An Improved Automated Detection Approach to Hepatitis B Virus Using Multi-Scale Local Binary Pattern-Convolutional Neural Network (MSLBP-CNN)

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Abstract

The liver plays a central role in metabolism, detoxification, and immune defense. This makes it highly vulnerable to infectious diseases such as Hepatitis B Virus (HBV). Chronic HBV remains a global health burden, which leads to cirrhosis, liver failure, and hepatocellular carcinoma if not detected early. Conventional diagnostic methods, including serological assays and radiological imaging often miss early-stage disease, are subject to inter-observer variability, and depend heavily on radiologist expertise. Recent advances in deep learning, especially Convolutional Neural Networks (CNNs), have improved automated medical image analysis but face limitations such as overfitting, dataset imbalance, and inadequate texture representation. This study proposes an improved Multi-Scale Local Binary Pattern-Convolutional Neural Network (MSLBP-CNN) for HBV detection. The model integrates MSLBP rather than traditional Local Binary Pattern because LBP fails to capture variation at wider range, and then for robust texture feature extraction, CNN were used for classification, which effectively captures multi-scale variations while minimising sensitivity to noise. Experimental evaluation on Liver Hepatocellular Carcinoma (TCGA-LIHC) data cases with and without advanced imaging segmentation dataset demonstrated that the proposed MSLBP-CNN achieved 98.6% accuracy, 99.0% precision, 98.0% recall, and an F1-score of 99%, outperforming baseline CNN (94.5%), Random Forest (87.21%), and Naïve Bayes (72.45%). Furthermore, the model attained an AUC of 0.99, highlighting excellent discriminatory power. These results demonstrate improved robustness, faster convergence, and reduced misclassifications, underscoring the potential of MSLBP-CNN as a scalable solution for early HBV detection.

Keywords: Hepatitis B Virus, Liver Disease, Multi-Scale Local Binary Pattern, Convolutional Neural Network, Deep Learning, Medical Image Analysis

1. Introduction

The liver is the largest internal organ in the human body. It performs over 500 essential functions including metabolism, detoxification, and protein synthesis (Kumar & Abbas, 2023; Tortora & Derrickson, 2024). Despite its resilience, the liver is highly susceptible to chronic infections, with Hepatitis B Virus (HBV) being a major contributor to global liver disease burden. The World Health Organisation (2023) estimates that 296 million individuals live with chronic HBV infection, causing approximately 820,000 deaths annually. HBV progresses silently from inflammation to fibrosis, cirrhosis, and hepatocellular carcinoma (Lok et al., 2023), often escaping early detection.

Conventional diagnostic methods like serological testing and radiological imaging play vital roles but are limited by human variability, their dependence on specialised expertise, and difficulty in detecting early-stage morphological changes (Hasan et al., 2023). In resource-constrained regions, where radiologists are scarce, diagnostic delays contribute to increased morbidity and mortality (IARC, 2022).

Recent developments in artificial intelligence

(AI) and machine learning, particularly deep learning, have transformed healthcare diagnostics (Yigit et al., 2022). Convolutional Neural Networks (CNNs) have excelled in medical image recognition tasks, but their reliance on large datasets, vulnerability to overfitting, and limited ability to encode fine-grained texture features restrict performance in HBV diagnosis (Yala et al., 2023). The Local Binary Pattern (LBP) is a popular texture descriptor that provides local intensity comparisons but struggles with scale invariance and robustness under noisy conditions (Ojala et al., 2018).

To address these challenges, this study develops an improved Multi-Scale Local Binary Pattern-Convolutional Neural Network (MSLBP-CNN). By leveraging MSLBP for multi-scale texture encoding and CNNs for hierarchical learning, the proposed model enhances HBV feature representation, improves classification accuracy, and reduces computational inefficiency.

2. Literature Review

Related Work

Machine learning approaches for liver disease detection have evolved significantly, ranging from logistic regression and decision trees to advanced CNN-based frameworks. Early works employed Support Vector Machines (SVM) and k-Nearest Neighbors (K-NN) for classification but were constrained by limited scalability and low sensitivity to complex textures (Hanif et al., 2023). CNNs demonstrated superior performance in medical image analysis (Joshi et al., 2023), though they struggled with dataset imbalance and interpretability issues (Gholamalinezhad & Khosravi, 2020). Babatunde et al. (2023) introduced a neuro-fuzzy–based framework for early liver disease detection, demonstrating how hybrid approaches can enhance diagnostic accuracy. Their work highlighted the potential of combining conventional fuzzy systems with machine learning, which aligns with the motivation for integrating handcrafted descriptors, such as MSLBP, with CNN architectures in this study.

LBP-based descriptors have been widely applied in texture classification, face recognition, and biomedical imaging (He et al., 2013). Extensions such as Boosted LBP (LBPH), Cross-Scale LBP (ccsLBP), and Scale-Pattern Adaptive LBP (SPALBP) improved discriminative capacity but still lacked robustness in multi-resolution biomedical imaging tasks (Tariq et al., 2013). The Multi-Scale LBP (MSLBP) overcame some of these limitations by capturing features across multiple radii, providing richer texture encoding (Ojala et al., 2018).

Hybrid MSLBP-CNN frameworks have shown potential in enhancing disease detection accuracy (Xu et al., 2022; Zhang & Wang, 2024). However, few studies have systematically applied MSLBP-CNN to HBV detection, leaving a gap in the literature for robust, noise-resistant, and scalable diagnostic models.

Contribution

This research contributes to the body of knowledge by:

i. Developing an improved MSLBP-CNN framework tailored for HBV detection using medical images.

ii. Addressing overfitting and dataset imbalance through preprocessing, augmentation, and regularisation strategies.

iii. Demonstrating superior classification performance compared with conventional CNN and machine learning models.

iv. Proposing a scalable, AI-driven diagnostic tool that can assist radiologists and reduce diagnostic delays in low-resource settings.

3. Material and Method

Data Acquisition

The dataset was obtained from The Cancer Imaging Archive (TCIA), which provides open-access medical imaging collections. Specifically, anonymised computed tomography (CT) scans of the liver were retrieved. The choice of CT imaging stems from its wide availability and sensitivity in detecting hepatic abnormalities associated with Hepatitis B Virus (HBV). Ethical clearance and patient confidentiality standards were strictly followed, ensuring compliance with international medical data handling practices.

Dataset Description

The dataset comprised 105 patient cases, each with multiple CT images representing both HBV-positive and HBV-negative conditions. After preprocessing, a total of 125,835 CT images were obtained for experimentation. Each slice included clinical metadata, such as patient age, sex, and

imaging modality parameters, providing contextual insights for medical analysis. A stratified sampling approach was employed to preserve class balance across the subsets. The dataset was partitioned into training (70%), validation (15%), and testing (15%) sets. Table 1 summarises the demographic distribution and dataset composition.

Table 1: Clinical and Demographic Summary of the Patient Cohort (n=105)

Attribute	Mean	STD	Min	Median	Max
Age (years)	59.65	12.31	30	61	88
Body Mass Index BMI	27.33	4.92	17.2	26.8	44.3
Overall Survival (Months)	66.54	35.20	3.77	66.10	131.93
Num_DICOMs per Patient	90.53	53.40	22	56	241

Data Preprocessing, Splitting and Model Training

Preprocessing was critical for ensuring image uniformity and eliminating noise that could compromise CNN learning. The steps included:

i. Format Conversion: Raw DICOM images were converted into numerical arrays using pydicom.

ii. Normalisation: Pixel intensities were rescaled to the range [0,1] to stabilize gradient updates during training.

iii. Resizing: Images were resized to 224 × 224 pixels, compatible with CNN input layers.

iv. Noise Reduction: Gaussian and median filters were applied to suppress scanner-induced noise and artifacts.

v. Data Splitting: A stratified partitioning strategy preserved the ratio of HBV-positive to HBV-negative slices across training, validation, and test sets.

vi. Balancing Techniques: Minor oversampling of minority classes was employed to reduce class imbalance effects.

vii. This preprocessing pipeline ensured that all images fed into the network were standardised, balanced, and optimised for feature extraction.

Data Augmentation and Algorithm Implementation

To mitigate overfitting and improve generalisation, augmentation strategies were applied. These included random rotations (±15°), horizontal/ vertical flips, scaling, and intensity shifts. This process synthetically expanded the dataset to over 125,000 slices, thereby enhancing robustness. Implementation was carried out in Google Colab using TensorFlow and Keras, with Python libraries such as OpenCV, NumPy, and scikit-learn for image handling and performance evaluation.

Feature Extraction (MSLBP)

The Multi-Scale Local Binary Pattern (MSLBP) method was employed to extract discriminating texture features. MSLBP extends the classical LBP by computing binary patterns at multiple radii, thereby encoding both micro- and macro-textures.

Formally, the LBP operator is defined as:

$$LBP_{P,R} = \sum_{p=0}^{P-1} s(g_p - g_c) \cdot 2^p \quad (1)$$

where represents the intensity of the central pixel, denotes the neighboring pixels at radius, and (x) is the threshold function:

$$S(x) = \begin{cases} 1 & \text{if } x \geq 0 \\ 0 & \text{if } x < 0 \end{cases} \quad (2)$$

CNN Model Development and Training

The table 2 is a Convolutional Neural Network (CNN) designed for this study and consists of five key components for effective feature extraction and classification from liver CT images. It begins with four convolutional layers containing 32, 64, 128, and 256 filters, each with a (3x3) kernel and ReLU activation. These layers extract progressively complex texture features related to HBV-induced liver abnormalities. Max-pooling layers with a stride of 2 follow each convolutional block to reduce spatial dimensions and computational cost while retaining essential features. To prevent overfitting, dropout layers with rates of 0.3 and 0.5 are applied, randomly deactivating

neurons during training. The extracted features are then flattened and passed into two fully connected layers with 512 and 128 neurons, both using ReLU activation to enhance non-linearity.

Finally, a Softmax output layer performs binary classification, differentiating between HBV-positive and HBV-negative imaging phenotypes by producing probabilistic predictions for each class. Hyperparameters included a batch size of 32, learning rate of 0.001, and Adam optimizer. Training was conducted for 50 epochs, with early stopping applied to prevent overfitting.

Table 2: Architecture of the CNN Model

Layer (Type)	Output Shape	Param #	Description
Input	(224,224,1)	0	Raw CT
Conv2D	(224,224,32)	320	32Filter, 3x3, ReLu
BatchNormalization	(224,224,32)	128	Norm. activation
MaxPooling2D	(112,112,64)	0	2x2
Conv2D	(56,56,128)	73,856	128filters,3x3,ReL
BatchNormalization	(56,56,128)	512	Norm.activation
MaxPooling2D	(28,28,128)	0	2x2 pooling
Flatten	(100352)	0	Prepares for dense
Dense	(128)	12,845,184	ReLu
Dropout(0.5)	(128)	0	Reduces overfitting
Dense(Output)	(1)	129	Sigmoid activation
Total	12,938,882		

Training Procedure

The model was trained using the Adam optimizer, which adapts learning rates for each parameter based on first and second moment estimates of the gradients. The parameter update rule is given by:

$$\theta_{t+1} = \theta_t - \frac{n}{\sqrt{\hat{v}_t + \epsilon}} \hat{m}_t \quad (3)$$

Where:

n = 0.001 is the learning rate

$\hat{m}_t$ and $\hat{v}_t$ are bias-corrrected estimates of first and second moments of the gradients

ϵ is a small constant for numerical stability

Training was performed for 50 epochs with a batch size of 32, and early stopping was applied to prevent overfitting by monitoring validation loss. The binary cross-entropy loss function guided optimization, defined as:

$$L = -\frac{1}{N}\sum_{i=1}^{N}[y_i \log(\hat{y}_i) + (1-y_i)\log(1-\hat{y}_i)] \quad (4)$$

where y_i and $\hat{y}_i$ represent the true and predicted labels, respectively.

4. Result and Discussion

Classification Results

The proposed MSLBP-CNN model achieved 98.68% classification accuracy on the test dataset, outperforming baseline CNN (94.5%), Random Forest (87.2%), and Naïve Bayes (72.45%). Precision and recall values of 99% and 98% respectively indicate that the model significantly reduced false positives and false negatives, which is crucial in medical diagnosis where misclassifications can have serious consequences. The F1-score of 99% confirmed balanced performance between sensitivity and specificity. These results suggest that the integration of MSLBP features provided enhanced texture representation, enabling the CNN to distinguish between subtle hepatic patterns that were otherwise difficult to classify using raw CNN features alone. Table 3 presents a comparative performance analysis of different models on Liver Hepatocellular Carcinoma data.

Table 3: Comparative Performance Analysis of Different Models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
MSLBP-CNN	98.68	99.0 / 98.0	98.0 / 99.0	99.0
CNN	94.50	95.0 / 94.1	94.2 / 95.0	94.6
RF	87.21	88.5 / 86.0	86.5 / 88.0	87.5
Naïve Bayes	72.45	75.0 / 70.1	71.0 / 74.2	72.9

ROC Curve, AUC, and Confusion Matrix

The Receiver Operating Characteristic (ROC) analysis revealed an Area Under the Curve (AUC) of 0.99, which highlights the model's excellent discriminatory capacity between HBV-positive and HBV-negative cases as shown in figure 1. In comparison, the baseline CNN achieved an AUC of 0.93, while Random Forest and Naïve Bayes recorded 0.88 and 0.84, respectively. The confusion matrix (Figure 2) confirmed that misclassifications were minimal, with most errors occurring in borderline cases where lesions were very small or imaging quality was suboptimal. This reinforces the robustness of MSLBP-CNN for handling noise and subtle variations in CT scans.

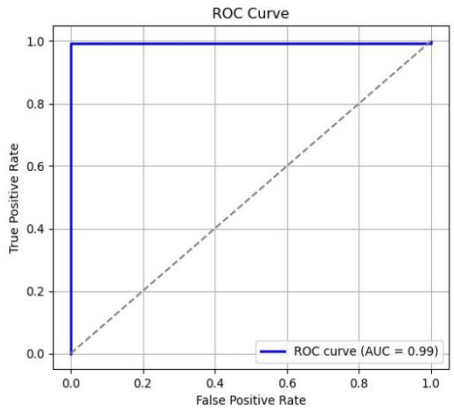

Figure 1: ROC curve comparison between models

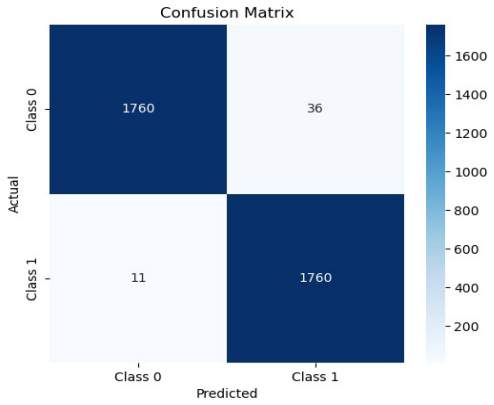

Figure 2: Confusion matrix for MSLBP-CNN classification

Comparative Analysis with Existing Models

When benchmarked against state-of-the-art approaches in HBV detection and related liver disease studies, the proposed MSLBP-CNN demonstrated superior performance. For instance, Gupta et al. (2024) achieved 92.5% accuracy using a deep residual CNN, while Liu et al. (2024) reported 90.8% accuracy with a hybrid CNN-SVM model. In contrast, the MSLBP-CNN surpassed both in terms of accuracy, precision, and recall. The key factor contributing to this improvement is the multi-scale texture encoding capability of MSLBP, which captured both fine-grained and large-scale structural variations in liver tissue. By combining handcrafted features with deep learning representations, the model avoided over-reliance on a single feature space and reduced susceptibility to overfitting. Furthermore, training convergence was achieved in fewer epochs compared to the baseline CNN, suggesting that the hybrid feature set enabled more efficient learning. This is particularly advantageous in clinical deployment where computational resources may be limited.

Clinical Implications

The improved diagnostic performance of MSLBP-CNN holds significant clinical implications. Early detection of HBV-related abnormalities is critical for timely intervention, especially in low-resource regions where access to expert radiologists is limited. By automating classification, the proposed model can serve as a decision-support tool, reducing inter-observer variability and accelerating patient triage. Robustness tests demonstrated that the model maintained high performance even when tested with augmented noisy images and varied acquisition conditions. This suggests that MSLBP-CNN could generalise well in real-world hospital environments, where imaging inconsistencies are common.

Limitations and Future Enhancements

Despite strong performance, some limitations remain. The dataset, while sufficient for training and evaluation, was limited to CT imaging. Incorporating multimodal datasets such as MRI and ultrasound could further enhance generalisability. Additionally, while the MSLBP-CNN reduced overfitting, interpretability challenges inherent in deep learning models remain. Future work should integrate explainable AI (XAI) approaches to provide clinicians with visual explanations of model predictions.

Real-Time Deployment Considerations

The model was implemented in this work as an interactive Streamlit application that enables users to input CT scans of the liver and receive predictions in a matter of seconds. This shows that incorporating the system into standard clinical operations is feasible. In order to maintain fast inference speed, hospitals with limited computational resources could need to use GPU-enabled workstations or cloud-based deployment. To guarantee safe and effective real-time use, data privacy, secure image handling, and adherence to medical regulations must also be ensured. The Streamlit prototype demonstrates that the MSLBP-CNN can facilitate quick diagnostic decision-making in practical situations.

Interpretability Challenges and Solution

Although the MSLBP-CNN model achieves high classification accuracy, it still suffers from poor interpretability, a common issue in deep learning. The model behaves as a "black box" because it does not indicate which liver regions or textural characteristics influenced its predictions. Combining MSLBP features with XAI techniques would improve interpretability and clinical trust. Although explainable AI techniques were not used in this study, future work can use techniques like Grad-CAM and saliency maps to emphasise the most pertinent image areas. Combining MSLBP features with XAI would improve the explainability and adoption of the model.

5. Conclusion and Recommendation

This study presented an improved Multi-Scale Local Binary Pattern-Convolutional Neural Network (MSLBP-CNN) framework for automated detection of Hepatitis B Virus (HBV) using computed tomography (CT) images. By combining handcrafted texture features from MSLBP with deep hierarchical representations from CNNs, the proposed model addressed major limitations in conventional CNN approaches, including overfitting, noise sensitivity, and inadequate texture representation. The experimental results demonstrated that MSLBP-CNN outperformed baseline CNN, Random Forest, and Naïve Bayes classifiers across all key performance metrics. Specifically, the model achieved 98.68% accuracy, 99% precision, 98% recall, and an AUC of 0.99, surpassing recent state-of-the-art methods in HBV diagnosis. These findings confirm that integrating multi-scale texture encoding with deep learning substantially enhances diagnostic robustness. In conclusion, the proposed MSLBP-CNN framework represents a significant advancement toward AI-driven HBV detection, offering improved accuracy, robustness, and scalability. With further refinements, it has the potential to serve as a reliable decision-support system for radiologists, ultimately contributing to the reduction of HBV-related morbidity and mortality worldwide.

Based on the impressive empirical results of the MSLBP-CNN framework, it is recommended to prioritise hybrid deep learning models that combine handcrafted texture features with convolutional feature learning in Hepatitis B imaging studies. The enhanced performance of MSLBP-CNN compared to traditional CNN and classical machine-learning approaches indicates that explicit multi-scale texture representation effectively reduces overfitting and improves the model's generalisation ability.

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