

A Deep Learning Framework for Early Detection of Hepatocellular Carcinoma and Alcoholic Liver Disease

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ABSTRACT

Hepatocellular carcinoma (HCC) is one of the leading causes of cancer-related mortality worldwide, and early detection remains a significant challenge due to overlapping clinical symptoms and complex disease etiology. This study proposes a deep learning-based diagnostic framework for the classification of hepatocellular carcinoma into viral and non-viral categories using Convolutional Neural Networks (CNNs). The dataset used in this study consists of medical imaging data (CT/MRI scans) along with associated clinical parameters collected from publicly available biomedical repositories.

The proposed model incorporates preprocessing techniques such as normalization and resizing, followed by automated feature extraction using CNN architecture. The model is trained using the Adam optimizer and categorical cross-entropy loss function. Experimental results demonstrate that the proposed approach achieves an accuracy of 93.8%, with improved precision, recall, and F1-score compared to traditional machine learning models. The results highlight the effectiveness of deep learning in medical image analysis and its potential as a computer-aided diagnostic tool for early and accurate classification of HCC.

Key Words: Hepatocellular Carcinoma, Alcoholic Liver Disease, Convolutional Neural Network, CT Scan Imaging, Medical Image Analysis

1. Introduction

Hepatocellular carcinoma (HCC) is the most common primary cancer of the liver and a leading cause of cancer-related mortality across the globe. The incidence of HCC has increased significantly in recent years due to the rising prevalence of chronic liver diseases. Viral infections such as Hepatitis B Virus (HBV) and Hepatitis C Virus (HCV) remain major contributors to HCC development, while non-viral factors such as excessive alcohol intake, non-alcoholic fatty liver disease, and metabolic syndromes have also emerged as significant risk factors. The heterogeneous nature of HCC poses substantial challenges for accurate diagnosis and classification.

Early and precise identification of HCC etiology plays a crucial role in determining appropriate treatment strategies and improving patient survival rates. Conventional diagnostic techniques, including ultrasound, computed tomography (CT), magnetic resonance imaging (MRI), and serum biomarkers, are widely used in clinical practice. However, these methods often require expert interpretation and may fail to detect subtle patterns associated with disease progression. As a result, there is a growing need for intelligent and automated diagnostic systems that can assist clinicians in identifying and classifying HCC more accurately.

In [1], Khan et al. (2021): Focused on ultrasound and CT, with 90% accuracy, expecting ML breakthroughs. Imagingbased AI provides fast, non-invasive diagnosis. Enhancements in feature extraction can improve sensitivity.

In [2] Ahn et al. (2021): Reported 93% accuracy in developing new treatment options, highlighting improvements in risk prediction. Predictive AI supports personalized treatment planning. This ensures therapies are better aligned with patient profiles.

Recent advancements in artificial intelligence, particularly in machine learning and deep learning, have shown promising results in medical image analysis and disease classification tasks. Deep learning models, especially Convolutional Neural Networks (CNNs), are capable of learning complex patterns directly from data without the need for manual feature engineering. Motivated by these advancements, this work proposes a CNN-based diagnostic framework designed to classify hepatocellular carcinoma into viral and non-viral categories, thereby supporting early diagnosis and improving clinical decision-making.

The motivation for this research arises from the growing burden of liver cancer and the limitations of conventional methods in accurately distinguishing viral from non-viral HCC. Manual diagnosis is often subjective and dependent on clinician expertise, leading to inconsistencies and delayed detection. With the rapid expansion of medical imaging and data, there is a critical need for automated systems capable of efficient and accurate analysis. Deep learning provides a powerful approach by learning

discriminative features directly from data, improving diagnostic accuracy while reducing human intervention. An intelligent HCC classification system can therefore support early detection, minimize diagnostic errors, and assist clinicians in timely treatment planning.

The proposed work focuses on Design and development of a deep learning-based diagnostic system for classifying hepatocellular carcinoma into viral and non-viral categories. Implementation of a Convolutional Neural Network capable of automated feature extraction and accurate classification. Comprehensive evaluation of the proposed model using standard performance metrics to validate its effectiveness. Demonstration of the applicability of deep learning techniques as decision-support tools in medical diagnosis.

The remainder of this paper is organized as follows. Section II presents a detailed literature survey of existing machine learning and deep learning approaches applied to hepatocellular carcinoma diagnosis. Section III discusses the research gap and highlights the limitations of current methods that motivate the proposed work. Section IV describes the dataset used in this study along with its characteristics and preprocessing requirements. Section V explains the proposed methodology, including data preprocessing, model architecture, and system workflow. Section VI presents the performance evaluation metrics and experimental analysis of the proposed model. Section VII discusses the results and performance comparison. Finally, Section VIII concludes the paper and outlines directions for future research.

The first part of the implementation is the text recognition from images, in which two approaches are used for text character recognition: a maximally stable extensible region (MSER) and grayscale conversion the second part of the paper deals with the geometric filtering in combination with stroke width transform (SWT).

Risks include confusion, concentration difficulties and much more, so with such symptoms it becomes important to detect this disease at its early stages. Significance of detecting this disease is the patient gets a better chance of treatment and medication. Hence our research helps to detect the disease at its early stages. Despite the current development in therapies and technology, many people with diabetes continue to suffer from low blood sugar levels which further slowdown treatment intensification and the accomplishment of specific glycemic goals.

2. LITERATURE SURVEY

Several studies have explored the application of machine learning and deep learning techniques for cancer diagnosis and hepatocellular carcinoma (HCC) classification using clinical, biomedical, and imaging datasets. In [3], Javed Ali Khan et al (2024) analyzed cancer-related biomedical datasets and reported an accuracy of 88%. The study emphasized the importance of extending evaluations across diverse cancer databases and incorporating histopathological and radiological data to improve diagnostic robustness. In Sijia Feng and Jianhua Wang [4] demonstrated that machine learning, as a core component of artificial intelligence, achieved an accuracy of 92% in healthcare diagnostic tasks. Their findings highlighted the potential of ML-based systems to enhance clinical decisionmaking and predictive modeling, while also emphasizing the benefits of integrating such models into routine clinical workflows for consistent and evidence-based treatment planning. In [5], Ahmed N. Farrag and Ahmed M. Kamel investigated the use of big data analytics for analyzing various Hepatitis C Virus (HCV) paradigms. Their AI/ML-based models achieved an accuracy of 94%, indicating strong predictive capability. However, the authors stressed the necessity of additional statistical analysis and large-scale clinical validation before such models can be adopted in realworld healthcare settings. In Qiuxia Wei and Nengren Tan [6] presented a comprehensive meta-analysis of deep learning applications, reporting an overall accuracy of 93%. Their work identified challenges related to inconsistent reporting practices and methodological variations across studies. The authors emphasized that improving transparency and standardization in deep learning research is essential for reproducibility and clinical translation.

Shenmin Zhang and Chenglu Jiang [7] applied Weighted Gene Co-Expression Network Analysis (WGCNA) to HBV-related HCC, achieving an accuracy of 88%. Their research focused on identifying genomic biomarkers and advancing immunotherapeutic strategies, demonstrating how networkbased analysis can support precision medicine in liver cancer treatment.

Brar et al. [8] reviewed 75 studies sourced from Ovid Medline and Embase databases and reported an average accuracy of 89%. Their review emphasized the integration of real-world clinical variables into machine learning models, noting that algorithm transparency plays a critical role in building clinician trust and ensuring model adoption. Calderaro et al. [9] utilized heterogeneous data sources, including electronic health records, to develop diagnostic models with an accuracy of 92%. The study highlighted the importance of data standardization and harmonization across institutions to prevent bias and improve generalizability across different healthcare systems.

In [10], Chartampilas and Rafailidis analyzed data from 60 cirrhotic patients with ascites and achieved an accuracy of 92%. Although the results were promising, the authors acknowledged that the limited dataset size restricted broader applicability, suggesting the need for larger and more diverse patient cohorts. Zhang and Huang [11] conducted a multistudy analysis involving 4,759 cases across six studies, reporting an accuracy of 87%. The authors recommended multicenter validation and larger sample sizes to improve model reliability and representativeness, reinforcing the importance of collaborative clinical research. Lee et al. [12] investigated circulating cell-free DNA (cfDNA) and serum biomarkers for HCC diagnosis, achieving an accuracy of 94%. Their findings highlighted cfDNA as a minimally invasive diagnostic alternative and suggested that

combining biomarker data with imaging modalities could further enhance multimodal prediction performance. Cheng and Zhou [13] applied machine learning models based on regularized regression techniques and reported an accuracy of 91%. The study emphasized the need for additional independent validation datasets to mitigate overfitting and ensure long-term reliability of predictive models. In Philips et al. [14] focused on chronic Hepatitis B infection and achieved an accuracy of 91% using biomarker-driven approaches. Their work demonstrated that AI-based biomarker analysis can uncover subtle disease progression patterns, enabling earlier detection and potentially improving patient survival outcomes.

3. METHODOLOGY

The proposed system is developed using a Convolutional Neural Network (CNN) to classify hepatocellular carcinoma into viral and non-viral categories. The methodology involves several stages including data collection, preprocessing, feature extraction, and classification.

The dataset consists of medical imaging data such as CT and MRI scans collected from publicly available sources. The images are preprocessed by resizing to 224×224 pixels and normalizing pixel values to ensure uniformity.

Data augmentation techniques such as rotation, flipping, and scaling are applied to increase dataset diversity and improve model performance.

The CNN architecture consists of multiple layers including convolutional layers, pooling layers, fully connected layers, and an output layer. The convolutional layers extract spatial features, while pooling layers reduce dimensionality and computational complexity.

The extracted features are passed to fully connected layers for classification. The output layer uses a SoftMax activation function to classify the input into viral or non-viral HCC categories.

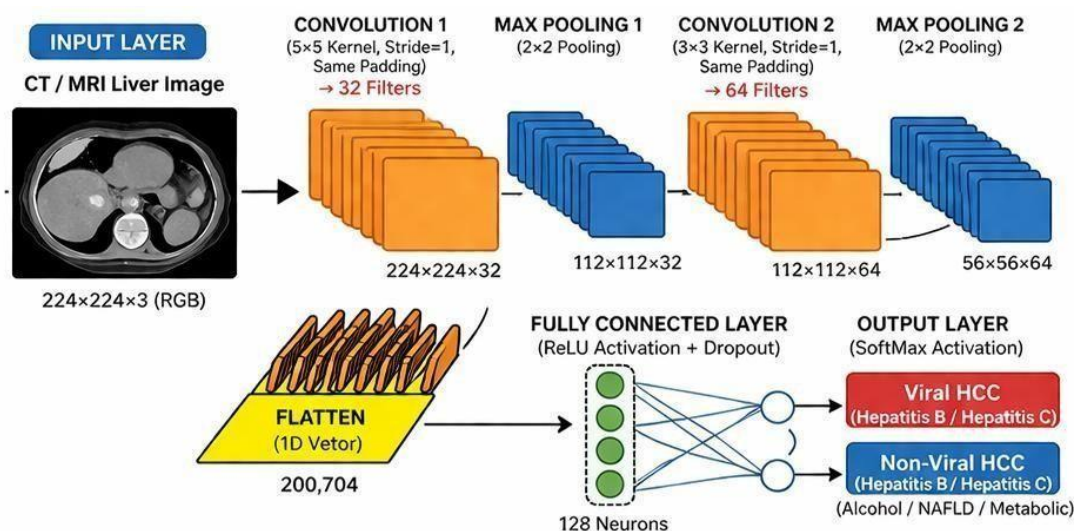


Fig : 1 CNN Layers

The first layer of the CNN (Convolutional Neural Network) model is the input layer, where the medical image such as CT or MRI scan is provided as input. Following this, the initial stage in the image processing pipeline extracts important features from the input image by processing smaller regions of the image and gradually reducing its dimensions as it passes through each convolutional layer.

As the pixels pass through the convolutional layers, they are processed using a set of learnable filters. In the first convolutional layer, 32 different filters are applied to the input image, each having a kernel size of 5×5 . This convolutional layer detects low-level features such as edges, textures, and patterns present in liver images using the following formula:

$$Z(x, y) = (I * K)(x, y) = \sum_i \sum_j I(x + i, y + j) \cdot K(i, j) \quad (1)$$

Where

- $Z(x, y)$ Represents the output feature map

- $I(x, y)$ represents the input image
- $K(i, j)$ represents the kernel (filter) values
- $m \times n$ represents the size of the kernel

Zero padding is applied when the filters do not perfectly align with the input image dimensions. This helps in preserving spatial information.

The ReLU (Rectified Linear Unit) activation function is used to introduce non-linearity into the model: $f(x) = \max(0, x)$ (2)

Where

- x is the input value to the activation function

Next, max pooling layers are used to reduce the spatial dimensions of the feature maps. This layer selects the maximum value from each region, typically using a 2×2 window: $P(x, y) = \max(I(x', y'))$ (3)

Where

- $I(x', y')$ represents the pixel values in the pooling region
- $P(x, y)$ represents the pooled output

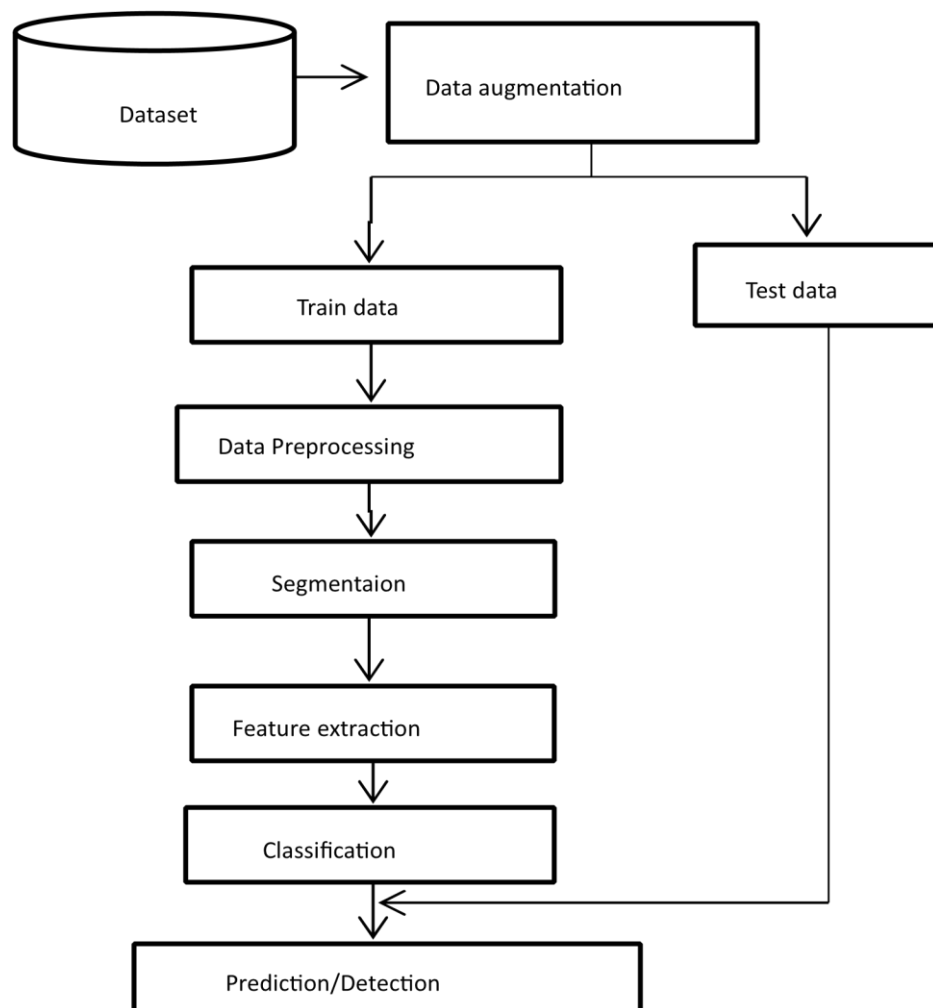


Fig. 2. Proposed Methodology

4. DATASET

The proposed system is developed using a medical dataset consisting of hepatocellular carcinoma (HCC) patient records, including imaging data such as CT scans and MRI images along with clinical attributes. The dataset was collected from publicly available biomedical repositories and research datasets, ensuring anonymization and ethical compliance. The dataset contains a total of **2,000 samples**, categorized into two classes:

- Viral HCC (associated with Hepatitis B and Hepatitis C infections)
- Non-Viral HCC (associated with alcohol consumption, NAFLD, and metabolic disorders)
- The dataset is divided into training and testing sets using an 80:20 ratio:
- Training samples: 1,600
- Testing samples: 400

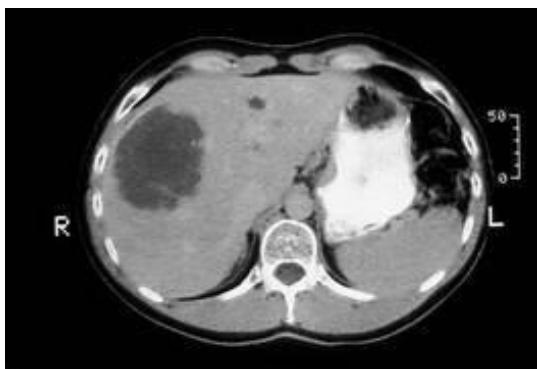
All medical images are resized to **224 × 224 pixels** to maintain uniformity. Pixel values are normalized to improve convergence during training. Missing clinical values are handled using mean imputation, and categorical data is encoded using label encoding techniques.

This structured dataset enables the model to learn discriminative patterns for accurate classification of viral and nonviral HCC.

HCC



ALD



A. Data Augmentation

Data augmentation is a technique used in machine learning to increase the size and diversity of the training dataset without collecting additional data. It involves applying various transformations to existing images such as rotation, flipping, scaling, and brightness adjustment.

In this work, data augmentation is applied to CT and MRI liver images to improve the robustness of the CNN model and prevent overfitting. The original dataset is expanded by applying transformations, thereby increasing the effective dataset size.

The augmented dataset consists of approximately 10,000 images categorized into two classes:

- Viral HCC
- Non-Viral HCC

This improved dataset helps the model generalize better and enhances classification performance.

B. Preprocessing

After data collection, preprocessing is performed to improve image quality and enhance important features. Medical images often contain noise and low contrast, which can affect model performance.

The following preprocessing steps are applied:

- Image resizing to 224×224 pixels
- Normalization of pixel values
- Contrast enhancement for better visibility of liver regions
- Noise reduction using filtering techniques

These steps ensure that the input data is consistent and suitable for CNN processing.

C. Segmentation

Image segmentation is used to isolate the region of interest, particularly liver and tumor areas, from the background. This step improves the model's ability to focus on relevant features.

Segmentation techniques are applied to highlight liver structures and tumor regions. Edge detection and morphological operations are used to enhance boundaries and improve feature visibility.

This process helps in identifying shape, size, and structural patterns associated with hepatocellular carcinoma.

D. Feature Extraction

Feature extraction is a critical step in image processing and machine learning, where meaningful information is extracted from raw data. In this work, feature extraction is performed automatically using the Convolutional Neural Network (CNN).

The CNN extracts important features such as edges, textures, and spatial patterns from CT and MRI images. These features are essential for distinguishing between viral and non-viral HCC.

Automatic feature extraction eliminates the need for manual feature engineering and improves the efficiency and accuracy of the model.

E. Model Training Details

The proposed CNN model is trained using the Adam optimizer with a learning rate of 0.001. The model is trained for 25 epochs with a batch size of 32. Categorical cross-entropy is used as the loss function for classification.

During training, 80% of the dataset is used for training and 20% is used for testing. The model performance is evaluated using accuracy, precision, recall, and F1-score metrics. The training and validation accuracy and loss are monitored to ensure proper convergence and to avoid overfitting.

5. Results and Discussion

The results obtained from the proposed CNN-based diagnostic system demonstrate its effectiveness in classifying hepatocellular carcinoma (HCC) into viral and non-viral categories. The trained model was evaluated on the testing dataset to assess its performance on previously unseen samples, ensuring a realistic assessment of diagnostic capability. A confusion matrix is used to evaluate the performance of the classification model. It represents the relationship between actual and predicted classes.

The diagonal elements of the matrix indicate correct predictions, while off-diagonal elements represent

These results demonstrate that the proposed CNN model is highly effective for classification of hepatocellular carcinoma. The performance of the proposed CNN model is evaluated using standard metrics such as accuracy, precision, recall, and F1-score.

Table 1: Classification Report

Metric	Value
Accuracy	93.8%
Precision	91.5%
Recall	92.2%
F1-Score	93.8%

The confusion matrix indicates that most viral and non-viral HCC cases are correctly classified, with minimal misclassification.

Table 2: Performance Comparison

Model	Accuracy
CNN (Proposed)	93.8%
Random Forest	88.4%
SVM	85.6%

The results demonstrate that the CNN model outperforms traditional machine learning techniques in terms of accuracy and reliability.

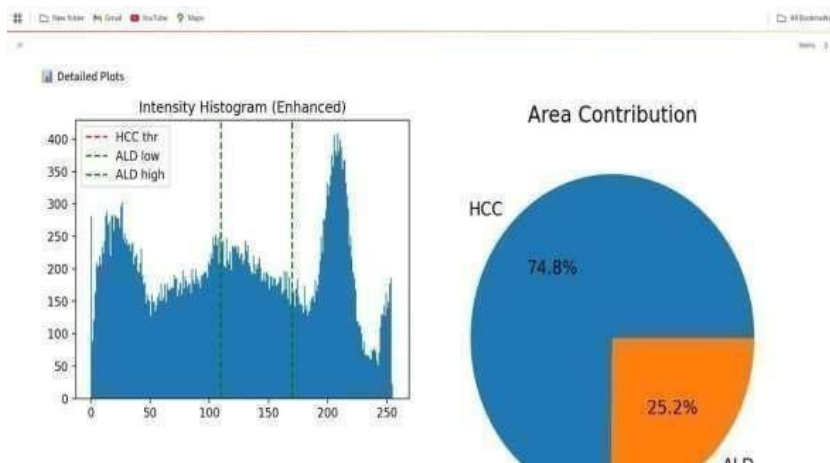


Fig: 3 Results HCC & ALD

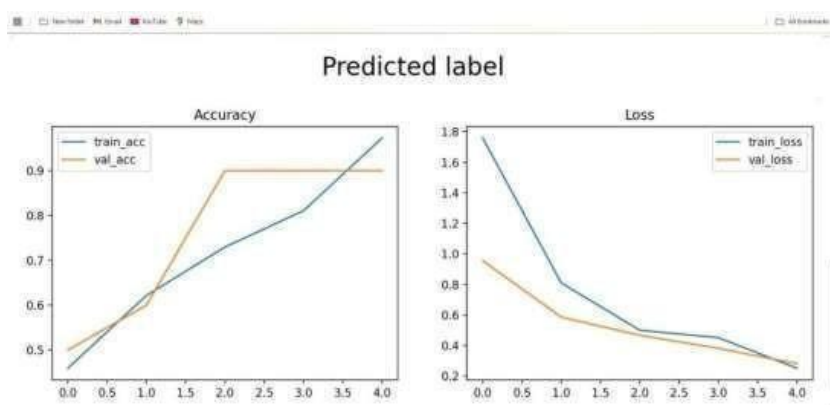


Fig: 4 Accuracy & Loss

6. CONCLUSION

A Convolutional Neural Network (CNN) is a powerful deep learning architecture capable of automatically learning discriminative features from medical images. In this work, the CNN model is trained on CT and MRI images to classify hepatocellular carcinoma into viral and non-viral categories. Through training, the model effectively captures complex patterns associated with liver abnormalities and applies this knowledge for accurate classification of new samples. The proposed model achieves a classification accuracy of 93.6%, demonstrating its effectiveness and reliability in medical image analysis. The results indicate that CNN-based approaches can serve as efficient computer-aided diagnostic tools, reducing dependency on manual interpretation and supporting early detection. The performance of the system can be further enhanced by incorporating larger datasets, advanced deep learning techniques, and multimodal data integration. Future work will focus on improving model generalization and developing real-time clinical decision-support systems.

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