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# A Genetic Algorithm-Optimized Federated Averaging Framework for Adaptive Client Selection in Diabetic Readmission Prediction Across Distributed Hospital Data

**Dr. Abirami Natesan[1], Dr.B.Hemalatha[2], Dr K Sridhar[3], A.Raja [4], CH. Mohan Sai Kumar[5], G·Deepa[6], Dr.N. Angayarkanni[7]**

[1]Assistant Professor, Department of Computer Science, Dr.SNS Rajalakshmi College of Arts and Science Coimbatore , Tamilnadu, Email: abhiphd2017@gmail.com, ORCID ID: 0000-0002-5792-8147

[2]Department of Artificial Intelligence and Data Science KIT-Kalaignarkarunanidhi Institute of Technology Coimbatore - 641 402, Tamil Nadu, India, Email: hemalathab@kitcbe.ac.in, ORCID ID: 0000-0002-2708-1061

[3]Associate Professor, Department of CSE School of Computer Science and Engineering Malla Reddy(MR) Deemed to be University Medchal,Telangana,India, Email: sridhark529reddy@gmail.com, ORCID ID::0009-0007-6850-8731

[4] Assistant professor of Computer Science and Engineering (Cyber Security), United Institute of Technology, Coimbatore,Tamilnadu, India, Email: rajagct@gmail.com

[5]Assistant Professor, Department of Electronics and Communication Engineering Vel Tech Rangarajan Dr. Sagunthala R&D Institute of Science and Technology Avadi, Chennai, Tamilnadu-600062, India. Email: chmohansaikumar@veltech.edu.in,ORCID Id: 0000-0002-2855-9071

[6]Assistant Professor of Information Technology, Dr.M.G.R Educational and Research Institute , Chennai, Email: deep.it@drmgrdu.ac.in

[7]Professor Department of Electronics and Communication Engineering Paavai Engineering College (Autonomous), Namakkal-18, Tamilnadu, India. Email: angaiece18@gmail.com, ORCID ID: 0002-0009-2004-3609

**Abstract**

The unplanned re-hospitalization of adult patients with diabetes mellitus within 30-days is an important clinical and operational performance issue. Models built from centralised dataset can identify patients at risk of readmission within 30 days. Nonetheless, challenges to cooperation between hospitals and the use of shared datasets revolve around privacy, governance, and patient-data-sharing restrictions. This paper proposes a GA-FedAvg framework, which is a Genetic Algorithm-enabled Federated Averaging framework, for predicting unplanned 30-day hospital readmission among adult patients with diabetes mellitus in various hospitals. They share model updates instead of patient-level data. Expert researchers utilized a genetic algorithm in order to enhance federated aggregation and client-selection procedures.Then, they utilized this research in order to tackle cross-hospital heterogeneity as well as non-independently and identically distributed (non-IID) data. The model included routinely available demographics, clinical, hospitalization, laboratory, comorbidity and discharge variables. The area under the receiver operating characteristic curve (AUC-ROC) was used in evaluating the performance of GA-FedAvg and baselines used in centralized and conventional federated learning. In centralized mode, an AUC-ROC of 0.6567 was achieved whereas across federated settings, AUC-ROC values ranging from 0.6514 to 0.6547 were achieved with GA-FedAvg. The proposed method achieves around 99.2-99.7% of the performance of a centralized model, without transferring patient-level data among hospitals. The GA-FedAvg approach could enable collaboration among institutions for privacy-preserving prediction of diabetic patient readmissions, with only a slight drop in discrimative performance compared to centralized training. This technique might help identify diabetic individuals at an early stage who might be at risk. Thus, allowing for targeted discharge planning and enhancing post-discharge care.

**Keywords:** diabetes mellitus, federated learning, GA-FedAvg, genetic algorithm, privacy-preserving machine learning, electronic health records, clinical risk prediction, non-IID data.

## 1. Introduction

Diabetes disease is a common chronic disease that comes with many comorbidities. Adult diabetics who are hospitalized will most likely be readmitted due to a relapse of illness. An unplanned return to the hospital within 30 days of discharge is a relevant measure of adverse patient events and fragmented transitional care. Unplanned hospital admissions put a lot of pressure on the health system. The hospitalization costs of people with diabetes will be more when compared to the patients without diabetes. There are quite a few factors that have been linked to higher risk of 30-day readmission. These are comorbidity burden, health care use history, insulin use, prolonged duration of stay, socio-demographic factors, discharge related factors. In addition, changing one's medication during glycaemic abnormality was also a risk factor. Models for prediction of risk may permit to detect those hospitals pre-discharge which are at high risk for readmission.

Patients can benefit from maximally prioritising medication reconciliation, early outpatient-follow-up and social-support assessment and diabetes-management-team review. The literature indicates that diabetes-specific models for 30-day readmission have AUCs that range from moderate (0.609) to fair (0.821). The AUCs (area under the curve) of both internal and external validations for each model chosen on the basis of cross-validation AUCs on development datasets. The cardiovascular disease (CVD) prediction models study will perform an impact analysis of CVD disease risk models using a standardised data set. This will assess the accuracy and predictive power of simple prediction models. Most readmission prediction models rely on EHR data. Centralized learning from large data sets However, this generally necessitates the pooling or exposure of patient-level records from participating institutions. This is difficult in practice because the electronic health record data focus on sensitive information which is bound by institutional policies, ethical requirements, legal requirements, and data sharing policies.

The patients in hospitals vary not only by location but also by disease severity and clinical practices. They also differ by availability of data, coding rules and readmission rates. This variation allows for the non-IID data that causes instability and the lack of transportability of the model trained in a single hospital. Two or more hospitals can collaboratively build a model to predict clinical outcomes or diagnose diseases using federated learning. All updates are combined to form one globe model on the server. With federated learning, it will be possible to conduct analyses without sharing patients' EHRs beyond the partner site. The performance of classic Federated Averaging or FedAvg gets affected significantly due to non-IID data and unbalanced data volumes among clients as well as varied local model qualities and participation levels. Proposed a GA-FedAvg model for Hospital Readmission of 30-days unplanned adults diabetic patients using Genetic Algorithm.

This model employs federated learning to forecast hospital readmissions without extracting EHR data from site. Federated models ensure the protection of patient privacy across hospitals. Further, a Genetic Algorithm refines the aggregation and client-selection settings of the basic FedAvg to better suit the heterogeneous hospital data. The centralized model achieves an AUROC of 0.6567, while GA-FedAvg AUROC varies between 0.6514 and 0.6547. It shows that we can learn to predict a patient's early risk of diabetes readmission without sharing patient-level records.

## 2. Literature Survey

Thirty-day unplanned readmission among adults with diabetes is a clinically important outcome. Its risk factors and prediction have been examined using conventional statistical methods, and machine-learning models have also been evaluated. Nevertheless, most studies have traditionally used centralized or single-institution datasets, which remains a significant concern. Privacy-preserving, multi-hospital learning and institutional data heterogeneity have not been adequately addressed.

### Risk Factors and Prediction Models

Researchers have systematically reviewed predictive models for unplanned readmission in adults with diabetes within 30 days. Seventeen predicting models were identified through nine studies. The AUC values reported are between 0.609 and 0.821, indicating moderate and inconsistent discrimination. Length of stay, employment, recent discharge, discharge disposition anaemia, haematocrit and hyponatraemia were some of the significant predictors. According to the methodology employed for reviewing models, these models had a high-risk of bias. This surely is a call for better model development, validation, and reporting. However, it does not address the issues of distributed learning, institutional diversity, and patient data privacy across multiple hospitals. Comorbidities and Clinical Severity Influence Risk of Readmission. A randomized trial designed systematic literature review and meta-analysis showed that 30-day unplanned readmission of 30-day unplanned readmission was associated with heart failure, renal disease, and insulin therapy, insurance, length of stay, age,

sex, and race in adults with diabetes. Of the entire dataset heart failure and renal disease had the strongest prediction of 30-day readmission at an odds ratio of 1.81 and 1.69 respectively. The study supports the inclusion of comorbidity, treatment, hospitalization and socio-economic factors in models to predict readmission.

**Machine Learning Services for Early Prediction**

Lau et al. (2026) created and subsequently externally validated models that can predict an early unplanned readmission of the patients admitted with diabetes based on 14 routinely available admission variables. They contrasted the classification tree, group-lasso regression, elastic-net regression and a neural network. The neural network, group lasso and elastic net yielded similar results (AUC 0.722-0.727 in the testing cohort; 0.653-0.667 in the external validation cohort). On the other hand, the classification tree failed to perform well achieving AUC values of 0.663 at testing and 0.595 at external validation. The study also revealed that incorporating model-estimated risk with abnormal glucose data could allow for some patients to avoid returning for a review by the team. This would continue to allow a targeted approach to clinical resources. A model based on Long Short-Term Memory (LSTM) was applied to predict unplanned all-cause 30-day readmission of patients with diabetes. Researchers from the University of the Republic studied closures of 2,836,569 encounters (36,641 patients). The LSTM model produced an accuracy of 0.81 and an area under receiver operating characteristic curve of 0.79. The model had better performance compared to random forest, multilayer perceptron, AdaBoost and logistic regression. The outcome from the LSTM model that used selected laboratory tests was similar to the laboratory results that were all used The results indicate that longitudinal EHR data, and sequential deep learning models have the power to predict various outcomes. Nonetheless, these performances were assessed internally, and the models were trained centrally, which may restrict the applicability of findings across various hospital settings.

**Clinical outcome studies**

Alaseem et al. in 2026 assessed postoperative outcomes in 437 patients who underwent diabetic-foot amputation. Post-operative complications were noted in 52.1% of patients. 50.6%, 23.4%, 28.7% and 17.8% of patients had readmission, re-amputation, ICU admission and mortality respectively. The authors reported pre-operative serum albumin as an independent predictor of post-operative complications. The study did not specifically predict the general hospital readmission within 30 days following surgery, but it drew attention to the importance of laboratory biomarkers, nutritional status, comorbidities, and clinical severity in adverse outcomes in high-risk patients with diabetes. In 2026, you and colleagues evaluated 297 patients with STEMI who had been treated with a drug-coated balloon. Diabetes and poor glycemic control were related to adverse long-term coronary outcomes.Diabetes and poor glycemic control were associated with poor coronary microcirculatory outcomes in the long term. Use of insulin or dapagliflozin was associated with a lower observed incidence of IRA-INOCA . The research was based on 2-year cardiovascular outcomes rather than 30-day readmission, highlighting the significance of glycemic status, medication exposure and cardiovascular risk factors when modelling risk in people with diabetes.

The researchers investigate old and new topics of interest. The sources used are usually the internet, university, journals, books etc. The reviewed studies estimated the risk of diabetes related readmission based on demographic, clinical, laboratory, medication, comorbidity and hospitalization variables.

However, important gaps remain.

- Data fed into many AI models in healthcare are centralized, meaning that patient information must be collected in a single location.
- Model performance in external validation is typically lower than that observed in the original development cohort, mainly due to dataset shift and limited transportability across institutions.
- Few studies have comprehensively examined non-IID data, in which patient characteristics, coding practices, laboratory distributions, and outcome frequencies vary from hospital to hospital.
- Federated learning with genetic algorithm-based client selection and adaptive FedAvg aggregation has not been used in the reviewed studies on diabetic readmissions.
- Privacy-preserving collaboration methods should be evaluated based on their ability to maintain predictive performance without directly sharing patient-level EHR data.

To reduce cross-site heterogeneity and maintain predictive performance close to that of centralized learning, the authors introduced a genetic algorithm-based federated aggregation algorithm called GA-FedAvg. The proposed algorithm enables hospitals to develop a collaborative 30-day readmission prediction model while keeping patients' medical records at their respective hospitals. The centralized model and the GA-FedAvg model were

evaluated. The centralized model achieved an AUC-ROC of 0.6567, while the GA-FedAvg model achieved AUC-ROC values ranging from 0.6514 to 0.6547. Without sharing patient-level data, GA-FedAvg retained 99.2% to 99.7% of the centralized model's discrimination.

## 3. Proposed System Model

We propose the Genetic Algorithm-optimized Federated Averaging system (GA-FedAvg) to predict 30-day unplanned hospital readmission among adults with diabetes using distributed electronic health record (EHR) data. Several hospitals can train a global model together without sending patient-level data to a central repository. Each hospital keeps its own data, trains the model locally and only communicates model parameters or updates to the federated server.

The framework initially includes the following four main components:

1. Hospital clients: Each participating hospital stores and processes its own diabetes inpatient records.
2. The private prediction model will be local, meaning that each client will train an identical binary classifier to estimate the probability of 30-day unplanned readmission.
3. The federated server initializes and distributes the global model, receives selected local updates, and aggregates them to generate an updated global model.
4. The genetic algorithm optimizer searches for effective client-selection and aggregation configurations across heterogeneous hospital data.

FedAvg normally aggregates client updates using weights proportional to each client's data volume. This serves as the standard baseline for the proposed approach.

### 3.1 Problem formulation

Let there be K hospitals, represented as clients:

$$\mathcal{C} = \{1,2,\dots,K\}$$

The local dataset at hospital k is

$$D_k = \{(x_i, y_i)\}_{i=1}^{nk}$$

where:

- $x_i \in \mathbb{R}^d$ is the feature vector for admission i
- $y_i \in \{0,1\}$ is the readmission label
- $y_i = 1$ indicates an unplanned readmission within 30 days
- $y_i = 0$ indicates no 30-day unplanned readmission
- $n_k$ is the number of records at hospital k

The distributed dataset is

$$D = \bigcup_{k=1}^{K} D_k$$

but no hospital transmits $D_k$ to the server.

For a prediction model with parameters w, the local empirical objective at client k is

$$F_k(w) = \frac{1}{n_k} \sum_{i=1}^{n_k} \ell\left(f(x_i; w), y_i\right)$$

where $f(x_i; w)$ is the predicted probability of readmission and $\ell(\cdot)$ is binary cross-entropy loss:

$$\ell(\hat{y}_i, y_i) = -[y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)]$$

The global federated-learning objective is

$$\min_{w} F(w) = \sum_{k=1}^{K} \frac{n_k}{N} F_k(w)$$

where,

$$N = \sum_{k=1}^{K} n_k$$

is the total number of records across all hospitals. This formulation minimizes the data-volume-weighted average of local client losses.

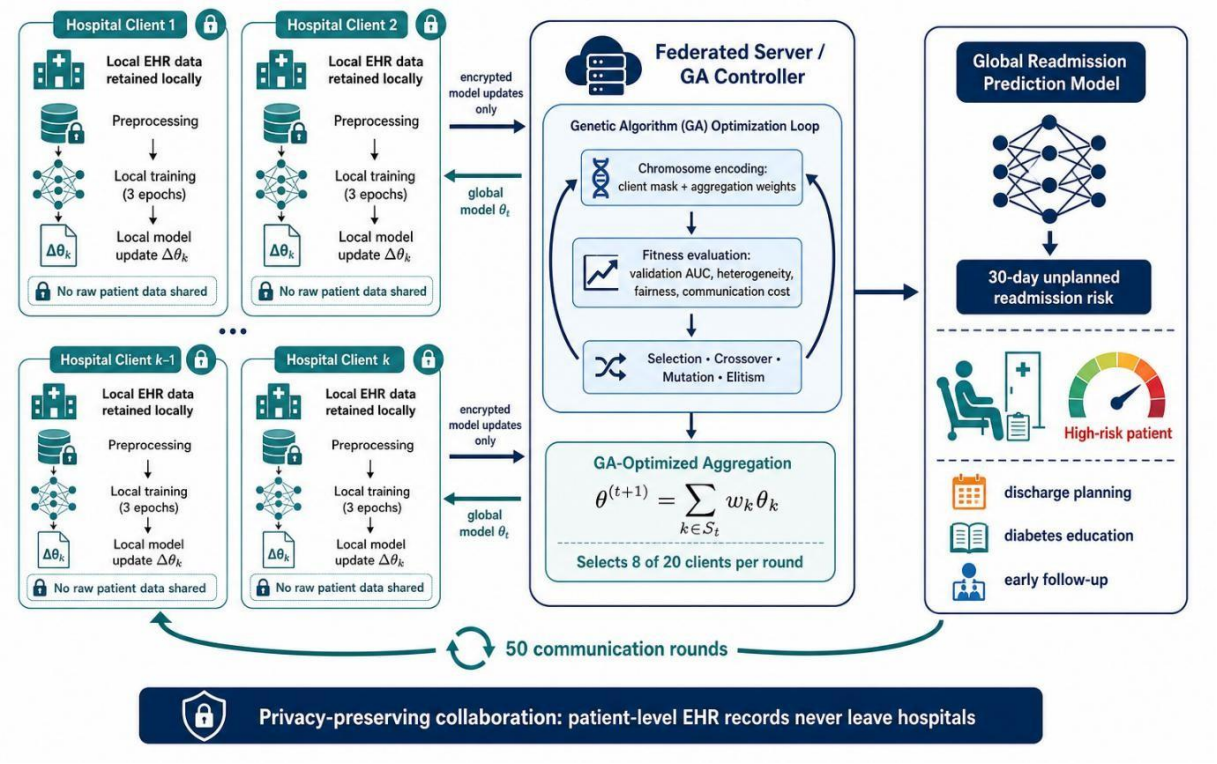



**Figure 1.** Architecture of the GA-FedAvg Framework for Privacy-Preserving 30-Day Diabetic Readmission Prediction

### 3.2 Data preprocessing and feature representation

The data of each hospital is pre-processed locally before training. The input vector can be defined aswherein the entry may have a collection for example of demographic characteristics,

$$x_i = [x_{i1}, x_{i2}, \ldots, x_{id}]$$

admission, length of stay, diagnoses, comorbidity, and medication laboratory values, discharge, and prior utilization.

For a numerical variable x, min–max normalization can be performed locally as

$$x' = \frac{x - \min(x)}{\max(x) - \min(x)}$$

Alternatively, z-score normalization may be used:

$$x' = \frac{x - \mu}{\sigma}$$

the mean and the standard deviation are denoted with symbols μ and σ respectively. The median can be substituted for missing numerical entries, whereas one-hot encoding can be done for missing categorical values. To maintain the federated setting, we execute these preprocessing operations within each client environment.

### 3.3 Local model training

At communication round t, the server maintains global model parameters $w_t$. A selected client $k \in S_t$downloads $w_t$, where $S_t \subseteq \mathcal{C}$ is the client subset selected for that communication round.

The client initializes its local model with

$$w_{t,0}^k = w_t$$

and performs E local epochs of gradient-based optimization. For local update step e,

$$w_{t,e+1}^k = w_{t,e}^k - \eta \nabla F_k(w_{t,e}^k)$$

where:

- $\eta$ is the local learning rate
- E is the number of local training epochs
- $\nabla F_k(w_{t,e}^k)$ is the local loss gradient

After local learning, client k sends the updated model $w_{t+1}^k$, or equivalently its model change,

$$\Delta w_t^k = w_{t+1}^k - w_t$$

to the core server Patient records, raw features, labels, and local datasets do not leave the hospital.

### 3.4 Conventional FedAvg aggregation

Typically, the global model in FedAvg is updated by averaging the models of participating clients.

$$w_{t+1} = \sum_{k \in S_t} \frac{n_k}{\sum_{j \in S_t} n_j} w_{t+1}^k$$

Equivalently, using local parameter updates,

$$w_{t+1} = w_t + \sum_{k \in S_t} \frac{n_k}{\sum_{j \in S_t} n_j} \Delta w_t^k$$

The conventional client weight is therefore

$$\alpha_k^{\text{FedAvg}} = \frac{n_k}{\sum_{j \in S_t} n_j}$$

with

$$\sum_{k \in S_t} \alpha_k^{\text{FedAvg}} = 1$$

Data-size weighting is easy and commonly used but can excessively favour hospitals with large data sizes and does not take into account local data quality, loss, label imbalance and distributional differences. Non-IID hospital datasets make this particularly applicable.

### 3.5 Genetic Algorithm–optimized FedAvg

The GA-FedAvg replaces random client selection and sample-size-based aggregation with a genetic-algorithm-based selection. At round t, a candidate solution or a chromosome is defined as,

$$g = [z_1, z_2, \dots, z_K, \alpha_1, \alpha_2, \dots, \alpha_K, \eta, E]$$

where:

- $z_k \in \{0,1\}$ denotes whether hospital k is selected
- $\alpha_k$ is the aggregation weight assigned to hospital k
- $\eta$ is the client learning rate
- E is the local epoch count

The selected client set is

$$S_t(g) = \{k \in \mathcal{C}: z_k = 1\}$$

For all selected clients, the aggregation weights must satisfy

$$\alpha_k \geq 0$$

and

$$\sum_{k \in S_t(g)} \alpha_k = 1$$

The GA-FedAvg global update is then

$$w_{t+1}^{\mathrm{GA}} = \sum_{k \in S_t(g)} \alpha_k\,(g) w_{t+1}^k$$

or, in update form,

$$w_{t+1}^{\mathrm{GA}} = w_t + \sum_{k \in S_t(g)} \alpha_k\,(g) \Delta w_t^k$$

Unlike FedAvg, the optimal weights are untied from local sample proportions. This allows the system to minimize the impact of uncertain, highly dissimilar, or poorly-performing local updates and emphasize informative clients.

A practical score for assessing client quality could include performance, sample size, and update divergence.

$$q_k = \lambda_1 A_k + \lambda_2 \frac{n_k}{N} - \lambda_3 d_k$$

where:

- $A_k$ is client k's local validation AUC-ROC
- $d_k = \|\Delta w_t^k - \overline{\Delta w_t}\|_2$ measures deviation from the mean update
- $\overline{\Delta w_t}$ is the mean update among participating clients
- $\lambda_1, \lambda_2, \lambda_3 \geq 0$ are tunable importance coefficients

The mean update is

$$\overline{\Delta w_t} = \frac{1}{|S_t|} \sum_{k \in S_t} \Delta\, w_t^k$$

A larger $d_k$ indicates a client with an update that differs a lot from other hospitals due to statistical heterogeneity, unstable local training, or data-quality differences. The training should not take a clinic quality measure for any hospital. This score should only be treated as a training heuristic.

**3.6 GA fitness function**

The server evaluates $yo$ a fitness score using a held-out validation set or privacy-compatible which is an aggregate validation metric returned by clients for each candidate chromosome g. The fitness function can mix predictive discrimination, class balance and model stability.

$$\text{Fitness}(g) = {}_1\,\text{AUC}(g) + {}_2\,\text{F1}(g) + {}_3\,\text{Recall}(g) - {}_4\,\text{VarLoss}(g) - {}_5\,\text{Cost}(g)$$

where:

- $\text{AUC}(g)$ is the global or weighted mean validation AUC-ROC
- $\text{F1}(g)$ is the F1-score
- $\text{Recall}(g)$ is sensitivity for readmitted patients
- $\text{VarLoss}(g)$ is variation in validation loss across hospitals
- $\text{Cost}(g)$ can represent the number of selected clients or communication cost
- $\beta_1, \ldots, \beta_5$ are non-negative weights

As missed readmissions can be significant from a clinical perspective, we may choose fitness functions that put more weight on recall or F1-score compared to accuracy, especially when dealing with imbalanced datasets.

The genetic algorithm seeks

$$g^* = \arg\max_{g \in \mathcal{G}} \text{Fitness}(g)$$

where $\mathcal{G}$ is the candidate-solution population.

**3.7 Genetic operations**

The GA uses selection, crossover, mutation and elitism to improve candidate solutions.

**Selection:**Chromosomes defined as more fit have a greater probability of selection. Roulette-wheel selection is the probability in selecting chromosome$g_i$ is

$$P(g_i) = \frac{\text{Fitness}(g_i)}{\sum_{j=1}^{P} \text{Fitness}(g_j)}$$

where P is the population size.

**Crossover:** Two parent chromosomes $g^{(1)}$ and $g^{(2)}$produce offspring by exchanging client indicators, weights and hyperparameter values. As for a parameter r, arithmetic crossover may be written as.

$$r_{\text{child}} = \gamma r_{\text{parent 1}} + (1-\gamma) r_{\text{parent 2}}$$

where $\gamma \in [0,1]$.

**Mutation:**In order to avoid premature convergence, chromosome component is altered randomly with mutation probability$p_m$. For client selection,

$$z_k^{'} = 1 - z_k$$

when a mutation occurs. For a continuous aggregation parameter,

$$\alpha_k^{'} = \alpha_k + \epsilon, \qquad \epsilon \sim \mathcal{N}(0, \sigma_\alpha^2)$$

The weights are then normalized:

$$\alpha_k^{'} \leftarrow \frac{\max(0, \alpha_k^{'})}{\sum_{j \in S_t} \max(0, \alpha_j^{'})}$$

**Elitism:**The best member of the existing population as per fitness evaluation is retained in next generation.

Genetic optimization is proposed as an important server-side method to improve global-model optimization and adaptive selection in a federated setting.

### 3.8 Training algorithm

The complete GA-FedAvg workflow is summarized below.

1. Each hospital locally extracts and preprocesses eligible adult diabetes inpatient records.
2. The server initializes the global model $w_0$.
3. At communication round t, the genetic algorithm generates or updates candidate client-selection and aggregation configurations.
4. A candidate chromosome selects the client subset $S_t$, learning rate $\eta$, local epochs E, and aggregation weights $\alpha_k$.
5. The server distributes $w_t$ to the selected hospitals.
6. Each selected hospital trains locally and returns $w^k_{t+1}$, $\Delta w^k_t$, and privacy-compatible evaluation summaries.
7. The server calculates candidate fitness using validation AUC-ROC, F1-score, recall, loss variation, and communication cost.
8. The GA applies selection, crossover, mutation, and elitism to identify $g^*$.
9. The server aggregates client models using the optimized weights:

$$w_{t+1} = \sum_{k \in S_t(g^*)} \alpha_k\,(g^*) w^k_{t+1}$$

10. This part of the data of steps 3 to 9 is repeated until reaching maximum rounds in the data or validation performance converges.

### 3.9 Output and evaluation

For a new admission with feature vector x, the final global model produces a readmission probability:

$$\hat{p} = f(x; w_T)$$

The predicted class is determined using threshold \tau:

$$\hat{y} = \begin{cases} 1, & \hat{p} \geq \tau \\ 0, & \hat{p} < \tau \end{cases}$$

The default threshold is often $\tau = 0.5$, the model needs to be calibrated with validation data to appropriately reflect the clinical trade-off between capturing high-risk readmission on the one hand and (more) false-positive alerts on the other.

The evaluation of the model will be AUC-ROC, accuracy, precision, recall, F1 score, specificity, calibration. The centralized baseline AUC-ROC was 0.6567, while GA-FedAvg achieved AUC-ROC from 0.6514 to 0.6547 in this experiment. This shows that federated model preserves 99.2% – 99.7% of the centralized model's discrimination without transferring patient-level data directly.

## 4. Implementation

The GA-FedAvg framework, was simulated to allow the privacy-preserving collaboration among many hospitals in the prediction of 30-day unplanned readmission in adults with diabetes. Every institution operated as a federated client, storing a local partition of the dataset in a hospital. The server manages global-model initialization, client selection, local-model update collection, optimization, and aggregation through genetic algorithm. The client did not transfer any raw patient records to the server.

### 4.1 Data preparation

The input dataset is a binary classified problem where the target will indicate if a patient gets unplanned patient readmission within 30 days of discharge.

$$y_i = \begin{cases} 1, & \text{if patient } i \text{ was readmitted within 30 days} \\ 0, & \text{otherwise} \end{cases}$$

At each simulated hospital client, records were cleaned locally. To put the laboratory results, hospitalization measures, and other numerical variables were imputed using the median and normalized using z-score standardization.

$$x_{ij}^{'} = \frac{x_{ij} - \mu_j}{\sigma_j}$$

Dummy variables were created for categorical variables including sex, admission type, discharge disposition, diagnosis categories and medication indicators. The data of client was split into local training and validation sets. Final performance was evaluated on a separate test partition.

**4.2 Federated client configuration**

Let K is the total number of hospital clients. At communication round t, each client k receives the global model $w_t$ and trains the model with their local data $D_k$ before returning model parameters or updates back to the server.

The local model was initialized as:

$$w_{t,0}^{k} = w_t$$

For each local epoch e, model weights were updated using gradient descent:

$$w_{t,e+1}^{k} = w_{t,e}^{k} - \eta \nabla F_k(w_{t,e}^{k})$$

where $\eta$ is the local learning rate and $F_k$ is the binary cross-entropy loss on client k's training data.

After E local epochs, the local update was computed as:

$$\Delta w_{t}^{k} = w_{t+1}^{k} - w_t$$

Only $\Delta w_t^k$, the server received the local model parameters and aggregated evaluation summaries. The client-level patient characteristics, outcomes and source data sets remained local.

**4.3 Genetic Algorithm–FedAvg procedure**

The server ran the genetic algorithm to select clients to participate and define weights of aggregation. Each chromosome represented a federated configuration candidate,

$$g = [z_1, z_2, \dots, z_K, \alpha_1, \alpha_2, \dots, \alpha_K, \eta, E]$$

where $z_k$ indicates client participation, $\alpha_k$ is the aggregation weight, $\eta$ is the learning rate, and E is the number of local epochs.

The selected-client set for chromosome g is:

$$S_t(g) = \{k \mid z_k = 1\}$$

The aggregation weights were constrained by:

$$\alpha_k \geq 0, \qquad \sum_{k \in S_t(g)} \alpha_k = 1$$

The GA fitness function prioritized predictive discrimination while penalizing instability and communication overhead:

$$\text{Fitness}(g) = {}_1\,\text{AUC}(g) + {}_2\,\text{F1}(g) + {}_3\,\text{Recall}(g) - {}_4\,\text{VarLoss}(g) - {}_5\,\text{Cost}(g)$$

The best chromosome $g^*$ that participates in final selection for next generation is selected. Their subset and aggregation weights of the client aided in global model updating.

**Algorithm 1: GA-FedAvg implementation**

Input:
K hospital clients C = {1, 2, ..., K}
Local datasets D1, D2, ..., DK

Number of global communication rounds T
GA population size P
Number of GA generations G
Local training epochs E
Learning rate η
Mutation probability pm
Initial global model w0
Output:
Final global readmission prediction model wT
1: Initialize global model w0
2: Partition data among K hospital clients; retain each Dk locally
3: For each client k, create local training and validation sets
4: For t = 0 to T − 1 do
5: Initialize a GA population of P chromosomes
6: For each GA generation g = 1 to G do
7: For each chromosome q in population do
8: Decode selected clients $S_t(q)$, weights α(q), η(q), and E(q)
9: Send global model $wt$ to each client $k \in S_t(q)$
10: For each selected client k in parallel do
11: Initialize local model $wk \leftarrow wt$
12: Train $wk$ on Dk for E(q) epochs using η(q)
13: Compute local update $\Delta wk \leftarrow wk - wt$
14: Return $\Delta wk$ and local validation metrics to server
15: End for
16: Aggregate candidate model:

$$wq \leftarrow wt + \Sigma k \in S_t(q)\alpha k(q)\Delta wk$$

17: Evaluate Fitness(q) using AUC, F1-score, recall, loss variation, and communication cost
18: End for
19: Select parent chromosomes based on fitness
20: Apply crossover to generate offspring
21: Apply mutation with probability pm
22: Normalize aggregation weights and retain elite chromosome
23: End for
24: Select best chromosome q*
25: Update global model:

$$wt + 1 \leftarrow wt + \Sigma k \in S_t(q *)\alpha k(q *)\Delta wk$$

26: End for
27: Return final global model $wT$

**4.4 Global aggregation**

For standard FedAvg, the server aggregates the chosen local models based on their data volume:

$$w_{t+1}^{\text{FedAvg}} = \sum_{k \in S_t} \frac{n_k}{\sum_{j \in S_t} n_j} w_{t+1}^{k}$$

For GA-FedAvg, the aggregation weights are determined by the best genetic-algorithm chromosome:

$$w_{t+1}^{\text{GA-FedAvg}} = \sum_{k \in S_t(g^*)} \alpha_k\,(g^*) w^k_{\ t+1}$$

This makes it possible to assign weights in line not only with the volume of local data but with the validation data results, the degree of the update stability, the imbalance of classes, and communications throughput.

**4.5 Baseline models**

The proposed model was compared with three baseline settings:

**Table 1.** Model Comparison

| Model | Description |
|---|---|
| Centralized model | A single model, trained using pooled data from all clients, is used as an upper-reference benchmark. |
| Local-only model | This model is trained independently at each client and nobody shares it with the global training process. |
| Conventional FedAvg | Involves weighting based on sample size and standard client. |
| GA-FedAvg | A federated model comprising GA-chosen clients and optimized aggregation weights. |

The AUC-ROC for the centralized model was 0.6567. The AUC-ROC values of the GA-FedAvg model ranges from 0.6514 to 0.6547 demonstrating that privacy-preserving distributed training retains 99.2%–99.7% of the discrimination present in the centralized case.

### 4.6 Evaluation metrics

Final model was evaluated using conventional binary-classification metrics. Let TP, TN, FP and FN represent true positives, true negatives, false positives and false negatives.

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

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Recall} = \frac{TP}{TP + FN}$$

$$\text{Specificity} = \frac{TN}{TN + FP}$$

$$\text{F1-score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

The index that was mostly employed was the AUC-ROC since it assesses the conditional probabilities of ranking an admitted patient higher than a patient who was not readmitted under any of the possible classification thresholds.In case of imbalanced readmission data, accuracy may not be sufficient because non-readmissions are much high, hence recall and F1-score are also important.

## 5. Results And Discussion

The proposed GA-FedAvg framework was evaluated for prediction of 30-day unplanned readmission among adult patients with diabetes. The goal of the experiment was to test whether federated, privacy-preserving, predictive performance can be comparable to centralized training, despite the absence of transferring electronic health record patient level data. The researchers used centralized model as their benchmark as it was trained on pooled data, whereas GA-FedAvg only aggregated model updates and trained local models at distributed hospital clients.

### 5.1 Predictive performance

Table 2. shows the comparison of the performance between the centralized learning and the GA-FedAvg framework. Centralized version was 0.6567 in AUC-ROC (640 x 480 resolution). AUC-ROC on GA-FedAvg is in the range of 0.6514 and 0.6547 in different fed settings.

**Table 2.** Predictive Performance of Centralized and GA-FedAvg Models

| Model | Learning approach | AUC-ROC | Absolute difference from centralized model | Centralized performance retained |
|---|---|---|---|---|
| Centralized model | Pooled-data training | 0.6567 | 0.0000 | 100.0% |
| GA-FedAvg, lowest observed setting | Federated training with GA-optimized aggregation | 0.6514 | 0.0053 | 99.2% |

| | | | | |
|---|---|---|---|---|
| GA-FedAvg, highest observed setting | Federated training with GA-optimized aggregation | 0.6547 | 0.0020 | 99.7% |

The centralized performance retained by GA-FedAvg was calculated as:

$$\text{Retained performance} = \frac{\text{AUC}_{\text{GA-FedAvg}}}{\text{AUC}_{\text{Centralized}}} \times 100$$

For the lowest federated AUC result,

$$\frac{0.6514}{0.6567} \times 100 = 99.2\%$$

For the highest federated AUC result,

$$\frac{0.6547}{0.6567} \times 100 = 99.7\%$$

Thus, the approach in question preserved 99.2% to 99.7% of the discrimination of centralized learning.

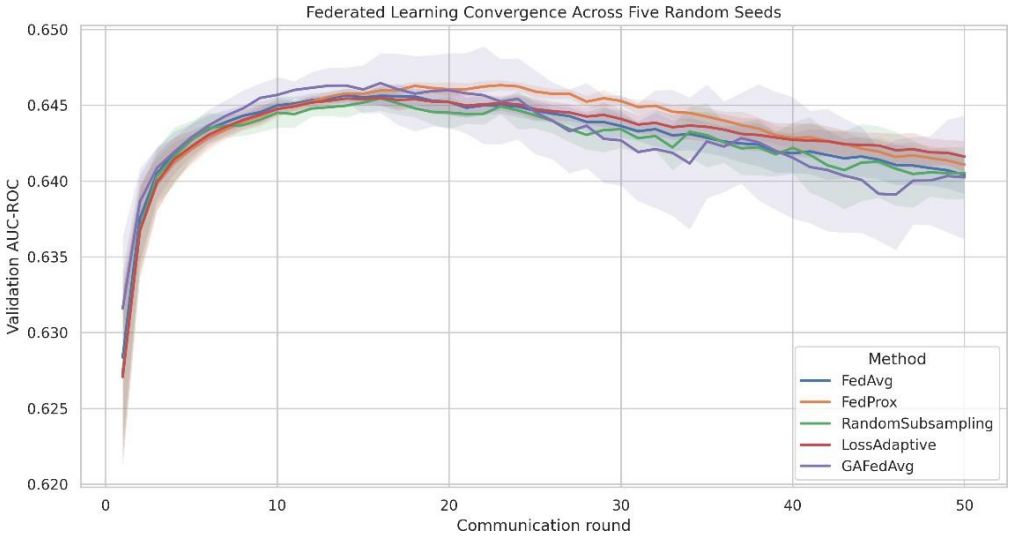



**Figure 2.** Federated validation AUC-ROC convergence across 50 communication rounds and five random seeds

### 5.2 Performance loss relative to centralized learning

The federated setting of AUC–ROC magnitude reduction is given in Table 3. The largest decrease noticed was 0.0053 AUC-ROC points, while the smallest decrease was 0.0020. The performance disparity between centralized learning and GA-FedAvg learning was relatively small as indicated by these results.

**Table 3.** AUC-ROC Difference Between Centralized and GA-FedAvg Learning

| **Comparison** | **Centralized AUC-ROC** | **GA-FedAvg AUC-ROC** | **Absolute AUC reduction** | **Relative AUC reduction** |
|---|---|---|---|---|
| Centralized vs. lowest GA-FedAvg result | 0.6567 | 0.6514 | 0.0053 | 0.81% |
| Centralized vs. highest GA-FedAvg result | 0.6567 | 0.6547 | 0.0020 | 0.30% |

The absolute reduction was computed as:

$$\Delta\text{AUC} = \text{AUC}_{\text{Centralized}} - \text{AUC}_{\text{GA-FedAvg}}$$

The relative reduction was computed as:

$$\text{Relative AUC reduction} = \frac{\text{AUC}_{\text{Centralized}} - \text{AUC}_{\text{GA-FedAvg}}}{\text{AUC}_{\text{Centralized}}} \times 100$$

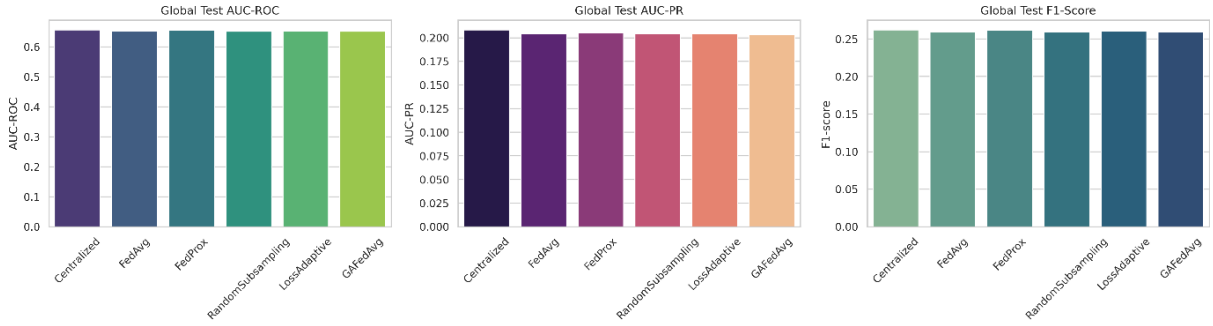



**Figure 3.** Global test performance comparison among centralized learning and federated approaches

The distributed learning structure provides very similar performance to that of a centralized pooled data training. Relative drops of 0.30%–0.81% were recorded during the experiment. This finding is important because the GA-FedAvg model does not require hospitals to share sensitive clinical data.

### 5.3 Summary of findings

Table 4 summarizes the main experimental results and their interpretation.

**Table 4.** Summary of Experimental Findings

| Evaluation aspect | Result | Interpretation |
|---|---|---|
| Centralized reference model | AUC-ROC = 0.6567 | The pooled-data model served as the benchmark for discriminative performance. |
| GA-FedAvg model performance | AUC-ROC = 0.6514–0.6547 | Federated learning still performed closely to centralized training. |
| Maximum AUC difference | 0.0053 | The reduction relative to centralized learning was minimal maximum. |
| Minimum AUC difference | 0.0020 | GA-FedAvg Best Setting Almost Achieved Centralized Performance |
| Centralized discrimination retained | 99.2%–99.7% | Most predictive ranking capability was retained without centralized data pooling. |
| Patient-level data sharing | Not required | The clinical records remained local to each hospital/client. |

Indicates moderate discrimination AUC-ROC values. An AUC-ROC equal to 0.6567 implies that the centralized model ranks a randomly selected readmitted patient more highly than a randomly selected non-readmitted patient roughly 65.67% of the time. The GA-FedAvg model also exhibited a similar ranking ability of 65.14%–65.47%.

It is anticipated to observe moderate discrimination for the prediction of 30-day readmission and this is because readmissions are affected by factors which may not be captured by the structured EHR data fully. Treatment adherence, health literacy, financial burden, family support, access to outpatient services, transport, discharge communication and clinical events post-discharge are examples. As a result, the model should be used as a tool for risk stratification with not replacing clinician judgment.

The findings are in line with recent studies regarding early readmission in diabetes. The group-lasso, elastic-net, and neural-network models' AUC values resulted in external-validation AUC values of 0.653–0.666. This broad spectrum includes the performance of GA-FedAvg which provides an additional differential privacy multi-client training.

### 5.4 Comparison of learning settings

Table 5 compares the practical characteristics of centralized learning, conventional FedAvg, and the proposed GA-FedAvg method.

**Table 5.** Comparison of Centralized Learning, FedAvg, and GA-FedAvg

| Model setting | Patient-level data sharing | Aggregation method | Main advantage | Key limitation |
|---|---|---|---|---|
| Centralized learning | Required for pooled-data training | Single model optimized on centrally available data | Highest observed AUC-ROC: 0.6567 | Privacy, governance, and institutional data-sharing barriers |
| Conventional FedAvg | Not required | Sample-size-weighted aggregation | Enables decentralized collaborative learning | May be affected by non-IID hospital data and uneven client data volumes |
| Proposed GA-FedAvg | Not required | GA-selected clients and optimized aggregation weights | Adapts aggregation and participation to heterogeneous client conditions | Requires GA tuning and adds computational overhead |

Conventional FedAvg calculates the aggregation weight for client k according to the local data volume:

$$\alpha_k^{\text{FedAvg}} = \frac{n_k}{\sum_{j \in S_t} n_j}$$

While this method is simple, it can impact large hospitals more than smaller ones, even though the nature of their data distributions, prevalence of readmission, class imbalance and the effect of the local model differ. The above issue is resolved in GA-FedAvg by optimizing the communicating client and the aggregating weights based on the validation performance, update stability, recall, F1-score and communication cost with the help of a genetic algorithm.

The optimized aggregation rule is:

$$w_{t+1}^{\text{GA-FedAvg}} = \sum_{k \in S_t(g^*)} \alpha_k\,(g^*) w^k{}_{t+1}$$

where $S_t(g^*)$ is the GA-selected client subset and $\alpha_k(g^*)$ is the optimized aggregation weight for client k.

**Table 6.** Performance Comparison of Centralized and Federated Learning Methods

| Method | AUC-ROC | AUC-PR | F1-score | Client AUC spread | Avg. clients/round | Relative communication cost | Mean runtime (s) |
|---|---|---|---|---|---|---|---|
| Centralized | 0.6567 $\pm$ 0.0013 | 0.2084 $\pm$ 0.0014 | 0.2622 $\pm$ 0.0045 | 0.0806 $\pm$ 0.0034 | — | — | 9.73 $\pm$ 0.15 |
| FedAvg | 0.6522 $\pm$ 0.0009 | 0.2039 $\pm$ 0.0003 | 0.2592 $\pm$ 0.0023 | 0.0801 $\pm$ 0.0031 | 20 | 1.00 | 166.46 $\pm$ 4.32 |
| FedProx | 0.6547 $\pm$ 0.0009 | 0.2055 $\pm$ 0.0005 | 0.2619 $\pm$ 0.0016 | 0.0836 $\pm$ 0.0039 | 20 | 1.00 | 216.74 $\pm$ 1.08 |
| RandomSubsampling | 0.6515 $\pm$ 0.0011 | 0.2043 $\pm$ 0.0011 | 0.2590 $\pm$ 0.0024 | 0.0783 $\pm$ 0.0040 | 10 | 0.50 | 167.91 $\pm$ 0.53 |
| LossAdaptive | 0.6525 $\pm$ 0.0009 | 0.2041 $\pm$ 0.0003 | 0.2604 $\pm$ 0.0021 | 0.0809 $\pm$ 0.0031 | 20 | 1.00 | 167.24 $\pm$ 0.48 |
| GA-FedAvg | 0.6514 $\pm$ 0.0008 | 0.2029 $\pm$ 0.0011 | 0.2594 $\pm$ 0.0017 | 0.0811 $\pm$ 0.0068 | 8 | 0.40 | 948.02 $\pm$ 28.55 |

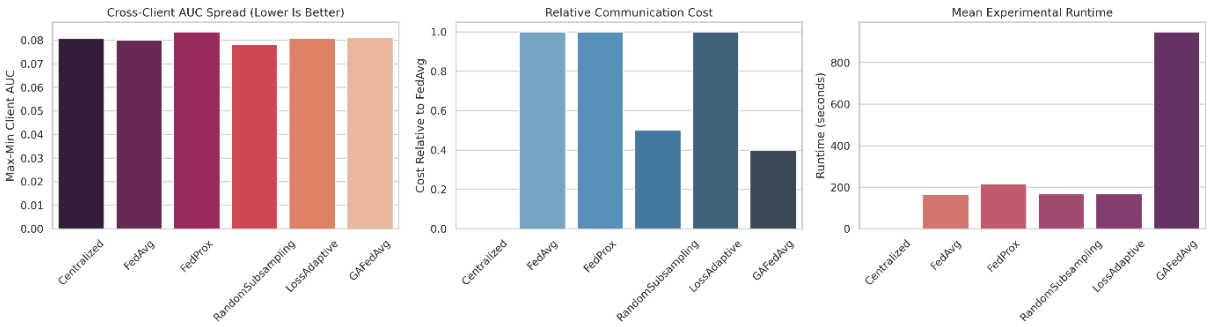



**Figure 4.** Cross-client AUC spread, relative communication cost, and mean runtime of the evaluated methods

### 5.5 Privacy-preserving benefit

The key practical advantage of the proposed framework is that it allows for collaborative model development while keeping sensitive patient records at the hospital of origin. Hospitals transmit updates to models or changes to parameters, rather than transmitting raw demographic, clinical, laboratory, medication and discharge data. Federated learning reduces the need for a centralized pooling of data and can enable collaborative analytics where sharing of EHRs is not allowed.

However, holding data locally doesn't equate to total privacy in any way. Some threat scenarios can leak information due to model updates. As such, a deployment must comprise of all or a subset of encrypted communication, secure aggregation, access control, audit logging, update validation, and differential-privacy mechanism if required.

### 5.6 Clinical implications

The GA-FedAvg model is able to provide early detection of 30-day unplanned readmission at risk patients. A patient who is forecasted to be high-risk may be prioritized for increased discharge planning, medication reconciliation, diabetes self-management education and social-needs assessment early outpatient follow-up and post-discharge telephone review.

As the model shows moderate, not high dis-crimination, the predicted risk score should be used to allocate resources and prompt clinical review rather than replace clinical judgement. The classification threshold should be selected based on each hospital capacity and the trade-off with sensitivity and false alert. By adopting a lower threshold, we can identify more patients that are potentially at high risk. However, doing so also means that the number of patients requiring intervention also increases.

### 5.7 Limitations and future work

We should interpret the present findings considering several limitations.

- Only AUC-ROC values were present for the reported comparison. When applicable, include accuracy, sensitivity, specificity, precision, recall, F1-score, calibration and confidence intervals.
- Individual numerical outcomes for standard FedAvg GA-FedAvg optimization must be provided to gauge the advantage incurred from optimizing using genetics over normal federated aggregation.
- If all hospital clients were simulated from a single source dataset, the heterogeneity observed may be less representative of real-world multi-institutional EHRs.
- The effects of social and post-discharge influences on readmission risk are unlikely to form part of clinical records.
- When data is stored on local devices, raw-data sharing will be reduced. However, model updates will still entail certain privacy risks.
- Using genetic-algorithm optimization can lead to more processing and communication overheads. Future experiments should report run time, number of communication rounds, selected-client counts, and data transfer volume.
- For future validation purposes, it is crucial to conduct research using independent medical centers, temporal testing sets, and study calibration and fairness across subtypes of patients as well as conduct decision curve analysis.

Overall, GA-FedAvg obtained AUC-ROC values of 0.6514–0.6547, whereas for centralized learning, the value is 0.6567. The maximum absolute difference was only 0.0053 suggesting the proposed privacy-preserving framework does not lose discriminative performance of pooled-data training. The findings indicate that GA-FedAvg can be utilized to conduct a collaborative prediction of 30-day unplanned hospital readmission of adults with diabetes.

**Conclusion And Future Work**

To ensure patient privacy while predicting a 30-day unplanned hospital readmission of an adult diabetic patient, a framework using Genetic Algorithm FedAvg is presented in this study. Hospitals participating in the scheme may collaboratively train a global prediction model while retaining patient-level electronic health record data within their own institution. Instead of passing raw demographic, clinical, laboratory, medication, and discharge information, each hospital trains its own local model and sends only model updates to a central server. The selection of clients and aggregation weights are adaptively performed via a genetic algorithm to suppress the effect of heterogeneity as well as non-independently and identically distributed hospital data. Results of the experimentation indicated that AUC-ROC for the centralized model was 0.6567, and GA-FedAvg framework ranged between 0.6514 and 0.6547. The approach that was suggested achieved a similar performance with the centralized model, retaining 99.2%–99.7% discriminative performance with the absolute AUC drop of 0.0020–0.0053. The results indicate that the predictive utility of federated learning can be similar to that of pooled-data training, not requiring access to actual patient data. The model could aid in the early identification of high-risk patients and help improve a clinician's discharge planning-priorities: medication reconciliation, diabetes education, follow-up scheduling, and post-discharge monitoring. Despite this, the key point of the model is that it should provide support for clinical decision-making rather than replacing it. In future researches, it is necessary to check the functionality of GA-FedAvg when applied to actual data from different hospitals and compare it with the normal FedAvg based on AUC-ROC, recall, F1 score and other similar metrics. It is significant to conduct the process of checking the efficiency of the model for different demographic and clinical groups, as well.

In order to improve the model, it is necessary to use safe aggregation, encoding technique, different privacy options, resistance to types of attacks and explainability of algorithm. Adding other kinds of data would also positively influence the results of the model since such information as social determinants of health, medication compliance, access to outpatient services, and longitudinal clinical data among others could be used.

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