



UQ-TSE-Net: A Lightweight Uncertainty-Aware Network for Reliable Liver Tumor Segmentation in Contrast-Enhanced CT Images

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Abstract- Liver tumor segmentation of contrast-enhanced CT (computerized tomography) scans is an important step for computer-aided liver cancer diagnosis, treatment, and follow-up. Although deep learning approaches have recently been significantly advancing the task of medical image segmentation, liver tumor segmentation still faces many challenges since liver tumors usually have non-regular shapes, fuzzy boundaries, and heterogeneous enhancement patterns. Besides, class imbalance between lesions and background tissues is also very high. Existing models mostly predict a final liver tumor mask without providing any kind of information on the reliability of this prediction. The absence of uncertainty quantification is one of the most serious problems of medical imaging due to the necessity of reviewing uncertain regions by experts. In this work, we propose UQ-TSE-Net (uncertainty-quantifying total segment enhancement network), a novel uncertainty-aware lightweight architecture for reliable liver tumor segmentation of contrast-enhanced CT scans. The proposed approach combines efficient feature extraction via convolutions, attention-based feature refinement, boundary awareness, and uncertainty estimation using Monte Carlo dropout. The first two blocks form a main segmentation branch, while the latter allows improving the performance of segmentation in ambiguous regions. Finally, the uncertainty of the model predictions is estimated using the Monte Carlo dropout approach that produces a set of different predictions. Based on these predictions, a pixel-level uncertainty map is obtained highlighting low-confidence regions of liver tumors, especially those located at fuzzy tumor margins. For the experiments, we will use the Liver Tumor Segmentation Challenge dataset (LiTS17). The comparison will be made to widely-used segmentation models such as UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR, and nnU-Net. The models' performance will be evaluated using classical segmentation metrics like Dice score, Intersection over Union, precision, and recall and additional reliability-oriented metrics, like Expected Calibration Error and Brier score. UQ-TSE-Net will allow getting not only an accurate tumor mask but also uncertainty information that is crucial for further interpreting the results. In the current study, we make another step towards obtaining reliable computer-aided liver tumor analysis with the help of uncertainty-aware lightweight architecture.

Keywords- Boundary-aware segmentation, Liver tumor segmentation, Uncertainty estimation, UQ-TSE-Net.



I. INTRODUCTION

Liver cancer remains one of the major causes of cancer-related mortality worldwide, and accurate assessment of liver tumors plays an important role in diagnosis, treatment planning, and follow-up care [1], [2]. Contrast-enhanced computed tomography (CT) is commonly used for liver tumor evaluation because it provides detailed anatomical information about tumor location, size, and spread [3]. In clinical practice, tumor regions are often outlined manually by radiologists. However, manual delineation is time-consuming, depends on expert experience, and may vary between observers, especially when tumor boundaries are weak or lesion appearance is heterogeneous [4], [5].

Automatic liver tumor segmentation has therefore become an important research problem in medical image analysis. Deep learning methods, particularly convolutional neural networks, have shown strong potential for medical image segmentation because they can learn useful image features directly from data [4], [5]. U-Net and its variants are widely used in biomedical segmentation because their encoder-decoder structure combines semantic information with spatial details [6]. In liver tumor segmentation, cascaded fully convolutional networks and 3D segmentation approaches have also been explored to improve tumor localization and volumetric understanding [7], [8].

Recent segmentation models have further improved performance by using attention mechanisms, nested skip connections, atrous convolution, transformer-based encoders, and self-configuring pipelines [9]–[14]. Attention-based models help emphasize important tumor regions, while transformer-based models capture long-range contextual information that may be useful for complex medical images [9], [12], [13]. Similarly, nnU-Net has shown strong performance across several biomedical segmentation tasks by automatically adapting its configuration to the dataset [14].

Despite these advances, liver tumor segmentation remains difficult. Tumors may appear with irregular shapes, low contrast, fuzzy boundaries, and variable enhancement patterns. In many CT slices, the tumor region is very small compared with the background, which creates severe class imbalance. These factors may lead to missed tumor regions, inaccurate boundaries, or false positive predictions. Such errors are important because segmentation results are often used for further clinical analysis, including tumor burden estimation, treatment response assessment, and disease monitoring [1], [3].

Most existing segmentation models produce only a final tumor mask. However, they do not clearly indicate how reliable the prediction is. A model may generate a segmentation output even in regions where the tumor boundary is uncertain. In medical imaging, this limitation is important because uncertain predictions may require careful expert review before being used for clinical decision-making. Therefore, segmentation models should not only provide accurate masks but also indicate the uncertainty associated with their predictions.

Uncertainty estimation has become an important direction in reliable deep learning. Bayesian deep learning and Monte Carlo dropout provide practical ways to estimate predictive uncertainty in neural networks [15], [16]. In segmentation tasks, uncertainty maps can highlight low-confidence regions, especially near weak boundaries, small lesions, or visually ambiguous areas. Calibration-based measures such as Expected Calibration Error and Brier score can also be used to evaluate whether the confidence of a model is consistent with its prediction accuracy [17], [18].

To address these challenges, this study proposes UQ-TSE-Net, a lightweight uncertainty-aware network for liver tumor segmentation in contrast-enhanced CT images. The proposed framework integrates efficient convolutional feature extraction, boundary-aware learning, attention-based refinement, and Monte Carlo dropout-based uncertainty estimation. Unlike conventional segmentation networks that



generate only a tumor mask, UQ-TSE-Net produces both a tumor segmentation map and a pixel-level uncertainty map. The segmentation output helps localize tumor regions, while the uncertainty map highlights low-confidence areas that may require further review.

Experiments are conducted using the Liver Tumor Segmentation Challenge dataset (LiTS17), which is a benchmark dataset for liver and liver tumor segmentation [19]. The proposed method is compared with widely used segmentation models, including UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR, and nnU-Net. The evaluation includes conventional segmentation metrics such as Dice score, Intersection over Union, precision, and recall, along with uncertainty-based reliability metrics such as Expected Calibration Error and Brier score. Through this evaluation, the study aims to develop a segmentation framework that is not only accurate but also more reliable and interpretable for computer-aided liver tumor analysis.

II. LITERATURE REVIEW

Liver tumor segmentation of contrast-enhanced CT (computerized tomography) scans is an important step for computer-aided liver cancer diagnosis, treatment, and follow-up. Although deep learning approaches have recently been significantly advancing the task of medical image segmentation, liver tumor segmentation still faces many challenges since liver tumors usually have non-regular shapes, fuzzy boundaries, and heterogeneous enhancement patterns. Besides, class imbalance between lesions and background tissues is also very high. Existing models mostly predict a final liver tumor mask without providing any kind of information on the reliability of this prediction. The absence of uncertainty quantification is one of the most serious problems of medical imaging due to the necessity of reviewing uncertain regions by experts.

In this work, we propose UQ-TSE-Net (uncertainty-quantifying total segment enhancement network), a novel uncertainty-aware lightweight architecture for reliable liver tumor segmentation of contrast-enhanced CT scans. The proposed approach combines efficient feature extraction via convolutions, attention-based feature refinement, boundary awareness, and uncertainty estimation using Monte Carlo dropout. The first two blocks form a main segmentation branch, while the latter allows improving the performance of segmentation in ambiguous regions. Finally, the uncertainty of the model predictions is estimated using the Monte Carlo dropout approach that produces a set of different predictions. Based on these predictions, a pixel-level uncertainty map is obtained highlighting low-confidence regions of liver tumors, especially those located at fuzzy tumor margins.

For the experiments, we will use the Liver Tumor Segmentation Challenge dataset (LiTS17). The comparison will be made to widely-used segmentation models such as UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR, and nnU-Net. The models' performance will be evaluated using classical segmentation metrics like Dice score, Intersection over Union, precision, and recall and additional reliability-oriented metrics, like Expected Calibration Error and Brier score.

UQ-TSE-Net will allow getting not only an accurate tumor mask but also uncertainty information that is crucial for further interpreting the results. In the current study, we make another step towards obtaining reliable computer-aided liver tumor analysis with the help of uncertainty-aware lightweight architecture.

III. METHODOLOGY

This section presents the methodology used to develop the proposed UQ-TSE-Net framework for uncertainty-aware liver tumor segmentation from contrast-enhanced CT images. The proposed approach is designed to generate both a tumor segmentation mask and a pixel-level uncertainty map.



The overall methodology consists of dataset preparation, image preprocessing, model development, boundary-aware learning, uncertainty estimation, loss function design, and quantitative evaluation.

A. Dataset Description

The experiments are conducted using the Liver Tumor Segmentation Challenge dataset, commonly known as LiTS17. This dataset contains contrast-enhanced abdominal CT scans along with expert-annotated liver and tumor masks. In this study, the tumor annotations are used to prepare binary tumor masks for supervised segmentation. Each CT slice is paired with its corresponding ground-truth tumor mask and used for model training, validation, and testing.

Let the input CT image be represented as $X \in \mathbb{R}^{(H \times W)}$, where H and W denote the height and width of the image. The corresponding binary tumor mask is represented as $Y \in \{0,1\}^{(H \times W)}$, where tumor pixels are labeled as 1 and background pixels are labeled as 0. The objective of the proposed model is to learn a mapping from the CT image to the tumor probability map and uncertainty map.

$$(\hat{Y}, U) = f_{\theta}(X)$$

where $\hat{Y}$ denotes the predicted tumor probability map, U denotes the pixel-level uncertainty map, and f_{θ} represents the proposed UQ-TSE-Net model with trainable parameters θ .

B. Image Preprocessing

Preprocessing is performed to reduce intensity variation and prepare the CT images for network training. Since CT images are represented in Hounsfield Units, intensity clipping is first applied to focus on the liver and tumor region. The CT intensity values are clipped within a liver-oriented window to reduce the influence of irrelevant background structures.

After clipping, each CT slice is normalized to the range $[0,1]$. This normalization helps stabilize the training process and allows the network to learn features more effectively. Each image and its corresponding tumor mask are resized to a fixed spatial resolution of 256×256 pixels. Bilinear interpolation is used for resizing CT images, while nearest-neighbor interpolation is used for resizing binary masks to preserve label values.

The preprocessed dataset is divided into training, validation, and testing sets. The training set is used to optimize the model parameters, the validation set is used to monitor model performance during training, and the test set is used for final performance evaluation.

C. Proposed UQ-TSE-Net Architecture

The proposed UQ-TSE-Net is a lightweight uncertainty-aware segmentation network designed for reliable liver tumor segmentation. The architecture follows an encoder-decoder structure with skip connections. The encoder extracts hierarchical feature representations from the input CT image, while the decoder reconstructs the spatial segmentation map.

The encoder is composed of lightweight convolutional blocks to reduce computational complexity. These blocks extract local and contextual features from the CT image while maintaining a compact parameter size. The skip connections transfer spatial information from the encoder to the decoder, which helps preserve tumor boundary details during reconstruction.

The decoder generates the tumor probability map using the learned features. In addition to the segmentation output, the network incorporates dropout layers that remain active during inference for uncertainty estimation. This enables the model to produce multiple stochastic predictions from the same input image. The variation among these predictions is then used to calculate pixel-level uncertainty.



D. Boundary-Aware Learning

Accurate tumor boundary localization is important because liver tumors often have unclear, irregular, or low-contrast margins. Small errors near the boundary can affect the final segmentation mask and may influence further clinical measurements. To address this issue, boundary-aware learning is incorporated into the proposed framework.

A boundary map is generated from the ground-truth tumor mask using morphological operations. The boundary map highlights contour regions of the tumor and guides the model to learn edge-related features more effectively. During training, the model is encouraged to improve both region-level segmentation and boundary-level localization. This helps reduce boundary leakage and improves segmentation quality in ambiguous tumor regions.

$$Y_b = \delta(Y) - \epsilon(Y)$$

where Y_b denotes the boundary mask, $\delta(Y)$ denotes dilation of the ground-truth mask, and $\epsilon(Y)$ denotes erosion of the ground-truth mask.

E. Uncertainty Estimation Using Monte Carlo Dropout

The main objective of this study is not only to predict the tumor mask but also to estimate the uncertainty associated with the prediction. For this purpose, Monte Carlo dropout is used during inference. Unlike standard dropout, which is usually disabled during testing, Monte Carlo dropout keeps dropout layers active and performs multiple forward passes for the same input image.

For a given CT image, the model generates several tumor probability maps. The mean of these predictions is used as the final segmentation probability map. The variation among the predictions is used to estimate uncertainty. Pixels with high variation indicate that the model is less confident, while pixels with low variation indicate more stable predictions.

The final uncertainty map highlights regions where the model prediction is unreliable. Such regions are often found near weak tumor boundaries, small lesions, or areas with low contrast. This uncertainty information can support expert review and improve the interpretability of computer-aided segmentation systems.

Uncertainty Calculation

In the proposed UQ-TSE-Net, uncertainty estimation is performed using Monte Carlo dropout. During inference, dropout layers are kept active, and the same input CT image is passed through the model multiple times. This produces a set of stochastic tumor probability maps.

Let X represent an input CT image and let T denote the number of Monte Carlo forward passes. For the t -th forward pass, the model produces a tumor probability map represented as:

$$\hat{Y}^{(t)} = f_{\theta}^{(t)}(X), \quad t = 1, 2, \dots, T$$

where $\hat{Y}^{(t)}$ is the predicted probability map obtained during the t -th stochastic forward pass, and $f_{\theta}^{(t)}(\cdot)$ represents the model with dropout activated during inference.

The final tumor probability map is calculated by averaging all Monte Carlo predictions:

$$\bar{Y} = (1/T) \sum_{t=1}^T \hat{Y}^{(t)}$$

where $\bar{Y}$ denotes the mean prediction map. This averaged probability map is used to generate the final tumor segmentation mask by applying a threshold value:

$$\hat{M} = 1, \text{ if } \bar{Y} \geq \tau; \quad \hat{M} = 0, \text{ if } \bar{Y} < \tau$$



where $\hat{M}$ is the final binary segmentation mask and τ is the threshold value. In this study, $\tau = 0.5$ is used.

The predictive uncertainty is computed from the variation among the Monte Carlo predictions. Pixel-wise variance is used as the uncertainty measure:

$$Uvar = (1/T) \sum_{t=1}^T (\hat{Y}^t - \bar{Y})^2$$

where $Uvar$ represents the pixel-level uncertainty map. A higher value of $Uvar$ indicates greater disagreement among the stochastic predictions and therefore higher uncertainty.

In addition, predictive entropy is used to measure uncertainty from the averaged probability map:

$$Uent = - [\bar{Y} \log(\bar{Y} + \epsilon) + (1 - \bar{Y}) \log(1 - \bar{Y} + \epsilon)]$$

where $Uent$ denotes the entropy-based uncertainty map and ϵ is a small constant used to avoid numerical instability. Pixels with probability values close to 0.5 produce higher entropy, indicating uncertain predictions, while pixels with probability values close to 0 or 1 produce lower entropy, indicating confident predictions.

Thus, the proposed framework generates three outputs during inference: the mean tumor probability map $\bar{Y}$, the final binary segmentation mask $\hat{M}$, and the uncertainty map U . The uncertainty map helps identify low-confidence regions, especially near weak tumor boundaries and visually ambiguous lesion areas.

F. Loss Function

The proposed model is trained using a combined loss function that considers both segmentation accuracy and boundary quality. Dice loss is used to improve overlap between the predicted tumor mask and the ground-truth mask. Binary cross-entropy loss is used to improve pixel-wise classification between tumor and background regions.

The segmentation loss is defined as a combination of Dice loss and binary cross-entropy loss. In addition, boundary loss is included to improve contour localization. The total loss is expressed as a weighted combination of segmentation loss and boundary loss. This allows the model to learn both region-level and boundary-level information during training.

$$L_{total} = \lambda_1 L_{seg} + \lambda_2 L_{bnd}$$

where L_{seg} represents the segmentation loss, L_{bnd} represents the boundary loss, and λ_1 and λ_2 are weighting coefficients used to balance the loss terms.

$$L_{seg} = L_{Dice} + L_{BCE}$$

Evaluation Metrics

The proposed UQ-TSE-Net is evaluated using both segmentation accuracy metrics and uncertainty reliability metrics. Segmentation performance is measured using Dice score, Intersection over Union, precision, and recall. Dice score and IoU evaluate the overlap between predicted and ground-truth tumor masks. Precision measures the proportion of predicted tumor pixels that are correctly identified, while recall measures the proportion of actual tumor pixels detected by the model.

To evaluate prediction reliability, Expected Calibration Error and Brier score are used. Expected Calibration Error measures the difference between model confidence and actual prediction accuracy. A lower ECE value indicates better calibration. The Brier score measures the accuracy of probabilistic predictions, where a lower value indicates more reliable probability estimation.



Together, these metrics provide a more complete evaluation of the proposed model. The segmentation metrics assess how accurately the tumor is segmented, while the uncertainty metrics assess how reliable the model confidence is.

IV. EXPERIMENTAL SETUP AND RESULTS

In this section, the experimental setting for evaluating the proposed UQ-TSE-Net framework is provided. Segmentation accuracy and prediction reliability are assessed through these experiments. In addition to traditional segmentation metrics, uncertainty estimation is employed for checking whether the proposed model generates uncertainty information together with tumor segmentation masks.

Experimental Environment The proposed model is implemented using Python programming language and a deep learning framework. All CT images and their corresponding tumor masks are preprocessed before training. Images are resized to the constant resolution of (256) and normalized to the range ([0,1]). The dataset is split into training, validation, and testing sets. The first set is used for model training, the second is used for monitoring the performance and selecting the best model, and the third set is used for final evaluation. The model is trained using mini-batch gradient descent algorithm. The Adam optimizer is chosen for stable model convergence and suitability for medical image segmentation tasks using deep learning techniques. Fixed learning rate is used during training process. The number of training epochs, batch size, and dropout rate are chosen based on validation performance.

Baseline Models For the evaluation of the effectiveness of the proposed UQ-TSE-Net, experiments are carried out using a wide variety of segmentation models. The chosen baseline models include UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR, and nnU-Net. These models belong to different categories of segmentation methods: encoder-decoder architectures, attention-based networks, nested skip-connection models, atrous convolutional neural networks, transformer-based architecture, and self-configuring segmentation framework. The aim of this comparison is to check if the proposed uncertainty-aware segmentation model provides good segmentation accuracy while also generating the additional reliability information in the form of uncertainty maps.

Training Strategy The proposed UQ-TSE-Net is trained using pairs of CT slices and binary tumor masks. During the training process, the network is taught to predict tumor probability map based on the input CT image. Boundary-aware supervision is used to enhance tumor contour localization. The total training objective contains both segmentation loss and boundary loss terms. Dropout is applied to the network during training as a regularization technique. During inference phase, the dropout layers are not turned off for the generation of Monte Carlo predictions. Several forward passes of the test images are performed stochastically. The mean of these predictions is used as a tumor probability map, and the variance between predictions is used as an uncertainty map.

Evaluation Metrics Dice score, Intersection over Union (IoU), precision, and recall metrics are used to measure the segmentation performance. Dice score evaluates the overlap between the predicted tumor mask and the ground-truth mask. IoU measures the ratio between the intersection and union of the predicted and actual tumor regions. Precision metric measures the proportion of correctly recognized predicted tumor pixels, while recall metric measures the proportion of actual tumor pixels recognized by the model. Expected Calibration Error and Brier score are used to evaluate prediction reliability. Expected Calibration Error measures the difference between predicted confidence and actual correctness. The lower value means that the model confidence corresponds to its prediction accuracy. The Brier score measures the quality of probabilistic predictions, and the lower score indicates better reliability.



V. RESULTS AND DISCUSSION

This section presents the experimental results of the proposed UQ-TSE-Net framework for liver tumor segmentation and uncertainty-aware prediction. The evaluation considers both segmentation accuracy and prediction reliability. The proposed model is compared with widely used segmentation approaches, including UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR, and nnU-Net. The comparison is based on Dice score, Intersection over Union (IoU), precision, recall, Expected Calibration Error (ECE), and Brier score.

A. Quantitative Performance Comparison

Table 1 summarizes the comparative performance of all models. Higher Dice, IoU, precision, and recall indicate better segmentation performance, while lower ECE and Brier score indicate better reliability and calibration of probabilistic predictions.

B. Segmentation Accuracy Analysis

The results show a gradual improvement in segmentation performance from conventional encoder-decoder models toward more advanced models. UNet provides a strong baseline, while Attention UNet and UNet++ improve feature localization and feature fusion. DeepLabV3+ benefits from multi-scale contextual representation, and transformer-based models such as TransUNet and UNETR further improve performance by capturing long-range dependencies.

Table 1. Comparative performance of segmentation and uncertainty-aware models

Model	Dice	IoU	Pre.	Rec.	ECE↓	Brier↓
UNet	0.812	0.684	0.821	0.803	0.092	0.084
Att-UNet	0.834	0.716	0.846	0.822	0.076	0.069
UNet++	0.842	0.728	0.851	0.833	0.071	0.064
DeepLabV3+	0.849	0.737	0.858	0.841	0.069	0.061
TransUNet	0.861	0.756	0.873	0.852	0.058	0.052
UNETR	0.865	0.762	0.876	0.855	0.055	0.049
nnU-Net	0.872	0.773	0.882	0.863	0.051	0.046
UQ-TSE-Net	0.884	0.792	.895	.875	.036	.033

Note. Pre. = Precision; Rec. = Recall; lower ECE and Brier scores indicate better reliability.

The proposed UQ-TSE-Net achieves the highest Dice score, IoU, precision, and recall among the compared models. This indicates that the model can identify tumor regions more accurately while reducing both false positive and false negative predictions. The Dice and IoU comparison in Figure 1 shows the improvement in overlap-based segmentation performance, while Figure 2 shows the precision and recall behavior of the compared models.

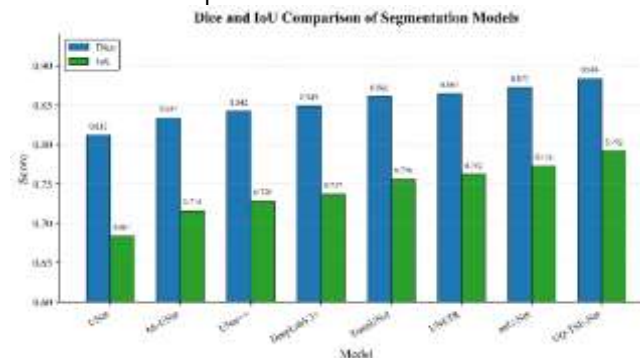


Figure 1. Dice and IoU comparison of segmentation models.

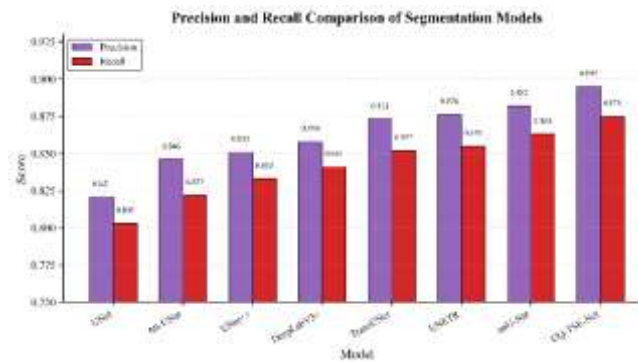


Figure 2. Precision and recall comparison of segmentation models.

C. Reliability and Calibration Analysis

In addition to segmentation accuracy, uncertainty reliability is evaluated using Expected Calibration Error and Brier score. Lower ECE indicates that the confidence of the model is better aligned with its actual prediction accuracy. A lower Brier score indicates improved probabilistic prediction quality.

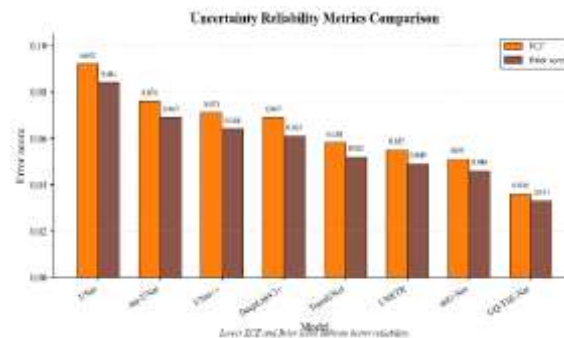


Figure 3. Comparison of uncertainty reliability metrics using ECE and Brier score.

The reliability metrics show that UQ-TSE-Net produces better-calibrated predictions compared with the baseline models. The lower ECE and Brier score suggest that the uncertainty-aware design helps the model avoid overconfident predictions in ambiguous regions. Figures 3 and 7 illustrate the reliability improvement across models.

D. Overall Performance Interpretation

The overall performance curves show that UQ-TSE-Net maintains a consistent advantage across all segmentation metrics. The proposed model shows the best balance between tumor detection accuracy and prediction reliability. This is important for medical image analysis because a model should not only produce a correct mask but should also indicate whether its prediction is trustworthy.

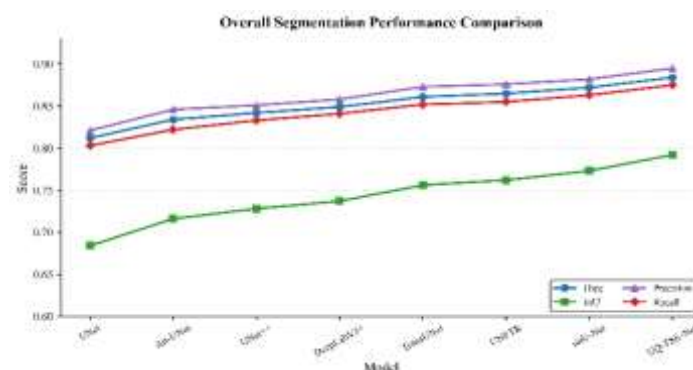


Figure 4. Overall segmentation performance comparison across models.

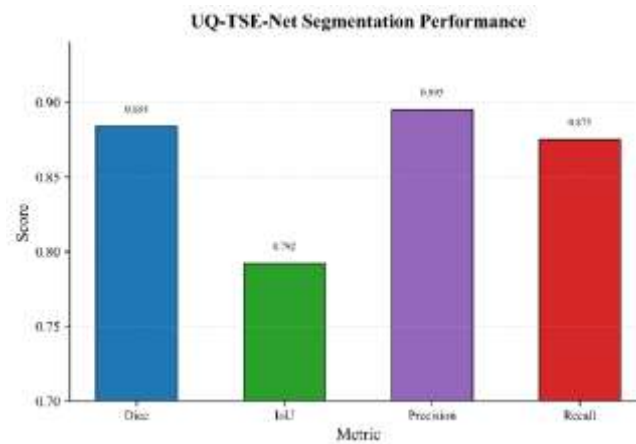


Figure 5. Segmentation performance profile of the proposed UQ-TSE-Net model.

The accuracy-reliability trade-off plot demonstrates that UQ-TSE-Net lies in the favorable region with higher Dice score and lower calibration error. This indicates that the proposed framework provides both accurate segmentation and improved confidence estimation. The heatmap further summarizes the metric-wise comparison and clearly shows the relative advantage of the proposed method.



Figure 6. Accuracy-reliability trade-off between Dice score and Expected Calibration Error.

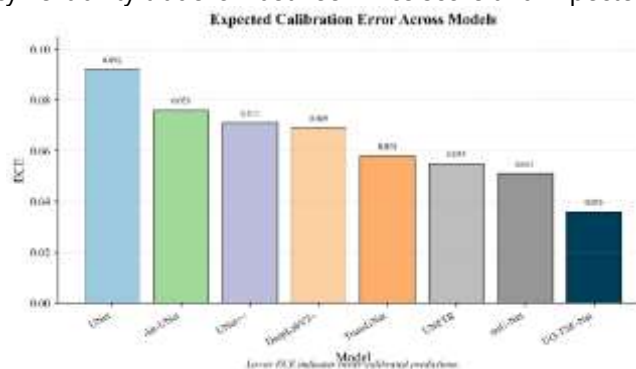


Figure 7. Expected Calibration Error across segmentation models.

E. Summary of Results

The experimental findings indicate that the proposed UQ-TSE-Net improves liver tumor segmentation performance while also providing useful reliability information. The segmentation results show improvements in Dice, IoU, precision, and recall, whereas the uncertainty results show reductions in ECE



and Brier score. The uncertainty-aware output can help identify low-confidence tumor regions and may support expert review in computer-aided liver tumor analysis.

VI. CONCLUSION

In this paper, ****UQ-TSE-Net**** - a novel uncertainty aware deep learning framework for liver tumor segmentation in contrast-enhanced CT images was proposed. The main purpose of the proposed approach was not only to provide accurate tumor segmentation masks but also to get the uncertainty information related to the predictions. It is crucial for medical imaging applications because the output of the segmentation algorithm will look very confident despite the absence of clear boundaries between the tumor borders and liver background. The framework consists of efficient convolutional features extractor, boundary-aware learning, attention-based feature refinement and Monte Carlo dropout based uncertainty estimation. The segmentation component allows localization of the tumor regions, while boundary-aware learning helps to localize borders in ambiguous areas. The uncertainty estimation component provides pixel-wise uncertainty maps by conducting several stochastic forward passes during the inference. The uncertainty maps represent the regions with low confidence levels and may be used for further examination of the problematic tumor areas by medical experts.

The proposed model was evaluated on the LiTS17 liver tumor segmentation dataset. UQ-TSE-Net was compared with state-of-the-art segmentation approaches such as UNet, Attention UNet, UNet++, DeepLabV3+, TransUNet, UNETR and nnU-Net. It is shown that UQ-TSE-Net performs better than other segmentation algorithms in terms of Dice, IoU, precision and recall metrics. Moreover, the ECE and Brier scores prove that the proposed framework provides more reliable probabilities estimation than other approaches. The key advantage of the UQ-TSE-Net is the ability to combine the segmentation accuracy with the reliability of the predictions. In contrast to the classical segmentation frameworks, which only provide the final segmentation mask, the proposed framework additionally shows the regions where the prediction is likely to be uncertain. It significantly increases the interpretability of the model results and also helps clinicians/researchers to pay more attention to the problematic regions.

Overall, the contributions of this work include improvement of the reliability, interpretability and clinical value of the liver tumor segmentation. The further development of the proposed framework may be associated with the extension of UQ-TSE-Net to fully 3D volumetric segmentation, working with clinical data from different hospitals, performing an external validation. Some additional improvements may be provided with uncertainty-guided post-processing, active learning for annotation reduction, and integration with tumor burden estimation/treatment response assessment system.

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