Comprehensive multi-phase 3D contrast-enhanced Ct imaging for primary liver cancer

July 1, 2025

1 INTRODUCTION

The work focuses on the implementation of a deep learning-based approach for segmenting liver tumors using contrast-enhanced CT (CECT) images. The reference research paper proposes a rich dataset with full four-phase CT imaging and annotations of both liver and tumor regions. The goal is to build and evaluate a U-Net based model for tumor segmentation.
CT images allow internal organs to be visualized non-invasively, and when enhanced with contrast agents (CECT), they reveal tumor vascularity and phase-based behavior essential for detection.

2 DATASET OVERVIEW

Each scan in this dataset includes four phases — Plain, Arterial, Venous, and Delayed — which help in differentiating liver cancer subtypes based on how they absorb contrast at different times.

- Source: Science Data Bank (publicly shared under CC BY 4.0)
- Total Cases: 278 liver cancer patients, 83 control patients
- Subtypes Covered: HCC, ICC, cHCC-CCA
- Selected Subset: 10 patients (40 CECT volumes)

- File Types: NIfTI (.nii/.nii.gz) images of CT scans, liver masks, and tumor masks
- Phases: Plain (P), Arterial (C1), Venous (C2), Delayed (C3)

3 Tools and Technologies

- Languages/Frameworks: Python, TensorFlow, NumPy, OpenCV
- Libraries: nibabel, matplotlib, pandas, sklearn, cv2
- Development Environment: Visual Studio Code (local machine)
- Visualization: Matplotlib

Tools like TensorFlow and OpenCV allow us to preprocess, train, and visualize medical image data efficiently within Python-based workflows.

4 Work Completed

4.1 File Preparation

- Extracted original cect.tar file and organized into folders
- Selected 10 patients, copied all 4-phase CT files, liver masks, and tumor masks
- Cleaned and subset $\text{patient}_data.csv$

4.2 Preprocessing

Preprocessing is essential to normalize image sizes and intensities, making them suitable for deep learning input and improving training performance.

- Resized all CT and mask slices from 512×512 to 256×256
- Normalized CT intensity values
- Converted to .npy format for model input
- Preprocessed 4,000 slices (7GB)

4.3 Data Visualization

- Visualized 2-panel overlays (CT + tumor mask)
- Visualized 3-panel (CT + tumor + liver mask)
- Saved sample overlays to overlays/ folder

4.4 Model Training (U-Net)

U-Net is a popular convolutional neural network architecture designed for biomedical image segmentation. It has a symmetrical encoder–decoder structure that captures context and enables precise localization.

- Model: 2D U-Net using TensorFlow/Keras
- Split: 80 % training, 20% validation
- Epochs Completed: 10
- Training Time: 0.4 hour per epoch
- Dice Coefficient: 0.8993 on validation

4.5 Prediction

Inference involves using the trained model to predict the tumor region from unseen CT slices, generating binary mask outputs per slice.

- Used trained model to predict tumor masks for a sample CT volume
- Saved 5 predictions from different slices as PNG overlay images

4.6 Evaluation

Dice Similarity Coefficient (DSC) is a metric used to measure the overlap between predicted and ground truth masks — a higher value means better segmentation performance.

- Calculated Dice Similarity Coefficient: 0.8993
- Visualized prediction vs. ground truth side-by-side

5 Results

- Model Accuracy: Improved consistently over 10 epochs
- Validation Accuracy: 99.7% by epoch 10
- Dice Score: 0.8993
- Overlay Output: 40 files in overlays folder, plus prediction images

5.1 Training Accuracy & Training Loss ....Validation Accuracy & Validation Loss

- Training Accuracy: How well your model performs on the training dataset.
- Training Loss: The error (or difference) between predicted and actual results during training.
- Validation Accuracy: How well your model performs on unseen validation data.
- Validation Loss: Error on the validation set.

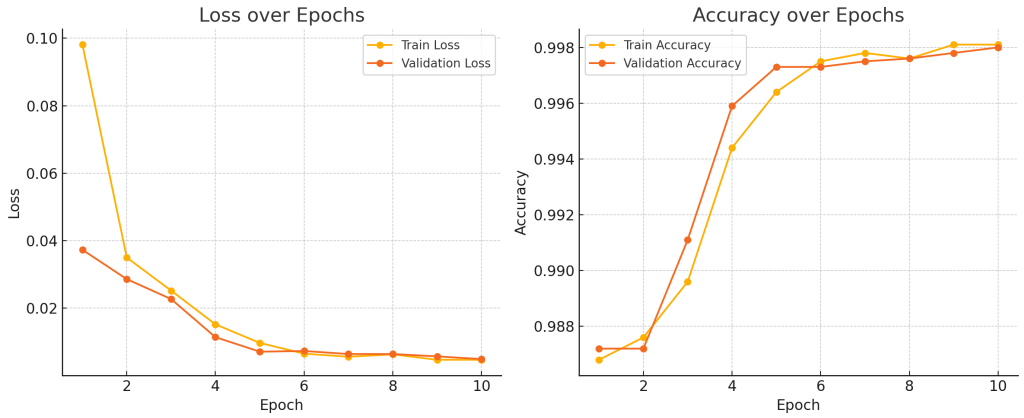

Figure 1: Training Accuracy Loss

5.2 Accuracy,Precision, Recall, F1-Score

- Precision: Out of all predicted tumor pixels, how many were correct.
- Recall: Out of all actual tumor pixels, how many were detected.
- F1 Score: Harmonic mean of precision and recall — balances both.

Accuracy: 0.9949
Precision: 0.7019
Recall: 0.6845
F1 Score: 0.6927

5.3 Confusion Matrix

Shows: True Positive, False Positive, True Negative, False Negative

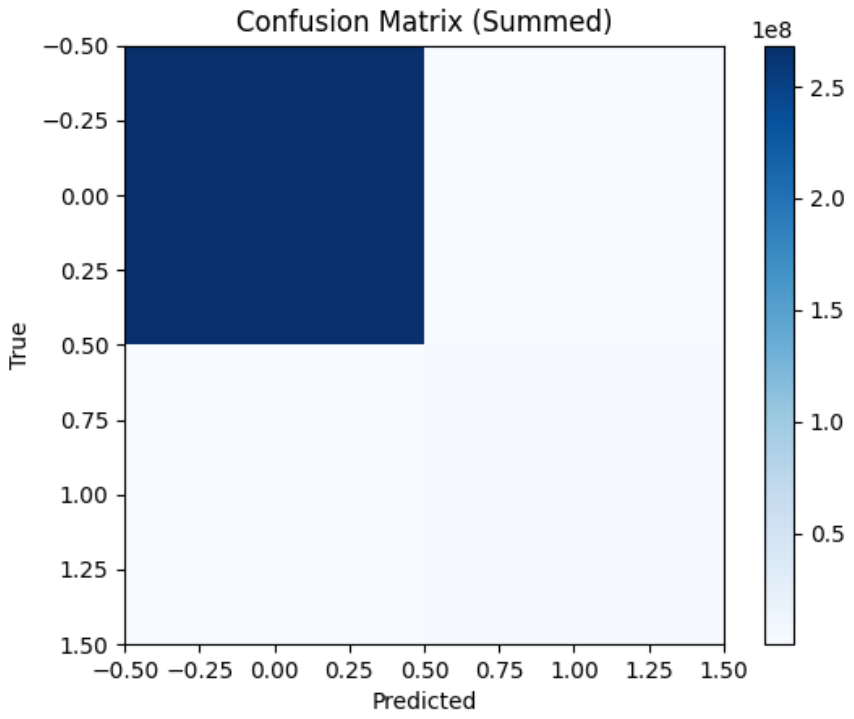

Figure 2: Confusion_Matrics

5.4 Hyperparameters

Table 1: Training Hyperparameters

Parameter	**Value**
Input Size	256 × 256
Epochs	10 (out of 10 planned)
Batch Size	8
Learning Rate	0.001 (Adam default)
Optimizer	Adam
Loss Function	Binary Cross Entropy
Train/Validation Split	80 / 20

6 Attachments section

6.1 Visualization OF 4 CT Phases

6.1.1 Artrial

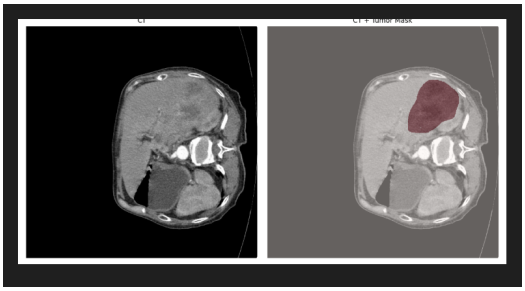

Figure 3: Artrial Phase

6.1.2 Venous

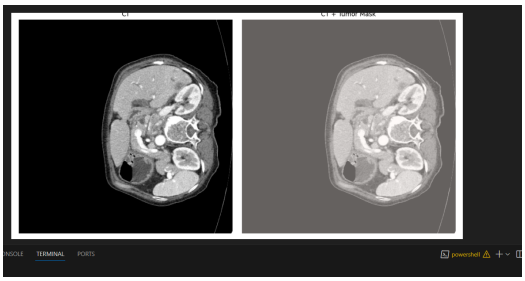

Figure 4: Venous Phase

6.1.3 Delayed

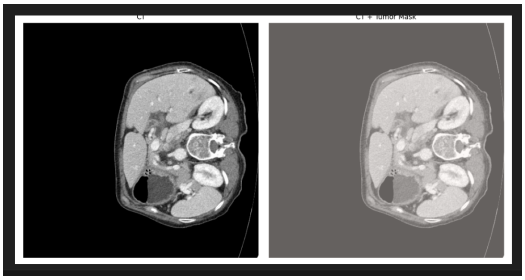

Figure 5: Delayed Phase

6.1.4 Plain

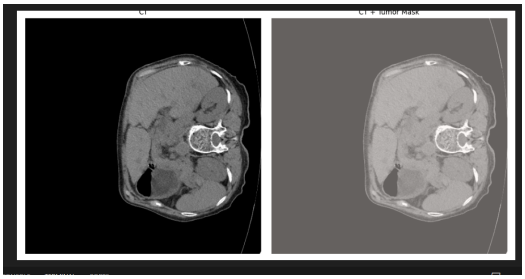

Figure 6: Plain Phase

6.2 Training Loss Curve

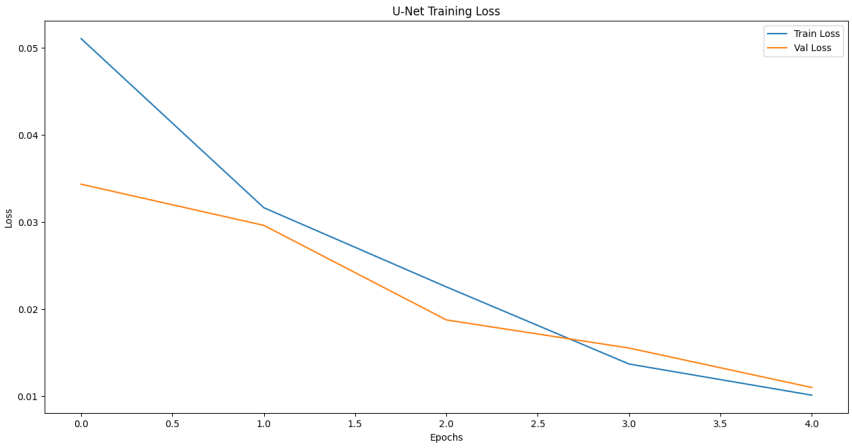

Figure 7: Training accuracy/loss over 5 epochs

6.3 Prediction

6.3.1 slice_000_overlay

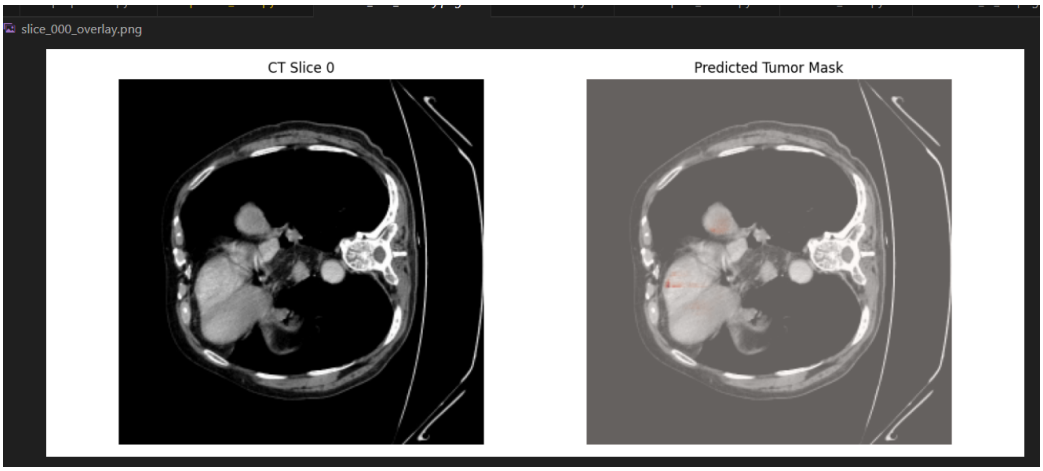

Figure 8: Prediction

6.3.2 slice_021_overlay

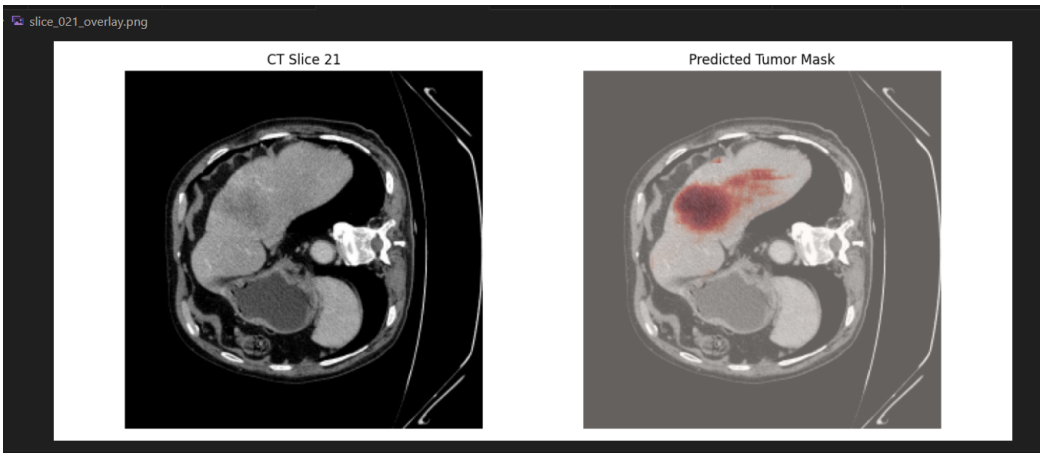

Figure 9: Prediction21

6.3.3 slice_042_overlay

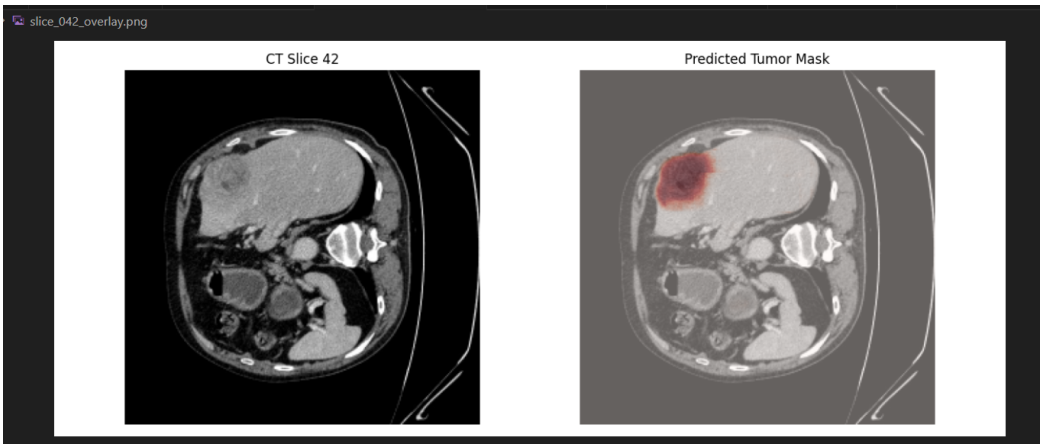

Figure 10: Prediction42

6.3.4 slice_084_overlay

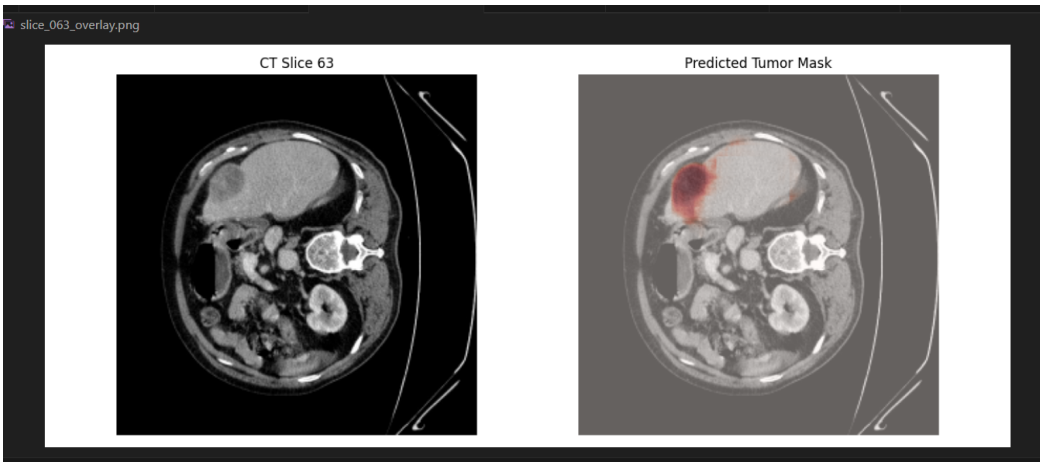

Figure 11: Prediction84

6.4 Dice Sampling Coefficient

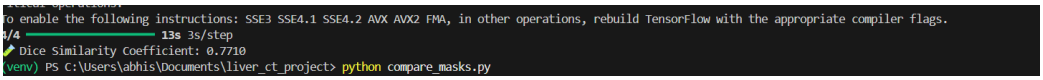

Figure 12: Dice Value

6.4.1 Comparison_Slice_65

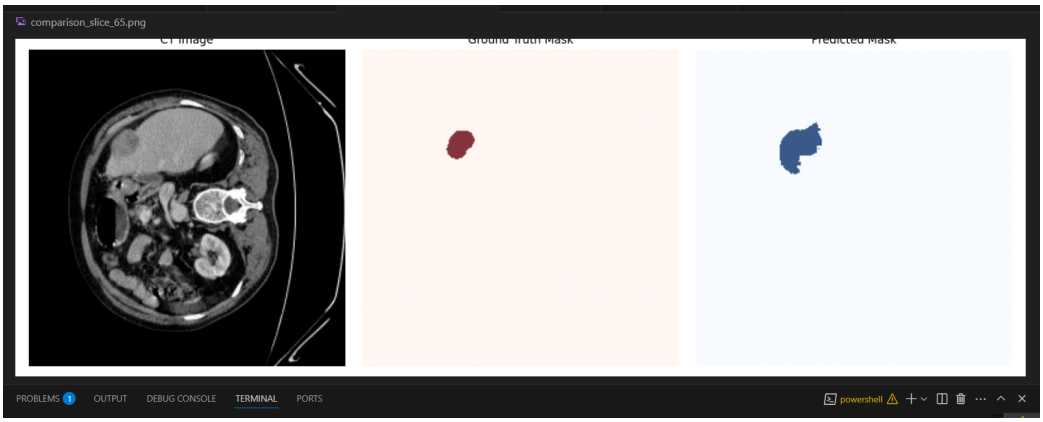

Figure 13: Comparison_Slice