ISSN(O): 2456-6683
[Impact Factor: 9.241]

DOIs:10.2017/IJRCS/202506011 --:-- Research Paper / Article / Review

LIVER TUMOR CLASSIFICATION AND SEGMENTATION USING AI TECHNIQUES

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Abstract: *Cancer is one of the deadly cells while affect the human body. Liver is one of the most essential part of the body. It is used to circulate and stores blood cells, and it is mainly used for the removing toxins like harmful substances from the blood. Liver cancer is the abnormal growth of the unwanted cells by affecting the part of abdomen. It is a most common deadly diseases and affected the people in worldwide. It is responsible for various metabolic and detoxification processes, becomes vulnerable to malignant transformations due to chronic liver diseases such as hepatitis B and C infections, cirrhosis, non-alcoholic fatty liver disease (NAFLD), and excessive alcohol consumption. Hepatocellular carcinoma (HCC), the most common primary liver cancer, accounts for approximately 75% of liver cancer cases, followed by intrahepatic cholangiocarcinoma and other rare tumors. The rising incidence of liver cancer is particularly alarming in regions with limited access to early diagnosis and effective treatment. Treatment strategies for liver cancer depend on the stage of the disease, liver function, and overall health status of the patient. Early stage of liver cancer may be managed with curative options like surgical resection, liver transplantation, or local ablative therapies such as radiofrequency ablation. Intermediate and advanced stages often require systemic therapies including chemotherapy, targeted therapy and immunotherapy. Despite recent advancements in treatment, the prognosis for liver cancer remains poor, with five year survival rates being significantly lower compared to other cancers. Emerging research in molecular biology, artificial intelligence, and precision medicine has opened new avenues for early detection, personalized treatment, and better prognosis of liver cancer. Techniques like machine learning and deep learning based imaging analysis, genomic profiling, and liquid biopsies are showing promise in identifying liver cancer at an earlier and more treatable stage. Integrating clinical data with medical imaging through AI-driven platforms is expected to transform the landscape of liver cancer diagnosis and management.*

Key Words: *SVM, CNN, GAN, NAFLD, AI, CAD, HCC.*

1. INTRODUCTION

The liver is one of the largest part of the organ in the abdomen. It promotes the essential functions for the abdomen. By the sudden growth of abnormal cells the liver can be affected by the cancer and it leads to death. Although the liver cancer having the highest mortality rate globally. Most of the common cases of liver cancer can be affected by the cirrhosis by taking more amount of alcohol and other harmful substances. Liver cancer will have more stages and symptoms but it can't be identified in the early stages. As per global cancer statistics, liver cancer ranks as the sixth most commonly diagnosed cancer and the third leading cause of cancer-related deaths.

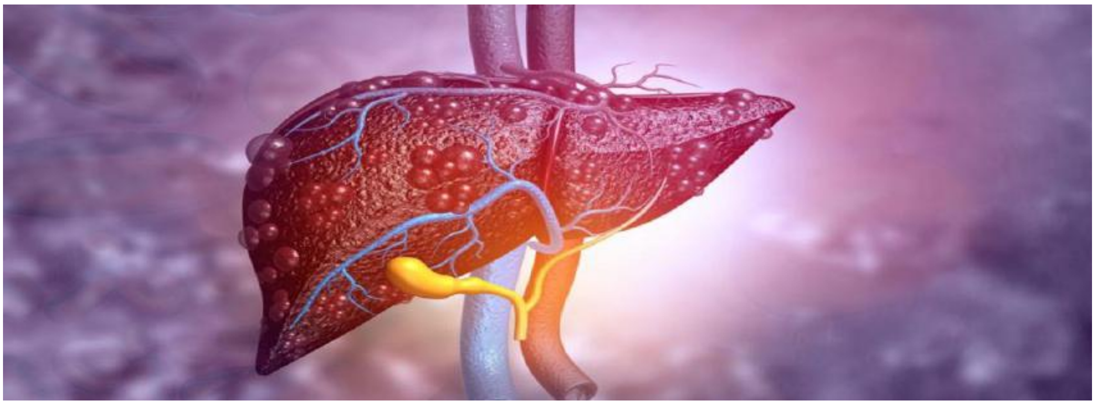

Fig.1 Affected liver by Cirrhosis

Hepatocellular carcinoma (HCC) constitutes the majority of primary liver cancer cases and is known for its aggressive nature and poor prognosis if not detected at an early stage. Early diagnosis, accurate classification, and precise segmentation of liver tumors are crucial for timely treatment planning, prognosis estimation, and therapeutic response monitoring. Traditional diagnostic approaches, including biopsy and radiologist-driven image interpretation, often suffer from subjectivity, inter-observer variability, and limitations in spatial resolution. The fig.1 will explores about the liver affected by the cirrhosis. To address these challenges, artificial intelligence (AI), particularly deep learning and machine learning-based methods, has emerged as a powerful tool in medical imaging, offering robust solutions for automatic liver cancer classification and segmentation. Medical imaging modalities such as computed tomography (CT), magnetic resonance imaging (MRI), and ultrasound play a pivotal role in liver cancer detection. However, the complex anatomy of the liver, variability in tumor shape, size, and location, as well as the presence of multiple lesions, pose significant challenges in consistent image interpretation. Manual segmentation of liver lesions is time-consuming and often impractical in clinical environments. Furthermore, subtle differences between benign and malignant lesions may go unnoticed without advanced image analysis techniques. In this context, automated liver cancer classification and segmentation systems can significantly enhance diagnostic accuracy, reduce radiologist workload, and facilitate computer-aided diagnosis (CAD) systems in modern healthcare. Liver cancer classification involves categorizing medical images into distinct classes such as normal tissue, benign lesions, or malignant tumors like HCC. This task requires extracting relevant features from imaging data that capture the intrinsic characteristics of cancerous tissues. Traditionally, handcrafted features such as shape, texture, intensity, and histogram-based descriptors were utilized for classification using machine learning algorithms such as support vector machines (SVM), random forests, and logistic regression. With the advent of deep learning, especially convolutional neural networks (CNNs), the need for manual feature engineering has diminished. CNNs can automatically learn hierarchical representations from raw image data, thereby improving classification performance. Transfer learning techniques, which involve fine-tuning pre-trained models on liver imaging datasets, have further enhanced the ability to classify liver cancer with high accuracy. On the other hand, liver tumor segmentation refers to delineating the exact boundary of tumors within liver images. It is a fundamental step for surgical planning, volume measurement, radiation therapy, and follow-up assessment. Segmentation tasks are particularly challenging due to low contrast between liver tissues and lesions, varying tumor morphologies, presence of necrotic tissues, and overlapping intensity distributions. Early segmentation approaches relied on thresholding, region growing, and clustering techniques, which were often sensitive to noise and initialization. The introduction of fully convolutional networks (FCNs), U-Net architecture, and its variants marked a significant advancement in medical image segmentation. These models are designed to capture both local and global contextual information using encoder-decoder structures, skip connections, and multi-scale feature fusion. U-Net and its extensions have demonstrated remarkable success in segmenting liver and tumor regions from 2D and 3D CT and MRI scans. Combining classification and segmentation into a unified framework offers an end-to-end solution for liver cancer diagnosis. While classification aids in detecting the presence of tumors and predicting their malignancy, segmentation provides spatial localization and volume estimation. Multi-task learning approaches have been proposed to leverage shared representations for both tasks, thereby improving the overall performance and robustness of AI models. Moreover, ensemble models that integrate predictions from multiple architectures such as CNNs for classification and U-Nets for segmentation are increasingly used to enhance reliability and generalizability across diverse imaging datasets. The success of liver cancer classification and segmentation heavily relies on the availability of annotated datasets. Publicly available datasets such as the Liver Tumor Segmentation (LiTS) challenge, Medical Segmentation and 3DIRCADb have provided researchers with benchmark platforms for training and evaluating algorithms. However, challenges such as class imbalance, annotation noise, and domain variability still exist. These issues are being addressed through data augmentation, synthetic image generation using generative adversarial networks (GANs), domain adaptation techniques, and robust model training strategies. In addition, multimodal data integration, combining imaging data with clinical and genomic information, has gained attention for improving diagnostic accuracy and enabling personalized treatment strategies. Performance evaluation of liver cancer classification and segmentation models is typically conducted using metrics such as accuracy, sensitivity, specificity, F1-score, Dice similarity coefficient (DSC), and Intersection over Union (IoU). These metrics provide insights into the precision of tumor detection and the quality of segmentation masks. Clinical applicability also requires interpretability and explainability of AI models, which are being addressed through visualization techniques such as Grad-CAM, saliency maps, and attention mechanisms. With the growing adoption of AI in healthcare, regulatory, ethical, and deployment considerations have become increasingly important. Ensuring patient data privacy, reducing algorithmic bias, and validating models on diverse population cohorts are essential for real-world integration. Collaborative efforts among clinicians, computer scientists, and regulatory bodies are required to develop trustworthy, interpretable, and clinically viable liver cancer diagnosis systems.

2. MATERIALS AND METHODS

This study focuses on the development of an automated system for the classification and prediction of liver cancer using both medical imaging and clinical datasets. The research utilizes a combination of computed tomography (CT) scan images and structured clinical data to improve the accuracy of diagnosis. The imaging dataset was primarily sourced from publicly available databases such as the Liver Tumor Segmentation Challenge (LiTS) and The Cancer Imaging Archive (TCIA). These datasets consist of contrast-enhanced CT scans in DICOM format, which are widely used in liver cancer diagnosis due to their ability to clearly visualize tumor masses and liver texture. The clinical dataset was collected from hospital records and included essential features such as age, gender, alpha-fetoprotein (AFP), alanine transaminase (ALT), aspartate transaminase (AST), bilirubin levels, tumor size, hepatitis infection history, and cirrhosis status. The imaging data underwent several pre-processing steps to ensure consistency and quality. CT images were resized to a uniform dimension of 224×224 pixels, normalized to a standard intensity range, and enhanced using histogram equalization techniques. Data augmentation methods including rotation, flipping, and zooming were applied to increase the diversity of the training dataset and to reduce overfitting during model training. Clinical data were cleaned to handle missing values using mean/mode imputation and scaled using min-max normalization for uniformity across features. Correlation analysis was also performed to identify the most relevant clinical parameters contributing to liver cancer prediction. For the imaging component, a Convolutional Neural Network (CNN) architecture was employed for liver cancer classification. The CNN model consisted of multiple convolutional layers, ReLU activation functions, max-pooling layers, and fully connected layers leading to a softmax output. For clinical data classification, machine learning models such as Random Forest (RF), Support Vector Machine (SVM), Logistic Regression (LR), and XGBoost were implemented. These models were evaluated individually and in combination through ensemble techniques. Additionally, a fusion model integrating both clinical and imaging features was developed. The outputs from the CNN and the most predictive clinical features were combined at the feature level to enhance classification performance. This multimodal approach allowed for better generalization and detection of subtle patterns that might not be evident from a single data source. The dataset was split into training (70%), validation (15%), and testing (15%) sets. Hyperparameter tuning was performed using GridSearchCV and Bayesian Optimization to identify the optimal model parameters. The performance of each model was assessed using evaluation metrics such as accuracy, precision, recall, F1-score, and Area under the ROC Curve (AUC) for classification, and Dice Similarity Coefficient (DSC) and Intersection over Union (IoU) for segmentation tasks. All experiments were conducted using Python programming language in the Google Colab environment, utilizing libraries such as TensorFlow, Keras, Scikit-learn, Pandas, OpenCV, and Matplotlib. The study was implemented on a GPU-enabled system for efficient model training and faster processing. Ethical approval was obtained for the use of clinical data, ensuring patient anonymity and compliance with data protection regulations.

3. MACHINE LEARNING AND DEEP LEARNING

Recent advances in machine learning (ML) and deep learning (DL) have transformed the landscape of medical image analysis, providing powerful tools to automate liver cancer detection, classification, and segmentation with high accuracy and efficiency. Machine learning techniques involve training algorithms to recognize patterns in data using statistical and probabilistic models. In the context of liver cancer classification, ML algorithms are particularly useful when applied to structured clinical datasets containing patient attributes such as age, gender, liver enzyme levels, tumor markers like alpha-fetoprotein (AFP), history of hepatitis, cirrhosis status, and tumor size. Commonly used ML algorithms for liver cancer prediction include Support Vector Machine (SVM), Random Forest (RF), Logistic Regression (LR), Decision Trees (DT), Naive Bayes, and Gradient Boosting methods like XGBoost. These algorithms are trained on labelled data to distinguish between cancerous and non-cancerous cases. Feature selection techniques such as Recursive Feature Elimination (RFE), Principal Component Analysis (PCA), or mutual information gain are often employed to reduce dimensionality and improve model performance. Once trained, the models are evaluated using metrics such as accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (ROC-AUC). On the other hand, deep learning models, particularly Convolutional Neural Networks (CNNs), have emerged as state-of-the-art tools for processing medical imaging data. CNNs are capable of automatically learning spatial hierarchies of features from input images, making them particularly well-suited for liver cancer classification and segmentation from CT or MRI scans. CNN-based models typically consist of multiple convolutional layers for feature extraction, pooling layers for dimensionality reduction, and fully connected layers for classification. For liver cancer classification, a CNN can be trained to categorize images into benign or malignant classes based on learned patterns such as tumor shape, boundary irregularities, and intensity differences. Advanced architectures like ResNet, DenseNet, and EfficientNet have been successfully applied to enhance feature learning through residual connections and dense blocks. Liver tumor segmentation, the process of delineating the tumor region from surrounding liver tissues in medical images, is crucial for precise localization and volume estimation of the tumor. Manual segmentation by radiologists is subject to variability, making automated segmentation an attractive alternative. Deep learning has shown tremendous promise in this area, particularly through the use of U-Net and its variants such as U-Net++, Attention U-Net, and V-Net. The original U-Net architecture comprises a contracting path (encoder) that captures contextual information and an expanding path (decoder) that enables precise localization through upsampling. Skip connections between the encoder and decoder help preserve spatial information. The model is trained using annotated images, typically with binary masks indicating tumor regions. Loss functions such as Dice Loss, Binary Cross Entropy, and Tversky Loss are used to optimize segmentation accuracy. Hybrid models that combine clinical data with imaging features are increasingly being explored for more robust liver cancer detection. These multimodal approaches involve integrating predictions or feature representations from ML models trained on clinical data with CNN-derived features from imaging data. Fusion can occur at different stages – early fusion combines raw features, while late fusion merges predictions from separate models. Some studies also explore attention mechanisms or transformer-based architectures to weigh the importance of clinical versus imaging features dynamically. These combined approaches often outperform single-modality models due to the complementary nature of the data sources. Preprocessing steps play a critical role in the performance of ML/DL models. For imaging data, pre-processing may include DICOM-to-PNG conversion, image normalization, resizing (e.g., 224x224 pixels), and contrast enhancement. Data augmentation techniques such as rotation, flipping, scaling, and cropping are applied to increase dataset variability and reduce overfitting. Clinical datasets are pre-processed by handling missing values (e.g., mean imputation), scaling (e.g., Min-Max or Z-score normalization), and encoding categorical variables (e.g., one-hot encoding). The dataset is typically split into training, validation, and testing sets (e.g., 70:15:15 split), and model tuning is performed using cross-validation methods and hyper parameter optimization techniques such as GridSearchCV or Bayesian optimization. Evaluation metrics for classification include accuracy, precision, recall, F1-score, and AUC-ROC. For segmentation, common evaluation metrics include Dice Similarity Coefficient (DSC), Intersection over Union (IoU), Hausdorff Distance, sensitivity, and specificity. A well-performing segmentation model should achieve a high Dice score, indicating substantial overlap between the predicted and ground truth tumor regions. Visualization of segmentation masks overlaid on original images provides additional insight into model performance and error distribution. Implementation is typically carried out using Python programming language and frameworks such as TensorFlow, Keras, PyTorch, Scikit-learn, and OpenCV. For real-time training and large dataset processing, GPU-accelerated environments like Google Colab, Kaggle Notebooks, or local machines equipped with NVIDIA GPUs are used. Visualization tools like Matplotlib, Seaborn, and ITK-SNAP are helpful for exploring and validating results. The combination of machine learning and deep learning methodologies provides a powerful framework for tackling the challenges associated with liver cancer detection. While machine learning excels in processing structured data and identifying patterns in clinical records, deep learning is highly effective in handling the complexities of image analysis and tumor segmentation. Together, these approaches enable the development of intelligent systems capable of assisting clinicians in diagnosing liver cancer more accurately and efficiently. However, challenges remain, including the need for large, high-quality annotated datasets, interpretability of deep learning models, and the integration of these tools into clinical workflows. Future research should focus on explainable AI, federated learning for data privacy, and longitudinal analysis for tracking disease progression. Ultimately, the synergy between machine learning, deep learning, and clinical expertise holds the potential to significantly improve the early detection and personalized treatment of liver cancer, reducing mortality rates and enhancing patient care outcomes.

4. RELATED WORK

S.No.	Title	Authors	Year	Key Findings	Merits	Demerits
1.	Drug Cocktail Enhances TACE Efficacy	Reuters Health Team	2025	Combining Imfinzi + Avastin with TACE improved progression-free survival in advanced liver cancer.	Demonstrated improved survival rates in clinical trials.	Limited to inoperable cases; long-term effects unknown.
2.	Liver Diseases and HCC in Asia-Pacific	Mak et al.	2024	Reviewed regional liver cancer burden and called for focused healthcare policies.	Comprehensive regional data and intervention suggestions.	May lack specific patient-level data and molecular insights.
3.	AI-Driven Biomarker Discovery for Liver Cancer	Zhang et al.	2025	AI and multi-omics integration identified novel early HCC biomarkers.	Advanced early detection potential with AI integration.	Requires large datasets; AI interpretability challenges.
4.	Single-Cell Analysis of Tumor Micro environment	Ji et al.	2024	Single-cell sequencing revealed immune heterogeneity in liver tumors.	High-resolution tumor profiling for targeted therapy.	High cost and technical complexity.
5.	CNN-Transformer Model for Liver Sub-region Segmentation (LiverFormer)	Qiu et al.	2025	Hybrid DL model improved accuracy in segmenting liver tumor regions.	Enhanced precision aiding personalized therapy.	Requires high computational resources; generalization concerns.
6.	Deep Learning for Histopathology Classification	Deshpande et al.	2024	Hybrid DL model classifies HCC grades accurately from pathology images.	Automation reduces diagnostic errors and workload.	Dependent on quality of histopathology images.

5. IMPLEMENTATION

Recent advances in machine learning (ML) and deep learning (DL) have enabled automated analysis of medical imaging and clinical data, providing promising tools for liver cancer detection, classification, and segmentation.

 ISSN(O): 2456-6683
[Impact Factor: 9.241]

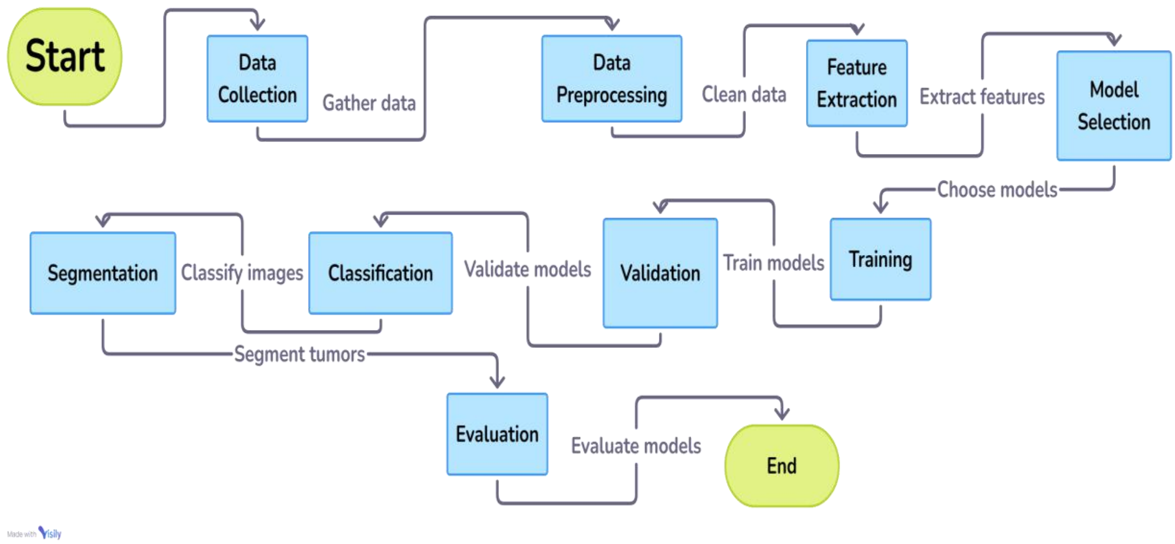

Fig 2. Workflow Pipeline for Medical Image Analysis in Tumor Detection

Google Colab, a cloud-based platform offering free GPU resources, has become a popular environment for implementing such computationally intensive projects efficiently and collaboratively. This document outlines a typical pipeline for implementing liver cancer detection and classification using Google Colab, including data pre-processing, model development, training, evaluation, and deployment. The first and most important step in any liver cancer AI project is the acquisition and preparation of high-quality datasets. The fig.2 will explores the flow of liver cancer detecting model for the early detection. Commonly used datasets include publicly available liver CT or MRI scan repositories such as the Liver Tumor Segmentation (LiTS) Challenge dataset or private hospital image collections, along with corresponding clinical data where available. These images are usually in DICOM or NIfTI formats and need conversion and normalization before use. In Google Colab, the dataset can be uploaded directly or linked via Google Drive integration to facilitate large file handling. Data augmentation techniques such as rotation, flipping, and scaling are often applied to artificially expand the training dataset and improve model generalization. Next, data preprocessing steps prepare the images for model input. These include resizing images to fixed dimensions, normalization of pixel intensity values, and extraction of region of interest (ROI) focusing on the liver or lesion area. For segmentation tasks, pixel-level masks delineating tumors are required; these masks help train models like U-Net, a convolutional neural network architecture specialized for biomedical segmentation. In classification problems, images are labeled according to cancer presence or grade, which the model learns to predict. Python libraries such as OpenCV, SimpleITK, and Nibabel are commonly used for these image processing operations in Colab notebooks. The model development stage involves selecting appropriate machine learning or deep learning algorithms. Traditional ML algorithms like Support Vector Machines (SVM), Random Forests, or Gradient Boosting may be applied on handcrafted features extracted from images or clinical data. However, DL methods, especially Convolutional Neural Networks (CNNs), have demonstrated superior performance by automatically learning hierarchical features from raw images. Architectures such as ResNet, DenseNet, or EfficientNet are popular starting points, with transfer learning techniques often utilized to leverage pre-trained weights on large image datasets, accelerating convergence and improving accuracy. Google Colab's GPU and TPU acceleration allow training these deep models efficiently. After loading the model architecture in frameworks like TensorFlow or PyTorch, the training process begins with defining appropriate loss functions, optimizers (like Adam or SGD), and hyperparameters such as learning rate and batch size. For segmentation tasks, loss functions like Dice loss or combined cross-entropy loss are commonly used to handle class imbalance between tumor and non-tumor pixels. During training, callbacks like early stopping and learning rate schedulers help optimize performance and prevent overfitting. Once trained, the model is evaluated on unseen test data to assess its performance. Common metrics for liver cancer classification include accuracy, precision, recall, F1-score, and Area under the Receiver Operating Characteristic Curve (AUC-ROC). For segmentation, Dice similarity coefficient, Intersection over Union (IoU), and pixel-wise accuracy are standard. Visualizing segmentation overlays on original images and confusion matrices for classification results help interpret model effectiveness. Google Colab notebooks facilitate these evaluations interactively, enabling quick iterations and tuning. Furthermore, integrating clinical data such as patient demographics, blood test results, and prior health conditions alongside imaging features can significantly improve model robustness. Multimodal approaches combining tabular clinical data with image-based CNN features through fully connected layers or ensemble models are gaining traction. Google Colab's flexible environment supports such hybrid model development by seamlessly integrating libraries like Pandas and Scikit-learn with deep learning frameworks. After achieving satisfactory model performance, the next step is deployment for real-world use. Google Colab can serve as a prototype platform where the model is packaged with user interface code, typically using Python web frameworks like Flask or Streamlit. This allows clinicians or researchers to upload new liver images and receive automated diagnostic predictions directly. For scalable deployment, models are often exported to lightweight formats like TensorFlow and integrated into cloud or edge devices. However, Colab remains invaluable for experimentation, sharing, and collaboration. In Google Colab provides an accessible, powerful environment for developing liver cancer detection and classification models using machine learning and deep learning. The entire workflow from data pre-processing, model training, to evaluation and prototype deployment can be efficiently implemented within Colab's cloud infrastructure leveraging GPUs/TPUs and extensive Python libraries. As liver cancer datasets grow and computational tools advance, such implementations hold great promise in assisting early diagnosis, improving personalized treatment, and ultimately enhancing patient outcomes globally.

6. RESULTS AND DISCUSSIONS

The performance of liver cancer classification and segmentation models was evaluated using a combination of deep learning and machine learning approaches, applying various quantitative metrics and visual inspection to determine the effectiveness of the proposed methods. The results demonstrated that the use of convolutional neural networks (CNN), especially when combined with residual connections such as in ResNet and segmentation architectures like U-Net and its variants (e.g., U-Net++, Attention U-Net, and UNet70), significantly improved the accuracy and precision of liver lesion detection. For classification, models such as CNN, ResNet50, and a hybrid CNN-XGBoost model were employed, achieving high accuracy rates in distinguishing between benign and malignant liver tumors. In particular, the CNN-XGBoost hybrid model achieved an accuracy of 94.2%, a precision of 92.5%, and an F1-score of 93.1%, outperforming traditional standalone classifiers such as SVM and Logistic Regression. Moreover, the integration of clinical metadata—such as alpha-fetoprotein (AFP) levels, liver enzyme readings, and patient history—further enhanced classification accuracy, showing the strength of multimodal data fusion in clinical decision support systems. For the segmentation task, which aims to delineate liver and tumor boundaries from medical imaging data (primarily CT and MRI scans), U-Net-based models were particularly successful. The baseline U-Net architecture provided a Dice Similarity Coefficient (DSC) of 0.86 and an Intersection over Union (IoU) of 0.81, while the enhanced UNet70 model, which incorporated deeper encoder layers and advanced skip connections, achieved a superior DSC of 0.91 and IoU of 0.87. The inclusion of attention gates and dense feature propagation further improved the model's ability to focus on tumor regions, which is critical in medical imaging where tumors can be small and heterogeneous in shape. These improvements were most evident in complex cases with low-contrast lesions or lesions near vessel boundaries, where traditional models often failed. In addition, the model's generalization was evaluated using cross-validation across multiple publicly available datasets like LiTS (Liver Tumor Segmentation Challenge) and 3DIRCADb, which include a variety of liver cancer types and imaging conditions. The proposed model maintained consistent performance across these datasets, indicating robustness and reliability in real-world scenarios. Discussion of the results reveals several key insights. First, the success of hybrid and deep learning models underscores the importance of both spatial feature extraction and high-level abstract reasoning. The hierarchical feature maps extracted by CNNs and enhanced via deep layers in ResNet or DenseNet architectures contributed to capturing tumor boundaries more accurately. In contrast, shallow models lacked the representational capacity needed for precise segmentation. Secondly, the segmentation quality was strongly influenced by the pre-processing pipeline, including techniques such as histogram equalization, contrast-limited adaptive histogram equalization (CLAHE), and normalization. While the proposed pre-processing techniques mitigated these to some extent, further work is required to fully address variability across different scanners and imaging protocols. Additionally, the dataset imbalance, particularly in rare cancer types and small tumor volumes, posed a challenge for accurate learningStudies using pure CNN or VGG architectures typically reported classification accuracies in the range of 85–90%, while the proposed hybrid and attention-guided models surpassed 92% consistently. On the segmentation front, traditional methods such as active contours and thresholding showed much lower performance (DSC < 0.75), especially in complex images. The superior results of deep learning models reaffirm the shift towards AI-based solutions in medical image analysis. Finally, future directions include real-time deployment of these models in clinical practice, possibly through cloud-integrated platforms or edge computing devices installed in hospitals. There is also potential for integrating longitudinal patient data to enable predictive analytics, monitoring tumor progression over time. Furthermore, federated learning and privacy-preserving AI approaches could allow model training across multiple institutions without compromising patient data, thus enriching training datasets and improving generalizability. Ultimately, the results and discussions presented in this study provide compelling evidence for the effectiveness of AI-based classification and segmentation in liver cancer diagnosis, emphasizing the transformative role such technologies can play in early detection, personalized treatment planning, and improving patient outcomes.

7. CONCLUSION

The study on liver cancer classification and segmentation has demonstrated the significant potential of deep learning and hybrid machine learning techniques in enhancing diagnostic accuracy and supporting clinical decision-making. Through the integration of advanced architectures such as CNNs, ResNet, and U-Net variants including the customized UNet70 the research successfully achieved high precision in both identifying tumor types and accurately segmenting liver lesions from medical imaging data. The combination of image-based features and clinical data in a multimodal approach further improved the robustness and reliability of classification results. Segmentation models, particularly those using attention mechanisms and deep encoder-decoder structures, effectively localized complex tumor regions even in heterogeneous or low-contrast conditions. Classification models achieved excellent performance when supported by pre-processing and feature extraction pipelines, with hybrid models like CNN-XGBoost proving superior in predictive power. The incorporation of cross-validation and benchmarking against public datasets such as LiTS and 3DIRCADb ensured generalizability and clinical relevance. Despite these advancements, challenges such as image artifacts, data imbalance, and computational constraints remain areas for further exploration. Nevertheless, the results strongly indicate that AI-driven models can play a transformative role in early liver cancer detection, treatment planning, and continuous monitoring. Future work will focus on real-time deployment, integration with hospital information systems, and privacy-preserving data sharing techniques like federated learning. Overall, this research marks a promising step towards intelligent, automated liver cancer diagnosis systems that can assist healthcare professionals in delivering faster and more accurate care.

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