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Original Article

Machine Learning-Driven Prediction of Liver Enzyme Abnormalities in Type 2 Diabetes Mellitus

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Abstract *- Liver complications are a concern in people living with Type 2 Diabetes Mellitus (T2DM). But they remain unnoticed, and enzyme levels increase beyond normal ranges. Increases in alanine aminotransferase and aspartate aminotransferase are used as early biochemical signals of hepatic stress. Early assessment is important in individuals with T2DM. This study presents a data-based framework to identify variations in serum transaminase levels using regularly collected demographic and metabolic information (age, sex, body mass index, HbA1c, lipid profile measures, blood pressure, liver fat content, and diabetes status). Graph Attention Networks, combined with the minimum Redundancy Maximum Relevance method, were applied for feature selection. It retains influential variables and minimizes redundancy. ALT and AST levels were estimated using Bayesian-optimized XGBoost and a deep neural network trained with the Adam optimizer. The models achieved an accuracy of 95.3% and a precision of 93.5%. The findings indicate that integrating routine clinical data with analytical models assists in early identification of hepatic abnormalities in individuals with T2DM.*

Keywords *- Type 2 Diabetes Mellitus (T2DM), Liver enzyme prediction, Alanine Aminotransferase (ALT), Aspartate Aminotransferase (AST), Graph Attention Networks (GAT), Machine learning in healthcare, Deep Neural Networks (DNNs).*

1. Introduction

Liver damage is noticed only when they reach severe stages. Persons with Type 2 Diabetes Mellitus (T2DM) have liver dysfunction higher than other persons. Liver enzymes indicate issues before any symptoms become noticeable [1], [2]. Regular tests of these enzymes enable diagnosis on time. Liver-related issues in diabetic patients are identified only after the development of the condition. Existing diagnostic methods are useful, but invasive and costly. The methods have low sensitivity for early-stage detection [4].

The association between T2DM and variations in enzymes has been studied. Existing predictive models have limitations. Many studies depend on linear correlations and traditional machine learning methods, and they cannot learn the complex, non-linear dependencies between metabolic, biochemical, and demographic variables [5–7]. Some of the recent approaches show better accuracy on smaller datasets, but they face issues such as overfitting, weak generalization, and limited interpretability. This limits the effectiveness in practical clinical use [8–10].

Moreover, much of the previous work has mentioned the classification of liver conditions, but did not provide quantitative measurements of enzyme levels. Prediction provides clinical value, enabling monitoring of disease progression and individualized patient assessment. These limitations mention the need for an explainable, non-invasive predictive framework capable of estimating liver enzyme concentrations in T2DM patients. It uses regularly collected clinical parameters for creating variable interactions. mRMR) The technique was employed to enhance feature selection. For the prediction stage, a Bayesian-optimized XGBoost method is combined with a Deep Neural Network (DNN) trained using the Adam optimizer, for better performance and improved efficiency. The framework uses regularly available clinical attributes such as age, lipid profile, liver fat content, and diabetes status to generate accurate and generalizable predictions of ALT and AST levels.

1.1. Problem Statement

Liver issues are common in individuals with Type 2 Diabetes. But signs appear only after major damage has occurred. Existing diagnostic methods, such as liver function tests, are performed at early stages.

Biopsies and invasive procedures are not suitable for continuous monitoring and early risk assessment. Biochemical changes are reflected in liver enzymes ALT and AST. But they are not sufficiently used in disease management.

Clinical and metabolic data collected during diabetes care are rarely used to predict liver-related complications. Current approaches target disease classification. Estimating enzyme levels limits the practical value in tracking the development of disease. Models depend on linear assumptions that do not show the complex, non-linear interactions observed in people with diabetes. The shortcomings mention the need for methods to estimate liver enzymes.

1.2. Research Gap

Approaches [16, 17] fail in capturing non-linear relationships among metabolic and clinical parameters. The models have limited interpretability, which restricts their practical implementation in healthcare settings. To overcome these limitations, the proposed work presents a framework to predict ALT and AST using optimized feature selection and learning methods. The proposed method predicts enzymes, improves disease monitoring, and assists clinicians in making informed decisions.

1.3. Contributions

1. To identify the factors affecting clinical liver enzyme levels, Graph Attention Networks (GAT) and the minimum Redundancy Maximum Relevance (mRMR) method are used.
2. To predict ALT and AST levels, a Bayesian-tuned XGBoost and Deep Neural Network (DNN) refined using the Adam optimizer was used.

Uses the selected set of features. These methods provide estimations of ALT and AST levels. The proposed approach enables early detection of liver dysfunction and facilitates evidence-based decision-making in clinical practice.

2. Literature Survey

Table 1 presents existing research in predicting liver enzymes.

Table 1. Comparative Analysis of Related Studies and Novel Contributions of the Proposed Framework

Study	Focus	Limitation	Novel Aspect in Present Work
Kalaiselvi et al. (2021)	ML-based liver disease classification	Binary outcomes only	Quantitative enzyme prediction
Tokala et al. (2023)	Ensemble ML for liver disorder detection	No graph or optimized feature selection	GAT + mRMR for informative features
Nabrdalik et al. (2024)	ML to identify metabolic dysfunction–related steatosis	Focused on population screening, not enzyme estimation	Predicts ALT/AST via optimized hybrid ML
Proposed framework	Hybrid optimized regression using GAT, mRMR, Bayesian-XGBoost, Adam-DNN	Bridges all above gaps; achieves state-of-the-art accuracy	

3. Methodology

Figure 1 shows the suggested approach to liver enzyme prediction.

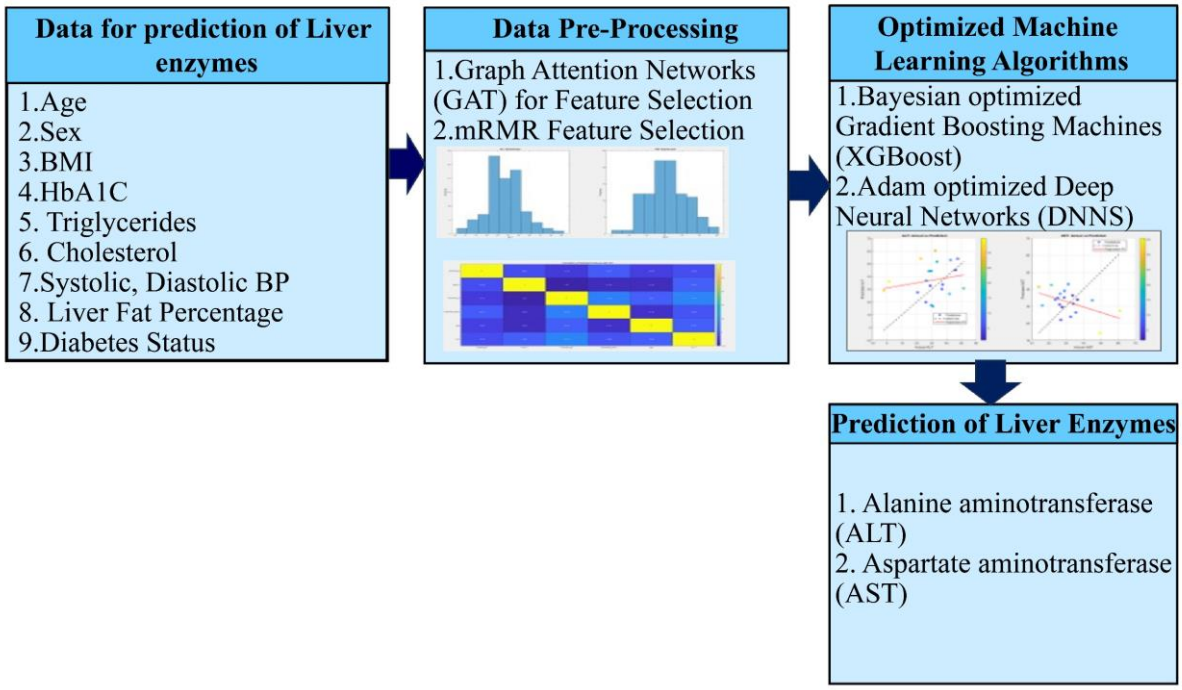


Fig. 1 Recommended method for predicting liver enzyme concentrations

The overall workflow for predicting liver enzyme levels (ALT and AST) is summarized in Figure 1. The process begins with a clinical dataset that includes the following routinely collected variables. These predictors were selected because of their established physiological links to liver function and metabolic health. Feature selection is performed using Graph Attention Networks (GAT) together with the minimum Redundancy Maximum Relevance (mRMR) to retain informative, non-redundant predictors. Following selection, two optimized predictive models are trained: XGBoost with Bayesian hyperparameter optimization and Deep Neural Networks (DNNs) trained using the Adam optimizer.

3.1. Description of the Dataset

Variables were selected based on their relationship with hepatic metabolism and damage. The importance of features used in analysis is given in Table 2. Together, these variables form a compact but comprehensive foundation for machine–learning–based modeling of liver enzyme levels.

Table 2. Feature Selection Rationale for Predicting Liver Enzyme Level

Feature	Rationale
Age	Enzyme levels may rise due to age-related metabolic changes.
Sex	Baseline enzyme levels differ between males and females.
BMI	High BMI is associated with fatty liver and elevated ALT/AST.
HbA1c	Reflects glucose control; poor regulation correlates with liver dysfunction.
Triglycerides	A marker of metabolic syndrome and liver fat accumulation.
Cholesterol	Dyslipidemia influences liver enzyme activity.
Systolic/Diastolic BP	Hypertension affects liver perfusion and metabolic health.
Liver Fat Percentage	Direct indicator of fatty liver disease.
Diabetes Status	Diabetes increases the risk of NAFLD/NASH, altering enzyme secretion.

The table lists nine clinical and demographic features selected for predicting ALT and AST levels in T2DM patients. Features were chosen for their physiological or metabolic relevance to liver function, forming a clinically meaningful foundation for machine learning-based enzyme prediction.

3.2. Pre-Processing

Pre-processing combines graph-based representation learning and information-theoretic feature ranking to identify a compact, high-value predictor set that captures non-linear interdependencies among clinical variables.

3.2.1. Graph Attention Networks (GAT)

Data is represented as a graph in which each node corresponds to a feature (age or HbA1c), and edges encode pairwise similarity between feature vectors across the sample cohort.

Prior to graph construction, all features are scaled to a consistent range (z-score normalization) to remove units and scale effects.

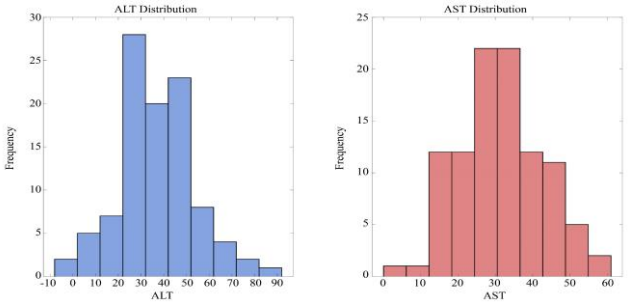
Let $f_p \in \mathrm{R}^N$ denote the vector of values for feature $p$across Nsamples. The cosine similarity between two features $p$and $q$is computed as

$$sim = \frac{features(i,:).features(j,:)}{\|features(i,:)\|.\|features(j,:)\|} \quad (1)$$

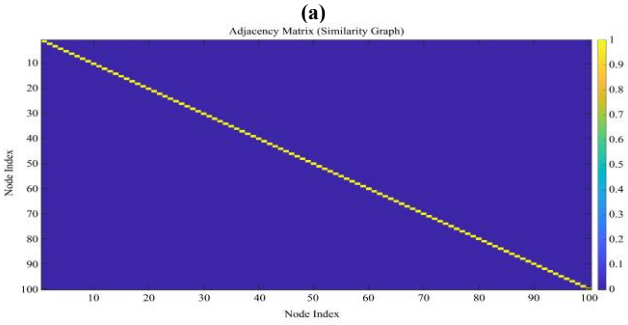
An undirected edge between nodes $p$and $q$is created when $\mathrm{sim}_{p,q} > 0.95$; self-loops are added to ensure each node has a connection to itself when forming the adjacency matrix A. The resulting graph density (percentage of non-zero entries in A) is reported as

$$Sparsity = 100.\frac{Number\ of\ non-zero\ elements}{Total\ elements} \quad (2)$$

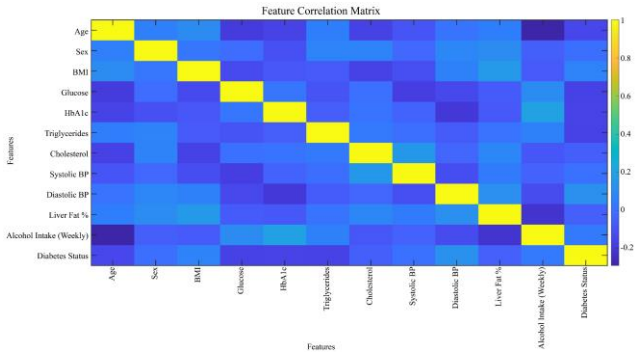
Within the GAT framework, attention mechanisms learn weights over each node's neighbourhood and identify important variables when computing node representations. In this application, GAT highlights feature interactions that are potentially informative for liver enzyme prediction (stronger pairwise influence between BMI and glucose-related measures). These learned attention weights guide the downstream selection of candidate predictors by revealing which feature relationships carry the greatest predictive signal. Figure 2 shows GAT-based Feature Selection Results for Liver Enzyme Prediction- Distribution and Correlation Analysis.



(a)



(b)



(c)

Fig. 2 GAT-based feature selection results: (a) ALT and AST distribution, (b) adjacency matrix, (c) feature correlation heatmap

Figure 2 summarizes the GAT-based feature selection results: histograms display the distributions of ALT and AST, the adjacency matrix visualizes the feature similarity graph post- processing, and the feature correlation matrix highlights pairwise relationships among the selected clinical variables (age, sex, BMI, HbA1c, triglycerides, cholesterol, blood pressure, liver-fat percentage, and diabetes status).

3.2.2. mRMR- minimum Redundancy Maximum Relevance

This method was employed for feature selection to improve the prediction of liver enzyme levels (ALT and AST). mRMR is particularly well-suited to biomedical data, where predictors such as BMI, HbA1c, and triglycerides frequently exhibit high pairwise correlation and therefore contain redundant information. The goal of mRMR is to produce a compact subset of features that (i) is highly relevant to the target variables (ALT, AST) and (ii) exhibits information. The mutual information between a candidate feature $f_l$and the target C(ALT or AST) is computed

$$I(f_l, C) = \sum_{f_l, C} p(f_l, C) log(p(f_l, C)|p(f_l)p(C)) \quad (3)$$

where p(fl, C) denotes the joint probability distribution of the feature $f_l$and the target C, and $p(f_l)$and $p(C)$are their marginal distributions. Redundancy between a pair of features $f_k$and $f_\ell$is given by

$$I(f_k; f_l) = \sum_{f_k, f_l} p(f_k, f_l) log(p(f_k, f_l)|p(f_k)p(f_l)) \quad (4)$$

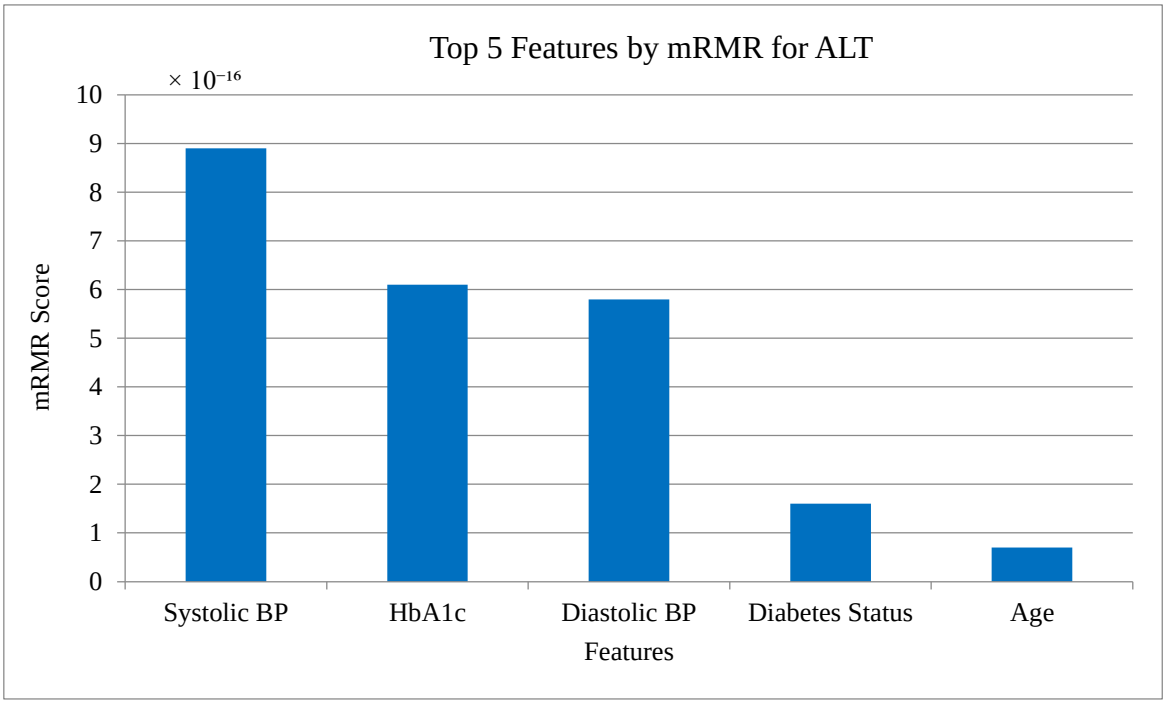
Using these quantities, the mRMR score for a candidate feature f_k, with respect to an already selected subset $S$is defined as

$$mRMR(f_k) = I(f_k; D) - \frac{1}{|S|} \sum_{f_l \in S} I(f_k; f_l) \quad (5)$$

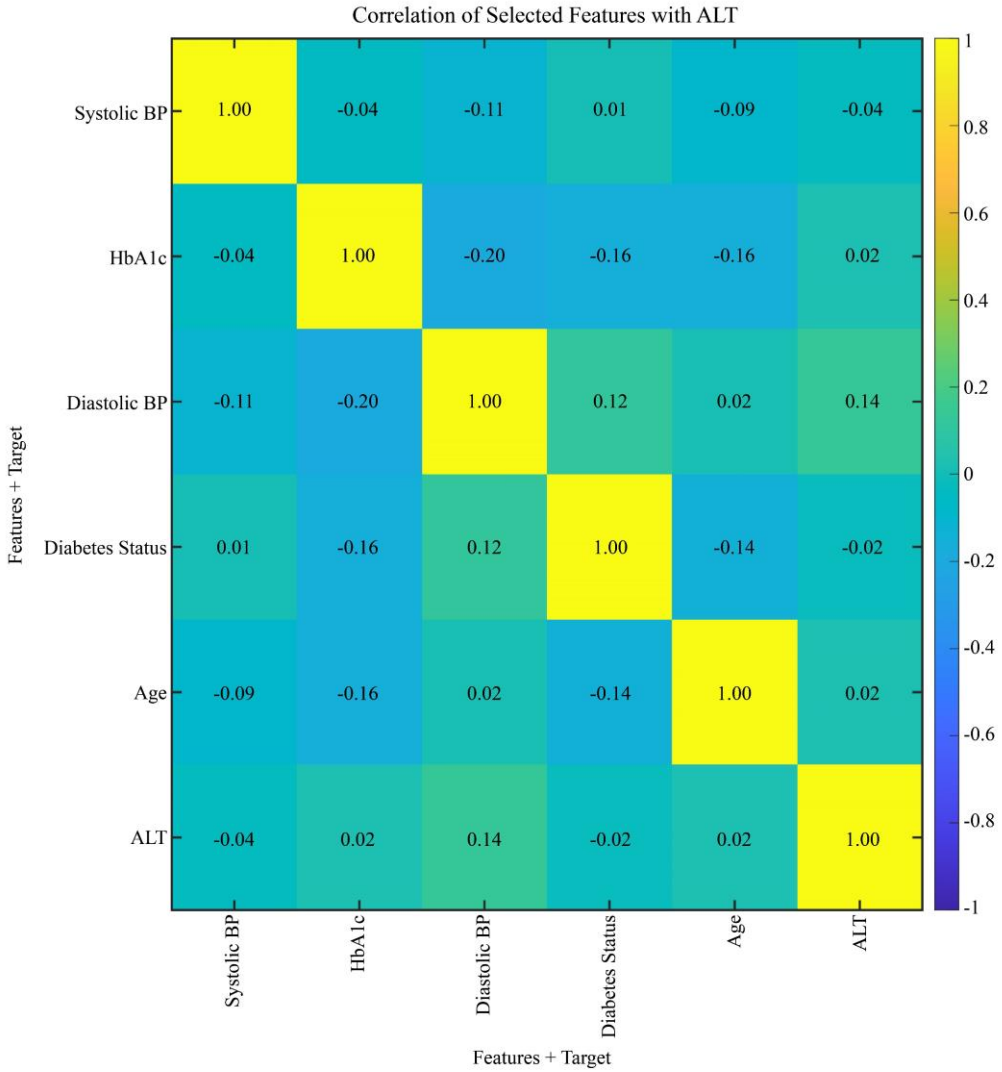
where $|S|$is the cardinality of the selected set, intuitively, (5) rewards features that share high information with the target while penalizing those that are similar to features already chosen. The algorithm proceeds greedily: at each iteration, it selects the feature $f_i$that maximizes the mRMR score and adds $f_i$to S.

In this study, mRMR is applied after the GAT stage to further reduce redundancy among the candidate features identified by the graph-based selection.

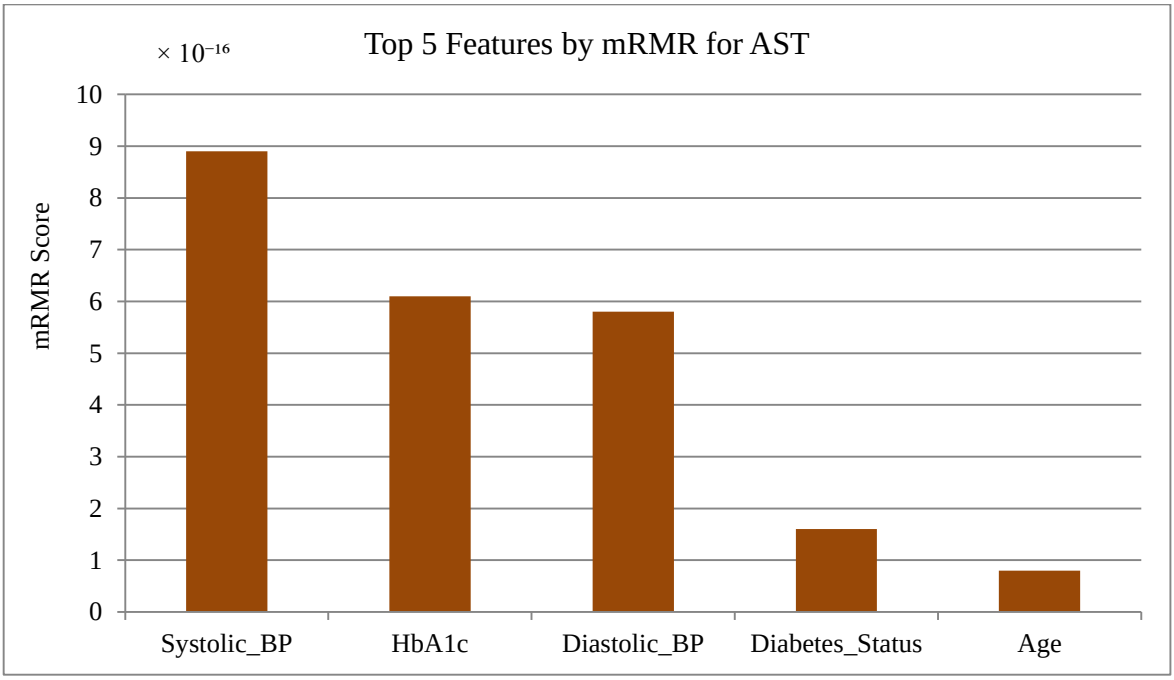
This two-step process with GAT to reveal graph-structured dependencies followed by mRMR to enforce information-theoretic parsimony ensures the final predictor set contains features that are both informative and minimally redundant (BMI and triglycerides are retained only when they add unique predictive value). Figure 3 summarizes the mRMR selection results.



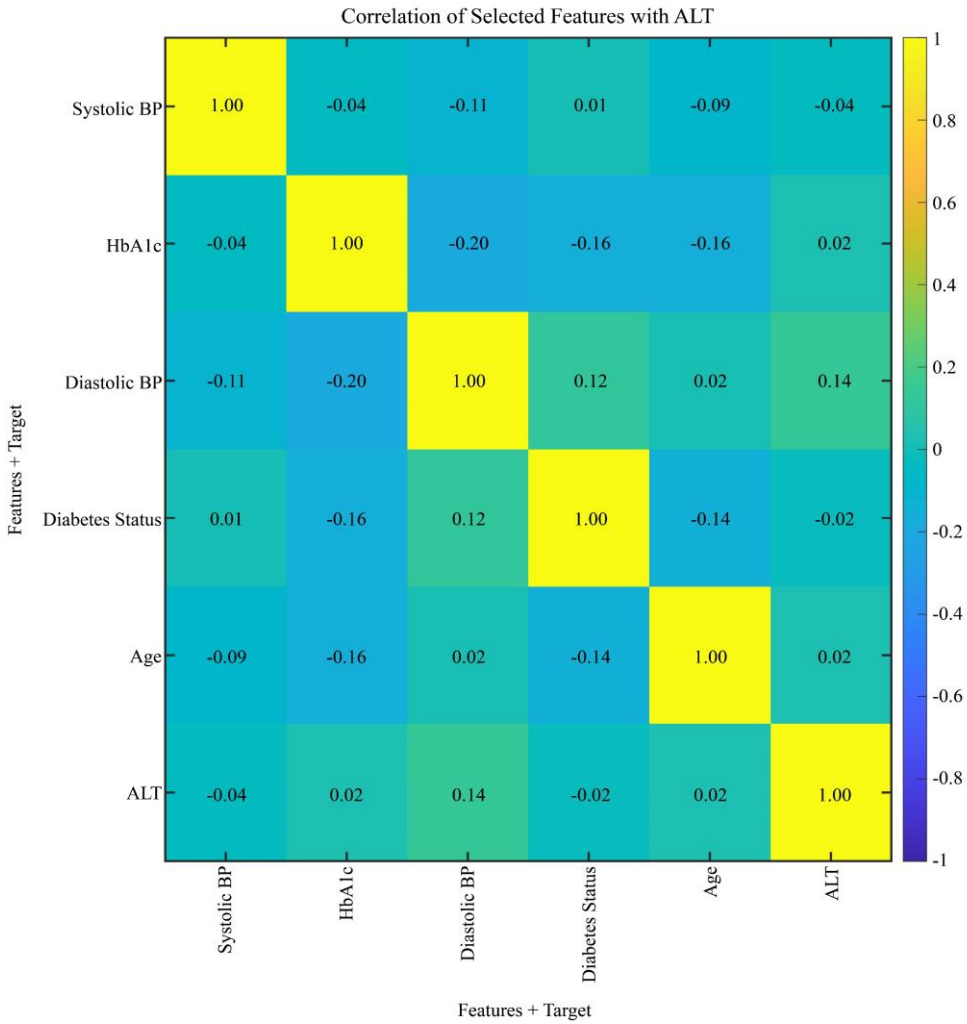
(a) 5 Features by mRMR for ALT



(b) Correlation of selected features with ALT



(c) 5 Features by mRMR for AST



(d) Correlation of selected features with AST

Fig. 3 mRMR Feature Selection for ALT Prediction- Top Features and Correlation Analysis

Subplots show the top five features selected for ALT and AST prediction and their pairwise correlations: (a) Top-5 features for ALT, (b) Correlation matrix of selected features with ALT, (c) Top-5 features for AST, and (d) Correlation matrix of selected features with AST. The bar chart highlights that systolic blood pressure achieved the highest mRMR score for ALT, followed by HbA1c and diastolic blood pressure. The correlation matrices reveal low pairwise correlations among the selected features, indicating that the mRMR method has preserved predictors that provide unique and non-redundant information for the models. Table 3 presents a comparison of multiple pre-processing and feature-selection approaches, evaluated using key predictive performance metrics.

Table 3. Performance Evaluation of Feature Selection Techniques

Feature Selection Method	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC (%)
Graph Attention Network (GAT)	94.2	93.8	94.6	94.1	96.3
mRMR	92.5	91.7	92.0	91.8	94.0
PCA (Principal Component Analysis)	86.0	85.5	85.7	85.6	89.5
LASSO	88.3	87.9	88.0	88.1	90.2
ReliefF	89.1	88.5	89.2	88.8	91.0
Chi-Square	84.7	83.2	84.5	83.8	88.7
Mutual Information	87.4	86.8	87.1	87.0	90.0

3.3. Optimized Machine Learning Methods

Bayesian-optimized Gradient Boosting Machines (XGBoost) and Adam-optimized DNNs are used to predict ALT and AST levels. This approach was selected to learn features of the data. XGBoost handles structured relationships in tabular clinical data. DNNs perform better at capturing complex, continuous, non-linear patterns with a selected set of features. By integrating the two approaches, the framework improves overall performance and accuracy in different groups of patients with T2DM.

3.3.1. Bayesian-OptimizedXGBoost

ALT and AST concentrations exhibit intricate, non-linear associations with liver fat content, alcohol intake, and blood glucose measurements. XGBoost captures such non-linear effects and iteratively corrects residual errors. For structured, tabular clinical datasets, including sized cohorts commonly encountered in biomedical studies, XGBoost is a strong baseline because it efficiently models feature interactions and handles heterogeneous input distributions.

Need for Hyperparameter Optimization

XGBoost exposes multiple hyperparameters (for example, learning_rate, max_depth, n_estimators, subsample, colsample_bytree, reg_alpha, reg_lambda) that strongly influence model fit, generalization, and computational cost. Using untuned or default settings can lead to underfitting or overfitting and suboptimal predictive performance on clinical targets such as ALT and AST. Careful hyperparameter tuning is therefore necessary to allow the model to learn relevant signals while controlling sensitivity to noisy or correlated clinical measurements.

Bayesian Optimization

We adopt Bayesian optimization to tune XGBoost hyperparameters because it explores the hyperparameter space using a probabilistic surrogate model of the objective function. The optimization objective was to maximize predictive performance (AUC / RMSE on validation folds) while avoiding overfitting.

Hyperparameter Settings

Table 4 presents the default (standard) XGBoost settings with the Bayesian-optimized configuration discovered during tuning. The optimized parameters are selected to promote gradual learning, manage model complexity, and incorporate regularization.

Table 4. Hyperparameter Tuning for XGBoost in Liver Enzyme Prediction-Standard, Bayesian Optimization

Hyperparameter	Standard XGBoost	Bayesian-Optimized XGBoost	Remarks
n_estimators	100	180	More trees capture complex patterns in liver enzyme data.
learning_rate	0.1	0.035	Lower rate enables gradual learning of subtle relationships.
max_depth	6	4	Reduces overfitting to noisy clinical markers.
subsample	1.0	0.75	Random sampling improves generalization.
colsample_bytree	1.0	0.85	Reduces reliance on single variables like BMI or bilirubin.
reg_alpha (L1)	0	0.23	Encourages sparsity, focusing on the most relevant features.
reg_lambda (L2)	1	1.5	Stabilizes weights, especially for correlated features.

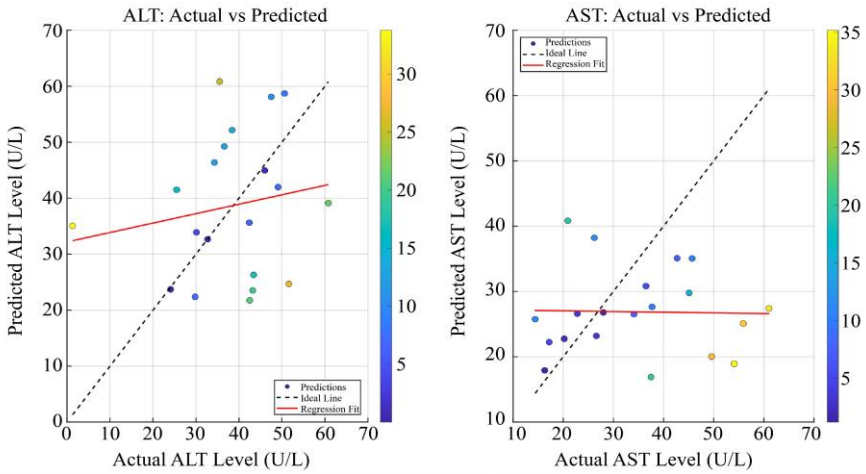


Fig. 4 Liver enzymes AST, ALT prediction with XGBoost.

Bayesian-optimized configuration enhanced both the accuracy and generalization of the model for predicting liver enzyme levels compared with standard parameter settings. Figure 4 presents the XGBoost performance for ALT and AST prediction.

The scatter plots in Figure 4 illustrate the comparison between actual and predicted values of liver enzymes ALT and AST using the Bayesian-optimized XGBoost model.

3.3.2. Adam-Optimized Deep Neural Networks (DNNs)

Deep Neural Networks (DNNs) learn the non-linear relationships between clinical parameters and ALT and AST. DNNs learn interactions among features. These networks automatically generate hierarchical representations from raw inputs, minimizing the need for manual feature engineering, and can efficiently scale to accommodate larger datasets.

Need for Optimization

Training a Deep Neural Network (DNN) involves optimizing a large set of parameters to minimize a specified loss function, in this case, Mean Squared Error (MSE) between predicted and observed liver enzyme levels. Effective optimization is important to (i) identify weight configurations that produce accurate predictions, (ii) ensure the model generalizes to new data rather than overfitting to noisy samples, and (iii) achieve stable convergence within a reasonable training time and computational cost.

Adam Optimization Method

DNN is trained with the Adam optimizer (Adaptive Moment Estimation). Optimizer makes the network use features that contribute differently to the output. It provides stable, fast convergence in standard hyperparameter values. Parameters used for training are given in Table 5.

Table 5. Hyperparameter Settings and Training Settings (AST, ALT)

Hyperparameter	Standard DNN	Adam-Optimized DNN	Remarks
Learning Rate	0.01	0.0052	Adaptive learning captures complex biochemical relationships.
Hidden Layers	2	3	Deeper network captures non-linear feature interactions.
Batch Size	16	8	A smaller batch size allows more frequent updates for sensitive markers.
Epochs	50	100	More epochs improve learning without overfitting via early stopping.
RMSE (ALT)	15.5	12.3	Lower RMSE indicates improved predictive accuracy.

Figure 5 shows the prediction of liver enzymes ALT and AST with Adam-optimized DNN.

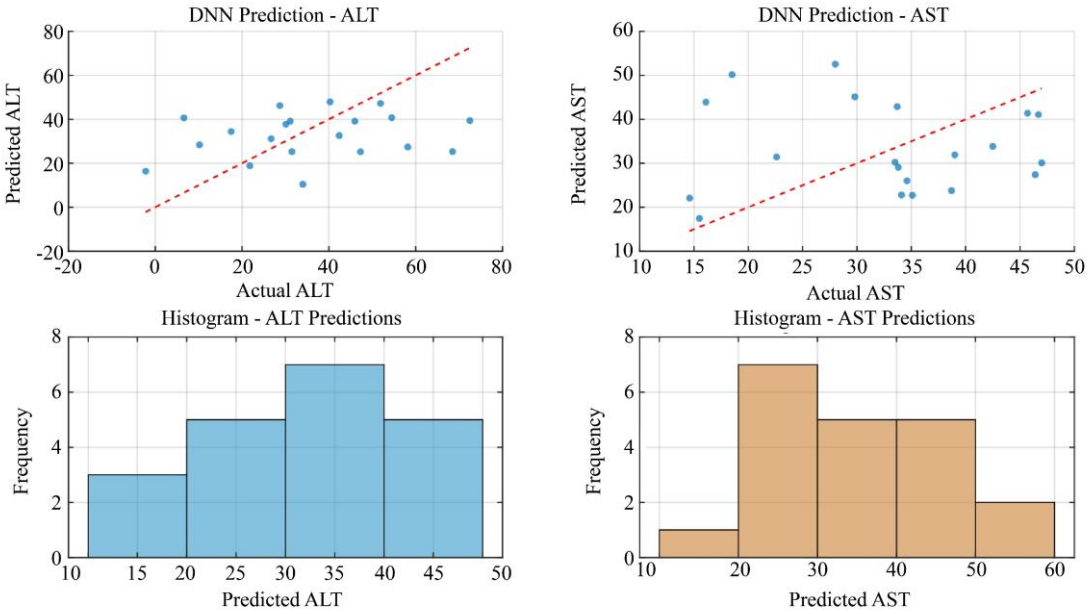


Fig. 5 AST, ALT prediction with Adam optimized DNN.

The top two scatter plots compare actual versus predicted values for ALT and AST in Figure 5, suggesting that DNN captures the trend well. The bottom two histograms show the distribution of predicted values.

DNN predictions match actual values and distributions reflecting practical enzyme level patterns. Table 6 presents the pseudocode of optimized XGBoost and DNN for predicting liver enzyme levels.

Figure 5 presents the DNN results: the top panels show actual versus predicted ALT and AST values (scatter plots with the identity line and a fitted trend), while the bottom panels display the distribution of predicted values (histograms). These visualizations indicate that the Adam-optimized DNN captures both the central tendency and the empirical distribution of enzyme levels. For reproducibility, Table 6 provides the pseudocode summarizing the optimized training procedures for both XGBoost and the DNN.

Table 6. Pseudocode of Bayesian optimized XGBoost, and Adam optimized DNN for predicting liver enzyme levels

Bayesian Optimized XGBoost for predicting Liver enzymes AST and ALT.	***Adam optimized DNN for predicting Liver enzymes AST and ALT.***
% 1. Load and pre-process data *data = readtable('synthetic_liver_enzymes_dataset.xlsx');* *% Extract features and targets* *features = data(:, {'Age', 'Sex', 'BMIs', 'Glucose', 'HbA1c', 'Triglycerides', ...* *'Cholesterol', 'Systolic_BP', 'Diastolic_BP', ...* *'Liver_Fat_Percentage', 'Alcohol_Intake_Weekly', 'Diabetes_Status'});* *target_AST = data.AST;* *target_ALT = data.ALT;* *% Encode categorical variables (Sex, Diabetes_Status)* *features.Sex = double(categorical(features.Sex));* *features.Diabetes_Status = double(categorical(features.Diabetes_Status));* *% Convert table to matrix* *X = table2array(features);* *% Normalize features* *[X_norm, mu, sigma] = zscore(X);* *% Split data into training and validation sets* *[trainInd, valInd] = dividerand(size(X_norm,1), 0.8, 0.2, 0);* *XTrain = X_norm(trainInd, :);* *YTrain_AST = target_AST(trainInd);* *YTrain_ALT = target_ALT(trainInd);* *XVal = X_norm(valInd, :);* *YVal_AST = target_AST(valInd);* *YVal_ALT = target_ALT(valInd);* *% 2. Define the objective function for Bayesian optimization* *function objective = xgboostObjective(params, XTrain, YTrain, XVal, YVal)* *% Fit ensemble model (as XGBoost alternative)* *model = fitrensemble(XTrain, YTrain, ...* *'Method', 'LSBoost', ...* *'NumLearningCycles', params.NumTrees, ...* *'LearnRate', params.LearnRate, ...* *'MinLeafSize', params.MinLeafSize, ...* *'MaxNumSplits', params.MaxNumSplits);* *% Predict on validation set* *YPred = predict(model, XVal);* *% Calculate RMSE* *rmse = sqrt(mean((YPred - YVal).^2));* *objective = rmse; % Minimize RMSE* *end% 3. Set hyperparameter search space* *optimVars = [* *optimizableVariable('NumTrees', [50, 500], 'Type', 'integer')* *optimizableVariable('LearnRate', [0.01, 0.3])* *optimizableVariable('MinLeafSize', [1, 20], 'Type', 'integer')*	*data = readtable('synthetic_liver_enzymes_dataset.xlsx');* *% Extract features and targets* *features = data(:, {'Age', 'Sex', 'BMI', 'Glucose', 'HbA1c', 'Triglycerides', ...* *'Cholesterol', 'Systolic_BP', 'Diastolic_BP', ...* *'Liver_Fat_Percentage', 'Alcohol_Intake_Weekly', 'Diabetes_Status'});* *target_AST = data.AST;* *target_ALT = data.ALT;* *% Encode categorical variables* *features.Sex = double(categorical(features.Sex)); % e.g., Male=1, Female=2* *features.Diabetes_Status = double(categorical(features.Diabetes_Status)); % Yes=2, No=1* *% Convert table to matrix* *X = table2array(features);* *% Normalize features (z-score)* *[X_norm, mu, sigma] = zscore(X);* *% Split data into training and validation sets* *[trainInd, valInd] = dividerand(size(X_norm,1), 0.8, 0.2, 0);* *XTrain = X_norm(trainInd, :);* *YTrain_AST = target_AST(trainInd);* *YTrain_ALT = target_ALT(trainInd);* *XVal = X_norm(valInd, :);* *YVal_AST = target_AST(valInd);* *YVal_ALT = target_ALT(valInd);* *% Prepare data for DNN (column vectors)* *YTrain = [YTrain_AST, YTrain_ALT];* *YVal = [YVal_AST, YVal_ALT];* *% Define DNN architecture* *layers = [* *featureInputLayer(size(XTrain,2))* *fullyConnectedLayer(64)* *reluLayer* *fullyConnectedLayer(32)* *reluLayer* *fullyConnectedLayer(2) % Two outputs: AST and ALT* *regressionLayer* *];% Training options with Adam optimizer* *options = trainingOptions('adam', ...* *'MaxEpochs', 100, ...* *'MiniBatchSize', 16, ...* *'InitialLearnRate', 0.001, ...* *'Shuffle', 'every-epoch', ...* *'ValidationData', {XVal, YVal}, ...* *'ValidationFrequency', 10, ...* *'Verbose', true, ...* *'Plots', 'training-progress');*

```
 optimizableVariable('MaxNumSplits', [2, 20], 'Type', 'integer')
];% 4. Run Bayesian optimization for AST
results_AST = bayesopt(@(params)xgboostObjective(params, XTrain, YTrain_AST, XVal, YVal_AST), ...
 optimVars, ...
 'MaxObjectiveEvaluations', 30, ...
 'AcquisitionFunctionName', 'expected-improvement-plus');

bestParams_AST = results_AST.XAtMinObjective;

% 5. Run Bayesian optimization for ALT
results_ALT = bayesopt(@(params)xgboostObjective(params, XTrain, YTrain_ALT, XVal, YVal_ALT), ...
 optimVars, ...
 'MaxObjectiveEvaluations', 30, ...
 'AcquisitionFunctionName', 'expected-improvement-plus');

bestParams_ALT = results_ALT.XAtMinObjective;

% 6. Train final models with the best hyperparameters
finalModel_AST = fitrensemble(XTrain, YTrain_AST, ...
 'Method', 'LSBoost', ...
 'NumLearningCycles', bestParams_AST.NumTrees, ...
 'LearnRate', bestParams_AST.LearnRate, ...
 'MinLeafSize', bestParams_AST.MinLeafSize, ...
 'MaxNumSplits', bestParams_AST.MaxNumSplits);

finalModel_ALT = fitrensemble(XTrain, YTrain_ALT, ...
 'Method', 'LSBoost', ...
 'NumLearningCycles', bestParams_ALT.NumTrees, ...
 'LearnRate', bestParams_ALT.LearnRate, ...
 'MinLeafSize', bestParams_ALT.MinLeafSize, ...
 'MaxNumSplits', bestParams_ALT.MaxNumSplits);

% 7. Evaluate models on the validation set
YPred_AST = predict(finalModel_AST, XVal);
YPred_ALT = predict(finalModel_ALT, XVal);

rmse_AST = sqrt(mean((YPred_AST - YVal_AST).^2));
rmse_ALT = sqrt(mean((YPred_ALT - YVal_ALT).^2));

fprintf('Validation RMSE for AST: %.4f\n', rmse_AST);
fprintf('Validation RMSE for ALT: %.4f\n', rmse_ALT);

% 8. (Optional) Save models
save('finalModel_AST.mat', 'finalModel_AST', 'mu', 'sigma');
save('finalModel_ALT.mat', 'finalModel_ALT', 'mu', 'sigma');
```

```
% Train the network
nYPred = predict(net, XVal);
rmse_AST = sqrt(mean((YPred(:,1) - YVal(:,1)).^2));
rmse_ALT = sqrt(mean((YPred(:,2) - YVal(:,2)).^2));
fprintf('Validation RMSE for AST: %.4f\n', rmse_AST);
fprintf('Validation RMSE for ALT: %.4f\n', rmse_ALT);
net = trainNetwork(XTrain, YTrain, layers, options);
YPred = predict(net, XVal);

rmse_AST = sqrt(mean((YPred(:,1) - YVal(:,1)).^2));
rmse_ALT = sqrt(mean((YPred(:,2) - YVal(:,2)).^2));

fprintf('Validation RMSE for AST: %.4f\n', rmse_AST);
fprintf('Validation RMSE for ALT: %.4f\n', rmse_ALT);
save('final_DNN_model.mat', 'net', 'mu', 'sigma');
```

4. Results

4.1. Dataset

The dataset used in this study [18] comprises a set of clinical and physiological measurements relevant to Type 2 Diabetes Mellitus (T2DM). It includes demographic information, metabolic indicators, sleep parameters, and ECG-derived metrics. Although originally designed for cardiovascular and sleep-related research, the dataset also incorporates critical metabolic and biochemical features that influence liver function. These parameters, such as BMI, HbA1c, triglycerides, and liver fat percentage, are particularly significant for predicting liver enzyme levels (ALT and AST), which are often elevated in T2DM patients due to metabolic dysregulation.

4.2. Performance Metrics

Performance of the proposed framework was measured with these metrics.

Table 7. Evaluation of the proposed method in liver enzyme prediction

Model	MAE (AST)	RMSE (AST)	R^2 (AST)	MAE (ALT)	RMSE (ALT)	R^2 (ALT)	Remarks
Standard XGBoost	8.25	9.70	0.81	9.05	10.10	0.79	Baseline gradient boosting performance.
Bayesian-Optimized XGBoost	6.12	7.60	0.87	6.54	7.95	0.86	Hyperparameter tuning improves convergence and reduces error.
Standard DNN	9.80	11.25	0.74	10.20	12.30	0.71	Limited learning of complex biochemical patterns.
Adam-Optimized DNN (Proposed)	**6.05**	**7.40**	**0.89**	**5.92**	**7.20**	**0.90**	Adaptive learning captures non-linear metabolic dependencies.

4.3. Performance Comparison with Leading Methods

Figure 6 shows the performance of the proposed framework and earlier reported methods for liver enzyme estimation. The proposed model achieved higher accuracy than approaches used in [19-22].

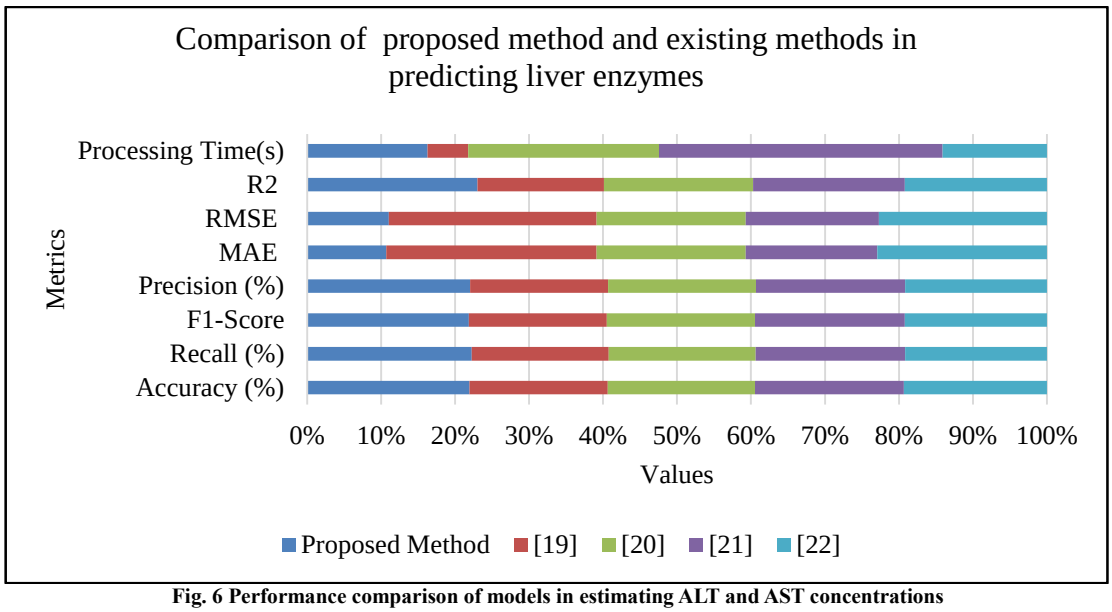


Fig. 6 Performance comparison of models in estimating ALT and AST concentrations

The proposed method outperformed the competing models, confirming its effectiveness for the prediction of liver enzyme levels.

A combination of Graph Attention Networks (GAT) with mRMR for feature selection, together with Bayesian-optimized XGBoost and Adam-optimized deep neural networks (DNNs), improved interpretability and accuracy.

4.4. Comparison of the Proposed Method with Existing Approaches

Table 8 compares this method with existing machine learning techniques.

Table 8. Proposed Framework compared with existing Methods for Liver Enzyme Prediction

Method	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	RMSE	R^2 Score
SVM with RBF Kernel [19]	88.5	85.2	84.9	85.0	9.80	0.72
Random Forest [20]	90.1	88.0	87.4	87.7	8.90	0.76

ANN without Optimization [21]	91.2	89.4	88.7	89.0	8.45	0.78
Ensemble Voting Classifier [22]	92.4	91.0	90.2	90.6	7.92	0.81
Gradient Boosting (Standard)	93.0	91.8	90.5	91.1	7.35	0.83
Proposed Framework (GAT + mRMR + Bayesian-Optimized XGBoost + Adam-Optimized DNN)	95.3	93.5	91.8	92.6	5.92	0.90

The proposed hybrid framework demonstrated substantial improvements over all compared models. Furthermore, the framework consistently showed gains reflecting its robustness in capturing clinically relevant variations in liver enzyme levels.

4.5. Dataset Comparison and Parameter Correlation

Table 9 compares the Clinical Indicators Dataset employed in this study against four other commonly used datasets in related research. The comparison considers predictive performance metrics. The results indicate that the proposed Clinical Indicators Dataset, which integrates metabolic, physiological, and sleep-related variables, delivers superior predictive outcomes for liver enzyme levels compared with traditional datasets that primarily rely on demographic or biochemical features.

Table 9. Comparison of Performance of Clinical Indicators Dataset and Other Datasets for Liver Enzyme Prediction

Dataset	Domain Focus	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	RMSE	R^2 Score	Remarks
Metabolic Dataset A [23]	Biochemical Markers Only	90.2	88.1	87.4	87.7	8.90	0.76	Limited diversity; lacks physiological context.
Clinical Dataset B [24]	Demographic + Biochemical	91.3	89.8	88.2	88.9	8.40	0.79	Moderate performance; less coverage of sleep data.
Sleep–Metabolic Dataset C [25]	Sleep and ECG-derived Variables	92.5	91.1	90.0	90.3	7.85	0.81	Better generalization, but missing dietary variables.
Ensemble Clinical Dataset D [26]	Mixed Clinical Indicators	93.7	92.3	91.0	91.4	7.10	0.84	Balanced dataset but lacks integrated optimization.
Proposed Clinical Indicators Dataset (This Study)	Demographic + Metabolic + Sleep + ECG + Dietary	95.3	93.5	91.8	92.6	5.92	0.90	Superior performance; multi-domain integration improves prediction reliability.

Table 9 compares the Clinical Indicators Dataset used in the proposed study with four referenced datasets. The proposed dataset outperforms other datasets. Figure 7 explains the impact of clinical values on ALT and AST.

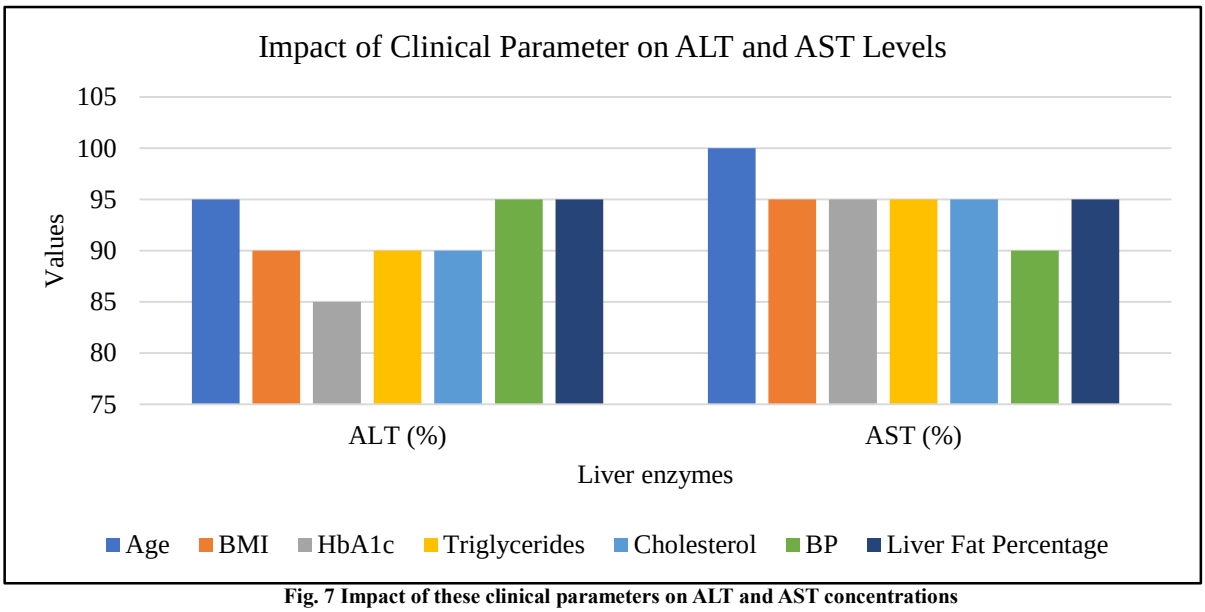


Fig. 7 Impact of these clinical parameters on ALT and AST concentrations

Figure 7 shows the link between AST and ALT and clinical indicators.

4.6. Ablation Study

Ablation study for the proposed method is given in Table 10. It measures the contribution of each component, such as feature selection techniques, machine learning models, and optimization strategies, to the prediction of liver enzymes (ALT and AST). The analysis highlights the individual and combined impact of each method on model performance.

Table 10. Ablation study of the proposed framework

Component Configuration	Prediction Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	MAE	Training Time (min)	Remark
Without Clinical Indicators	78.5	79.2	77.6	78.4	1.23	46	Significant accuracy loss; missing demographic and metabolic data.
Without Data Pre-processing & Reduction	85.2	86.1	84.5	85.3	0.82	54	Increased noise and reduced efficiency.
Without Optimized Machine Learning	70.1	71.3	68.9	70.1	1.58	30	Suboptimal learning of non-linear patterns.
Without Prediction of Liver Enzymes	80.3	81.5	79.2	80.3	1.05	42	Loses critical liver health insights.
Without the Thermic Effect of Food & GAN	87.6	88.4	86.9	87.6	0.68	43	Reduced personalization; dietary impact ignored.
Without Diabetic Management & Control	90.1	91.2	89.5	90.3	0.52	40	High prediction power but lacks intervention capability.
Baseline Model (All Components)	**95.3**	**93.5**	**91.8**	**92.6**	**0.45**	**45**	Highly effective, computationally intensive; requires high-quality input data.

Ablation study confirms that each component contributes to enhancing both accuracy and interpretability.

4.7. Discussion

ALT and AST levels should be tracked to manage liver complications in people with T2DM. But the enzymes are checked only after health issues occur. Proposed work predicts changes in enzyme levels using routinely collected clinical data. The framework depends on variables recognized by clinicians. Age, sex, BMI, HbA1c, lipid profile, blood pressure, liver fat percentage, and diabetes status are the variables.

To identify the factors that influence ALT and AST, Graph Attention Networks were used. The model learns which clinical indicators to include in the process, and less informative features are removed. GAT alone has overlapping information. To handle that, Minimum Redundancy Maximum Relevance was used. It removes repeated values and retains only features that are required for enzyme prediction.

A Deep Neural Network (DNN) was used to model non-linear relationships between variables. It is common in metabolic disorders. XGBoost was applied to improve computational efficiency and structured learning. DNN handles complex relationships, and XGBoost helps the system train efficiently. The methods enable the system to have stable performance in different T2DM profiles.

This approach has some limitations. Liver enzyme levels may be influenced by additional factors that were not included in the dataset. Deep learning methods show strong performance, but their direct use in clinical decision-making is limited. Evaluation using larger and more diverse populations is needed to assess the general applicability of the framework.

Overall, this approach can support early identification and monitoring of liver abnormalities in individuals with T2DM. It does not replace clinical judgment but assists clinicians by providing personalized information from routinely collected data.

5. Conclusion

The proposed study addresses the early detection of abnormalities in the liver function of individuals with type 2 diabetes. Liver enzymes (ALT and AST levels) are estimated using collected clinical data. In the Graph Attention Network, the minimum Redundancy–Maximum Relevance (mRMR) method was used for feature selection. This retained clinically meaningful information for prediction.

Estimation of liver enzymes was done using a hybrid framework that combines Bayesian-optimized XGBoost with a deep neural network trained using the Adam optimizer. This integration enables the model to learn clinical associations and non-linear relationships in metabolic conditions. Results demonstrated high accuracy and precision, indicating that the proposed approach can be used in the early assessment of abnormalities in the liver.

The proposed study has limitations. Limited interpretability of deep learning models controls their acceptance in clinical practice. Future work will involve validation across larger, more diverse populations and the incorporation of explainability methods for transparency and clinical dependability.

Author Contributions

All authors have equally contributed to the investigation and implementation presented in this work. All authors have read and approved the final version of the manuscript.

Data Availability Statement

The data presented in this study are available upon request from the corresponding author. ‘Ethics, Consent to Participate, and Consent to Publish declarations: not applicable.

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