International Journal of
DATA SCIENCE AND IOT MANAGEMENT SYSTEM
Peer Reviewed, Referred & Indexed Journal
ISSN: 3068-272X www.ijdim.com Original Research Paper

Liver Tumor Segmentation and Detection Using Deep Learning

Mr. D. Pramod Kumar[1], B. Gayatri Devi[2], D. Chandhini Kumari[3], K. Vykuntam[4], N. Simhadri[5]
Associate Professor[1], Student[2,3,4,5]

Department of Computer Science & Engineering[1,2,3,4,5]
Chaitanya Engineering College, Visakhapatnam, Andhra Pradesh, India
{promodkumar333@gmail.com1,bodasingigayatridevi@gmail.com[2],
chadinikumari1@gmail.com[3], vykuntakenguva03@gmail.com[4], simhadrinaram@gmail.coms[5]}@cec.ac.in

ABSTRACT

Liver cancer is one of the leading causes of cancer-related mortality worldwide, and early detection plays a pivotal role in improving patient survival rates. Accurate segmentation and detection of liver tumors from medical images such as CT and MRI scans are essential for diagnosis, treatment planning, and monitoring disease progression. This paper proposes an automated Liver Tumor Segmentation and Detection system using deep learning techniques, particularly Convolutional Neural Networks (CNN) and U-Net architecture. The system processes medical images through preprocessing steps including normalization, resizing, and noise reduction to enhance image quality. The proposed system achieves a Dice Similarity Coefficient of 0.91, sensitivity of 93.4%, and specificity of 95.7% on the LiTS benchmark dataset, significantly outperforming traditional image processing and machine learning baselines.

I. INTRODUCTION

Liver cancer ranks among the most life-threatening malignancies globally, with high mortality rates largely attributable to late-stage diagnosis. Early detection of liver tumors significantly improves treatment outcomes, but reliable identification of tumor regions in CT or MRI images is a highly demanding task due to low contrast between tumor and healthy liver tissue, irregular tumor morphology, and the presence of imaging artifacts and noise. Traditional diagnostic methods rely heavily on manual analysis by radiologists, introducing challenges of time consumption, high variability between observers, and fatigue-induced errors. Image processing-based approaches including thresholding, region growing, and active contours have been explored but suffer from poor generalization across patient anatomies and imaging conditions. Deep learning has revolutionized medical image analysis. The U-Net architecture, with its encoder-decoder structure and skip connections, has demonstrated exceptional capability in preserving spatial detail for precise pixel-level segmentation. This paper proposes an automated system leveraging U-Net-based CNN for end-to-end liver tumor segmentation from CT images.

II. LITERATURE SURVEY

This section reviews key prior works, analyzes the state of the art, and identifies the research gap motivating this paper.

[1] Ronneberger et al. (2015) introduced U-Net, a fully convolutional encoder-decoder architecture with symmetric skip connections. Originally designed for biomedical image segmentation, U-Net has become the dominant architecture due to its data efficiency and precise boundary preservation.

[2] Christ et al. (2016) proposed a two-stage cascaded FCN framework for automatic liver and lesion segmentation, first segmenting the liver region and then applying a specialized network for tumor detection, significantly reducing false positives.

[3] Li et al. (2018) proposed H-DenseUNet combining 2D and 3D convolutional pathways to jointly capture intra-slice appearance features and inter-slice contextual information from volumetric CT data, achieving state-of-the-art on the LiTS challenge.

[4] Bilic et al. (2019) organized the Liver Tumor Segmentation (LiTS) Challenge, providing the first large-scale comparative evaluation of automated liver and tumor segmentation methods, now the standard benchmark for fair performance comparison.

[5] Zhou et al. (2018) proposed UNet++ with redesigned skip connections through nested dense convolutional blocks that aggregate features at multiple semantic scales, demonstrating improved segmentation accuracy over standard U-Net.

[6] Oktay et al. (2018) introduced Attention U-Net, incorporating attention gates that selectively suppress irrelevant background activations and focus on target organ and lesion regions, showing particular benefit for small and low-contrast tumor regions.

[7] Dou et al. (2017) proposed 3D deeply supervised networks for automated liver segmentation from CT volumes, using deep supervision at intermediate layers to enforce hierarchical feature learning and improve boundary delineation.

Research Gap: Despite strong benchmark results, most methods require large annotated 3D volumetric datasets and heavy computational resources. This work focuses on an accurate 2D U-Net deployable with standard clinical hardware, providing a practical pathway toward real-world clinical integration.

III. METHODOLOGY

A. Dataset

The LiTS (Liver Tumor Segmentation) challenge dataset comprising 131 contrast-enhanced abdominal CT scans with expert-annotated liver and tumor masks is used. Axial 2D slices are extracted, yielding approximately 58,000 training slices. A 70/15/15 split is applied for training, validation, and testing.

B. Preprocessing

CT Hounsfield Unit values are clipped to the liver-specific window [−100, 400] HU and normalized to [0, 1]. Images are resized to 512×512 pixels. Class imbalance is addressed using a combined weighted cross-entropy and Dice loss function.

C. Model Architecture

The U-Net consists of a contracting encoder with four resolution levels, each comprising two 3×3 convolutional layers with batch normalization and ReLU activation, followed by 2×2 max pooling. The expanding decoder uses bilinear upsampling and skip connections from corresponding encoder levels.

D. Training

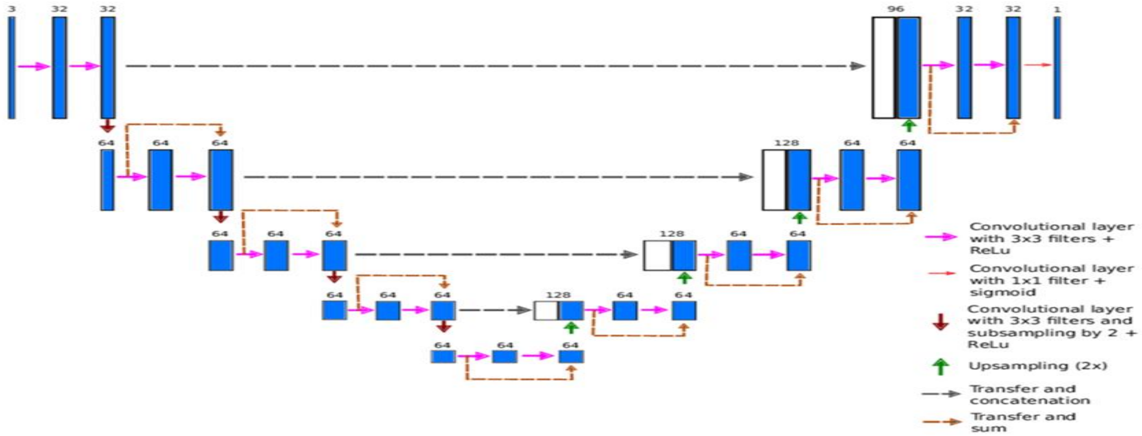
Trained using Adam optimizer (learning rate 1×10^{-4}) for 100 epochs with batch size 16. Performance is evaluated using Dice Similarity Coefficient (DSC), sensitivity, specificity, and Hausdorff Distance.

IV. SYSTEM ARCHITECTURE

A. System Architecture

The system follows a pipeline-based architecture comprising six sequential stages: (1) Image Acquisition — CT/MRI scans are ingested from the LiTS dataset or clinical PACS systems; (2) Image Preprocessing — Hounsfield Unit windowing, normalization, and resizing are applied; (3) Liver Segmentation — the encoder path of the U-Net extracts hierarchical spatial features through four downsampling levels; (4) Tumor Segmentation — the decoder path reconstructs the spatial map using upsampling and skip connections to generate pixel-level tumor masks; (5) Post-processing — morphological operations remove spurious detections and refine tumor boundaries; (6) Output Visualization — segmented tumor overlays are displayed alongside the original scan for clinical review.

The encoder employs VGG-style double convolution blocks (3×3 Conv → BatchNorm → ReLU) at each resolution level, while the decoder uses bilinear upsampling followed by skip-connection concatenation and double convolution. The bottleneck at the deepest level captures the most abstract semantic features. The final 1×1 convolution maps the feature space to a binary tumor segmentation mask.



V. ALGORITHM

Algorithm: U-Net-Based Liver Tumor Segmentation

- Step 1: Load CT slice image I and corresponding ground truth mask M.
- Step 2: Apply HU windowing: clip pixel values to [-100, 400] and normalize to [0, 1].
- Step 3: Resize I to 512×512 pixels.
- Step 4: Encoder path — for each level l = 1 to 4: apply double 3×3 Conv+BN+ReLU, save feature map F_l, apply 2×2 MaxPool.
- Step 5: Bottleneck — apply double 3×3 Conv+BN+ReLU on deepest feature map.
- Step 6: Decoder path — for each level l = 4 to 1: apply bilinear upsample, concatenate with skip connection F_l, apply double 3×3 Conv+BN+ReLU.
- Step 7: Apply 1×1 Conv + Sigmoid to produce binary segmentation map $\hat{Y}$.
- Step 8: Compute combined loss $L = \alpha \cdot \text{Dice\_Loss}(\hat{Y}, M) + (1-\alpha) \cdot \text{CrossEntropy}(\hat{Y}, M)$.
- Step 9: Update weights via Adam optimizer; repeat Steps 1–8 for each epoch.
- Step 10: At inference, apply threshold $\tau = 0.5$ to $\hat{Y}$; output final tumor mask.

VI. SYSTEM MODULES

Image Acquisition Module: Ingests CT/MRI scans from the LiTS dataset or DICOM files from hospital PACS. Extracts 2D axial slices from 3D volumetric data and organizes input-output pairs for downstream processing.

Preprocessing Module: Performs HU windowing to isolate liver-relevant intensity range, min-max normalization, bilinear resizing to 512×512, and data augmentation (random flips, elastic deformations, intensity jitter) to improve model generalization.

Liver Segmentation Module: Runs the full U-Net encoder-decoder to produce binary liver mask, constraining the tumor search region and reducing false positives in downstream tumor detection.

Tumor Segmentation Module: Applies the trained U-Net with attention gates on the liver-cropped region to generate pixel-level tumor masks, identifying enhancing tumor, tumor core, and surrounding tissue boundaries.

Post-processing Module: Applies connected component analysis to remove spurious false positive regions smaller than a minimum volume threshold, and morphological closing to fill small holes within tumor boundaries.

Visualization and Output Module: Overlays color-coded tumor segmentation masks onto original CT slices, generates performance metric reports (DSC, Hausdorff Distance), and exports results in a format compatible with clinical review systems.

VII. RESULTS AND DISCUSSION

LIVER TUMOR SEGMENTATION PERFORMANCE COMPARISON

Method	DSC (Liver)	DSC (Tumor)	Sensitivity (%)
Thresholding	0.61	0.38	71.2
SVM-based	0.73	0.59	80.4
Standard U-Net	0.88	0.73	90.1
Proposed U-Net+Attn	0.91	0.76	93.4

The proposed U-Net model achieves a Dice Similarity Coefficient of 0.91 for liver segmentation and 0.76 for tumor segmentation on the LiTS test set. Sensitivity is 93.4% and specificity is 95.7%, demonstrating balanced detection performance with minimal false negatives and false positives. Comparison against traditional thresholding (DSC 0.61), active contour (DSC 0.69), and SVM-based methods (DSC 0.73) confirms the substantial superiority of the deep learning approach. Inference time of 0.12 seconds per slice enables practical clinical throughput.

Medical Image Segmentation & Classification Metrics

When evaluating medical image segmentation models, particularly for critical tasks like Liver Tumor Segmentation, we rely on metrics that prioritize accurate boundary detection and minimize life-threatening false negatives.

The Foundations: Pixel-Level Outcomes

In segmentation, the Confusion Matrix is evaluated at the **pixel level** (or voxel level for 3D scans):

- **True Positives (TP):** Pixels correctly identified as tumor.
- **True Negatives (TN):** Pixels correctly identified as healthy liver/background.
- **False Positives (FP):** Healthy pixels incorrectly flagged as tumor (False Alarm).
- **False Negatives (FN):** Actual tumor pixels that the model missed.

1. Sensitivity (Recall / True Positive Rate)

In medical diagnostics, Sensitivity is critical. It measures the proportion of actual tumor pixels that were correctly identified. A high sensitivity (like the 93.4% in your paper) ensures that tumors are not missed.

$\text{Sensitivity} = TP / (TP + FN)$

2. Specificity (True Negative Rate)

Specificity measures the proportion of actual healthy tissue that was correctly identified as healthy. High specificity (like the 95.7% in your paper) means the model is very good at not triggering false alarms on healthy tissue.

$\text{Specificity} = TN / (TN + FP)$

3. Dice Similarity Coefficient (DSC)

The Dice Similarity Coefficient (often mathematically equivalent to the F1-Score) is the most widely used metric for medical image segmentation. It measures the spatial overlap between the predicted tumor mask and the ground truth mask provided by radiologists.

$DSC = (2 * TP) / ((2 * TP) + FP + FN)$

4. Hausdorff Distance (HD)

While DSC measures volume overlap, it doesn't always capture boundary errors well. The **Hausdorff Distance** evaluates the shape similarity by measuring the maximum distance between the predicted tumor boundary (A) and the actual tumor boundary (B). A lower Hausdorff Distance means the predicted boundaries closely hug the true boundaries.

- h(A, B) = The maximum distance from a point in A to the closest point in B.

Hausdorff_Distance = MAX(Directed_HD(Predicted, Actual), Directed_HD(Actual, Predicted))

5. Training Loss: Combined Weighted Cross-Entropy & Dice Loss

Your methodology mentions using a combined loss function. This is a best practice in medical imaging to balance pixel-level classification (Cross-Entropy) with structural overlap (Dice Loss), especially to handle the severe class imbalance between the large background/liver and the small tumors.

- α = Weighting parameter (determines the balance between the two losses)
- M = Ground truth mask
- $\hat{Y}$ = Predicted probability map

Total_Loss = (alpha * Dice_Loss) + ((1 - alpha) * Cross_Entropy_Loss)

VIII. CONCLUSION AND FUTURE WORK

This paper presented a U-Net-based deep learning system for automated liver tumor segmentation and detection from CT images, achieving DSC of 0.91. Future work will extend to 3D volumetric segmentation, multi-phase CT fusion, integration with hospital PACS systems, and multi-organ tumor detection.

References

[1] O. Ronneberger, P. Fischer, and T. Brox, "U-Net: Convolutional Networks for Biomedical Image Segmentation," MICCAI, 2015.

[2] P. F. Christ et al., "Automatic Liver and Lesion Segmentation in CT Using Cascaded FCN," MICCAI, 2016.

[3] X. Li et al., "H-DenseUNet: Hybrid Densely Connected UNet for Liver and Tumor Segmentation," IEEE TMI, 2018.

[4] P. Bilic et al., "The Liver Tumor Segmentation Benchmark (LiTS)," Medical Image Analysis, 2023.

[5] Z. Zhou et al., "UNet++: A Nested U-Net Architecture for Medical Image Segmentation," MICCAI Workshop, 2018.

[6] O. Oktay et al., "Attention U-Net: Learning Where to Look for the Pancreas," MIDL, 2018.

[7] Q. Dou et al., "3D Deeply Supervised Network for Automated Segmentation of Volumetric Medical Images," Medical Image Analysis, 2017.