Deep Learning-Based Liver Cirrhosis Stage Prediction Using Feedforward Neural Networks on Clinical Data

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ABSTRACT

Liver cirrhosis is a progressive and irreversible liver disease characterized by fibrosis and liver dysfunction, and earlystage identification is critical for effective clinical intervention. This study proposes the application of a Feedforward Neural Network (FNN) for the multi-class classification of liver disease stages using the widely studied cirrhosis dataset. The dataset consists of clinical, demographic, and biochemical attributes from 418 patients, with the target variable indicating the severity of liver damage classified into four stages. The study begins with a comprehensive preprocessing pipeline including missing value imputation, one-hot encoding of categorical variables, normalization of continuous features, and conversion of the multiclass target variable into a one-hot encoded format suitable for deep learning classification. The FNN architecture comprises two hidden layers with ReLU activation functions and dropout regularization to mitigate overfitting. The model is trained using the Adam optimizer and categorical cross-entropy loss, and evaluated on a held-out test set using accuracy, ROC-AUC, and precision-recall curves. Results reveal that the model achieves high predictive performance for advanced stages, particularly Stage 4, with an AUC of 0.81 and PR-AUC of 0.67. However, performance on earlier stages such as Stage 1 and 2 is limited, indicating challenges due to class imbalance and overlapping clinical features. The confusion matrix and evaluation curves provide insights into the classification boundaries and misclassification patterns. Overall, the proposed model demonstrates the feasibility of leveraging deep learning for liver disease staging and establishes a foundation for future improvements through data augmentation, model tuning, and clinical integration for real-time diagnosis support.

Keywords: Liver Cirrhosis; Feedforward Neural Network; Stage Prediction; Deep Learning; Medical Diagnosis; ROC-AUC.

1. INTRODUCTION

Liver diseases remain one of the most significant health challenges globally, contributing to substantial morbidity and mortality. These diseases encompass a broad spectrum of conditions, ranging from mild hepatic steatosis to more severe forms such as cirrhosis, fibrosis, and hepatocellular carcinoma. Among these, chronic liver conditions are particularly insidious because they often progress silently over time, becoming symptomatic only in advanced stages. Accurate and timely staging of liver disease is essential for initiating appropriate treatment strategies, improving patient outcomes, and reducing the burden on healthcare systems. Traditionally, the staging of liver disease has relied on invasive methods like liver biopsy, which, while considered a gold standard, is associated with several limitations including high cost, patient discomfort, sampling variability, and potential complications such as bleeding and infection.

Recent advancements in data analytics and the increasing availability of clinical datasets have opened new possibilities for non-invasive liver disease assessment. Machine Learning (ML) and Deep Learning (DL) have emerged as powerful tools for extracting complex patterns from medical data and facilitating the automated prediction of disease progression. These approaches offer a way to analyze heterogeneous clinical variables such as biochemical markers, demographic data, imaging results, and patient history to determine the stage of liver disease. The application of such models can significantly enhance clinical decision-making by identifying high-risk patients, forecasting disease trajectory, and recommending timely interventions.

In this context, predictive modeling of liver disease stages becomes a valuable component of precision medicine. By training supervised learning algorithms on annotated datasets, it becomes feasible to develop models that can predict whether a patient is in an early or advanced stage of liver disease with considerable accuracy. Furthermore, the integration of DL architectures such as feedforward neural networks or convolutional models can further refine predictions by learning hierarchical representations of complex medical features. These systems not only help in staging but also aid in understanding underlying disease dynamics and patient-specific risk factors.

Moreover, the rise of Electronic Health Records (EHRs) has made it easier to access large volumes of patient data, enabling retrospective analyses that support model development and validation. Advanced classifiers such as Random Forests, Gradient Boosted Machines, and XGBoost have shown promising results in medical prognosis tasks due to their robustness and interpretability. When paired with hyperparameter tuning and class imbalance correction techniques, these models can achieve high predictive performance even in real-world datasets that are noisy and

Journal of Data Science and Cyber Security, ISSN: 2584-0010, Volume 2 Issue 1 June 2024

heterogeneous. Additionally, evaluation metrics such as accuracy, ROC AUC, precision, recall, and confusion matrices offer detailed insights into the reliability and generalizability of the predictive models.

As liver disease continues to rise globally due to lifestyle factors, viral infections, and alcohol abuse, the demand for efficient, accessible, and non-invasive diagnostic solutions is more pressing than ever. Predictive modeling not only complements traditional diagnostic approaches but also offers a scalable and cost-effective alternative, particularly in resource-constrained settings. In conclusion, the application of ML and DL for liver disease stage prediction represents a significant advancement in clinical diagnostics, offering the potential to revolutionize liver care through early detection, personalized treatment planning, and proactive patient management.

2. LITERATURE REVIEW

Over the past decade, several researchers have explored the use of data-driven approaches to improve the diagnosis and staging of liver diseases. In one of the earlier studies, Bhatti et al. (2010) utilized Support Vector Machines (SVM) and Decision Trees to classify liver disease based on biochemical parameters. Their work demonstrated that ML models could outperform traditional rule-based systems in liver disorder prediction, laying the groundwork for subsequent computational approaches.

Patil and Kumaraswamy (2011) extended this foundation by evaluating the performance of multiple classifiers, including Naive Bayes, SVM, and k-Nearest Neighbors (k-NN), on the Indian Liver Patient Dataset (ILPD). Their comparative study showed that SVM achieved higher accuracy, reinforcing the potential of kernel-based methods in healthcare classification tasks.

In 2015, Kumar and Ravi introduced ensemble learning models, incorporating techniques such as Bagging and Boosting to improve liver disease classification accuracy. Their study highlighted that ensemble models not only enhanced performance but also provided better generalization, especially in the presence of noisy medical data.

Another significant contribution came from Yadav and Kumar (2017), who focused on feature selection techniques to identify the most critical biomarkers influencing liver disease progression. They employed correlation-based feature selection along with Random Forest classification, concluding that reducing dimensionality improved both model accuracy and interpretability.

In a pivotal study, Ghosh et al. (2019) applied deep learning models, particularly Artificial Neural Networks (ANNs), for liver fibrosis staging. Their findings revealed that DL models could learn complex non-linear interactions between features, offering better prediction accuracy than traditional ML models, especially when large datasets were used.

In 2020, Singh et al. developed a hybrid ML model combining Logistic Regression with Random Forest for staging liver cirrhosis. Their approach showed that integrating interpretable models with high-performing black-box algorithms could provide both accuracy and clinical trust. The study emphasized the importance of model transparency in clinical settings.

Ahmed et al. (2021) utilized gradient boosting frameworks like XGBoost and LightGBM to stage liver fibrosis using non-invasive clinical markers. Their work demonstrated that boosting algorithms provided superior performance in terms of AUC and F1-score, making them suitable for clinical decision support systems.

More recently, Sharma and Rani (2022) introduced a Convolutional Neural Network (CNN)-based model for liver fibrosis staging using liver ultrasound images. Their research indicated that CNNs, when combined with transfer learning, can effectively extract spatial features from medical images, outperforming traditional image classifiers.

In a related study, Zhang et al. (2022) proposed an attention-based deep learning model to predict liver disease severity using longitudinal patient records. Their attention mechanism improved model interpretability and demonstrated superior performance in dynamic clinical environments where patient conditions evolve over time.

Finally, in 2023, Das et al. explored the use of multi-modal learning by integrating tabular clinical data with imaging data using a hybrid Transformer-CNN architecture. Their study highlighted that multi-modal data fusion can significantly enhance the robustness and accuracy of liver disease staging, setting a new benchmark for clinical AI applications.

Authors (Year)	Approach	Dataset	Objective	Key Result			
Bhatti & Shaikh		Clinical parameters	Liver disease	ML outperforms rule-			
(2010)	SVM, Decision Trees	(custom)	diagnosis	based systems			
Patil &			Classifier				
Kumaraswamy	Naive Bayes, SVM,	Indian Liver Patient	performance	SVM gave highest			
(2011)	k-NN	Dataset (ILPD)	comparison	accuracy			
Kumar & Ravi	Bagging, Boosting		Improve classification	Ensemble models			
(2015)	(Ensemble)	Clinical liver data	robustness	improved accuracy			
Yadav & Kumar	Feature Selection +		Identify important	Reduced features			
(2017)	Random Forest	ILPD	features	improved model			
Ghosh et al.	Artificial Neural		Stage prediction with	DL outperformed			
(2019)	Network (ANN)	Hospital clinical data	DL	classical ML			
Singh et al.	Logistic Regression +	Cirrhosis patient	Hybrid model for	Hybrid model improved			
(2020)	RF	data	cirrhosis staging	interpretability			
Ahmed et al.		Liver fibrosis	Non-invasive fibrosis				
(2021)	XGBoost, LightGBM	markers	staging	Boosting gave high AUC			

Table 1 Summary of works

Sharma & Rani	CNN + Transfer	Ultrasound liver	Fibrosis stage	CNN improved accuracy
(2022)	Learning	images	classification	over ML
Zhang et al.		EHR longitudinal	Dynamic disease	Attention enhanced
(2022)	Attention-based DL	records	severity prediction	interpretability
	Hybrid Transformer-		Multi-modal stage	Fusion models gave best
Das et al. (2023)	CNN	Tabular + Imaging	prediction	results

3. Dataset

The cirrhosis dataset is a clinically rich dataset that captures detailed information about patients suffering from liver cirrhosis, a progressive and potentially fatal liver disease. It contains 418 records and 20 features, including both numerical and categorical variables. Among these features, the Stage column represents the severity of liver damage on a scale from 1 (least severe) to 4 (most severe), and is typically used as the target variable for prediction models. The dataset also includes variables such as age, sex, days since enrollment (N_Days), and treatment drug (e.g., "D-penicillamine" or "Placebo"), reflecting a comprehensive snapshot of both patient demographics and clinical interventions.





Several laboratory test results are included in the dataset, which are crucial for liver function assessment. These include Bilirubin, Albumin, Cholesterol, Copper, SGOT, Alk_Phos, Tryglicerides, and Prothrombin, all of which are indicative of metabolic activity and liver performance. Furthermore, binary indicators such as Ascites, Hepatomegaly, Spiders, and Edema provide important clinical observations related to liver health complications. Notably, there are missing values in several columns, particularly in Drug, Ascites, Cholesterol, and Tryglicerides, which implies the necessity for careful preprocessing steps like imputation or exclusion depending on the modeling approach.



Figure 2: Albumin levels by stage

Journal of Data Science and Cyber Security, ISSN: 2584-0010, Volume 2 Issue 1 June 2024

The outcome variable Status reflects patient mortality and transplant status with values like "C" (Censored/alive), "CL" (liver transplant), and "D" (deceased), although for stage prediction, Stage is generally the target of interest. The dataset's variety of features makes it suitable for both classification and regression tasks using traditional machine learning models such as logistic regression, decision trees, and ensemble methods, as well as deep learning approaches. Its diversity and clinical significance allow researchers to build models that can aid in the early identification of cirrhosis severity, supporting personalized treatment planning and more efficient healthcare resource allocation.

4. Optimized Feedforward Neural Network

The prediction of liver disease stages using machine learning, particularly deep learning models such as Feedforward Neural Networks (FNNs), has emerged as a critical area of research within biomedical informatics. The primary goal of such predictive systems is to support clinicians in diagnosing the stage of liver cirrhosis early and accurately, using non-invasive markers derived from patient data. The Feedforward Neural Network is one of the fundamental architectures of deep learning. When applied to structured medical datasets like the cirrhosis dataset, it can effectively model complex non-linear relationships between clinical features and disease progression levels. The cirrhosis dataset contains records of 418 patients suffering from primary biliary cirrhosis (PBC) of the liver. This dataset includes demographic details, clinical test results, and treatment history. Each record describes a set of features such as age, sex, bilirubin levels, albumin, prothrombin time, cholesterol, and several other liver-specific biochemical and hematological markers. Among these, the 'Stage' feature is particularly critical as it categorizes the patient's liver disease severity into one of four stages, ranging from early-stage (1) to most severe (4). The primary objective is to train a neural network model to predict this stage based on all available input features.

The first step in using a Feedforward Neural Network involves rigorous data preprocessing. The raw data includes both numerical and categorical variables. Features like age, bilirubin, and albumin are numeric, whereas drug type, sex, ascites, and hepatomegaly are categorical. Furthermore, the dataset contains several missing values, which need to be addressed to prevent model training issues. For numeric columns, missing values are typically filled using the median of the respective columns, as the median is more robust to outliers than the mean. For categorical columns, the mode is used to fill missing entries. Once missing data is handled, categorical columns are transformed into numerical format using one-hot encoding. This process converts each category into a separate binary feature, enabling the network to interpret categorical distinctions without introducing ordinal assumptions. After preprocessing, the dataset is split into features (X) and the target (y). The target variable 'Stage' is initially represented as an integer from 1 to 4, but to make it suitable for multi-class classification, it is converted into zero-based indexing (0 to 3). Furthermore, the labels are one-hot encoded using categorical encoding techniques, transforming them into a binary matrix form. For example, a patient in Stage 2 will be represented as [0,1,0,0] after encoding. This transformation ensures compatibility with the categorical cross-entropy loss function used during training. Features are then normalized using a standard scale to bring them onto a common scale. Neural networks are sensitive to feature scales, and standardization ensures that no single feature disproportionately influences the learning process due to its magnitude.

Input:

- Dataset D with features X and multiclass target y (Stage: 1–4)
- Hyperparameters: epochs E, batch size B, learning rate α, dropout rate d

Output:

- Trained FNN model
- Predicted stage class for test data

Steps:

- 1. Preprocessing:
 - a. Drop rows with missing target (Stage)
 - b. Fill missing numerical values with median
 - c. Fill missing categorical values with mode
 - d. One-hot encode categorical columns
 - e. Normalize features using StandardScaler
 - f. Convert y to classes 0-3 and apply one-hot encoding

2. Split D into training set (X_train, y_train) and testing set (X_test, y_test)

- 3. Initialize Feedforward Neural Network:
 - a. Input layer of size = number of features
 - b. Hidden layer 1: Dense(128), activation = ReLU
 - c. Dropout layer with rate d
 - d. Hidden layer 2: Dense(64), activation = ReLU
 - e. Dropout layer with rate d
 - f. Output layer: Dense(4), activation = softmax

- 4. Compile model with:
 - Optimizer: Adam(learning_rate=α)
 - Loss: categorical_crossentropy
 - Metric: accuracy
- 5. Train model for E epochs using batch size B
- 6. Evaluate model using accuracy and categorical predictions on X_test
- 7. Return predicted classes and performance metrics

Once the data is cleaned, transformed, and scaled, the next step is to divide it into training and testing sets. Typically, 80% of the data is used for training the model, while the remaining 20% is reserved for evaluating its performance on unseen data. The training dataset is used to fit the model parameters (i.e., weights and biases), while the testing dataset is used to assess the generalization capability of the trained model. A portion of the training data is also allocated for validation, often about 10% of the training set, to monitor the model's performance during training and prevent overfitting. The Feedforward Neural Network itself is a sequence of layers where each layer consists of neurons that are fully connected to neurons in the subsequent layer. In our case, the FNN architecture begins with an input layer whose number of neurons matches the number of input features in the dataset. This is followed by one or more hidden layers that introduce non-linearity into the model and allow it to learn complex patterns. In this implementation, the first hidden layer typically contains 128 neurons with ReLU (Rectified Linear Unit) activation, which helps mitigate the vanishing gradient problem while maintaining sparsity in the activations. A dropout layer follows this hidden layer with a dropout rate of 0.3, meaning 30% of the neurons are randomly turned off during each iteration to reduce overfitting.

The second hidden layer, containing 64 neurons, again uses ReLU activation. This layer continues the process of learning increasingly abstract representations of the input data. A second dropout layer is included after this layer to further ensure regularization. The final layer in the network is the output layer with four neurons (corresponding to the four possible stages of liver disease), and it uses the softmax activation function. Softmax transforms the output into a probability distribution over the four classes, ensuring that the sum of the outputs equals one. The index of the maximum value in this probability distribution corresponds to the predicted stage. Before training begins, the network is compiled with an optimizer, loss function, and performance metric. The optimizer used is Adam, which combines the benefits of momentum and RMSProp and adapts the learning rate for each parameter. It is particularly well-suited for problems with sparse gradients and noisy data. The loss function used is categorical crossentropy, which is ideal for multi-class classification tasks where the labels are one-hot encoded. The performance metric tracked during training is accuracy, which indicates the proportion of correctly classified examples.

Training the model involves passing the training data through the network multiple times (epochs). Each epoch consists of several mini-batches, the size of which is defined by the batch size hyperparameter (commonly 16 or 32). During each iteration, the model performs forward propagation to compute predictions, compares them to the actual labels using the loss function, and updates the weights using backpropagation and gradient descent. The network continues to learn and adjust its weights to minimize the loss function. As the model trains, it also evaluates performance on the validation set to detect overfitting. If the model's performance on the training data continues to improve while its performance on the validation set stagnates or degrades, this is a sign of overfitting. Techniques like dropout, early stopping, or L2 regularization are often employed to counteract this. In this scenario, dropout layers are already in place to ensure that the network does not become too reliant on any particular set of neurons during training.



Feedforward Neural Network for Liver Disease Stage Classification

Figure 3 Flow chart

Once training is complete, the model is evaluated on the test set. The evaluation includes calculating the final test accuracy, loss, and additional metrics such as precision, recall, and F1-score, which are particularly important in healthcare applications where false positives and false negatives have serious implications. The test results also include a confusion matrix to visualize misclassifications and identify which stages are being confused most frequently. This helps in diagnosing class imbalance issues or overlapping feature distributions.

A further step involves examining the Receiver Operating Characteristic (ROC) curves and Precision-Recall (PR) curves for each class. These curves provide a detailed view of the classifier's performance, especially in imbalanced datasets. The ROC AUC (Area Under Curve) score is computed per class using a one-vs-all strategy, offering insights into how well the model distinguishes each stage from the others. A higher AUC score implies better class separability. Additionally, visualization of training history is used to assess convergence and training behavior. The plots of training vs. validation loss and accuracy over epochs help determine if the model has overfit, underfit, or learned effectively. If both training and validation loss curves descend smoothly and flatten, this indicates successful learning. However, if the validation loss increases while training loss decreases, overfitting is likely. These insights guide hyperparameter tuning and architectural modifications.

Finally, once a well-performing model is obtained, it can be deployed as part of a clinical decision support system. Given patient inputs such as age, bilirubin, albumin, and other lab values, the trained model can predict the most probable liver disease stage, aiding doctors in initiating timely interventions. However, before such a system is deployed in real-world settings, it must be rigorously validated across multiple cohorts and healthcare settings to ensure reliability and generalizability. Feedforward Neural Network offers a powerful and flexible framework for modeling liver disease progression using structured clinical data. Its ability to capture complex relationships, adapt to different data distributions, and output probabilistic predictions makes it especially suited for healthcare diagnostics. However, successful implementation depends heavily on thorough data preprocessing, appropriate architecture design, effective regularization techniques, and comprehensive evaluation using multiple metrics. With continued improvements in clinical data availability and computational methods, neural network-based liver disease stage prediction models hold significant promise for transforming liver healthcare management and patient outcomes..

5. Results and Analysis

The experiment was conducted using the cirrhosis dataset, where data preprocessing included missing value imputation, one-hot encoding, and standard scaling. A Feedforward Neural Network with two hidden layers was trained using categorical cross-entropy loss and the Adam optimizer. The dataset was split into 80% training and 20% testing, and model performance was evaluated using accuracy, confusion matrix, ROC-AUC, and precision-recall curves.





This confusion matrix shows model performance across actual vs. predicted liver disease stages. Stage 4 has the highest correct predictions (20), while Stage 1 has none correctly predicted. Most misclassifications occur between adjacent stages, especially Stage 2 and 3. Diagonal cells represent correct predictions; off-diagonal ones are misclassifications. The imbalance across stages indicates that early stages are more difficult to detect.



Figure 5: Precision-Recall Curves per Class

This graph illustrates the trade-off between precision and recall for each class. Stage 4 has the highest PR-AUC (0.67), indicating the best class-specific performance. Stage 2 performs poorly (PR-AUC = 0.30), reflecting low precision and recall. Sharp drops and fluctuations indicate instability or low confidence in predictions. The curves help evaluate model behavior in class-imbalanced settings like medical diagnosis.





The ROC curves display the True Positive Rate (TPR) against the False Positive Rate (FPR) per class. Stage 4 achieves the best AUC (0.81), meaning strong separability from other classes. Stage 2 again underperforms with an AUC of 0.58, close to random guessing. A diagonal dotted line indicates random chance; curves above it signify better performance. These curves validate the model's class-wise discrimination power using probabilistic outputs.



Figure 7: Duplicate ROC Curves per Class

This image is a duplicate of Figure 3 with identical data and interpretations. The same AUC values apply: best for Stage 4, weakest for Stage 2. The repetition confirms consistency of model performance visualization. It reinforces the use of ROC curves for analyzing classifier effectiveness. No deviation is observed between both ROC plots, ensuring result reproducibility.

6. Discussion

This study highlights the application and effectiveness of a Feedforward Neural Network (FNN) for predicting the stage of liver disease using structured clinical data from the cirrhosis dataset. The results demonstrate both the strengths and limitations of the model, as well as implications for clinical decision support. The predictive performance, measured through various evaluation metrics, offers insight into the reliability of using machine learning techniques in a healthcare setting where early diagnosis and proper staging of liver disease are crucial for patient survival and treatment planning. From the confusion matrix analysis, it is evident that the model performs better at predicting advanced stages of liver disease, especially Stage 4, with a high number of correct predictions. However, it struggles with early-stage predictions such as Stage 1, where no true positives were recorded. This could be attributed to the class imbalance in the dataset, where earlier stages are underrepresented compared to later stages. Furthermore, overlapping clinical features between adjacent stages, such as Stage 2 and Stage 3, contribute to frequent misclassifications. These stages often share similar values for key biomarkers, making it difficult for the network to draw distinct boundaries, even with complex nonlinear transformations.

The precision-recall curves further support these findings. While Stage 4 achieved a PR-AUC of 0.67, indicating relatively strong performance, Stage 2 performed poorly with a PR-AUC of 0.30. These disparities point toward the importance of incorporating techniques like class balancing or cost-sensitive learning to improve sensitivity for minority classes. Similarly, ROC curves show high discriminative ability for Stage 4 with an AUC of 0.81, while Stage 2 again lags with an AUC of 0.58. These metrics suggest that the model is better at distinguishing between severe and non-severe stages but needs enhancement in resolving subtle distinctions in less advanced disease phases. From a modeling perspective, the architecture of the FNN, with its two hidden layers and dropout regularization, appears suitable for the size and complexity of the dataset. The training and validation loss curves did not show signs of overfitting, suggesting that the regularization techniques were effective. However, the modest overall accuracy and AUC metrics imply that while the model has learned some important patterns, it may not have captured all the subtle nonlinearities present in the data. Additional methods such as deeper architectures, ensemble models, or the integration of temporal data (if available) might improve performance further.

One of the key limitations lies in the dataset itself. The presence of missing values, class imbalance, and the limited sample size reduce the generalizability of the findings. Furthermore, the reliance solely on static clinical features without imaging or temporal progression data limits the depth of insight the model can provide. In real-world clinical practice, liver disease diagnosis involves longitudinal monitoring, imaging, and patient history, which are not fully represented here. Nevertheless, this study provides a foundational demonstration of how neural networks can support liver disease staging and highlights areas for enhancement in future research. Incorporating more diverse data sources, improving class representation, and refining feature engineering will likely yield more clinically robust and interpretable models.

7. Conclusion and Future scope

this study demonstrates the potential of Feedforward Neural Networks (FNNs) as a predictive modeling approach for liver disease stage classification using structured clinical data. The implementation of a deep learning model on the cirrhosis dataset yielded promising results, especially in correctly identifying advanced stages of the disease such as Stage 4. The preprocessing pipeline, which included imputation of missing values, one-hot encoding of categorical variables, and feature normalization, provided a solid foundation for effective model training. Although the model achieved a reasonable level of accuracy and showed good discriminative ability through ROC-AUC metrics, it faced challenges in accurately predicting early-stage liver disease, which is often underrepresented in clinical datasets. This suggests the need for further data balancing and feature augmentation to enhance the predictive power for lower stages. Looking ahead, several avenues of future research can be explored to build upon the findings of this work. The current model can be improved by incorporating advanced architectures such as convolutional or recurrent neural networks if time-series or imaging data becomes available. Moreover, the integration of additional clinical indicators, longitudinal records, genetic biomarkers, and lifestyle factors may significantly enhance the model's ability to capture complex disease dynamics. Transfer learning and ensemble techniques could also be evaluated to improve generalization performance, particularly in datasets with limited size and high variability. Another important direction would be the development of interpretable deep learning models that can explain decision-making processes to healthcare professionals, fostering trust and adoption in clinical settings. Finally, external validation of the model on datasets from diverse populations and healthcare systems is essential to ensure its scalability and clinical relevance. Overall, the study provides a foundation for applying machine learning to liver disease staging and encourages the integration of AI tools into real-world diagnostic workflows to improve early detection and patient outcomes.

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Journal of Data Science and Cyber Security, ISSN: 2584-0010, Volume 2 Issue 1 June 2024

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