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# A Comparative Machine Learning Framework for Early Prediction of Liver Cancer Using Clinical Attributes

Diksha Goyal[1], Surendra Kumar Yadav[2,*], Shalini Sharma[1]

***Abstract***

*One of the main causes of cancer-related death globally is liver cancer, and improving patient outcomes depends heavily on early detection. However, low contrast, noise, organ similarity, and tumor shape and size variability make it difficult to accurately identify and segment liver tumors from medical imaging. Automated liver cancer diagnosis, segmentation, and prognosis have been greatly improved by recent developments in artificial intelligence (AI), especially deep learning. This work presents a thorough, effective method for liver tumor analysis by combining knowledge from image-processing-based MRI tumor detection, CT-based deep learning segmentation models, and AI-driven diagnostic frameworks. Otsu's thresholding for image enhancement, marker-controlled watershed and active contor models for MRI-based segmentation, and sophisticated deep networks – including U-Net variants, ResNet hybrids, and graph convolutional networks (GCN) – for CT-based liver and tumor segmentation are among the methods highlighted in this work. Notably, SLIC superpixel clustering in conjunction with GCN architecture has shown state-of-the-art performance with high Dice scores, accuracy, and robustness in noisy environments. Furthermore, new AI systems that combine clinical parameters with multi-modal imaging (CT, MRI, and US) show promise in predicting tumor characteristics and treatment response. Overall, the review emphasizes how AI-powered models outperform conventional techniques in terms of accuracy, consistency, and automation, providing a solid basis for creating dependable computer-aided systems for clinical decision support, tumor segmentation, and early liver cancer detection.*

**Keywords:** Convolutional neural networks, graph convolutional networks, radiomics, CT, MRI, machine learning, deep learning, hepatocellular carcinoma, and liver cancer

## INTRODUCTION

An estimated 17 million cases of liver cancer will be diagnosed by 2022, making it one of the deadliest illnesses in the world. Therefore, increasing survival rates requires early and accurate detection [1]. Despite their effectiveness, traditional diagnostic methods are frequently constrained by tumor variability, low contrast in medical images, and a significant dependence on professional interpretation. Researchers from various fields are increasingly using machine learning (ML) and computational intelligence (AI) methods to improve medical diagnosis to overcome these obstacles [2, 3]. Numerous studies have shown how ML can be used to predict and classify cancer – such as Wang et al.'s [4] tumor classification framework, Zhang et al.'s [3] Extreme Learning Machine (ELM) for multiple microarray cancer datasets, and Stokowy et al.'s [2] gene-expression-based diagnosis of thyroid nodules – showing notable increases in accuracy over traditional techniques. To carry out tasks – like classification, prediction, and pattern recognition – machine learning, a fundamental area of artificial intelligence, learns from both historical and current data. Modern computational techniques are becoming increasingly

***Author for Correspondence**
Surendra Kumar Yadav
E-mail: surendrakumar.yadav@jecrcu.edu.in

[1]Research Scholar, Department of Computer Science, JECRC University, Ramchandrapura Industrial Area, Jaipur, Rajasthan, India
[2]Professor, Department of Computer Science Engineering, JECRC University, Ramchandrapura Industrial Area, Jaipur, Rajasthan, India

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capable of attaining superior diagnostic performance thanks to developments in machine learning and the availability of a variety of clinical datasets (Figure 1).

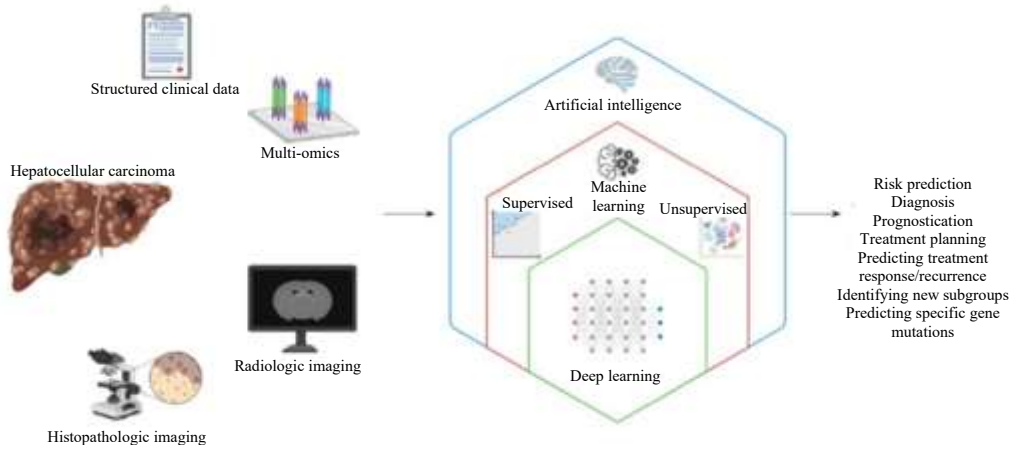


**Figure 1.** AI-based approaches for diagnosis and prognosis of hepatocellular carcinoma.

Simultaneously, automated liver tumor segmentation from CT and MRI images has greatly improved thanks to deep learning techniques like graph convolutional networks (GCNs), U-Net variants, and ResNet-based architecture. MRI-based tumor localization is further improved by techniques like Otsu's thresholding, marker-controlled watershed segmentation, and active contor models. Recent methods that combine Chebyshev graph convolution layers with SLIC superpixel clustering have demonstrated high accuracy, robustness, and Dice coefficients even in noisy imaging scenarios. Additionally, multi-modal AI systems that integrate clinical parameters with imaging data have the potential to forecast treatment response, tumor behavior, and overall prognosis.

By applying machine learning algorithms to actual datasets involving thyroid, liver, and colon cancer, assessing their efficacy, and examining their diagnostic potential, this study unifies these advancements. A thorough analysis of related work, a description of the dataset, methodology, experimental findings, and potential future research avenues are presented in the remaining sections. All things considered, this work demonstrates the revolutionary role that AI-driven models play in improving the accuracy of cancer detection, assisting clinical decision-making, and opening the door to more dependable, automated healthcare solutions.

## LITERATURE REVIEW

A deep learning (DL)-based survival prediction model that can accurately differentiate between patient subgroups with different survival probabilities across six separate cohorts was created by Kumar deep Chaudhary et al. [7]. The authors created a survival-sensitive DL framework using information from the Cancer Genome Atlas (TCGA), including RNA sequencing (RNA-Seq), microRNA sequencing (miRNA-Seq), and DNA methylation profiles for 360 patients with hepatocellular carcinoma (HCC). To increase prognostic accuracy, this model incorporates clinical and genomic variables in addition to accurately predicting patient outcomes.

Watershed Gaussian-based Deep Learning (WGDL), a novel method for precisely identifying liver cancer lesions in CT images, was presented by Amit Das et al. [8]. Their method uses a deep neural network (DNN) classifier that, after 200 training iterations, demonstrated both precision and robustness with a classification accuracy of 99.38% and a Jaccard index of 98.18% while maintaining a remarkably low validation loss of 0.062.8 Convolutional neural networks (CNNs) were used in another important study by Shi-hui Zhen et al. [9] to create seven-way, binary, and three-way tumor malignancy classifiers trained on 31,608 images gathered from 1,210 liver cancer patients. These models' efficacy was validated on a sizable external cohort of 201 patients (6,816 images), with the CNN obtaining an AUC

 

of 95% in differentiating between benign and malignant liver tumors – even without the use of sophisticated image enhancement techniques. Additionally, the classification performance for both HCC and metastatic tumors was improved by merging raw imaging data with clinical information.

A specialized CNN architecture was proposed by Charlie A. Hamm et al. [10] and improved through iterative network structure and training sample optimization. Three convolutional layers, two max-pooling layers, and two fully connected layers make up their model. The model obtained an overall accuracy of 92%, with a sensitivity of 92% and specificity of 98%, using 434 hepatic lesions from six diagnostic categories for training and an extra 60 for testing. The model's strong generalization ability was demonstrated by average sensitivity and specificity of 90% and 98%, respectively, in single-run evaluations on previously unseen cases.

## MATERIALS AND METHODS

### Dataset

According to [11], the dataset used in this study is made up of patient records related to liver cancer. Each of the 450 patient entries has one target variable (where "Y" denotes the presence of liver cancer and "N" denotes its absence) and 26 predictive characteristics pertinent to the diagnosis of liver cancer. Several machine learning models are trained and assessed using this dataset.

### Methodology

According to [11], the dataset used in this study is made up of patient records related to liver cancer. Each of the 450 patient entries has one target variable (where "Y" denotes the presence of liver cancer and "N" denotes its absence) and 26 predictive characteristics pertinent to the diagnosis of liver cancer. Several machine learning models are trained and assessed using this dataset. A 10-fold cross-validation approach was employed to reliably assess the performance and generalization capability of all machine-learning models (Figure 2).

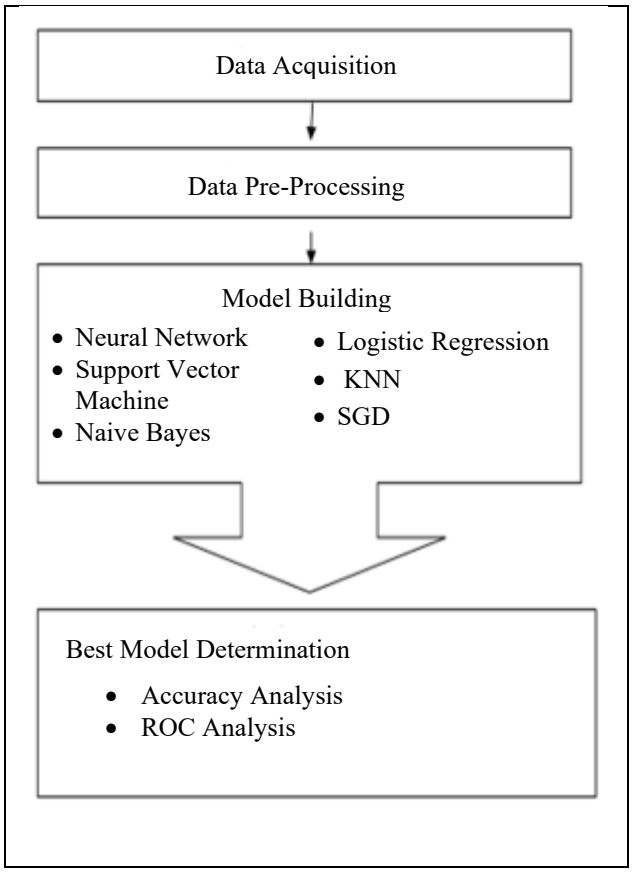


**Figure 2**. Flowchart of the machine learning model development and evaluation process.

 

**Model Training**

The following machine learning algorithms were implemented for classification:

***Artificial Neural Network (ANN)***

Artificial Neural Networks are computational models inspired by biological neurons. Each artificial neuron performs mathematical operations such as weighted summation and activation. Inputs are multiplied by adjustable weights, combined with biases, and passed through an activation (transfer) function to generate an output [12].

The Multilayer Perceptron (MLP), a commonly used ANN architecture, consists of an input layer, one or more hidden layers, and an output layer. Each neuron in a hidden or output layer computes a weighted sum of its inputs and applies an activation function. ANNs are widely used in prediction systems, financial modeling, and medical bioinformatics due to their capability to learn complex nonlinear relationships [13].

***Support Vector Machine (SVM)***

Support Vector Machines are powerful machine-learning models used for classification and prediction. SVM aims to identify the optimal separating hyperplane that maximizes the margin between classes. SVMs assist in lowering overfitting by using structural risk minimization.

Nonlinear classification is enabled through kernel functions, which transform data into higher dimensions using techniques such as RBF or polynomial kernels. Slack variables are incorporated to make SVMs robust to noise and outliers [14].

***Naïve Bayes Classifier***

Naïve Bayes (NB) is a probabilistic classifier based on Bayes' theorem and assumes independence among predictor variables. It uses a directed acyclic graph structure where nodes represent variables and edges denote dependencies. The model is simple, computationally efficient, and performs well on well-labeled, moderately preprocessed datasets [15, 16].

***Logistic Regression***

Logistic Regression is a discriminative model used for binary and multiclass classification tasks. It estimates the probability of a binary outcome using a logistic (sigmoid) function applied to a linear combination of input features. Logistic regression is particularly effective when relationships between predictors and the target are approximately linear [17].

***k-Nearest Neighbor (kNN)***

kNN is an instance-based learning algorithm that does not build an explicit model. Instead, it classifies a new data point based on the majority class among its k-nearest neighbors in the feature space. Although simple and intuitive, the performance of kNN largely depends on the choice of k and the distance metric applied [18, 19].

***Stochastic Gradient Descent (SGD)***

Stochastic Gradient Descent is an iterative optimization technique used to minimize differentiable objective functions. Instead of computing the gradient over the entire dataset, SGD updates model parameters using randomly selected batches, resulting in faster iterations though with slower convergence. It is especially useful for large-scale, high-dimensional problems [20].

**Classification Performance Measurement**

Six supervised machine-learning algorithms were applied to classify liver cancer samples. To assess their efficacy, a 10-fold cross-validation scheme was employed. To guarantee a thorough assessment, performance was evaluated using eight quality metrics.

- "Positive" in the classification setup denotes samples that are free of cancer.
- "Negative" describes samples found to have cancer.

 

### Performance Evaluation Metrics

Standard metrics – such as accuracy, precision, recall, and F1-score – were used to assess the model's performance [21]. These metrics aid in verifying the accuracy of forecasts and guaranteeing that classification outcomes are not deceptive because of skewed distributions, a problem that is usually evaluated using the confusion matrix.

## FINDINGS AND ANALYSIS

This study assesses the effectiveness of six machine-learning classifiers for liver cancer prediction based on the 26 predictive attributes previously discussed. To ensure dependable training and testing performance, a cross-validation approach was used, dividing the dataset into twenty subsets (Tables 1–3).

**Table 1.** Comparison of model complexity and training efficiency.

| Model | Training time | Model complexity | Hyper parameter sensitivity | Interpretability | Scalability |
|---|---|---|---|---|---|
| kNN | Low (no training) | Very Low | Low | High | Poor (slow with large data). |
| SVM | Medium | Medium | High (C, Kernel, Gamma) | Medium | Good. |
| SGD | Very Low | Low | Medium | Medium | Excellent. |
| ANN | High | High | High (layers, neurons, LR) | Low | Excellent. |
| Naïve Bayes | Very Low | Very Low | Low | High | Excellent. |
| Logistic Regression | Low | Low | Low–Medium | High | Good. |

**Table 2.** Strengths and weaknesses of ML algorithms.

| Model | Strengths | Weaknesses |
|---|---|---|
| kNN | Simple, no training required, good for small datasets | Very slow for large datasets, sensitive to noisy features. |
| SVM | Works well on high-dimensional data, robust margin | Requires heavy tuning; kernel selection is difficult. |
| SGD | Fast for large-scale problems, efficient online learning | Convergence may be unstable; sensitive to learning rate. |
| ANN | Learns complex nonlinear patterns, highest accuracy | Requires more data, long training time, less interpretable. |
| Naïve Bayes | Fast, performs well with categorical data, easy to interpret | Assumes feature independence; poor with correlated data. |
| Logistic Regression | Good baseline model, interpretable coefficients | Poor performance on nonlinear relationships. |

**Table 3.** Feature handling & data requirements.

| Model | Handles nonlinearity | Feature scaling required | Handles noisy data | Works well with small dataset | Feature engineering needs |
|---|---|---|---|---|---|
| kNN | Yes (implicitly) | Yes | Low | Yes | High. |
| SVM | Yes (with kernel) | Yes | Medium | Yes | Medium. |
| SGD | Limited | Yes | Medium | Yes | Medium. |
| ANN | Yes (very strongly) | Yes | Medium–High | No (requires large data) | Low. |
| Naïve Bayes | Limited | No | High | Yes | Low. |
| Logistic Regression | Limited | Yes | Medium | Yes | Medium. |

The comparison tables presented above offer a deeper understanding of the behavior of different machine-learning models beyond their prediction accuracy. While performance metrics – like precision,

 

recall, and F1-score – demonstrate how well a model performs on the dataset, other factors – like model complexity, interpretability, scalability, and feature-handling capability – are just as crucial for determining which algorithm is best for medical diagnosis applications.

**Comparison Based on Model Complexity and Training Efficiency**

Traditional linear models – like Logistic Regression and probabilistic models like Naïve Bayes – are computationally light and can be trained quickly, even on modest hardware, as Table A illustrates. On the other hand, because of its multi-layered architecture, which lengthens training times and necessitates hyperparameter tuning, the Artificial Neural Network (ANN) has a much higher computational cost. But this added complexity enables ANN to discover more intricate and nonlinear patterns in the data, which eventually results in higher accuracy.

Complexity and performance are balanced by the Support Vector Machine (SVM). The model is very sensitive to parameter choices because its efficacy primarily depends on choosing the appropriate kernel and fine-tuning hyperparameters like the regularization parameter and gamma. Despite its simplicity, kNN does not scale well with large datasets and becomes computationally demanding during prediction.

**Strengths and Weaknesses of Algorithms**

The intrinsic advantages and disadvantages of each model are shown in Table B. Because of its probabilistic nature, Naïve Bayes, for example, exhibits strong resilience to noisy features, making it appropriate for preliminary screening systems where data quality may vary. Nevertheless, its performance is limited for clinical datasets where attributes are frequently correlated due to its assumption of feature independence.

However, SVM and ANN are very successful at classifying cancer because they can identify intricate relationships in medical features and imaging data. However, their increased computational load and decreased interpretability – a crucial component in clinical decision-making where transparency is crucial – come at the expense of their greater modelling capability.

Although kNN is still a simple and intuitive algorithm, this study shows that it performs poorly in high-dimensional datasets. Because of its dependence on distance computations, it is less appropriate for medical datasets due to its sensitivity to redundant attributes and feature scaling.

**Feature Handling and Data Requirements**

Table C assesses the models based on preprocessing requirements and data characteristics. When dealing with nonlinear relationships – a common feature in medical datasets where symptoms interact in intricate ways – ANN and SVM (with kernel) are effective tools. However, extensive tuning and careful feature scaling are necessary for these models.

On the other hand, logistic regression and naïve bayes are much simpler to use and do not need extensive preprocessing. They are advantageous in medical research scenarios where large annotated datasets are not always available because they perform reliably even with smaller datasets.

Lastly, despite its flexibility, kNN performs poorly when dealing with noisy or unnormalized data. It is less appropriate for diagnostic datasets with many correlated variables because its accuracy drastically decreases in high-dimensional spaces. Figure 3 displays machine learning-generated classifications.

**ROC for Performance Evaluation**

Plotting the True Positive Rate (TPR) against the False Positive Rate (FPR) in Receiver Operating Characteristic (ROC) analysis offers a thorough method of assessing classifier performance. The trade-off between sensitivity and specificity at different threshold settings is depicted by the ROC curve. Because it is unaffected by unequal sample distributions, this evaluation is especially useful in medical datasets where class imbalance is prevalent.

 

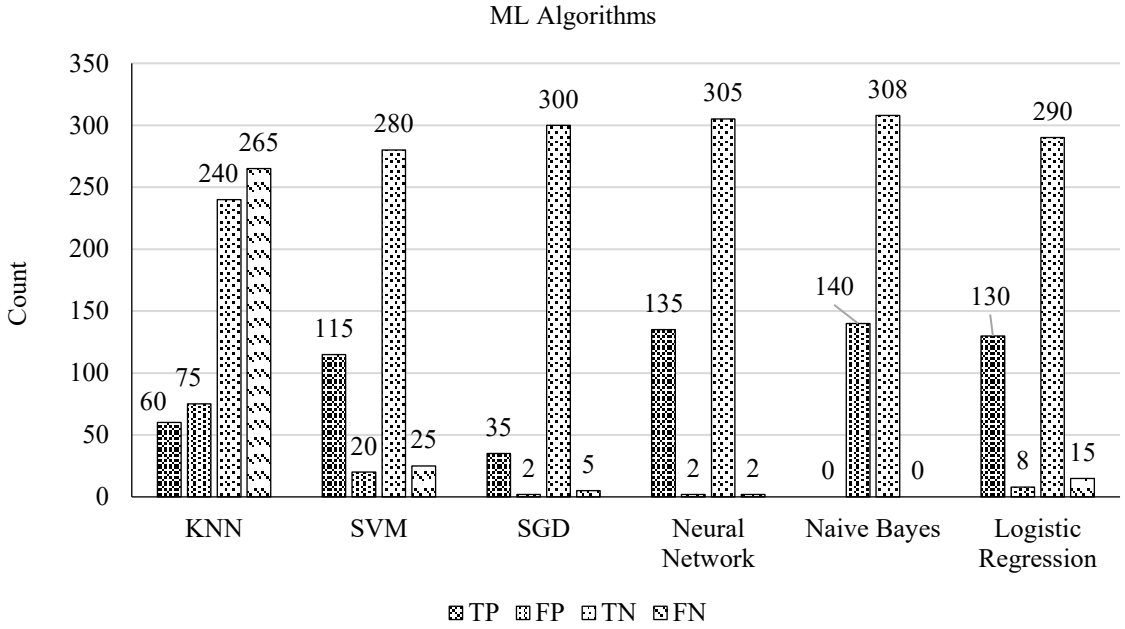


**Figure 3.** In-depth analysis of ML algorithms.

The Area Under the Curve (AUC) provides a single-value summary of performance, and a model with a ROC curve closer to the top-left corner exhibits greater discriminative power. An outstanding classifier with strong predictive power is indicated by an AUC score that is close to 1.0. The neural network model achieves the highest ROC area among all evaluated algorithms, as shown in Figures 4 & 5, demonstrating its superior ability to distinguish between cases of liver cancer and non-cancer. The neural network also generated the highest accuracy, precision, recall, and F1 values, which further supports the previous findings.

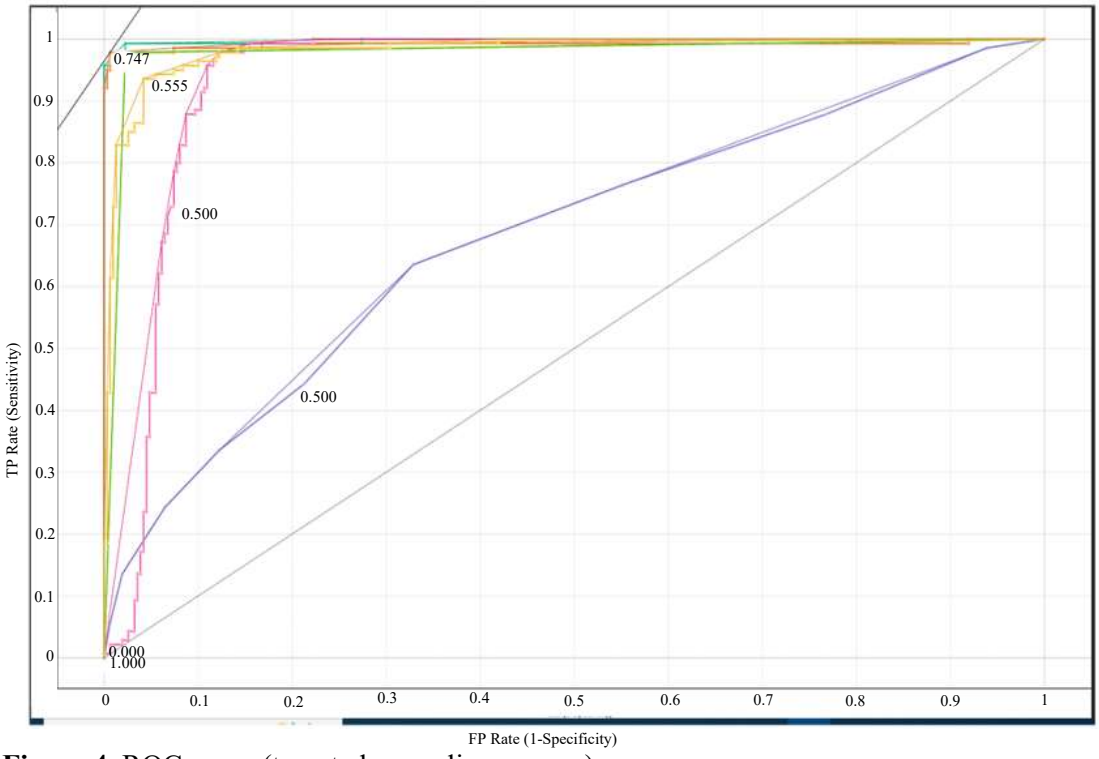


**Figure 4.** ROC curve (target class no liver cancer).

 

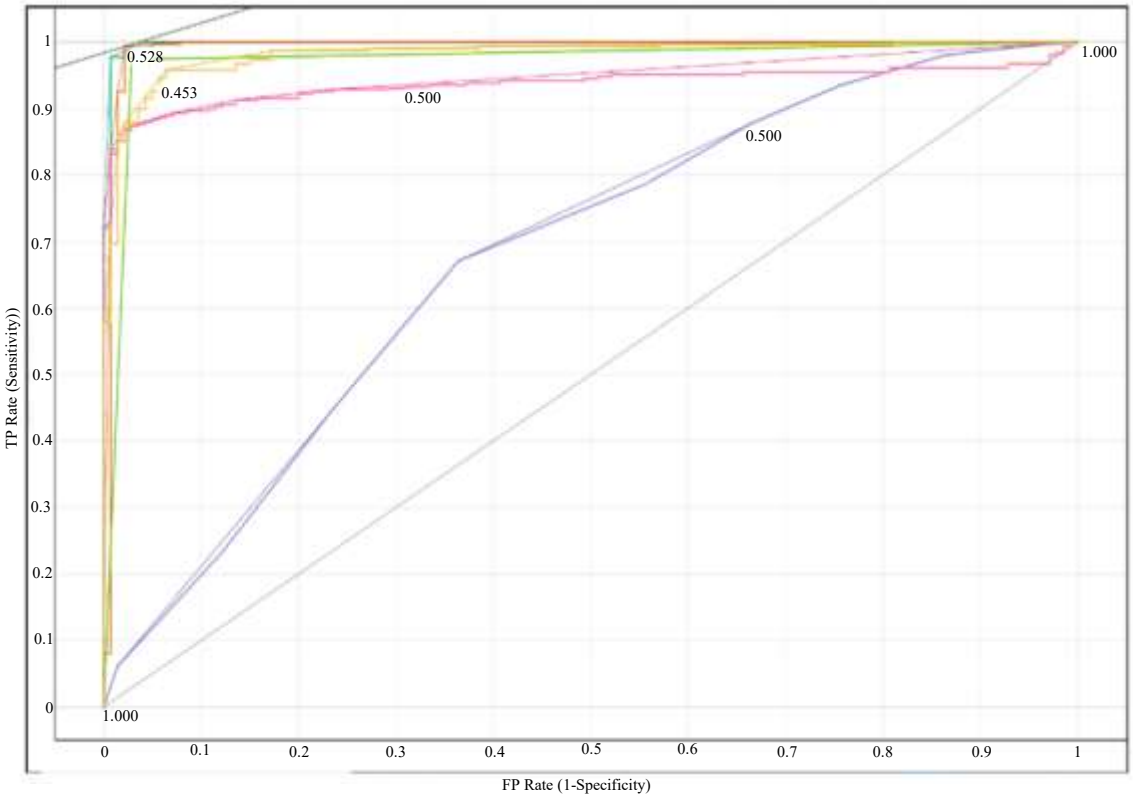


**Figure 5.** ROC curve (liver cancer).

## CONCLUSION

Improving patient survival and facilitating prompt and efficient treatment planning depend on an early and accurate diagnosis of liver cancer. This study shows how machine learning methods can be used to accurately predict liver cancer based on clinical characteristics. With an accuracy of 98.8% and strong precision, recall, F1-score, and AUC values, the Artificial Neural Network (ANN) outperformed the other six supervised models that were assessed. Machine learning offers a strong basis for automated liver cancer diagnosis, as demonstrated by the competitive performance of other classifiers like SVM, Logistic Regression, and SGD.

The results show that the ANN model is the most successful of all tested algorithms because of its capacity to discover intricate, nonlinear relationships in the data. However, the comparative performance analysis also demonstrates that more straightforward models, like Naïve Bayes and Logistic Regression, can still be useful, particularly in diagnostic environments that are interpretable or have limited resources.

By adding more clinically relevant features, extracting more sophisticated characteristics from the current dataset, and increasing the size of the dataset, future work will concentrate on improving model accuracy and generalizability. Additionally, using a wider range of deep learning and machine learning techniques, like ensemble learning, transfer learning, and sophisticated neural architectures, may improve diagnostic performance and facilitate practical implementation in healthcare systems.

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