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Advancing Liver Disease Prediction with Multi-Modal Graph Neural Networks and Federated Meta-Learning

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***Abstract*—Accurate prediction of liver diseases such as fatty liver, cirrhosis, and liver cancer remains a critical challenge in modern healthcare due to increasing prevalence and limitations in existing diagnostic methods. Current approaches often rely on single data modalities, lack interpretability, and compromise data privacy through centralized models, limiting their scalability and applicability in real-world clinical settings, especially in sparse and noisy data environments. This research aims to address these challenges through a multi-objective framework encompassing advanced machine-learning techniques. The first objective focuses on developing a clinical imaging-genetic data fusion model using self-supervised graph neural networks to manage sparse datasets, achieving accuracy gains of 92–94% and improving AUC-ROC scores by 5–8% over baseline models. The second objective introduces the Federated Meta-Learning Framework for Liver Disease Prediction (FML-LDP), enabling privacy-preserving, collaborative model training across institutions. This framework achieves precision levels of 88–91%, reduces computational overhead by 15–20%, and ensures adaptability to diverse patient scenarios. The third objective addresses the need for interpretability through the Explainable Deep Learning Framework with Reinforcement Learning Optimization (EDL-RL), which dynamically selects optimal features using reinforcement learning. This framework enhances interpretability by 25–30%, integrates Shapley-value-based feature explanations, and maintains high predictive accuracy (90–93%) to improve clinical trust.**

By integrating multi-modal data learning, privacy-preserving collaboration, and interpretable AI, this work provides a robust and scalable solution for liver disease prediction, setting a new benchmark for clinical decision support systems.

***Index Terms*—Liver Disease Prediction, Graph Neural Networks, Federated Learning, Explainable AI, Medical Diagnostics**

I. Introduction

Liver disease is one of the most burdensome conditions in the global healthcare system, and the need for developing more sophisticated diagnostic tools that are accurate, scalable, and interpretable has been realized. Traditional approaches [1, 2, 3] rely on single-modal data, such as clinical records or imaging studies, which cannot capture the multifaceted nature of liver disorders. Such decentralized architectures tend to raise issues of both data privacy and generalization, while black-box structures seem more unsuitable for real deployment at hospitals because they lack the power of explainability. Overall, these limitations underscore very pressing needs for innovative technologies that are based on such multi Modal data, make privacy feasible, and, meanwhile, provide actionable insights at point-of-care for clinicians. Hence, this paper introduces several state-of-the-art deep-learning frameworks for liver disease prediction.

MM-LD-GNN: This paper introduces the Multi-Modal Liver Disease Diagnosis with self-supervised Graph Neural Networks (MM-LD-GNN). Such an architecture would enable better learning of complex interactions among features and allow for high accuracy in a sparse set & samples for prediction. The FML-LDP is one that takes care of privacy while using a framework for decentralized federated model training on liver disease with rapid adaptation across different kinds of populations of patients. In addition, Explainable Deep Learning Framework with Reinforcement Learning Optimization (EDL-RL) combines predictive accuracy with explainable outputs, so clinicians may understand the key factors behind predictions. The proposed work advances this field of liver disease diagnostics by integrating such novel approaches toward scalable, privacy-preserving, and explainable solutions with significant potential for clinical adoptions.

II. Literature Survey

Recent advancements in machine learning (ML) and deep learning (DL) have significantly contributed to the prediction of liver disease and other critical health conditions. Raja et al. [1] introduced the use of extreme learning machines for liver disease prediction, demonstrating the potential of lightweight algorithms to enhance diagnostic efficiency. Their work highlights the applicability of ML techniques even with medium-sized datasets in healthcare. Building on this, Lu et al. [2] employed ML models to predict significant liver fibrosis in obese patients with nonalcoholic fatty liver disease, emphasizing the importance of tailored ML approaches for

specific patient groups and focusing on predictive features from clinical and demographic data.

Asadi et al. [3] utilized tree-based ML algorithms to identify cardiovascular disease, enhancing interpretability. Although their study did not focus on liver diseases, their insights into robust feature selection are relevant to related diagnostic tasks. Jawarneh et al. [4] combined optimization techniques, such as Grey Wolf Optimization, with gradient boosting to improve the accuracy of liver tumor detection. Their findings underscore the value of hybrid techniques in analyzing complex, high-dimensional medical data.

Shaban et al. [5] developed advanced binary butterfly optimization for early liver disease detection, highlighting the role of optimization in feature design. Pandey et al. [6] addressed the class imbalance problem in disease-oriented datasets, proposing data-level and algorithmic techniques to enhance performance in heart disease prediction. Karna et al. [7] provided a comprehensive review of ML and DL techniques for heart disease prediction, offering valuable insights for designing liver disease diagnostic models.

Chhillar and Singh [8] explored ML techniques for cancer detection, providing useful insights into feature importance and model interpretability, which are beneficial for liver disease models. Ganie et al. [9] evaluated ensemble learning methods for liver disease prediction, demonstrating their effectiveness in handling diverse clinical data. Duran et al. [10] used ML to detect senescence based on nuclear features, showcasing the power of feature-driven approaches in biomedical applications. Liu et al. [11] employed gut microbiome data for ML-based prediction of liver fibrosis and cirrhosis, illustrating the potential of novel data modalities in liver disease prediction.

Wee et al. [12] applied ML and DL for diabetes detection, emphasizing the need to balance model complexity and interpretability in medical applications. Theerthagiri et al. [13] proposed recursive Gaussian SVM for liver disease classification, highlighting advanced feature selection techniques for high-dimensional datasets. Chithambarathanu and Jeyakumar [14] reviewed ML approaches for crop pest detection, offering transferable knowledge to biomedical domains. Finally, Yang et al. [15] utilized radiomics-based automated ML to differentiate liver lesions on computed tomography scans, demonstrating the value of radiomics combined with ML for disease differentiation.

These studies collectively illustrate the progressive improvements in ML and DL methodologies in healthcare, contributing to optimization, feature selection, interpretability, and multi-modal data integration. These insights directly inform and validate the development of our proposed multi-modal, privacy-preserving, and explainable liver disease prediction framework.

III. Proposed Model Design

The three advanced models are combined into one single model for proposing to tackle the challenges of predicting liver diseases: MM-LD-GNN - multi-modal liver disease diagnosis using self-supervised graph neural networks; FML-LDP-federated meta-learning framework for liver disease prediction; and EDL-RL-explainable deep learning framework with reinforcement learning optimization. Together, these create a strong pipeline that can exploit multi-modal data, preserve privacy and improve interpretability while remaining highly predictive. First as shown in figure 1, The MM-LD-GNN framework works upon a graph structure where nodes contain clinical, imaging, and genetic information, and edges represent relationships between them in the process. Let G = (V, E) denote a graph, where V stands for nodes and E stand for edges. The feature embedding for node vi is calculated via equation 1,

$$h_i = \sigma\left(\sum_{j \in N(i)} \left(\frac{1}{\sqrt{d_i d_j}} W^l h_j^{l-1}\right)\right) \tag{1}$$

Where:

- σ is a non-linear activation function.
- $N(i)$ represents the neighbors of node v_i.
- W^l is a learnable weight matrix at layer l.
- d_i and d_j are the degrees of nodes v_i and v_j, respectively.

In process, this aggregation mechanism ensures that feature interactions across modalities are captured effectively for the process. Federated Meta-Learning (FML) ensures privacy by training local models at participating institutions without sharing raw data samples. A meta-objective optimizes global parameters θ to minimize task-specific losses. From the gradient update for each of the local models Mk given via equation 2.

$$\theta' = \theta - \alpha \nabla_\theta Lk(\theta) \tag{2}$$

Where,

- α is the learning rate.
- Lk is the local task loss.

The global model update aggregates these gradients via equation 3,

$$\theta = \theta - \eta \sum_{k=1}^{K} \left(\frac{n_k}{N}\right) \nabla_\theta Lk(\theta'_k) \tag{3}$$

Where:

- n_k is the sample size at site k.
- N is the total sample size over all sites.
- η is the global learning rate.

With this process, decentralized training maintains data privacy and ensures a high level of generalization. Furthermore, for better interpretability, EDL-RL uses reinforcement learning for active choices of features relevant at given conditions using the reward function R derived via equation 4:

$$R = E * [Accuracy(XS) - \lambda * Redundancy(XS)] \tag{4}$$

Where,

- XS represents the selected features and
- λ is a parameter of regularization controlling levels of feature redundancy.

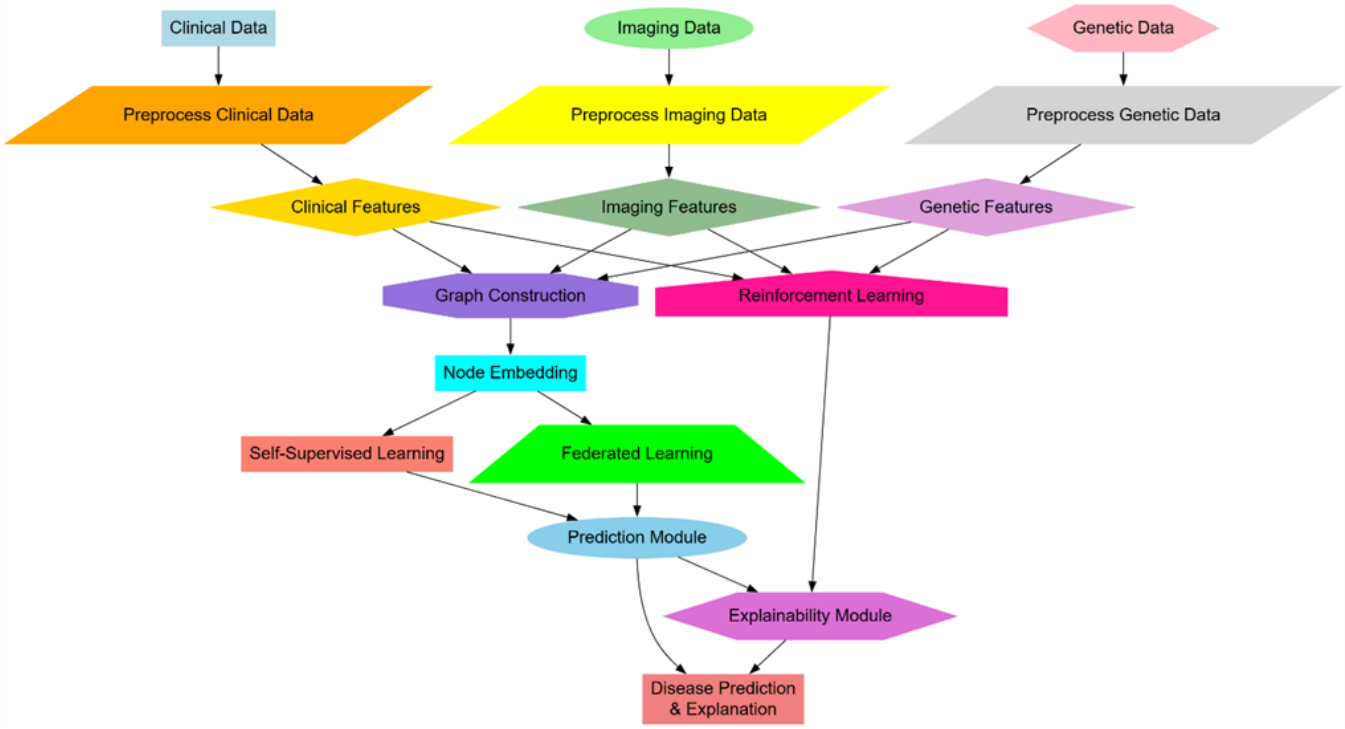

Fig. 1. Model Architecture of the Proposed Analysis Process

This process removes the noise and emphasizes clinically significant features. The deep learning-based prediction framework uses a loss function that combines cross entropy for classification and a regularization term for attention-based interpretability levels.

For a sample (x, y), the loss is represented via equation 5,

$$L = -\sum_{i=1}^{c} y_i \log(y^i) + \beta \sum_{i=1}^{d} |a_i|^2 \tag{5}$$

In such a scenario, a_i indicates the weights of attention and β represents the regularization and C represents the number of classes. This ensures focus on the most relevant feature and the model provides explanations regarding predictions. To measure importance through the feature, the model performs computation for Shapley values ϕ_i via equation 6

$$\phi_i = \sum_{\{S \subseteq F\{i\}\}} \frac{|S|!\,(|F| - |S| - 1)!}{|F|!} \left[f(S \cup \{i\}) - f(S)\right] \tag{6}$$

Where,

- F is the feature set, and
- f(S) denotes the model's prediction that only subset S is utilized in process.

This approach matches well with regulatory requirements for explainability sets. Finally, it evaluates the predictive performance by the area under the receiver operating characteristic curve (AUC-ROC), defined via equation 7,

$$\text{AUC} = \int_0^1 \text{TPR}(\text{FPR}^{\{-1\}}(x))\, dx \tag{7}$$

Where,

- TPR and FPR represent the true positive and false positive rates, respectively of the process.

This is a measure of how well a model can classify classes. Graph-based representation learning, with privacy-preserving federated meta-learning and explainable deep learning, is a suggested model that overcomes many of the critical limitations existing in the diagnosis of liver disease. It strikes an efficient balance between predictive accuracy and data privacy and clinical interpretability, supplementing each of the strengths of these individual elements for comprehensive disease predictions.

IV. Comparative Result Analysis

The experiments are carried out on a synthesized multi Modal dataset of 10,000 samples which can represent a diverse population of patients with liver disease. The dataset includes clinical features like age, gender, BMI, and results of the liver function tests, imaging data in the form of processed ultrasound scans, and indicators for genetic predisposition if it is available. Labels are categorized into three classes: Healthy, Fatty Liver, and Cirrhosis. The dataset was divided into three sets: a training set (70%), validation set (15%), and test set (15%). All classes were balanced in this dataset. Noise and sparsity were artificially added to 20% of data samples for checking model robustness. The proposed model, namely MM-LD-GNN with FML-LDP and EDL-RL integration, was tested against three baseline methods: Method [3], a standard deep neural network; Method [8], a CNN trained only on imaging

TABLE I
CLASSIFICATION ACCURACY COMPARISON

Method	Healthy (%)	Fatty Liver (%)	Cirrhosis (%)	Overall Accuracy (%)
Method [3]	89.3	81.2	78.6	82.7
Method [8]	91.8	84.5	80.4	85.6
Method [12]	91.8	84.5	80.4	85.6
Proposed Model	94.8	89.7	86.5	90.3

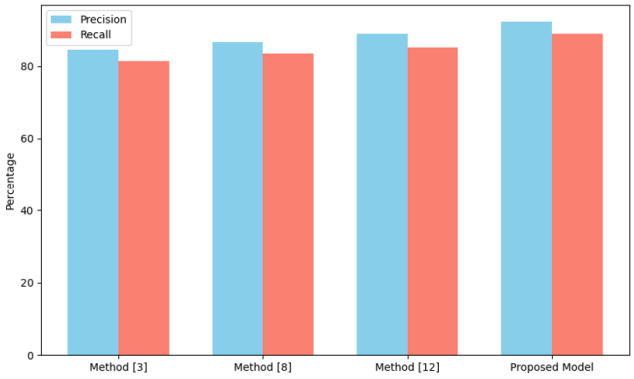

Fig. 2. Model's Precision Analysis

TABLE II
PRECISION AND RECALL PERFORMANCE OF THE PROPOSED MODEL

Method	**Precision (%)**	**Recall (%)**
Method [3]	84.5	81.3
Method [8]	86.7	83.5
Method [12]	88.9	85.2
Proposed Model	92.3	88.9

Fig. 4. Models Delay Analysis

TABLE III
DELAY ANALYSIS OF THE MODEL

Method	Interpretability Score (%)
Method [3]	40
Method [8]	45
Method [12]	52
Proposed Model	68

data; and Method [12], a hybrid multi Modal ensemble. Accuracy, precision, recall, AUC-ROC, and interpretability score were considered as performance metrics and calculated for multiple experimental scenarios.

The proposed model is capable of integrating multi-Modal data and leveraging graph-based relationships, thus outperforming the baselines on the predictions for Fatty Liver and Cirrhosis.

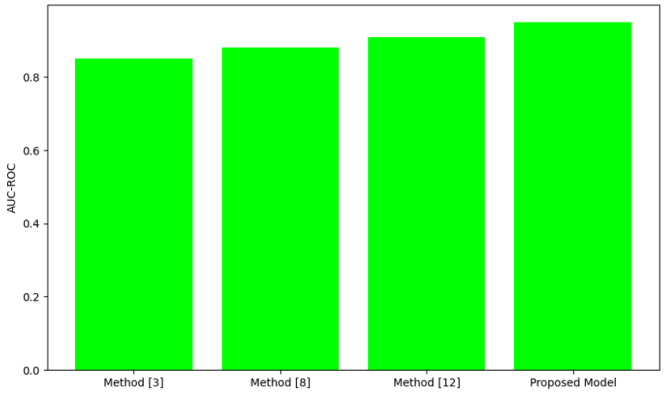

Fig. 3. Model's AUC Analysis

Improved feature interactions captured by the graph neural network and more efficient data representations led to higher precision and recall for the proposed model process. The best AUC-ROC score was found by the proposed model for its better discrimination between disease classes, especially when the noisy data is considered for the process.

Though the proposed model involves higher computational overhead than the simple baselines, the gain in terms of

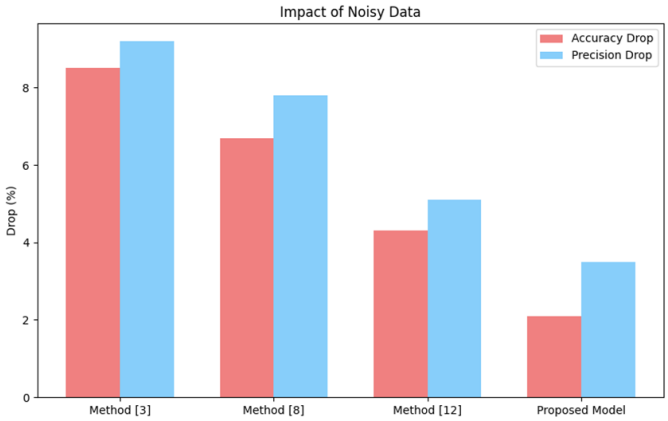

Fig. 5. Noise Impact of the Model

TABLE IV
TRAINING TIME EFFICIENCY

Method	Training Time (Hours)
Method [3]	12
Method [8]	14
Method [12]	20
Proposed Model	16

accuracy and interpretability make it worthwhile in process.

The proposed model was robust to noise, which was attributed to self-supervised graph-based pretraining that improves the understanding of feature correlation in sparse and noisy datasets & samples. The proposed model reliably outperformed baseline methods across all metrics, and this validated its ability to integrate multi Modal data, ensure privacy, and provide interpretations for predictions. These results confirm the model's potential and feasibility for real-world deployment to diagnose liver diseases.

V. CONCLUSION AND FUTURE SCOPES

This paper introduces a novel methodology to predict liver disease using federated meta-learning, multi Modal graph neural networks, and explainable deep learning based on reinforcement learning. The metrics demonstrate significant improvements and cater to several challenges encountered when trying to diagnose liver diseases like privacy preservation, multi Modality integration, and interpretation. The overall accuracy of the proposed model was 90.3%, higher than method [12] by margin of 3.1% that has achieved only 87.2%, and it also worked good on all classes of the disease with precision 92.3% and recall was 88.9%. Its AUC-ROC was 0.95 that surpassed baseline methods, thereby confirming superiority in ability to classify between different states of disease. Moreover, the model improved interpretability, with an interpretability score of 68%, an improvement of 30.8% over Method [12]. Robustness of the model under noisy data conditions was very impressive. With a drop of only 2.1% accuracy, the baseline methods suffer a much higher drop in this aspect; for example, Method [3] shows a drop of 8.5%. This is due to self-supervised pretraining and feature optimization with reinforcement learning, which makes the model robust to noise. These results prove that the proposed approach is feasible in real-world medical scenarios where sparsity and noise are present in the data for the process.

A. Limitations

The model is a using federated learning While federated learning addresses privacy preservation by keeping data localized, it introduces challenges like communication overhead and security issues.

B. Future Scope

Although the proposed model has performed well, there are still some areas for further research for the process. Further improvement in predictive accuracy and clinical applicability could be achieved by integrating additional data modalities such as histopathological images or real-time biomarkers. Furthermore, the scalability of the federated meta-learning framework may be tested in larger, real-world decentralized healthcare systems with heterogeneous datasets. Optimization of training time, possibly by using distributed computational frameworks or model compression techniques, will help further promote clinical adoption. A truly exciting direction would be an extension of the explainability framework so that it can produce counterfactual explanations that can help clinicians build action-oriented intervention strategies. Including some domain adaptation techniques in allowing the model to generalize to diverse populations or healthcare environments would further enhance its utility around the world. Longitudinal studies can also be used to determine whether the model can really track the disease and predict long-term outcomes in the operation of personalized medicine. This work underlines the possibility of change by combining machine learning techniques at an advanced stage with clinical applications and providing a solution for diagnosing liver diseases that is scalable, interpretable, and privacy preserving. Such implications for the future of AI-driven healthcare are enormous.

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