstrated high accuracy in segmenting multiple organs at risk (OARs) in abdominal MRI scans, achieving dice similarity coefficients (DSCs) as high as 0.96 for certain organs. Similarly, approaches like deep multi-planar co-training (DMPCT) have been proposed to leverage consensus information from multiple planes in CT scans, further enhancing the reliability of segmentation outcomes [2].

The adoption of these ML techniques in abdominal imaging is driven by their ability to process large datasets, learn complex patterns, and generalize well to new data. This capability is particularly important given the high anatomical variability and the presence of weak boundaries between adjacent organs in abdominal images. For example, the use of dense V-networks has shown promise in improving segmentation accuracy without the need for inter-subject image registration, a step that is often challenging in abdominal images due to variability in anatomy [3].

Precise multi-organ division is critical for various clinical applications, including surgical planning, disease diagnosis, and radiation therapy. The ability to precisely delineate multiple organs within the abdomen enables clinicians to better assess the extent of disease, plan appropriate interventions, and monitor treatment outcomes. In radiation therapy, for example, precise organ segmentation is at risk is essential to minimize damage to healthy tissues while delivering the maximum therapeutic dose to the target area [4].

Moreover, automated multi-organ segmentation facilitates the analysis of large-scale clinical datasets, paving the way for more personalized and data-driven approaches to healthcare. Techniques such as atlas-based methods, where segmentation is guided by pre-labeled anatomical templates, and more recent techniques of DL have demonstrated significant improvements in handling the complexities of abdominal anatomy. For instance, the combination of atlas-based segmentation with context learning has been used to enhance the accuracy of multi-organ segmentation on clinically acquired CT scans, demonstrating robust performance across different patient populations [5].

Conze *et al.* [6] explored a cascaded DL model with adversarial networks for CT and MRI segmentation. This method outperformed traditional encoder-decoder architectures for the spleen, kidneys, and liver. Wolz *et al.* [7] proposed a weighting scheme and atlas registration for fully automated segmentation. This method demonstrated competitive results for liver, kidneys, pancreas, and spleen. Lee *et al.* [8] developed Siamese learning to improve segmentation by capturing both global and local contexts. This method achieved a 2% improvement in dice score coefficients compared to existing methods.

A multi-sequence DL method was presented by Amjad *et al.* [9] for automatic abdominal segmentation in MRIs used to schedule radiation therapy. To improve segmentation accuracy, there model makes use of data from several MRI sequences. T1 and T2 weighted MRI sequences are used to test and train the model, which works on a 3DResUnet network. The results of the investigation showed that the model could accurately and effectively create outlines for 12 upper abdominal organs, by the DSC of 0.87. The study emphasizes how crucial multi-sequence MRI is for enhancing the precision of organ segmentation in clinical practice, especially when it comes to tumors of the abdomen. To accomplish segmentation of images. Kakeya *et al.* [10] presented a DL scheme, 3D U-JAPA-Net, which integrates transfer learning with a probabilistic atlas of organs for CT-based abdominal multi-organ segmentation. This method improved upon traditional 3D U-net by addressing errors associated with local volumetric data, thereby enhancing segmentation accuracy. The study achieved higher dice scores compared to conventional 2D and 3D U-nets, underscoring the effectiveness of incorporating probabilistic atlases into DL frameworks for organ segmentation. Wang *et al.* [11] developed the cross-convolutional transformer (C2Former) network to enhance the generalization and accuracy of organ segmentation across various medical imaging modalities. The study applied this method to CT images of abdominal organs, MRI of cardiac structures, and skin cancer images, achieving high performance in all datasets. The C2Former effectively integrates local and global contexts, making it a robust solution for diverse medical imaging challenges. In order to enhance abdominal segmentation from CT images. Irshad *et al.* [12] suggested a technique which utilizes prediction of organ-boundary as a supplemental job. The technique demonstrated the benefit of multi-task learning in managing complicated abdominal anatomy by exhibiting notable gains.

Liang *et al.* [13] developed a hybrid model (HDM) combined with fusion network to enhance segmentation accuracy of abdominal CT scans. The HDM addresses the limitations of rigid or affine transformations by incorporating both inter-patient and intra-patient deformations, thus capturing subtle organ deformations more effectively. The strategy beat current cutting-edge methodologies, using 0.852 as the average DSC across various organs. Hu *et al.* [14] created a completely automated multi-organ segmentation approach that combines deep CNNs with time-implicit level sets. This approach was highly accurate, with dice overlap ratios of 96.0%, 94.2%, and 95.4% for spleen, kidneys and liver respectively, proving its resilience and efficiency in clinical situations. Wang *et al.* [15] studied organ segmentation of abdominal CT images based on organ networks with reverse connections. This method enhances organ discrimination by focusing on local background reduction and structural similarity, which are critical in complex anatomical regions. The approach outperformed traditional 2D and 3D patch-based methods with regard to mean surface distances and DSCs, establishing itself as a leading method in accurate abdominal organ segmentation. In order to enhance segmentation, Tong *et al.* [16] presented the DenseNet, which uses a dense connection block. Self-paced DenseNet attained dice coefficient of 84.46% across eight organs, surpassing previous methods, especially for challenging structures like the duodenum and gallbladder. Tang *et al.* [17] developed a random network technique for resolution of 3D abdominal. This method addresses the memory limitations of GPU-based networks by using a patch-based approach. The given technique significantly improves accuracy of segmentation, achieving dice coefficient of 0.856, outperforming conventional coarse baseline technique.

Abdominal multi-organ segmentation has seen recent progress using U-Net, dense V-networks, atlas-based methods, and DMPCT. U-Net and dense V-networks are able to segment large, well-defined organs but struggle to segment smaller structures with weak boundaries. Methods that rely on atlas-based approaches do well where there is consistency of the anatomical shapes, but are challenged by variability. Although DMPCT requires high computational resources, using DMPCT with limited annotation can significantly increase the accuracy of the detector. However, these techniques suffer from common limitations; they can operate on smaller organs, handle weak inter-organ boundaries, and be computationally efficient, but there is a need for more innovation [18].

The current challenges in abdominal multi-organ segmentation include managing anatomical variability, segmenting organs with weak boundaries, and ensuring computational efficiency. While existing models have made progress, gaps remain, particularly in handling complex anatomy and maintaining efficiency. The ResUnet model addresses these issues by combining the DL strengths of residual networks with U-Net's effective localization. This architecture improves the model's ability to handle anatomical diversity, accurately segment organs with weak boundaries, and remain computationally efficient; this renders it ideal for use in medical clinics [19].

2. METHOD

2.1. Datasets

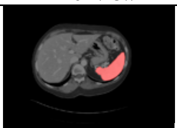
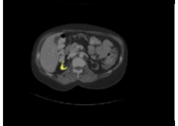
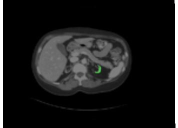
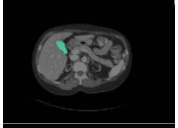
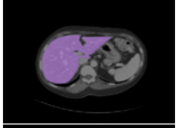
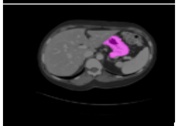
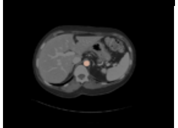
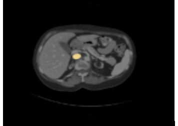
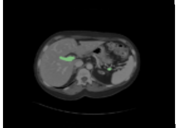
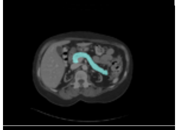
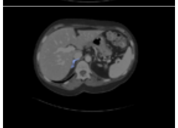
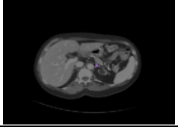
Datasets are essential for the advancement and assessment of ML models, especially in the field of medical imaging. This study exclusively utilized standard, publicly available datasets, widely recognized in the domain of multi-organ segmentation. The datasets include standardized and annotated photos, enabling researchers to evaluate and validate their algorithms using a shared reference. The subsequent datasets are often employed in the domain and are crucial for evaluating and verifying segmentation models. The beyond the cranial vault (BTCV) dataset includes 30 fully annotated CT scans of many organs, such as the liver, kidneys, pancreas, and spleen. The complete coverage of abdominal organs in this study is generally acknowledged, making it a typical reference point in segmentation research [20]. The combined healthy abdominal organ segmentation (CHAOS) dataset contains 40 annotated CT volumes, complemented by MRI scans for multi-modality segmentation have been annotated to identify organs such as the liver, spleen, and kidneys. This dataset is highly relevant for investigations involving the segmentation of many modalities. It has been widely utilized in challenges and contests to assess the performance of models [21]. In addition, the liver tumour segmentation (LiTS) dataset includes 130 annotated CT volumes, primarily focusing on liver and tumor segmentation, but with additional organ annotations primarily focusses on segmenting the liver and tumours, but it also provides a substantial number of CT scans that have been annotated. The dataset is of great significance for training models that use liver segmentation as a component of a multi-organ strategy [22].

The total dataset size for this study was 200 annotated CT volumes. These were divided into training, validation, and testing subsets using a 70:20:10 split to identify several abdominal organs, such as the spleen, kidneys, gallbladder, liver, stomach, and others as shown in Table 1. The spatial resolution of the CT scans varies across datasets but was standardized during preprocessing to ensure uniform input dimensions. Key features extracted from the images include pixel intensities normalized to the range [0, 1] and anatomical structure boundaries represented in the segmentation masks. The imaging technique offers full visualizations of each organ, including detailed axial views. The dataset's comprehensive annotations make it well-suited for training and assessing ML models that specialize in multi-organ segmentation. This guarantees precision and dependability in accurately delineating organs across several anatomical planes [23].

2.2. Model development

We develop the ResUnet model for abdominal organ segmentation in a systematic fashion by incorporating novel preprocessing, training, and evaluation strategies. Performance of the model is benchmarked using advanced metrics for robustness and accuracy.

Table 1. Dataset comprising CT images used for several abdominal organs

Name of the organ	Axial view
Spleen	
Right kidney	
Left kidney	
Gallbladder	
Esophagus	
Liver	
Stomach	
Aorta	
Poor vena cava	
Splenic vein and portal vein	
Pancreas	
Right adrenal gland	
Left adrenal gland	

2.2.1. Data pre-processing

Several preprocessing steps are taken to standardize input data and to improve model performance prior to using the CT dataset for model training. To rescale the CT image intensity values between 0 to 1 uniformly the CT image intensity values are performed intensity normalization and the same is expressed by (1);

$$I_{normalised} = \frac{I - I_{min}}{I_{max} - I_{min}} \quad (1)$$

where I is the default intensity value, and I_{min} and I_{max} are the maximum and minimum intensity figures in datasets.

In order to maintain constant input dimensions for the model, all photos in the dataset are resampled to a uniform resolution, ensuring homogeneity throughout. To enhance the variety and resilience of the model, the training data undergoes several techniques like rotation, scaling, flipping, and elastic deformations. Data augmentation can be expressed quantitatively as [24],

$$T_{(x)} = A_{(x)} + \in \quad (2)$$

where, $T_{(x)}$ denotes transformed image, $A_{(x)}$ denotes augmented operation and $\in$ is the random noise or can be termed as perturbations.

2.2.2. Model training

The ResUnet model integrates the residual learning technique with architecture of U-Net. The conventional U-Net is enhanced by residual connections, which can be formally defined as,

$$y = F(x, \{W_i\}) + x \quad (3)$$

where, x indicates input given to layer, $F(x, \{Wi\})$ indicates output of block and y denotes layer output post residual connection. The reason the loss function is used is to optimization which is more compatible for segmentation task. The coefficient of dice is given as [25],

$$Dice = \frac{2\,|P \cap G|}{|P| + |G|} \quad (4)$$

where, P used for segmentation and G is truth segmentation. Model minimized the dice loss which is given by,

$$LOSSDice = 1 - Dice \quad (5)$$

the input CT images were normalized to the range [0,1] to ensure uniformity in intensity values, as given by,

$$I_{normalized} = \frac{I - I_{min}}{I_{max} - I_{min}} \quad (6)$$

where, I represent the intensity of pixel and I_{min} and I_{max} denote the minimum and maximum pixel intensities in the dataset respectively. Resampling ensured that all images had consistent dimensions, critical for maintaining uniformity in input across the network.

The stochastic gradient descent (SGD) optimizer was employed, selected for its efficiency and ability to generalize well on segmentation tasks. A momentum factor of 0.9 was used to accelerate convergence and reduce oscillations during training. The ResUnet model was trained with an initial learning rate of 0.01 that was dynamically modified using a step decay schedule to ensure smooth convergence. In particular, the learning rate was decreased by 0.1 after every 10 epochs, which enabled the model to improve its performance gradually as training progressed. In order to optimize the model's generalization capabilities and computational efficiency, a sample size of 16 was chosen. The high-resolution character of the CT images in the dataset also influenced this decision, as well as the GPU memory requirements. The training was conducted over 100 epochs, which allowed for a sufficient number of iterations to accomplish convergence while reducing the likelihood of overfitting. In addition, an early halting mechanism was implemented to terminate training if the validation loss did not improve for 10 consecutive epochs, thereby preventing unnecessary overtraining and ensuring the efficient use of computational resources.

2.3. Model validation

To rigorously evaluate the generalization capabilities of the ResUnet model, we adopted a 5-fold cross-validation protocol. In this established approach, the entire dataset was partitioned into five subsets (or 'folds') of comparable size. The experimental procedure was repeated five times: during each iteration, one subset was reserved as the holdout validation set, while the other four subsets were utilized for model training. This methodical rotation ensured that every data point was included in the validation phase exactly once.

For a robust assessment of the model's segmentation performance, we calculated and reported the average results of key performance metrics across all five folds. These metrics included the DSC, the Hausdorff distance (HD), and the average surface distance (ASD). The selection of the K=5 configuration was strategically made to achieve an optimal balance between the depth of model evaluation and the constraints of computational efficiency, given the inherent size and complexity of our image dataset.

3. RESULTS AND DISCUSSION

This section introduces the quantitative results derived from the segmentation task, focusing on the ResUnet model's ability to accurately delineate various abdominal organs. We primarily use the DSC as our main performance indicator. The DSC is a well-established, standard metric within medical image analysis, designed to precisely quantify the degree of spatial overlap between the model's predicted segmentation and the manually annotated ground truth. It is interpreted such that higher values indicate superior segmentation accuracy, with a perfect score of 1.0 representing complete and perfect alignment with the true organ boundaries.

The results in Table 2 clearly show that the ResUnet model's ability to separate organs is very different from one another. The model did a great job of separating the spleen into its parts. It got a high mean DSC of 0.8299, which means it was accurate in all of its tests. This good result is probably because the spleen is bigger and has clear edges, which makes it easier for the model to find and divide correctly. The model also did a good job with the kidneys. The right kidney had a mean DSC value of 0.7452 and the left kidney had a value of 0.7124. There was some variation in the results, especially for the left kidney, but the total performance is good enough for most clinical uses, like finding kidney tumours or making plans for surgeries. The model had a hard time with the gallbladder, though. Its mean DSC value was only 0.1433, which means it wasn't very good at segmenting. This problem probably happens because the gallbladder is small, has an odd shape, and doesn't have clear edges, which makes it hard for the model to tell it apart from other cells nearby. A mean DSC value of 0.0004 for the oesophagus, which was the hardest organ to separate, shows that the model did not do a good job of it. This bad performance may have been caused by the esophagus's narrow, tubular shape and its closeness to other body parts. This suggests that the ResUnet model, in its current form, might not be good for tasks that require segmenting the oesophagus.

Table 2. DSC for different city scans

Organ name	img0037.nii	img0030.nii	img0007.nii	img0039.nii	img0024.nii
Spleen	0.8073	0.8658	0.6368	0.9288	0.9106
Right kidney	0.7913	0.7283	0.7038	0.6921	0.8106
Left kidney	0.7304	0.8175	0.5990	0.6191	0.7957
Gallbladder	0.3702	0.1529	0.0789	0.1134	0.0009
Oesophagus	0.0009	0.0003	0.0005	0.0002	0.0003
Liver	0.8623	0.8245	0.8722	0.9172	0.9215
Stomach	0.4041	0.7655	0.5754	0.8108	0.7154
Aorta	0.7619	0.7656	0.5089	0.5781	0.8134
Inferior vena cava	0.6663	0.7614	0.6574	0.5543	0.3849
Portal vein and splenic vein	0.5257	0.5916	0.4141	0.3750	0.5927
Pancreas	0.3938	0.6492	0.1667	0.5072	0.4297
Right adrenal gland	0.1147	0.2617	0.0005	0.0640	0.0051
Left adrenal gland	0.0205	0.2801	0.0000	0.0487	0.2040

The Figures 1 and 2 demonstrates how the working speed of the ResUnet model changes with the number of slices for different CT scan files, including img0037.nii, img0039.nii, img0007.nii, img0024.nii, and img0030.nii. The speed, which is given in slices per second, tells you how fast the model processes each scan, and the form tells you how many slices are in each CT scan. The research shows that the processing speed changes a lot from one scan to the next. As an example, img0007.nii is handled the fastest, at 16.317 slices per second, even though it has the most slices (163). If we compare this to img0030.nii, which has 124 slices, it is handled more slowly, at 12.038 slices per second. This shows that the processing speed is not directly related to the number of slices. Instead, how quickly the model can segment the images may depend on other factors. It's interesting that img0024.nii, the scan with the fewest slices (90), doesn't handle data the fastest. Instead, it moves at a slower rate of 12.075 slices per second. This suggests that the complexity of the anatomical structures, the sharpness of the organ boundaries, and maybe even how well the model can be computed might have a bigger effect on processing speed than just the number of slices. The overall results show that there is some interaction between the number of slices and the working speed, but it's not a simple one. The high processing speed of the scan with the most slices shows that the ResUnet model can handle bigger datasets well. But the model's success is affected by more than just the size of the dataset. This shows how difficult it is to separate parts of medical images.

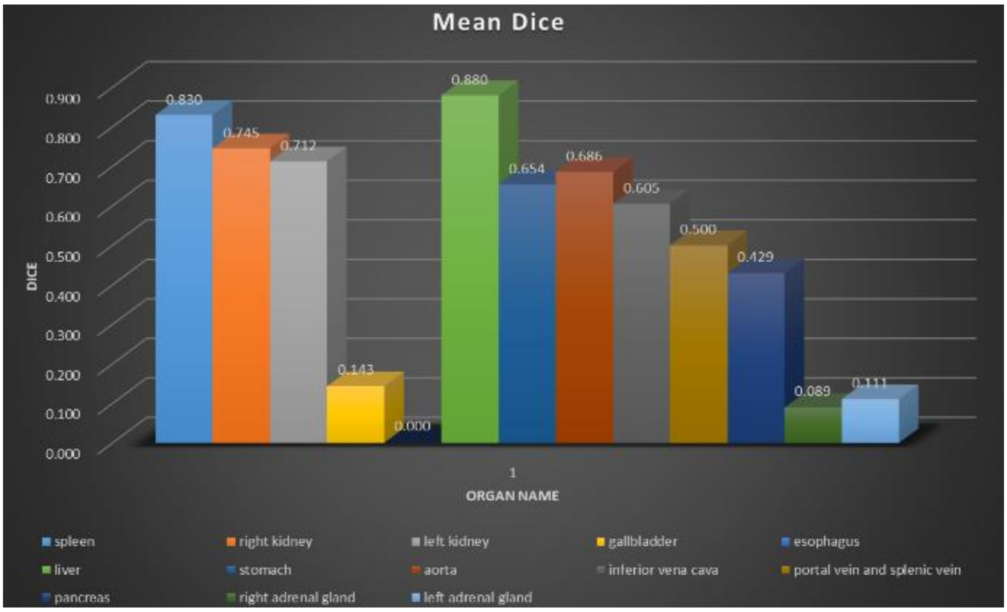


Figure 1. Mean dice values plot for different organs chosen in the study

Figure 2. Relationship between shape and speed for different CT scan images

4. CONCLUSION AND FUTURE DIRECTION

The study specifically attempted to identify the model's capabilities and constraints while dealing with varied anatomical structures. The ResUnet model exhibited exceptional segmentation precision when applied to bigger organs characterized by well delineated borders. The liver attained the highest average DSC of 0.880, whereas the spleen obtained an average DSC of 0.830. The high scores suggest that the model is very suitable for accurately dividing big, clearly defined organs into separate segments.

The right kidney had a satisfactory performance, with a mean DSC of 0.745. Conversely, the left kidney exhibited a slightly lower mean DSC of 0.712, indicating consistent performance in kidney segmentation despite minor variations. These findings indicate that although the model has efficacy in segmenting larger organs, it encounters difficulties when segmenting organs that are encompassed by intricate anatomical structures or possess varying forms.

The gallbladder had a mean DSC of 0.143, indicating a low level of similarity, while the pancreas achieved a DSC score of 0.429. The process of dividing the right and left adrenal glands into separate segments was found to be difficult, as shown by the mean DSCs of 0.089 and 0.111, respectively. The segmentation of the oesophagus exhibited a significant limitation, as seen by a mean DSC of 0.000. This indicates that the model was unable to accurately segment this particular organ.

Improving the model's concentration on critical regions, such as SE blocks or self-attention layers, can improve segmentation accuracy for smaller and less distinct organs by incorporating attention modules. The model's generalization to a variety of anatomical structures can be enhanced by the expansion of augmentation techniques, such as synthetic data generation through GANs, which can help resolve data scarcity. The efficacy of complex segmentation tasks could be enhanced by integrating features from multi-scale feature fusion networks or combining ResUnet with state-of-the-art models such as transformers.

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FUNDING INFORMATION

We, the authors of the manuscript titled "Advanced ML for enhanced abdominal organ segmentation" (Authors: Rohini Pawar, Dr. Rohini Jadhav, Dr. Rohit Jadhav), hereby declare that no external funding was received for this research. The work described in the paper was conducted solely using the institutional resources available at the authors' respective departments within Bharati Vidyapeeth (Deemed to be University), Pune, India. We confirm that this declaration is accurate and complete.

AUTHOR CONTRIBUTIONS STATEMENT

We, the authors, confirm that we have all contributed significantly to the research and preparation of the manuscript titled "Advanced ML for enhanced abdominal organ segmentation" and agree to its submission to the International Journal of Informatics and Communication Technology (IJ-ICT). The following table details the specific contributions of each author.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Rohini Pawar	✓	✓	✓	✓	✓	✓		✓	✓	✓				
Rohini Jadhav	✓	✓		✓	✓	✓	✓	✓		✓	✓	✓		
Rohit Jadhav	✓	✓	✓		✓	✓	✓			✓	✓		✓	

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

We, the authors of the manuscript titled "Advanced ML for enhanced abdominal organ segmentation" (Rohini Pawar, Dr. Rohini Jadhav, and Dr. Rohit Jadhav), hereby declare that no conflicts of interest exist, either financial or otherwise, that could be construed as influencing the results, integrity, or interpretations presented in this manuscript. Specifically, the authors affirm that, we have no commercial or associative interest that represents a conflict of interest in connection with the work submitted. We have not received any funds, grants, or financial support from any organization that would benefit from the publication of this manuscript. All authors have seen and approved the final version of the manuscript and the submission of this declaration.

INFORMED CONSENT

Regarding our manuscript titled “Advanced ML for enhanced abdominal organ segmentation,” authored by Rohini Pawar, Dr. Rohini Jadhav, and Dr. Rohit Jadhav, we affirm our commitment to ethical research standards. We recognize that the protection of privacy is a legal right that must not be breached without individual informed consent. Our study ensures that no personal identifying information is disclosed, maintaining the highest level of confidentiality. We strictly followed the institutional guidelines and legal frameworks required for the use of datasets in scientific research.

ETHICAL APPROVAL

Regarding our manuscript titled “Advanced ML for enhanced abdominal organ segmentation,” authored by Rohini Pawar, Dr. Rohini Jadhav, and Dr. Rohit Jadhav, we confirm that this research strictly adheres to all ethical guidelines. The study was conducted in full compliance with the relevant national regulations and institutional policies in accordance with the tenets of the Helsinki Declaration. We formally state that the research has been approved by the Institutional Review Board of Bharati Vidyapeeth (Deemed to be University) College of Engineering, Pune.

DATA AVAILABILITY

Regarding our manuscript titled “Advanced ML for enhanced abdominal organ segmentation,” we are committed to promoting transparency and reproducibility in our research. The data that support the findings of this study are available from the corresponding author, upon reasonable request. We maintain the supporting evidence and raw processed data securely within our institutional records at Bharati Vidyapeeth. Interested researchers may contact the authors for the purpose of study. This availability is subject to ethical considerations and the restrictions established during the initial data collection phase. We affirm that all evidence supporting the findings presented in this article remains accessible for legitimate scientific inquiry.

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