Proceedings of the 7th Latin American Conference on Industrial Engineering and Operations Management
Panama City, Panama, August 4-6, 2026

Proceedings of the International Conference on Industrial Engineering and Operations Management

Publisher: IEOM Society International, USA DOI: 10.46254/SA07.20260135
Published: August 4, 2026

An AI-Assisted Multimodal Framework for Hepatocellular Carcinoma Prediction and Tumor Grading Using ANP-Based Biomarker Prioritization and MRI/CT Image Analysis

Amala Maria Kuruvilla
Department of Computer Science and Engineering
Rajiv Gandhi Institute of Technology
Kottayam, Kerala, India
amalamaria012@gmail.com

K. Sunil Kumar
Professor
Department of Mechanical Engineering
Rajiv Gandhi Institute of Technology
Kottayam, Kerala, India
ksk_sunil@rit.ac.in

Shabeerali T. U
Senior Consultant, HPB and Liver Transplant
KIMSHEALTH
Thiruvananthapuram, Kerala, India
drshabeeralitu@gmail.com

Abstract

Hepatocellular Carcinoma (HCC) is among the most common and aggressive forms of primary liver cancer, contributing significantly to cancer-related deaths worldwide. Because the disease often develops without obvious symptoms during its early stages, timely diagnosis and accurate assessment of tumour severity are essential for improving treatment outcomes and patient survival. Current diagnostic methods, particularly liver biopsy, are invasive and may not always provide a complete representation of tumor characteristics due to sampling limitations. Although recent advances in artificial intelligence have improved computer-aided diagnosis, most existing approaches focus either on clinical biomarkers or on medical imaging, with limited attention to integrating both sources of information or to analysing the relationships among clinical variables. This research presents an AI-assisted multimodal framework for predicting and grading Hepatocellular Carcinoma by combining clinical biomarker analysis with MRI and CT image analysis. To better represent the influence of individual biomarkers, the Analytic Network Process (ANP) was employed to evaluate their interdependencies and determine their relative importance. The resulting biomarker weights were incorporated into a Logistic Regression model to estimate the probability of HCC occurrence, producing

© IEOM Society International

an R^2 value of 0.97. The prioritized biomarkers were further used to train a Random Forest classifier for stage-wise disease prediction, which achieved an overall classification accuracy of 99.71%**.** For imaging-based tumour grading, a Convolutional Neural Network (CNN) was developed to automatically learn discriminative features from MRI and CT images, resulting in a grading accuracy of 96.2%**.** By integrating biomarker prioritization, probabilistic disease prediction, stage classification, and image-based tumour grading within a single framework, the proposed approach provides a comprehensive and non-invasive method for HCC assessment. The integration of clinical biomarker and imaging information improves diagnostic consistency, supports early detection and accurate tumor grading, and provides a practical clinical decision support tool to assist clinicians in treatment planning and patient management.

Keywords
Hepatocellular Carcinoma (HCC), Artificial Intelligence, Biomarker Analysis, Analytic Network Process (ANP), Clinical Decision Support

1. Introduction
Liver diseases continue to pose a significant global healthcare challenge due to their increasing prevalence and high mortality rates. The liver plays a vital role in metabolism, detoxification, protein synthesis, and maintaining biochemical homeostasis. Consequently, liver dysfunction can adversely affect multiple organ systems and lead to severe health complications. Liver diseases account for nearly two million deaths annually worldwide, with cirrhosis and liver cancer representing major causes of liver-related mortality (Asrani et al. 2022). Among primary liver malignancies, Hepatocellular Carcinoma (HCC) constitutes approximately 75–80% of all liver cancer cases and remains one of the leading causes of cancer-related deaths worldwide. The incidence of HCC has been steadily increasing, particularly among patients suffering from chronic liver diseases such as hepatitis B, hepatitis C, liver cirrhosis, and non-alcoholic fatty liver disease. Early diagnosis and accurate assessment of disease progression are therefore essential for improving patient survival and selecting appropriate treatment strategies.

Conventional diagnostic approaches for HCC rely primarily on serum biomarker evaluation, radiological imaging using Computed Tomography (CT) and Magnetic Resonance Imaging (MRI), and histopathological examination through liver biopsy. Although biopsy remains the clinical gold standard for tumor grading, it is invasive, time consuming, expensive, and susceptible to sampling errors due to tumor heterogeneity. In addition, manual interpretation of MRI and CT images depends heavily on clinical expertise and may fail to identify subtle imaging characteristics associated with tumor differentiation and disease progression. These limitations often delay diagnosis and reduce the effectiveness of clinical decision-making.

Recent advancements in Artificial Intelligence (AI), Machine Learning (ML), and Deep Learning (DL) have demonstrated significant potential in addressing these challenges by enabling automated analysis of complex clinical and imaging data. Machine learning techniques can effectively identify relationships among multiple biomarkers and generate predictive models for disease diagnosis, while deep learning architectures such as Convolutional Neural Networks (CNNs) have achieved remarkable success in extracting discriminative features from medical images for tumor classification and grading. However, most existing studies focus either on biomarker-based prediction or imaging-based analysis independently, with limited efforts devoted to integrating both sources of information into a unified diagnostic framework. Furthermore, many biomarker-based models neglect the interdependencies among clinical variables, potentially reducing prediction accuracy.

Motivated by the growing need for accurate, non-invasive, and intelligent clinical decision-support systems, this research proposes an AI-assisted multimodal framework that combines clinical biomarker analysis with MRI/CT image-based tumor grading for comprehensive Hepatocellular Carcinoma diagnosis. The proposed framework employs the Analytic Network Process (ANP) to evaluate the relative importance and interdependencies among clinically significant biomarkers. The prioritized biomarkers are subsequently utilized by Logistic Regression for HCC prediction and a Random Forest classifier for stage-wise disease classification. In parallel, a Convolutional Neural Network is developed to perform automated tumor grading from MRI/CT images by learning complex imaging features associated with different stages of HCC.

The primary problem addressed in this research is the absence of an integrated, non-invasive framework capable of simultaneously predicting HCC occurrence, estimating disease stage, and grading tumors using complementary

© IEOM Society International

clinical biomarkers and medical imaging data. By integrating machine learning, deep learning, and biomarker prioritization within a single clinical decision-support system, the proposed approach aims to improve diagnostic accuracy, reduce dependence on invasive biopsy procedures, facilitate early disease detection, and support personalized treatment planning for patients with Hepatocellular Carcinoma.

1.1 Objectives

The primary objective of this research is to develop an Artificial Intelligence-assisted multimodal framework for the accurate prediction and grading of Hepatocellular Carcinoma (HCC) by integrating clinical biomarker analysis with MRI/CT medical imaging. Specifically, the study aims to identify and prioritize the key clinical biomarkers associated with HCC progression by analyzing their interdependencies using the Analytic Network Process (ANP). Based on the prioritized biomarkers, machine learning models, namely Logistic Regression and Random Forest, are employed to predict the occurrence of HCC and perform stage-wise disease classification. Furthermore, a Convolutional Neural Network (CNN) is developed to automatically analyze MRI/CT images for tumor grading by extracting discriminative imaging features. Finally, the proposed framework seeks to integrate biomarker-based prediction and medical image analysis into a unified clinical decision-support system that facilitates non-invasive diagnosis, improves early disease detection, enhances diagnostic accuracy, and supports personalized treatment planning for patients with Hepatocellular Carcinoma.

2. Literature Review

Hepatocellular Carcinoma (HCC) remains one of the most aggressive forms of primary liver cancer and is a leading contributor to cancer-related mortality worldwide. Owing to its asymptomatic progression during the early stages, timely diagnosis and accurate staging remain challenging. Conventional diagnostic approaches, including serum biomarker evaluation, medical imaging, and histopathological examination, each possess inherent limitations that may affect diagnostic accuracy when used independently. Consequently, increasing research efforts have focused on integrating Artificial Intelligence (AI) techniques with clinical biomarkers and medical imaging to develop more accurate, non-invasive, and reliable diagnostic frameworks for HCC. Recent advancements in machine learning, deep learning, and radiomics have further accelerated the development of intelligent clinical decision-support systems for HCC detection, staging, and tumor grading. This section reviews the existing literature on biomarker-based diagnosis, medical imaging, machine learning, deep learning, and multimodal diagnostic frameworks for HCC.

Several studies have investigated the role of clinical biomarkers in improving the early diagnosis of HCC. Acharya (2014) discussed the epidemiology and increasing burden of hepatocellular carcinoma in India and emphasized that delayed diagnosis remains one of the major factors affecting patient survival. Similarly, Mondal et al. (2022) reported that metabolic disorders such as obesity, diabetes, and fatty liver disease considerably increase the risk of HCC development. Giri and Singh (2024) further highlighted that chronic hepatitis B, hepatitis C, liver cirrhosis, and metabolic syndrome are among the principal clinical factors responsible for HCC progression. These studies collectively demonstrate the importance of biomarker-based screening for early disease detection.

The emergence of radiomics has substantially enhanced medical image analysis by enabling the extraction of quantitative imaging features from CT and MRI scans. Yao et al. (2021) demonstrated that radiomic features such as texture, intensity, and tumor heterogeneity improve diagnostic accuracy and recurrence prediction in HCC patients. Likewise, Le et al. (2025) reported that radiomics provides clinically relevant information that is often not readily visible through conventional radiological assessment. Furthermore, Wu et al. (2025) integrated CT-based radiomic features with serum biomarkers, including Alpha-fetoprotein (AFP) and Protein Induced by Vitamin K Absence-II (PIVKA-II), resulting in improved preoperative prediction of pathological tumor grade. Huang et al. (2024) also confirmed that combining radiomic features with clinical variables significantly enhances diagnostic performance compared with imaging-only approaches.

Magnetic Resonance Imaging (MRI) has become increasingly important for evaluating liver tumors because of its superior soft-tissue contrast and ability to characterize tumor morphology. Wei et al. (2024) demonstrated that multiphase MRI combined with automated image analysis provides valuable information for predicting recurrence and disease progression following treatment. Despite these advances, histopathological examination obtained through liver biopsy remains the clinical gold standard for tumor grading. However, El Jabbour et al. (2019) and Martins-Filho et al. (2017) observed that biopsy is invasive, susceptible to sampling errors, and frequently fails to represent the

© IEOM Society International

heterogeneous characteristics of the entire tumor, thereby motivating the development of reliable non-invasive diagnostic alternatives.

Artificial Intelligence has increasingly been applied in medical image analysis, enabling automated feature extraction and pattern recognition for disease diagnosis and classification. Litjens et al. (2017) presented one of the earliest comprehensive reviews demonstrating the effectiveness of deep learning across multiple medical imaging applications. Subsequently, Salehi et al. (2023) showed that transfer learning substantially improves Convolutional Neural Network (CNN) performance when limited annotated medical images are available. Chen et al. (2025) reviewed recent convolutional neural network-based methods for medical image classification and highlighted the effectiveness of advanced architectures, including residual learning and attention mechanisms, for improving feature extraction and classification performance. Nevertheless, Rashed and Popescu (2022) emphasized that many existing deep learning models still suffer from limited generalizability because of insufficient external validation and heterogeneous imaging datasets.

Machine learning techniques have also demonstrated considerable success in HCC prediction using clinical variables. Nishida and Kudo (2023) reviewed various AI applications in hepatology and concluded that machine learning models can achieve diagnostic performance comparable to that of experienced clinicians. Kuo et al. (2019) demonstrated that ensemble learning algorithms effectively capture nonlinear relationships among clinical variables, thereby improving survival prediction. Similarly, Wang et al. (2020) developed a Random Forest model for predicting postoperative HCC recurrence and identified Alpha-fetoprotein level, tumor size, and vascular invasion as the most influential predictive variables. Collectively, these studies demonstrate that machine learning models provide robust predictive capabilities for HCC diagnosis, prognosis, and disease-stage prediction by effectively capturing complex relationships among clinical variables.

Recent research has increasingly focused on multimodal diagnostic systems that combine clinical information with medical imaging. Several studies have demonstrated the diagnostic significance of individual biomarkers, including VEGF (Zhu et al., 2008), IL-6 (Naugler et al., 2007), microRNAs (Ji et al., 2009), circulating tumor DNA (Labgaa et al., 2017), and serum biomarkers such as AFP and AFP-L3 (Sherman, 2009). Collectively, these studies suggest that integrating multiple complementary biomarkers can improve diagnostic performance compared with relying on individual biomarkers alone. Likewise, Balsano et al. (2023) highlighted that integrating imaging data with clinical biomarkers has the potential to improve diagnostic reliability while identifying challenges related to dataset diversity, model interpretability, and clinical deployment. Žigutytė et al. (2024) further emphasized the importance of explainable Artificial Intelligence for increasing clinician trust and facilitating the adoption of AI-assisted diagnostic systems in healthcare environments.

Although considerable progress has been achieved in biomarker analysis, radiomics, machine learning, and deep learning, most existing studies investigate these components independently. Biomarker-based models often overlook the complex interrelationships among clinical variables, whereas imaging-based approaches generally ignore complementary clinical information. Furthermore, only limited emphasis has been placed on prioritizing clinically significant biomarkers before predictive modeling, which may reduce model interpretability and affect decision-making in real-world clinical settings. Moreover, only a limited number of studies provide an integrated framework capable of simultaneously performing disease prediction, stage classification, and tumor grading within a single clinical decision-support system. Motivated by these research gaps, the present study proposes a multimodal Artificial Intelligence-assisted framework that combines Analytic Network Process (ANP)-based biomarker prioritization, Logistic Regression for HCC prediction, Random Forest for stage-wise disease classification, and Convolutional Neural Networks for MRI/CT-based tumor grading within a unified clinical decision-support framework. The proposed integration of prioritized clinical biomarkers and medical imaging is expected to improve diagnostic accuracy, support non-invasive HCC diagnosis, enhance disease-stage prediction and tumor grading, and facilitate personalized treatment planning.

3. Methods

The proposed methodology presents an Artificial Intelligence-assisted multimodal framework for predicting and grading Hepatocellular Carcinoma (HCC) by integrating clinical biomarker analysis with MRI/CT image analysis. Figure 1 illustrates the overall workflow of the proposed AI-assisted framework for Hepatocellular Carcinoma prediction and grading. The methodology consists of sequential stages, including data collection, clinical variable

© IEOM Society International

selection, biomarker prioritization using the Analytic Network Process (ANP), machine learning-based HCC prediction, CNN-based tumor grading, and performance evaluation.

Initially, relevant clinical and imaging data were collected from publicly available datasets and supplemented through an extensive review of the literature and consultation with clinical experts. Based on their clinical relevance and reported association with HCC progression, eight key biomarkers—AFP, AFP-L3, DCP (PIVKA-II), VEGF, IL-6, TNF-α, miR-21, and miR-122—were selected for further analysis. In parallel, MRI and CT images of liver tumors were acquired to facilitate automated tumor grading using deep learning techniques

To account for the complex relationships among clinical variables, the Analytic Network Process (ANP) was employed to prioritize the selected biomarkers. Unlike conventional weighting techniques, ANP considers interdependencies and feedback relationships among biomarkers through pairwise comparison analysis and super matrix computation. The resulting normalized weights were used to determine the relative importance of each biomarker and served as inputs for the subsequent prediction models.

Pairwise comparison matrices were constructed using Saaty's 1–9 fundamental scale, and the priority weights were computed using the principal eigenvector method (Saaty 2004). The consistency of each pairwise comparison matrix was evaluated using the Consistency Ratio (CR). All matrices satisfied the acceptable consistency criterion (CR < 0.10), indicating that the pairwise judgments were sufficiently consistent for reliable biomarker prioritization. The normalized weights obtained from the ANP limit super matrix were subsequently used as inputs for the machine learning models.



Figure 1. Workflow of the Proposed System

The prioritized biomarker data were utilized to develop machine learning models for HCC prediction. A Logistic Regression model was first implemented to estimate the probability of HCC occurrence using weighted clinical variables, providing an interpretable probability-based prediction framework. Subsequently, a Random Forest classifier was employed to perform stage-wise classification of HCC. Owing to its ensemble learning mechanism, Random Forest effectively captures nonlinear relationships among biomarkers and estimates the probabilities corresponding to different disease stages, namely Normal, Early HCC, Intermediate HCC, and Advanced HCC.

For imaging-based analysis, MRI and CT images were preprocessed through resizing and normalization to ensure consistency across the dataset. A Convolutional Neural Network (CNN) was then developed to automatically learn discriminative imaging features without requiring manual feature engineering. The CNN extracted complex spatial characteristics related to tumor texture, intensity distribution, and morphological patterns to classify liver tumors into their respective grades.

© IEOM Society International

The proposed framework was implemented in Python. Machine learning models, including Logistic Regression and Random Forest, were developed using the Scikit-learn library, while the CNN model was implemented using TensorFlow/Keras for automated medical image analysis and tumor grading.

The developed models were evaluated using standard machine learning performance metrics. The Logistic Regression model was evaluated using the coefficient of determination (R^2) to measure the agreement between the predicted and observed outcomes. The Random Forest and CNN models were evaluated using classification accuracy, which represents the proportion of correctly classified samples. These evaluation metrics provided a quantitative assessment of the proposed framework for HCC probability prediction, disease stage classification, and tumor grading.

The evaluation results obtained from the Logistic Regression, Random Forest, and CNN models were subsequently analyzed to assess HCC probability prediction, disease stage classification, and tumor grading performance. The integration of ANP-based biomarker prioritization with machine learning and deep learning techniques provides a comprehensive, non-invasive clinical decision-support framework for the prediction and grading of Hepatocellular Carcinoma.

4. Data Collection

The proposed framework was developed using both clinical biomarker data and medical imaging data related to Hepatocellular Carcinoma (HCC). The collected datasets were intended to support biomarker-based disease prediction as well as image-based tumor grading within a unified Artificial Intelligence framework.

The clinical dataset consisted of approximately 500 patient records obtained from a publicly available HCC-related dataset used for model development and evaluation. The dataset included fourteen clinically relevant biomarkers associated with HCC diagnosis and progression, namely Alpha-Fetoprotein (AFP), AFP-L3, Des-gamma-carboxy Prothrombin (DCP/PIVKA-II), Vascular Endothelial Growth Factor (VEGF), Interleukin-6 (IL-6), Tumor Necrosis Factor-alpha (TNF-α), miR-21, miR-122, C-Reactive Protein (CRP), Lactate Dehydrogenase (LDH), circulating tumor DNA (ctDNA), Heat Shock Protein 70 (HSP70), Tissue Inhibitor of Metalloproteinase-1 (TIMP1), and Hyaluronic Acid. These biomarkers were selected based on published clinical studies and expert consultation due to their established roles in liver inflammation, fibrosis, angiogenesis, tumor progression, and HCC diagnosis.

To support automated tumor grading, CT images were obtained from the Liver Tumor Segmentation (LiTS) Challenge dataset, a publicly available benchmark dataset for liver tumor analysis (Bilic et al. 2023). The dataset contains annotated liver tumor images collected from multiple clinical institutions and provides segmentation masks for tumor localization and analysis. The dataset comprises approximately 200 liver scan cases along with corresponding segmentation masks that facilitate accurate localization and characterization of tumor regions. The imaging data provide valuable information regarding tumor morphology, texture, boundary characteristics, and structural variations required for deep learning-based classification. The combination of clinical biomarker data and medical imaging data provides a comprehensive foundation for developing and evaluating the proposed multimodal HCC prediction and grading framework**.** For model development and performance evaluation, the datasets were divided into training and testing subsets using an 80:20 ratio to evaluate the generalization capability of the proposed machine learning and deep learning models.

5. Results and Discussion

5.1 Numerical Results

The proposed multimodal framework was evaluated using both clinical biomarker data and MRI/CT imaging data to assess its effectiveness in the prediction and grading of Hepatocellular Carcinoma (HCC). The performance of the framework was analyzed through biomarker prioritization, probability prediction, disease stage classification, and image-based tumor grading.

Initially, the Analytic Network Process (ANP) was employed to determine the relative importance of the selected biomarkers by considering the interdependencies among clinical variables. Pairwise comparison matrices were constructed based on clinical expertise and published medical literature, followed by super matrix computation to obtain the global priority weights of each biomarker. The consistency analysis confirmed that all pairwise comparison

© IEOM Society International

matrices satisfied the acceptable threshold (CR < 0.10), validating the reliability of the ANP-based biomarker prioritization process.

The numerical values obtained are summarized in Table 1. Among the selected biomarkers, Alpha-Fetoprotein (AFP) obtained the highest global weight (0.22383), followed by VEGF (0.12842) and AFP-L3 (0.09566), indicating their significant contribution to HCC prediction. Biomarkers such as CRP, IL-6, miR-21, and DCP exhibited moderate importance, whereas TIMP1, TNF-α, LDH, ctDNA, HSP70, Hyaluronic Acid, and miR-122 received comparatively lower priority weights. Although 14 biomarkers were initially considered, eight clinically dominant biomarkers identified through ANP prioritization were selected as inputs for predictive modelling.

Table 1. Prioritized clinical biomarkers for Hepatocellular Carcinoma using ANP

Biomarker	Global Weight
AFP	0.22383
VEGF	0.12842
AFP-L3	0.09566
CRP	0.07796
IL-6	0.07557
miR-21	0.07151
DCP (PIVKA-II)	0.06184
TIMP1	0.04995
TNF-α	0.04648
LDH	0.04588
ctDNA	0.04208
HSP70	0.02822
Hyaluronic Acid	0.02672
miR-122	0.02588

The ANP-derived biomarker weights were subsequently utilized in the Logistic Regression model to estimate the probability of HCC occurrence. The developed Logistic Regression model is given in Equation (1), where the coefficients represent the contribution of each biomarker to HCC prediction.

$$\begin{aligned}\text{logit}(p) = {} & -4.6637 + (0.0015 \times \text{AFP}) + (0.0884 \times \text{AFP-L3}) + (0.0077 \times \text{DCP}) \\ & + (0.0104 \times \text{VEGF}) + (0.5229 \times \text{IL-6}) + (0.5420 \times \text{TNF-}\alpha) \\ & + (1.0540 \times \text{miR-21}) - (0.3590 \times \text{miR-122})\end{aligned} \quad (1)$$

The Logistic Regression model achieved an $\boldsymbol{R^2}$ value of 0.97, indicating excellent agreement between the predicted and observed outcomes. The high coefficient of determination demonstrates the effectiveness of integrating ANP-based biomarker prioritization with Logistic Regression for reliable HCC probability prediction.

For disease stage prediction, the Random Forest classifier was trained using the prioritized biomarkers. The classifier successfully categorized patients into Normal**,** Early HCC**,** Intermediate HCC**,** and Advanced HCC stages with an overall classification accuracy of 99.71%. The reported accuracy was obtained using the independent testing subset after an 80:20 train-test split to evaluate model generalization In addition to stage prediction, the model generated probability estimates for each disease stage, providing a comprehensive assessment of disease progression.

Tumor grading was performed using a Convolutional Neural Network (CNN) trained on CT liver images. The CNN automatically extracted discriminative imaging features associated with tumor morphology, texture, and intensity patterns, achieving an overall grading accuracy of 96.2%.

© IEOM Society International

The overall performance of the developed models is summarized in Table 2. The obtained results demonstrate that combining ANP-based biomarker prioritization with machine learning and deep learning techniques provides a reliable and accurate framework for non-invasive HCC prediction, disease stage classification, and tumor grading.

Table 2. Performance comparison of the developed models

Model	Task	Evaluation Metric	Result
Logistic Regression	HCC probability prediction	R^2	0.97
Random Forest	Disease stage classification	Accuracy	99.71%
CNN	Tumor grading from MRI/CT	Accuracy	96.20%

5.2 Graphical Results

The graphical results demonstrate the implementation of the proposed AI-assisted framework through a user-friendly web application developed using the Streamlit. The application integrates clinical biomarker analysis and medical image-based prediction into a single interface, allowing users to perform HCC diagnosis and grading in an efficient and interactive manner. The graphical interface was designed to simplify data entry, automate prediction, and present the results in an easily interpretable format, making the framework suitable for clinical decision-support applications.

Figure 2 illustrates the graphical user interface (GUI) developed. The interface provides separate input fields for clinically significant biomarkers, including AFP, AFP-L3, DCP (PIVKA-II), VEGF, IL-6, TNF-α, miR-21, and miR-122. To improve usability and minimize input errors, each biomarker is accompanied by its corresponding clinical reference range. The interface also includes options for uploading MRI or CT images for tumor grading and provides controls for initiating the prediction process. The simple and intuitive layout enables clinicians and healthcare professionals to interact with the system without requiring technical expertise.

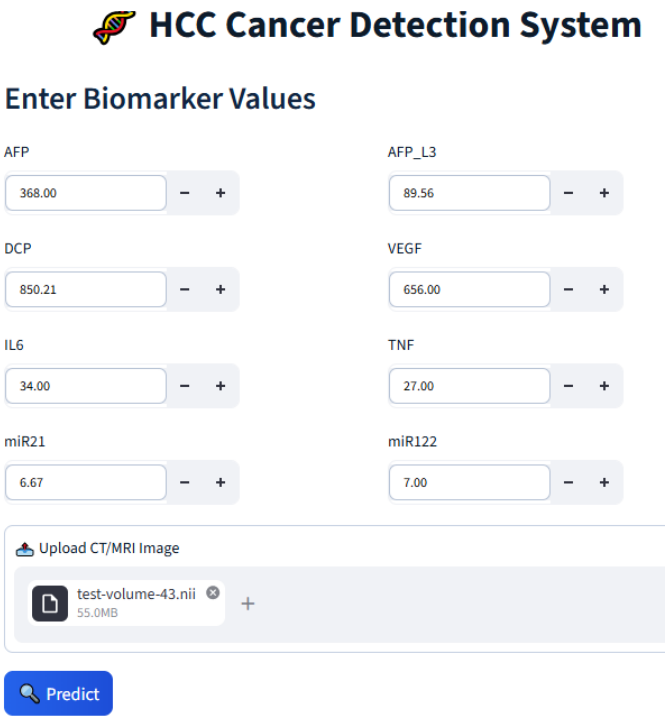


Figure 2. Streamlit-based graphical UI for the proposed HCC prediction framework

© IEOM Society International

The graphical interface demonstrates the practical implementation of the proposed multimodal framework by integrating biomarker-based prediction and image-based tumor grading within a single application. The centralized design facilitates efficient data entry, reduces manual processing, and supports real-time clinical decision making.

Figure 3 presents the prediction results generated by the proposed framework after processing the entered biomarker values and image. The interface displays the predicted HCC stage together with the corresponding BCLC classification and the probability associated with each disease stage. In addition, the application allows users to generate and download a comprehensive PDF report containing the prediction results and the entered biomarker values. Presenting both categorical predictions and probability estimates provides clinicians with additional confidence in interpreting the model outputs and supports informed treatment planning.

The graphical results demonstrate that the proposed framework successfully integrates machine learning, deep learning, and clinical biomarker analysis into a practical decision-support application. The Streamlit implementation provides an interactive environment for data input, automated prediction, and report generation, thereby improving accessibility and supporting non-invasive diagnosis and grading of Hepatocellular Carcinoma. The developed interface highlights the feasibility of deploying the proposed framework as a real-time clinical decision support tool for assisting healthcare professionals in HCC diagnosis, disease staging, and treatment planning.

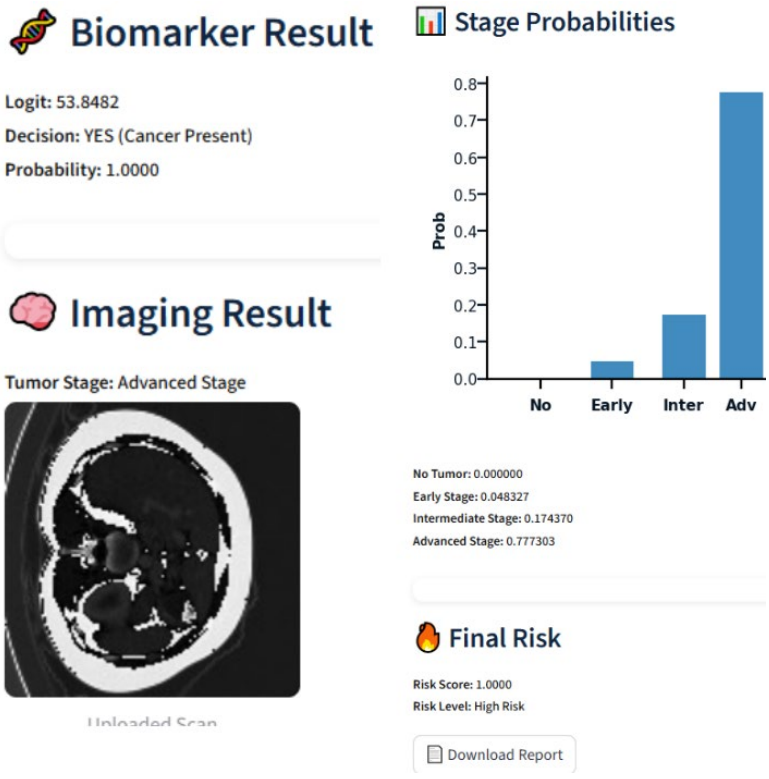


Figure 3. Prediction output generated by the proposed AI-assisted HCC prediction system

5.3 Proposed Improvements

Although the proposed multimodal framework demonstrated promising performance in the prediction and grading of Hepatocellular Carcinoma (HCC), several improvements can further enhance its clinical applicability, robustness, and generalizability. The present study was developed using publicly available biomarker and MRI/CT datasets; therefore, future work should focus on collecting larger, multi-institutional clinical datasets containing diverse patient populations and imaging conditions. Increasing the dataset size is expected to improve model generalization, reduce prediction bias, and enable more reliable evaluation of the framework under real-world clinical scenarios.

© IEOM Society International

The proposed framework can be further enhanced by incorporating additional clinical variables, including patient medical history, liver function parameters, genomic information, and advanced radiomics features extracted from medical images. The integration of these complementary data sources may provide a more comprehensive representation of disease characteristics and improve predictive performance. Furthermore, advanced multimodal learning techniques can be explored to automatically identify complex relationships between clinical biomarkers and imaging features.

Another important improvement is the integration of Explainable Artificial Intelligence (XAI) techniques. Methods such as SHAP can be incorporated to interpret biomarker contributions, while Grad-CAM can be applied to visualize important regions influencing CNN-based tumor grading decisions. These explainability approaches can improve model transparency, enhance clinician confidence, and facilitate the adoption of AI-assisted diagnostic systems in healthcare environments.

From an implementation perspective, the developed web-based application can be extended into a real-time clinical decision-support system by integrating it with hospital information systems and electronic health records. Future studies can also investigate longitudinal monitoring using sequential biomarker measurements and follow-up MRI/CT scans to support treatment response assessment, recurrence prediction, and personalized patient management.

The expected improvements include enhanced prediction reliability, improved clinical interpretability, and stronger validation through independent datasets. These developments would further strengthen the proposed framework as a practical, non-invasive, and clinically applicable solution for HCC diagnosis, disease staging, and tumor grading.

5.4 Validation

To validate the proposed framework, its methodology and outcomes were compared with representative studies reported in the literature. Previous research has primarily focused on biomarker-based prediction, machine learning-based prognosis, or medical image analysis independently. For example, Wang et al. (2020) demonstrated the effectiveness of Random Forest models for predicting HCC recurrence using clinical variables, highlighting the ability of ensemble learning methods to capture complex relationships among patient characteristics. Nishida and Kudo (2023) reviewed artificial intelligence applications in hepatology and reported the potential of AI models for improving liver disease diagnosis and management. Similarly, Wu et al. (2025) showed that combining CT-based radiomics features with laboratory biomarkers such as AFP and PIVKA-II improved pathological grade prediction of HCC.

Compared with these existing approaches, the proposed framework provides an integrated multimodal solution by combining ANP-based biomarker prioritization, Logistic Regression-based HCC probability prediction, Random Forest-based disease stage classification, and CNN-based MRI/CT tumor grading within a unified AI-assisted clinical decision-support framework. The incorporation of ANP enables the identification and prioritization of clinically significant biomarkers by considering their interdependencies before predictive modelling, thereby improving model interpretability.

The proposed framework achieved an R^2 value of 0.97 for HCC probability prediction, 99.71% accuracy for disease stage classification, and 96.2% accuracy for MRI/CT-based tumor grading. These results demonstrate that the integration of clinical biomarkers and medical imaging provides a more comprehensive assessment of HCC compared with single-modality approaches. Additionally, the consistency of the ANP pairwise comparison judgments was evaluated using the Consistency Ratio (CR), ensuring the reliability of biomarker prioritization.

The comparative evaluation with representative studies from the literature demonstrates that the proposed multimodal framework effectively integrates biomarker prioritization, disease prediction, stage classification, and MRI/CT-based tumor grading within a unified decision-support system. The obtained performance metrics indicate that the proposed framework is capable of providing accurate and reliable predictions while improving interpretability through ANP-based biomarker prioritization. Although the present validation is based on comparative performance analysis and internal evaluation, future work will include statistical hypothesis testing and validation using larger independent multi-center clinical datasets to further establish the robustness and generalizability of the proposed framework.

© IEOM Society International

6. Conclusion

The present study proposed an AI-assisted multimodal framework for the prediction and grading of Hepatocellular Carcinoma (HCC) by integrating clinical biomarker analysis with MRI/CT image analysis. The proposed framework combines the Analytic Network Process (ANP) for biomarker prioritization, Logistic Regression for HCC probability prediction, Random Forest for disease stage classification, and a Convolutional Neural Network (CNN) for image-based tumor grading. This integrated approach provides a comprehensive and non-invasive solution for supporting HCC diagnosis and clinical decision-making.

The objectives of the study were successfully achieved by identifying and prioritizing clinically significant biomarkers associated with HCC progression through ANP-based interdependency analysis. The prioritized biomarkers were incorporated into machine learning models for estimating HCC probability and predicting disease stages. Furthermore, the CNN-based image analysis model effectively extracted relevant imaging features from MRI/CT scans to perform automated tumor grading.

The experimental results demonstrated the effectiveness of the proposed framework. The Logistic Regression model achieved an R^2 value of 0.97 for HCC probability prediction, the Random Forest classifier achieved an overall accuracy of 99.71% for disease stage classification, and the CNN model achieved a tumor grading accuracy of 96.2%. These results indicate that the proposed framework can effectively analyze both clinical biomarker information and medical imaging data for comprehensive HCC assessment.

The major contribution of this research is the development of a unified AI-assisted multimodal framework that integrates biomarker prioritization, disease prediction, stage classification, and tumor grading within a single clinical decision-support system. Unlike conventional approaches that analyze biomarkers or medical images independently, the proposed framework combines complementary clinical and imaging information to provide a more holistic assessment of HCC. The incorporation of ANP improves the interpretability of biomarker importance by considering relationships among clinical variables before predictive modeling. Additionally, the Streamlit-based implementation demonstrates the practical applicability of the proposed framework by enabling automated prediction, tumor grading, visualization of results, and report generation through an interactive interface.

Overall, the proposed framework demonstrates the potential of integrating machine learning, deep learning, and clinical biomarker analysis for supporting early HCC detection, disease staging, and tumor grading. The developed approach provides a foundation for future clinical decision-support systems and may assist healthcare professionals in treatment planning and personalized patient management. Further validation using larger, multi-institutional datasets will enhance its clinical reliability and generalizability.

References

Acharya, S. K., Epidemiology of hepatocellular carcinoma in India, *Journal of Clinical and Experimental Hepatology*, vol. 4, Suppl. 3, pp. S27-S33, 2014.

Asrani, S. K., Devarbhavi, H., Eaton, J. and Kamath, P. S., Burden of liver diseases in the world, *Journal of Hepatology*, vol. 77, no. 4, pp. 1000-1022, 2022, https://doi.org/10.1016/j.jhep.2022.06.002.

Balsano, C., Burra, P. and Duvoux, C., Artificial intelligence and liver: Opportunities and barriers, *Digestive and Liver Disease*, vol. 55, no. 11, pp. 1455-1461, 2023.

Bilic, P., Christ, P. F., Li, H. B. et al., The Liver Tumor Segmentation Benchmark (LiTS), *Medical Image Analysis*, vol. 84, p. 102680, 2023, https://doi.org/10.1016/j.media.2022.102680.

Chen, C., Isa, N. A. M. and Liu, X., A review of convolutional neural network-based methods for medical image classification, *Computers in Biology and Medicine*, vol. 185, p. 109507, 2025.

El Jabbour, T., Lagana, S. M. and Lee, H., Update on hepatocellular carcinoma: Pathologists' review, *World Journal of Gastroenterology*, vol. 25, no. 14, pp. 1653-1665, 2019.

Giri, S. and Singh, A., Epidemiology of hepatocellular carcinoma in India: An updated review for 2024, *Journal of Clinical and Experimental Hepatology*, vol. 14, no. 6, p. 101447, 2024.

Huang, Y., Chen, L. and Ding, Q., CT-based radiomics for predicting pathological grade in hepatocellular carcinoma, *Frontiers in Oncology*, vol. 14, p. 1295575, 2024.

Ji, J., Shi, J., Budhu, A. et al., MicroRNA expression, survival, and response to interferon in liver cancer, *New England Journal of Medicine*, vol. 361, no. 15, pp. 1437-1447, 2009.

© IEOM Society International

Kuo, Y. H., Lu, S. N., Chen, C. L. et al., Application of a machine learning approach to predict survival outcomes in patients with hepatocellular carcinoma, *Scientific Reports*, vol. 9, p. 15720, 2019.
Labgaa, J., Villanueva, A., Dormond, O. et al., Circulating tumor DNA in hepatocellular carcinoma, *Nature Reviews Gastroenterology and Hepatology*, vol. 14, no. 11, pp. 641-652, 2017.
Le, M. H. N., Kha, H. Q., Tran, N. M. et al., Radiomics in liver research: A paradigm shift in disease detection and staging, *European Journal of Radiology Artificial Intelligence*, vol. 2, p. 100016, 2025.
Litjens, G., Kooi, T., Bejnordi, B. E. et al., A survey on deep learning in medical image analysis, *Medical Image Analysis*, vol. 42, pp. 60-88, 2017.
Martins-Filho, S. N., Paiva, C., Azevedo, R. S. and Alves, V. A. F., Histological grading of hepatocellular carcinoma: A systematic review of literature, *Frontiers in Medicine*, vol. 4, p. 193, 2017.
Mondal, D., Das, K. and Chowdhury, A., Epidemiology of liver diseases in India, *Clinical Liver Disease*, vol. 19, no. 3, pp. 114-117, 2022.
Naugler, T., Sakurai, T., Kim, S. et al., Gender disparity in liver cancer due to IL-6 signaling, *Science*, vol. 317, no. 5834, pp. 121-124, 2007.
Nishida, N. and Kudo, M., Artificial intelligence models for the diagnosis and management of liver diseases, *Ultrasonography*, vol. 42, no. 1, pp. 10-19, 2023.
Rashed, B. M. and Popescu, N., Critical analysis of the current medical image-based processing techniques for automatic disease evaluation: Systematic literature review, *Sensors*, vol. 22, no. 18, p. 7065, 2022.
Saaty, T. L., Fundamentals of the analytic network process—Dependence and feedback in decision-making with a single network, *Journal of Systems Science and Systems Engineering*, vol. 13, no. 2, pp. 129-157, 2004.
Salehi, A. W., Khan, S., Gupta, G. et al., A study of CNN and transfer learning in medical imaging: Advantages, challenges, future scope, *Sustainability*, vol. 15, no. 7, p. 5930, 2023.
Sherman, M., Serum biomarkers for hepatocellular carcinoma, *Cancer*, vol. 115, no. 3, pp. 565-574, 2009.
Wang, Y., Li, Z., Xu, P. et al., Random forest model for predicting early recurrence of hepatocellular carcinoma after surgical resection, *BMC Cancer*, vol. 20, p. 1230, 2020.
Wei, H., Zheng, T., Zhang, X. et al., MRI radiomics based on deep learning automated segmentation to predict early recurrence of hepatocellular carcinoma, *Insights into Imaging*, vol. 15, p. 120, 2024.
Wu, M., Yu, H., Pang, S. et al., Application of CT-based radiomics combined with laboratory tests such as AFP and PIVKA-II in preoperative prediction of pathologic grade of hepatocellular carcinoma, *BMC Medical Imaging*, vol. 25, p. 51, 2025.
Yao, S., Ye, Z., Wei, Y., Jiang, H. Y. and Song, B., Radiomics in hepatocellular carcinoma: A state-of-the-art review, *World Journal of Gastrointestinal Oncology*, vol. 13, no. 11, pp. 1599-1615, 2021.
Zhu, L., Huang, P. and Zhang, Y. et al., Role of VEGF in hepatocellular carcinoma, *Journal of Clinical Oncology*, vol. 26, no. 18, pp. 3004-3009, 2008.
Žigutytė, L., Sorz-Nechay, T., Clusmann, J. N. and Kather, J. N., Use of artificial intelligence for liver diseases: A survey from the EASL Congress 2024, *JHEP Reports*, vol. 6, no. 12, p. 101209, 2024.

.

Biographies

Amala Maria Kuruvilla is currently pursuing the MTech degree in Data Science at Rajiv Gandhi Institute of Technology, Kottayam, Kerala, India. She received her BTech degree in Computer Science and Engineering with Honors and also completed a Minor Degree in Robotics and Automation. Her research interests include Artificial Intelligence, Machine Learning, Deep Learning, Data Analytics, and Image Analysis.

Dr. K. Sunil Kumar is a Professor in the Department of Mechanical Engineering at Rajiv Gandhi Institute of Technology, Kottayam, Kerala, India. He has extensive teaching, research, and academic experience in Industrial Engineering, Operations Research, Optimization Techniques, Manufacturing Systems, and Artificial Intelligence applications. He has guided several undergraduate and postgraduate research projects and has published research articles in reputed national and international journals and conferences.

Dr. Shabeerali T. U is a Senior Consultant in the Department of HPB Surgery and Liver Transplantation at KIMSHEALTH, Thiruvananthapuram, Kerala, India. He specializes in hepatobiliary surgery, liver transplantation, liver oncology, and the management of complex liver diseases. He has extensive clinical experience in the diagnosis and treatment of Hepatocellular Carcinoma and has been actively involved in multidisciplinary research aimed at improving liver cancer diagnosis and patient care.

© IEOM Society International