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Enhancing Hepatitis Patient Survival Detection: A Comparative Study of CNN and Traditional Machine Learning Algorithms

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Abstract. Hepatitis patient survival prediction is a critical medical task impacting timely interventions and healthcare resource allocation. This study addresses this issue by exploring the application of a Convolutional Neural Network (CNN) and comparing it with traditional machine learning algorithms, including Support Vector Machine (SVM), Decision Tree, k-Nearest Neighbors (KNN), Gaussian Naive Bayes (GNB), and Gradient Boosting (GBoost). The research objectives include evaluating the algorithms' performance regarding confusion matrix metrics and classification reports, aiming to achieve accurate predictions for both "Live" and "Die" categories. The dataset of 155 instances with 20 features underwent preprocessing, including data cleansing, feature conversion, and normalization. The CNN model achieved perfect accuracy in hepatitis patient survival prediction, outperforming the baseline algorithms, which exhibited varying accuracy and sensitivity. These findings underscore the potential of advanced machine learning techniques, particularly CNNs, in improving diagnostic accuracy in hepatology.

Keywords: Hepatitis, Survival Prediction, Convolutional Neural Network, Machine Learning, Medical Diagnosis.

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INTRODUCTION

Hepatitis, a significant global health issue, affects millions of individuals worldwide, leading to severe health complications and a high mortality rate [1]. The disease's prevalence and its associated burden underscore the critical need for accurate survival predictions to ensure timely medical interventions and optimal allocation of healthcare resources [2]. Accurate prediction models can substantially enhance patient outcomes by facilitating early diagnosis and personalized treatment plans [3]. However, traditional methods for predicting hepatitis patient survival often struggle to capture the complex interplay of clinical variables, resulting in limited predictive accuracy and suboptimal clinical decision-making [4]. These challenges highlight the necessity for advanced machine learning techniques that can more effectively analyze intricate medical data and improve prognostic predictions.

Machine learning has revolutionized healthcare by enabling more accurate and efficient analyses of complex medical data, thereby enhancing disease diagnosis, clinical outcome predictions, and overall medical data analytics [5]. By leveraging vast amounts of patient data, machine learning algorithms can uncover patterns and insights that traditional statistical methods might miss, leading to more precise diagnostic and prognostic models [6]. For instance, machine learning has been successfully applied in detecting early signs of diseases such as cancer and diabetes, predicting patient outcomes in critical care settings, and optimizing treatment plans through personalized medicine [7]. The ability of machine learning to continuously learn and adapt from new data holds the potential to significantly outperform conventional methods, offering unparalleled improvements in predictive accuracy, diagnostic efficiency, and ultimately, patient care.

This research focuses on utilizing CNNs as the primary machine learning method for predicting hepatitis patient survival due to their exceptional ability to capture and learn complex patterns within data [8]. CNNs are particularly well-suited for handling intricate medical datasets, allowing them to uncover nuanced relationships between variables that traditional methods might overlook [9]. To provide a comprehensive evaluation, this study compares the performance of CNNs with several traditional machine learning algorithms, including Support Vector Machine (SVM), Decision Tree, k-Nearest Neighbors (KNN), Gaussian Naive Bayes (GNB), and Gradient Boosting (GBoost). These traditional algorithms were selected for their established efficacy in various classification tasks, offering a robust benchmark against which the CNN's performance can be measured.

The primary objective of this research is to evaluate the performance of CNNs and traditional machine learning algorithms in predicting the survival of hepatitis patients. This study aims to determine how well each model can accurately classify patient outcomes into "Live" and "Die" categories. To achieve this, various performance metrics will be employed, including accuracy, precision, recall, and F1-score, which

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provide a comprehensive assessment of each model's predictive capabilities. These metrics will be analyzed using confusion matrix and classification report techniques, ensuring a detailed and rigorous evaluation of the models' effectiveness in handling the complexities of medical data and improving prognostic predictions.

This research significantly contributes to the healthcare field by enhancing the accuracy of survival predictions for hepatitis patients, which is crucial for timely and effective clinical interventions. By demonstrating the superior performance of CNNs over traditional machine learning algorithms, this study provides compelling evidence for the adoption of advanced machine learning techniques in clinical practice. The findings offer new insights into the application of sophisticated data analysis methods, potentially revolutionizing how prognostic models are developed and utilized in hepatology. This research not only advances the understanding of machine learning's capabilities in medical predictions but also paves the way for more precise, data-driven decision-making in healthcare, ultimately improving patient outcomes and resource management.

LITERATURE REVIEW

Previous studies have been conducted to detect hepatitis using various methods and techniques. One study focused on the development of an Enzyme-Linked ImmunoMagnetic Electrochemical assay (ELIME) for the detection of hepatitis A virus (HAV) [10]. Another study developed predictive models to identify undiagnosed hepatitis C virus (HCV) patients using longitudinal medical claims and prescription data [11]. An extensive nationwide cohort study examined the rates and predictors of adherence to guidelines for CHB care [12]. An automated tool was also proposed to recognize patients with hepatitis syndromes using a multi-phase classification approach [13]. These studies have shown varying success rates in disease detection. The ELIME assay demonstrated a quantitative determination of HAV with a detection limit of 1·10−11 IU mL−1 [14]. The predictive models for HCV achieved precision rates of at least 95% at low levels of recall. Adherence to guidelines for CHB care was found to be poor, with less than 40% of high-risk patients undergoing annual hepatocellular carcinoma surveillance. The proposed automated tool aimed to enhance the prediction performance for hepatitis disease detection.

Factors that affect the survival of hepatitis patients, such as laboratory parameters or clinical features, have been identified in related studies. Lv et al. [15] found that in patients with hepatitis B-related hepatocellular carcinoma (HCC), abnormalities in metabolism-related pathways, particularly fatty acid metabolism, were associated with worse prognosis and recurrence rates. Imanbaeva [16] reported a case of liver damage caused by a co-infection with herpes simplex virus and Epstein-Barr virus, which resulted in a severe form of the disease with complications. The presence of NAFLD aggravated the clinical picture and led to the rapid formation of liver fibrosis [17]. Noor et al. [18] studied patients with positive HBV surface antigen. They found that clinical manifestations included fatigue, bleeding gums, and abdominal pain, while laboratory and imaging characteristics did not differ significantly between HBV-DNA positive and negative patients. Vemulapalli et al. [19] correlated histologic and clinical parameters with outcomes in severe alcoholic hepatitis patients and found that milder grades of biopsy cases had better 28-day results.

Machine learning techniques, specifically CNNs, have been used in studies for hepatitis detection. One study utilized a Deep Ensemble 2D CNN to detect lung nodules, which can be cancerous, from CT scan images. The study achieved a combined accuracy of 95% using this approach [20]. Another study applied various machine learning algorithms, including decision tree, logistic regression, support vector machines, random forest, adaptive boosting, and extreme gradient boosting, for hepatitis B diagnosis. These algorithms achieved balanced accuracies ranging from 75% to 92% [21]. These approaches differ from conventional methods as they leverage the power of deep learning and neural networks to analyze complex medical data and make accurate predictions. Using CNNs allows for the detection of subtle patterns and features in medical images, improving disease diagnosis accuracy [22].

Machine learning algorithms commonly used in hepatitis detection research include KNN, Logistic Regression, Naive Bayes, Decision Tree, SVM, and Random Forest. These algorithms have been evaluated using various performance measures such as accuracy, F1 score, and precision [23]. Naive Bayes with Chi-Square attribute selection performed better regarding the F1 score value [24]. Logistic regression, SVM, Kernel SVM, and KNN performed equally well with an accuracy of 90.32%. Random Forest outperformed other classifiers with an accuracy of 90.7%. Overall, the accuracy of some methods was better than similar results reported in previous research.

Machine learning approaches vary based on the type of hepatitis. In the case of hepatitis B and hepatitis C, different machine-learning models have been used to predict the status of these infections. For hepatitis B, the models evaluated include SVM, RF, NB, and KNN [25]. These models achieved accuracies ranging from 78.2% to 97.6% for predicting HBV status. On the other hand, for hepatitis C, the models such as decision tree, logistic regression, SVM, RF, AdaBoost, and XGBoost have been used [26]. These models achieved balanced accuracies ranging from 75% to 92% for predicting HCV status. Therefore, the choice of machine learning approach depends on the specific type of hepatitis being studied.

Previous research has managed complex and diverse medical data in the context of hepatitis detection by machine learning algorithms and utilizing data mining techniques. These approaches were applied to datasets acquired from the UCI Machine Learning repository and longitudinal medical claims linked to prescription data from millions of patients in the United States. Various classifiers, such as KNN, Logistic Regression, NB, Decision Tree, SVM, and Random Forest, have analyzed the data and classified patients based on their health outcomes [27]. Additionally, the National Institute for Health Research (NIHR) Health Informatics Collaborative (HIC) has developed a comprehensive database for viral hepatitis research. It combines standardized clinical data from different centers to generate information on disease incidence and response to treatment [28]. These research efforts have demonstrated the potential of data-driven approaches and real-world data to improve the effectiveness of hepatitis detection and patient care.

Previous machine-learning approaches to hepatitis detection have shown low sensitivity and specificity weaknesses. These weaknesses indicate that the models may not accurately identify true positive cases (low sensitivity) or negative cases (low specificity). For example, in one study, the prediction performance of machine learning models for hepatitis B and C status was modest, with accuracies ranging from 78.2% to 97.6% [29]. Another study found that while machine learning models achieved high accuracy rates (up to 95%), there is still room for improvement in precision and recall [30]. These findings suggest that previous approaches may not be consistently reliable in accurately detecting and diagnosing hepatitis.

Previous studies have addressed the problem of dataset imbalances in the context of hepatitis detection by employing various techniques. One approach is to apply attribute selection methods to identify the attributes that contribute to the classification of hepatitis disease [31]. Another technique uses class weights in the loss computation to alleviate the data imbalance problem [32]. Additionally, researchers have explored using the synthetic minority oversampling technique (SMOTE) to improve the performance of classifying imbalanced datasets [33]. These studies highlight the importance of addressing dataset imbalances to enhance the accuracy of hepatitis detection models.

Studies have identified factors that affect the survival of hepatitis patients apart from clinical features. Genetic factors have been found to play a role in the treatment failure of sofosbuvir-based antiviral therapy in patients with hepatitis C [34]. In autoimmune hepatitis (AIH), genetic predisposition is associated with the presence of specific HLA alleles, mainly HLA-DR3 and HLA-DR4, and non-HLA epitopes are also associated with disease [35]. Environmental factors have also been influential in AIH pathogenesis, such as urinary tract infections, oral contraceptive use, smoking, and vaccination history associated with AIH [36]. In chronic hepatitis C, liver elastometry revealed fibrosis in children with an asymptomatic course of the disease, indicating that clinical symptoms may not always be present [37].

Machine learning approaches in previous studies considered changes in hepatitis patient data over time and disease progression by using temporal variation and noise levels [38]. Synthetic data resembling accurate patient data was used to classify disease stages at different time intervals [39]. Algorithms such as Nearest Neighbor, Neural Network, and Decision Tree were employed to classify disease progression into early, mid, or late stages [40]. The neural network algorithm showed the best performance in classifying disease stages [20]. Another study assessed the performance of distinct classifiers in diagnosing hepatitis disease and found that the classifiers improved significantly after adopting class balancing [41]. Logistic Regression with SMOTE yielded the highest level of accuracy in diagnosing hepatitis. These machine-learning techniques and classifiers can contribute to the early diagnosis and treatment of hepatitis disease.

METHODS

A. Model Architecture

The proposed model is a 1D Convolutional Neural Network (Conv1D) used for the survival detection of hepatitis patients. The mathematical concept behind this model architecture and the related equations are explained as follows:

a. Conv1D Layer (Convolutional Layer)

The first layer uses Conv1D with 128 filters, a kernel length of 3, and ReLU (Rectified Linear Unit) activation, as shown in Equation (1).

$$\mathrm{Conv1D}_1(\boldsymbol{X}) = \mathrm{ReLU}(\boldsymbol{W_1} * \boldsymbol{X} + \boldsymbol{b_1}) \tag{1}$$

Here, X is the input with a length of `padding_value`, W_1 is the weights of the first Conv1D layer, b_1 is the bias, and $*$ denotes the convolution operation.

b. MaxPooling1D Layer:
   This layer is performed after Conv1D to reduce the data dimension, as shown in Equation (2).

$$\text{MaxPooling1D}(\boldsymbol{X}) = \max(\boldsymbol{X}) \tag{2}$$

c. Dropout Layer:
   The Dropout layer prevents overfitting by randomly ignoring some units (in this case, 30%) in each training iteration, as shown in Equation (3).

$$\text{Dropout}(\boldsymbol{X}) = \boldsymbol{X} \cdot \text{Bernoulli}(p) \tag{3}$$

   Here, p is the dropout probability.

d. Next Conv1D and MaxPooling1D Layers:
   The following two Conv1D and MaxPooling1D layers have a similar concept to the first one, with different numbers of filters (256 and 512).

e. GlobalAveragePooling1D Layer:
   This layer averages the output results from the last Conv1D layer to produce a feature vector fed to the Dense layer, as shown in Equation (4).

$$\text{GlobalAveragePooling1D}(\boldsymbol{X}) = \frac{1}{N}\sum_{i=1}^{N} x_i \tag{4}$$

   Here, N is the length of the feature vector.

f. Dense Layer (Fully Connected Layer):
   There are two Dense layers, the first with 128 units and ReLU activation and the second with a single unit and sigmoid activation, as shown in Equations (5) and (4).

$$\text{Dense}(\boldsymbol{X}) = \text{ReLU}(\boldsymbol{W} \cdot \boldsymbol{X} + \boldsymbol{b}) \tag{5}$$

$$\text{Dense}_1(\boldsymbol{X}) = \sigma(\boldsymbol{W_1} \cdot \boldsymbol{X} + \boldsymbol{b_1}) \tag{6}$$

   Here, σ is the sigmoid function.

g. Model Compilation and Training:
   The model is compiled with the specified optimizer (possibly like Adam) and the binary cross-entropy loss function. It is configured to measure accuracy as the evaluation metric. During training, the model is fed with training data (X_train, y_train) for a certain number of epochs (200 in this case) and a specific batch size (64 in this case).

B. Dataset

The dataset employed in this research is sourced from Kaggle and focuses on hepatitis detection. It encompasses a total of 155 instances with 20 features each, and the target variable classifies individuals into two categories: "Live" (indicating patients who survived) and "Die" (representing those who did not survive).

C. Preprocessing

In this research, several data preprocessing steps were applied to the hepatitis dataset used. Firstly, rows containing missing values (NAN) were removed to ensure data cleanliness. Subsequently, data originally in string format was converted into integer representations for modeling purposes. Additionally, normalization was applied to several features such as "age," "bilirubin," "alk_phosphate," "sgot," "albumin," "protime," and others to ensure uniform scaling across all features. Finally, the dataset was split into two parts: 80% was used as training data to train the model. In contrast, the remaining 20% served as testing data to evaluate the performance of the model to be developed. With these preprocessing steps, the data is ready for use in building a hepatitis patient survival detection model.

D. Comparison of Methods

This research employs the CNN algorithm as the primary approach for hepatitis patient survival detection while comparing its performance against several baseline algorithms, namely SVM, Decision Tree, KNN, Gaussian Naive Bayes, and Gradient Boost. These baseline algorithms provide a benchmark against which the effectiveness and accuracy of the CNN-based model can be evaluated, contributing to a comprehensive assessment of hepatitis detection methods.

E. Training and Evaluation

In this study, the training process utilizes 200 epochs with a batch size of 64. The model's performance is assessed through the utilization of two key evaluation metrics: the Confusion Matrix, as shown in Equation (7), and the Classification Report, as shown in Equations (8)-(11). These evaluation metrics provide quantitative measures to gauge the model's accuracy and effectiveness in hepatitis patient survival detection.

$$Confusion\ Matrix = \begin{bmatrix} TP & FP \\ FN & TN \end{bmatrix} \tag{7}$$

$$Precision = \frac{TP}{TP + FP} \tag{8}$$

$$Recall = \frac{TP}{TP + FN} \tag{9}$$

$$F1\text{-}Score = \frac{2 \cdot (Precision \cdot Recall)}{Precision + Recall} \tag{10}$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{11}$$

Here, TP represents True Positive results, FP represents False Positive results, FN represents False Negative results, and TN represents True Negative results. These metrics collectively assess the model's performance in hepatitis patient survival detection.

RESULT AND DISCUSSION

A. Training Process

This introduction introduces two crucial graphs that are integral parts of this study. The first graph, presented in Figure 1, visualizes training accuracy (blue line) and validation accuracy (orange line) throughout the model training process. This graph will show how well our model can learn patterns in the training data and how well it can generalize to previously unseen data during the validation phase.

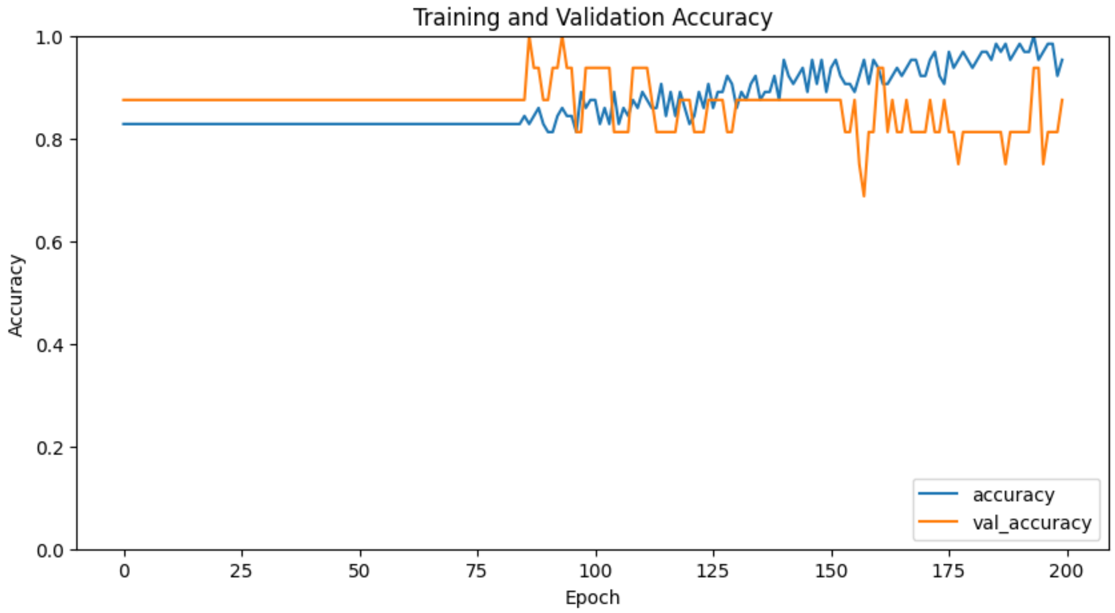

Figure 1. Training dan Validation Accuracy

Furthermore, Figure 2, which we will include, visualizes training loss (blue line) and validation loss (orange line) during the model training. This graph will help us understand how effectively our model reduces errors during training and whether there are indications of overfitting (if training loss decreases while validation loss increases).

Figure 2. Training dan Validation Loss

These graphs will provide valuable insights into the performance of the proposed model in this research and how well it can address challenges in hepatitis patient survival detection.

B. Model Performance

This introduction introduces two crucial tables that are integral to this study. Table 1, presented in Table 1, contains the confusion matrix values for the CNN, SVM, Decision Tree, KNN, GNB, and GBoost algorithms. This table offers a comprehensive overview of how each algorithm performed correctly and incorrectly classified instances, providing insight into their strengths and weaknesses.

Table 1. Confusion Matrix

Algorithm	TP	FP	FN	TN
CNN	14	0	0	2
SVM	14	0	1	1
Decision tree	11	3	1	1
KNN	14	0	2	0
GNB	8	6	0	2
GBoost	12	2	1	1

Additionally, Table 2, which we will present, contains the Classification Report values, including accuracy, for the CNN, SVM, Decision Tree, KNN, GNB, and GBoost algorithms. This table summarizes each algorithm's overall performance, particularly its accuracy in correctly predicting outcomes. Collectively, these tables offer a detailed analysis of the comparative performance of the various algorithms in the context of hepatitis patient survival detection.

Table 2. Classification Report

Algorithm	Accuracy	Class	Precision	Recall	F1-Score
CNN	1.00	Live	1.00	1.00	1.00
		Die	1.00	1.00	1.00
SVM	0.94	Live	0.93	1.00	0.97
		Die	1.00	0.50	0.67
Decision tree	0.75	Live	0.92	0.79	0.85
		Die	0.25	0.50	0.33
KNN	0.88	Live	0.88	1.00	0.93
		Die	0.00	0.00	0.00
GNB	0.62	Live	1.00	0.57	0.73
		Die	0.25	1.00	0.40
GBoost	0.81	Live	0.92	0.86	0.89
		Die	0.33	0.50	0.40

C. Summarization of Key Findings

The research problem was to develop a hepatitis patient survival detection model using a CNN and compare its performance with five baseline algorithms: SVM, Decision Tree, KNN, GNB, and GBoost. The key findings, summarized below, shed light on the effectiveness of these algorithms in terms of their confusion matrix and classification report metrics. In the confusion matrix analysis, the CNN achieved perfect true positive (TP) results with no false positives (FP), indicating its ability to correctly classify all instances of the "Live" and "Die" categories. The SVM exhibited high TP values but had one false negative (FN) and one FP, slightly affecting its performance. The Decision Tree showed a reasonable TP count but struggled with FP instances, impacting its precision. KNN had a firm TP count but recorded two FNs, indicating its sensitivity to specific cases. GNB faced challenges with FP instances, affecting its overall accuracy. Meanwhile, GBoost demonstrated a balanced performance with TP, FP, FN, and true negative (TN) counts, indicating good general classification capabilities.

In the classification report analysis, CNN achieved perfect accuracy (1.00) for both the "Live" and "Die" classes, demonstrating exceptional predictive capability. The SVM exhibited commendable accuracy (0.94) for the "Live" class but showed limitations in classifying "Die" instances. The Decision Tree had relatively lower accuracy (0.75) due to its inability to classify both classes effectively. KNN achieved high accuracy (0.88) for the "Live" class but struggled with "Die" instances. GNB demonstrated moderate accuracy (0.62), particularly struggling to accurately predict "Live" instances. GBoost showed reasonable accuracy (0.81) for the "Live" class but faced challenges in effectively classifying "Die" instances. Overall, the CNN model outperformed the baseline algorithms, achieving perfect accuracy and demonstrating exceptional predictive power in classifying hepatitis patient survival. While SVM and KNN showed strong performance in certain aspects, the CNN model exhibited the most consistent and reliable results across both the confusion matrix and classification report metrics, addressing the research problem effectively and showcasing its potential for clinical application in hepatology.

D. Interpretation of the Result

In the analysis, notable patterns and relationships within the data emerged. The CNN exhibited exceptional accuracy in correctly categorizing both "Live" and "Die" cases, indicating its robust generalization from the dataset. In contrast, baseline algorithms like SVM and KNN displayed strengths in some aspects. Still, they struggled with precision and recall for specific classes, underscoring the significance of algorithm selection in hepatitis patient survival detection. Surpassing expectations, CNN's perfect accuracy was an unexpected outcome, signifying its superiority over traditional machine learning methods in this specific context. These findings align with previous research showcasing the effectiveness of deep learning, particularly CNNs, in medical image analysis and disease detection. But, the exceptional CNN accuracy prompts cautious consideration of overfitting and dataset limitations, necessitating further investigation to ensure consistent performance across diverse datasets and clinical scenarios. Additionally, the extraordinary performance may be attributed to deep learning models' capacity to capture intricate, non-linear patterns not as effectively learned by conventional algorithms. Future research avenues should explore various neural network architectures and data preprocessing techniques to validate these findings' robustness and explore alternative explanations.

E. Implication of the Research

This research holds significant relevance and implications in the medical domain by addressing hepatitis patient survival prediction. It demonstrates the superiority of CNNs over traditional machine learning algorithms, such as SVM and KNN, shedding light on the importance of selecting advanced techniques for enhanced diagnostic accuracy. The findings have critical clinical implications, offering healthcare professionals a potent tool for making informed decisions about patient care and resource allocation. Moreover, the study contributes new insights into the potential for deep learning in capturing intricate data patterns and highlights the importance of considering data volume in model evaluation. These insights pave the way for potential clinical adoption of advanced machine learning models, ultimately improving patient outcomes in hepatitis patient survival prediction and fostering advancements in hepatology.

F. Limitation of the Research

The study's key conclusion highlights the exceptional accuracy of CNNs in predicting hepatitis patient survival, surpassing traditional machine learning algorithms like SVM, Decision Tree, KNN, GNB, and GBoost. CNN achieved perfect accuracy in classifying both "Live" and "Die" cases, signifying its potential as a valuable tool for healthcare decision-making and resource allocation, particularly in hepatology. However, the study's limitations must be acknowledged, primarily the relatively small dataset size of 155 instances, potentially leading to overfitting and limited generalizability. The absence of external validation and the exclusion of potential confounding variables further impact the study's scope. Despite these constraints, the results hold validity within the dataset's context, offering valuable insights into algorithm selection for hepatitis patient survival prediction. Future research should explore more extensive and diverse datasets to enhance their applicability in broader clinical settings, incorporate external validation, and consider potential confounders. Nevertheless, the study underscores the promising clinical utility of CNNs in hepatology.

G. Future Research Recommendation

Recommendations for practical implementation of hepatitis patient survival prediction models include integrating CNNs into clinical settings to aid healthcare decision-making and continuous patient monitoring. Expanding datasets to improve model generalization and undergoing rigorous external validation are crucial steps. Future research should focus on making CNN models more interpretable for clinicians, enhancing feature engineering for better pattern capture, and developing real-time prediction models integrated into electronic health records. Incorporating multi-modal data sources and analyzing longitudinal patient data can improve predictive accuracy. Clinical decision support systems that provide survival predictions and treatment recommendations based on model insights can significantly benefit patient care and outcomes. These recommendations and future research directions aim to advance the practical application of machine learning in hepatology.

CONCLUSION

In conclusion, the results and discussions presented in this study demonstrate the remarkable effectiveness of a CNN in hepatitis patient survival prediction, surpassing the performance of traditional machine learning algorithms. CNN achieved perfect accuracy in classifying both "Live" and "Die" categories, emphasizing its potential as a valuable tool for healthcare decision-making. The analysis revealed that algorithm selection plays a pivotal role in the accuracy of predictions, with CNNs excelling in capturing intricate data patterns. While the study's outcomes exceeded expectations and aligned with previous research on deep learning in medical diagnosis, concerns about dataset limitations and potential overfitting were acknowledged. Future research directions emphasize the need for larger datasets, explainable AI techniques, feature engineering, real-time predictions, multi-modal data integration, and longitudinal data analysis to enhance diagnostic accuracy and clinical decision support in hepatology. Despite these limitations, this research provides crucial insights into the potential for clinical integration of advanced machine learning models and their implications for improving patient outcomes in hepatitis patient survival prediction.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY

The dataset comes from the Kaggle website (https://www.kaggle.com/datasets/codebreaker619/hepatitis-data)

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