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Balancing Interpretability and Performance: Optimizing Random Forest Algorithm Based on Point-to-Point Federated Learning

Abstract: - Federated learning is extensively applied in collaborative data scenarios involving multiple data owners. While the majority of state-of-the-art federated learning algorithms are currently black-box models, making it challenging for users to comprehend how decisions are made. Random forest models are extensively utilized in medical contexts owing to their exceptional interpretability. However, when faced with multicenter data, the heterogeneity of data from each center often leads to its predictive performance falling short of expectations. To mitigate this challenge, the present study introduces DFLRF (Decentralized Federated Learning Random Forest), a federated learning algorithm based on random forests. Expanding on conventional random forests, DFLRF employs federated learning to disseminate decision tree models. It assesses and consolidates tree models from all client sites, thereby comprehensively addressing data disparities across various centers. The algorithm selects the optimal decision tree model based on the magnitude of model loss to guarantee the predictive performance of the final federated random forest model. The algorithm undergoes testing on a public dataset. Experimental results demonstrate that, compared to baseline algorithms, DFLRF enhances the AUC by 1.5% and the recall rate by 6%, while also ensuring superior interpretability.

Keywords: Federated Learning; Random Forest; Interpretability; Big Data Healthcare.

I INTRODUCTION

The rapid development of big data[1] and medical information technology[2,3] has led to the generation of a substantial amount of data. Machine learning, leveraging these data, has been applied in the realm of intelligent healthcare. Traditional machine learning typically necessitates the centralization of data from various data centers onto a large server for centralized training.However, as more users become aware of data security and privacy[4] issues, data centralization faces significant challenges[5]. In recent years, federated learning, proposed by Google, has gained increasing attention. It allows for the establishment of a shared global machine learning model among multiple hospitals while keeping users' data local. The most initial algorithm in federated learning is the Federated Averaging algorithm[6] (FedAvg), which mainly follows three steps in each communication iteration: (a) the server sends the latest global model to clients; (b) clients receive the global model, train it based on their local datasets, then send gradient updates back to the server; (c) the server aggregates these gradient updates to form a new global model. These steps are repeated until convergence.

In certain scenarios, such as healthcare[7], Model interpretability[8,9] is also an issue in evaluating the merits of predictive models. The application of machine learning typically outputs business decisions, and the level of interpretability refers to the extent to which model users can understand why a decision was made. The better the model's interpretability, the deeper people's understanding of the decisions made by the model. Decision tree models[10], known for their good interpretability, allow for statistical causal analysis of the model, ensuring the rationality of model predictions. Compared to traditional machine learning algorithms, neural net-

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work algorithms[11], even if more accurate in prediction results, suffer from reduced interpretability due to increased complexity. When using black-box models[7], like neural networks, it becomes difficult to interpret the model, and the feasibility and rationality of model predictions cannot be discerned, greatly limiting the practical application scenarios of the model and reducing its actual benefits. In contrast random forest model[12] have a certain interpretability advantage over deep neural networks[13,14]. Random forest models are particularly suited to medical data modeling scenarios and have been proven very effective in precisely modeling biomedical data for various tasks[15]. Random forests can discover the relationship between prediction results and data information based on the branching, nodes, and weight parameters in the model's tree structure. Additionally, tree models can identify the contribution of all features to the model's prediction results, which is crucial for the model's interpretability. Most importantly, tree models allow for the visualization and analysis of the entire tree structure, ensuring model performance while providing high interpretability. Currently, most heterogeneous optimization algorithms for federated learning rely heavily on deep learning, which often results in poor interpretability,while federated learning based on the random forest model often fails to meet performance expectations, and the construction algorithm is complex.

Addressing the above issues,We propose a novel federated random forest algorithm, improving the interpretability issue of mainstream federated learning algorithms and enhancing the predictive performance of random forest models in federated scenarios. The main contributions are as follows:

1. Combining traditional random forest algorithms with horizontal federated learning to propose a peer-to-peer federated random forest modeling method.
2. Introducing a loss matrix in the federated random forest modeling process to balance model complexity and performance, making it suitable for cross-silo multi-center horizontal federated learning scenarios and enhancing model interpretability while ensuring model performance compared to mainstream federated algorithms.
3. We conducted a set of experiments on real datasets, where our federated random forest model significantly improved in AUC and Recall compared to baseline algorithms; we visualized the model and analyzed feature importance to explain the performance improvement of our algorithm.

II RELATED WORKS

Interpretability is generally defined as the extent to which humans can understand the attribution of decisions made by ML models. As machine learning applications continue to expand and deepen, the algorithms used become increasingly complex, leading to a "black box effect" that raises questions and concerns about the predictions made by machines. Consequently, there is a growing demand for model interpretability. Interpretable models include decision trees, linear regression, and random forests, whereas less interpretable or "black box" models typically involve complex models focused on outcomes, such as deep neural networks.

In the medical field, models with better interpretability are often traditional machine learning models like linear regression and decision tree models. These allow for statistical causal analysis to ensure the rationality of model predictions. For instance, Otunaiya et al. have used simple logistic regression models to predict chronic kidney disease; Zhang et al. [16]developed a prediction model for urinary toxicity using a naive Bayes classifier. Models like linear regression, naive Bayes, and decision trees, which are highly interpretable and conceptually simple to understand, are still used in different healthcare domains, even if their predictive performance is lower. Compared to traditional machine learning algorithms, neural network algorithms may be more accurate in prediction results, but their increased complexity reduces model interpretability. The use of black-box models, such as neural networks, makes it difficult to interpret the model, and the feasibility and rationality of model predictions cannot be discerned, greatly limiting the practical application scenarios of the model and reducing its actual benefits. Kwon

B C et al.[17]used Recurrent Neural Networks (RNN) to establish predictive models for patients with heart failure and cataract symptoms on electronic medical records, and used a visualization analysis tool named RetainVis to interpret the model. Cheng J et al.[18] used deep neural network models based on preoperative multimodal MRI images to grade glioma, adopting SHapley Additive exPlanations (SHAP) for quantitative interpretation and analysis of the impact of important features on classification. This shows that interpreting complex black-box models requires introducing model-agnostic explanation techniques, such as model visualization tools, feature importance, SHAP[19], etc., to better explain how predictions are influenced by features.

In ensemble models, such as random forest algorithms, there is a certain interpretability advantage compared to deep neural networks. Random forest models are particularly suited to medical data modeling scenarios and have been proven very effective in precisely modeling biomedical data for various tasks. Qiu et al. [20]utilized data from 7188 cycles of initial IVF-ET treatment in infertile women to establish a predictive model for cumulative live birth rate per ovarian stimulation cycle. The study employed interpretable machine learning algorithms such as Random Forest and Extreme Gradient Boosting[21] (XGBoost); Hou et al. [22]combined vertical federated learning with a random forest model and proposed a verifiable privacy protection scheme for Vertical Federated Random forests (VPRF) based on multi-key homomorphic encryption for homomorphic comparison and voting statistics algorithms. Liu et al. [23]proposed a federated random forest algorithm tailored for vertical federated learning, aiming to align and match shared users with different features among participating parties while preserving data privacy. Subsequently, all participants jointly learn a global shared random forest model based on privacy-preserving protocols. SM Jalal et al. [24]presented a random forest algorithm based on horizontal federated learning to detect heart disease among patients from distributed hospitals. This federated random forest algorithm integrates the updating processes of both the federated central server model and client-side models, requiring the server to possess data and iterate the server model across client data for updates.

III METHOD

A. Transfer Strategy for Tree Models

Inspired by the parameter passing process of the FedAvg federated learning strategy, this paper introduces a novel federated learning-based Random Forest algorithm. Building upon traditional Random Forest methods, this algorithm enables the secure sharing of complete, unencrypted decision tree models through federated learning, thereby facilitating the creation of local Random Forests without introducing latency and noise associated with encrypted message exchanges. By collectively modeling data from multiple clients, this approach not only enhances predictive performance but also improves the interpretability of tree models.

Random Forest is not a singular machine learning model; rather, it constructs multiple decision tree models on the dataset and then integrates all the decision tree models. Therefore, in the federated process of our algorithm, each client sends its constructed decision tree model to other clients, eliminating the need for centralized model aggregation. Instead, the best model is selected from the received foundational models. Through this process, all clients have a premier foundational model, thereby ensuring the effectiveness of the final integrated model. Since decision tree models are transmitted during the federated process, a certain level of security can be ensured, and the complexities of homomorphic encryption can be avoided. Consequently, there is no model parameter aggregation process, meaning there is no need for a central server, making the algorithm based on peer-to-peer federated learning.

B. DFLRF：Decentralized Federated Learning Random Forest Algorithm

Traditional Random Forest algorithms have achieved commendable success in numerous application scenarios. However, they encounter challenges when addressing issues related to multi-center data, as encountered in this

study. In the conventional Random Forest algorithm, each tree's generation involves randomly selecting a certain proportion of data and feature subsets from the local training dataset. This methodology effectively ensures model accuracy and mitigates overfitting. However, in federated settings, model training should leverage data from all clients, a requirement that the traditional Random Forest algorithm fails to meet.

This research builds upon the traditional Random Forest framework by integrating the transmission of decision tree models through federated learning, evaluating, and integrating tree models from all clients. This approach meticulously addresses the data variances distributed across different centers. During the learning process, the optimal decision tree model is selected based on model loss, ensuring the final model's accuracy. In the Federated Random Forest algorithm, each tree is generated by randomly selecting a certain proportion of data on the client side while utilizing all features of the data, thereby maximizing the retention of client information. Each round, clients train a decision tree based on their local data, which may not ensure optimal performance across all clients. A loss matrix is used to select the best tree. Figure 1 depicts the workflow of the proposed Federated Random Forest algorithm.

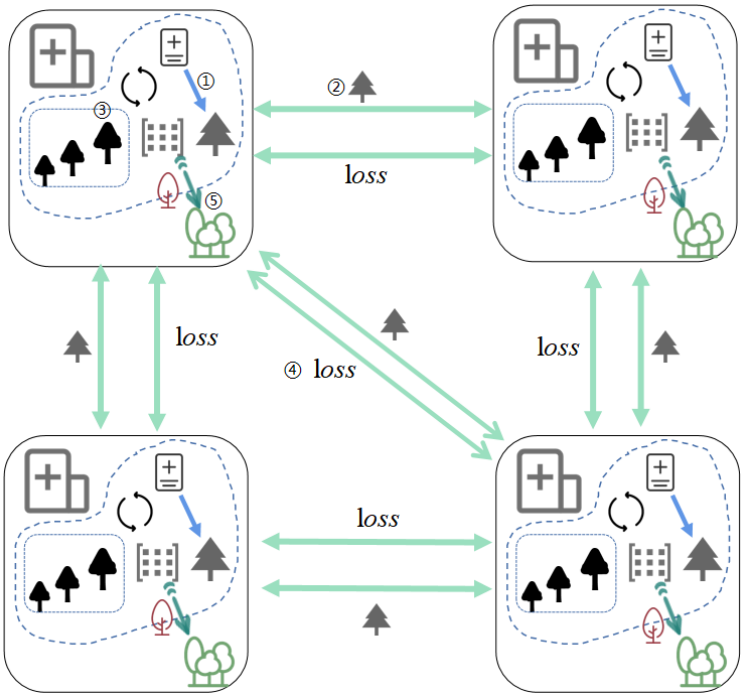


Figure 1 *The Workflow of Federated Random Forest.*

The DFLRF algorithm is presented in Algorithm 1. Each tree in the Federated Random Forest is specifically the best-performing tree learned from all participating clients, effectively capturing knowledge from data distributed across multiple centers. The Federated Random Forest algorithm delineates the federated learning process into four main stages:

Algorithm 1: DFLRF algorithm

Input：1) N, Local data user count；2) $D=\{D_1,\cdots,D_N\}$, sample sets from each client；3) T, maximum communication rounds；4) h, height of Decision Trees；

Output: Random Forest $F=\{f_{tree}^1, f_{tree}^2,\cdots f_{tree}^T\}$

1: for $t \leftarrow 1$ *to* T *do*

2: for c = 1, 2, …N in parallel **do:**

3: $f_{tree}^{i} \leftarrow DecisionTree(D_i, h)$

4: Send f_{tree}^{i} to all clients

5: end for

6: Receiving f_{tree}^{j} from Other Clients

7: for j=1,2,...N:

8: Compute Log Loss: $l_i^j = \log loss(f_{tree}^{j}, D_i)$

9: Sending the every model loss l_i to other clients

10: Receiving loss from other clients and combining into loss matrix $|\sum|$

11: $$|\sum| = \begin{bmatrix} l_1^1 & l_1^2 & \cdots & l_1^j \\ \vdots & \ddots & & l_2^j \\ \vdots & & \ddots & \\ l_i^1 & l_1^2 & & l_i^j \end{bmatrix}$$

12: Selecting the tree model with the minimum Loss: $f_{tree}^{\min loss} = \min\_loss(|\sum|)$ Adding to the random forest

13: end for

(1) Client T(1) Training:Each client conducts random sampling with replacement on their local data and trains a decision tree model f_{tree}^{i} using all features, subsequently disseminating the model to all clients.

(2) Loss Matrix Calculation: Each client receives the decision tree model f_{tree}^{j} from other clients and then calculates the model's loss on its local data. The loss l_i^j represents the loss of thej^{th} client's tree model on the i^{th} client's test set. Subsequently, the losses l_i from all models are shared with all clients.

(3) Selecting the Best Tree: Each client receives model losses from other clients and compiles them into a loss matrix $|\sum|$. Through this matrix, a tree model $f_{tree}^{\min loss}$ with the lowest average loss is identified. This tree model is then integrated into the random forest as one of its trees.

(4) Model Integration: The Federated Random Forest, as an ensemble model, is easily integrated. The set $\left\{f_{tree}^{\min loss}(1), f_{tree}^{\min loss}(2),\cdots f_{tree}^{\min loss}(T)\right\}$ represents the collection of optimal decision trees with the least loss selected from the loss matrix in each communication round $t = \{1,2,\cdots T\}$

IV EVALUATION

A. Federated Dataset

This research employs electronic medical record data derived from the eICU database, which is openly accessible to the public. Originated from Philips Healthcare, the eICU database integrates data from a telehealth system, aggregating information from numerous ICUs across more than 200 United States hospitals, specifically focusing on patient admissions throughout 2014 to 2015. To legally access and utilize the eICU dataset, you must submit an application to the official website of the eICU Collaborative Research Database. This application should include a detailed research plan and institutional information, along with the signing of the requisite data usage agreement.Encompassing a wide array of information, the database includes patient demographics, diagnostic details, Glasgow Coma Scale (GCS) scores, results of laboratory tests, pharmacological interventions, nursing notes, and APACHE IV scores, among others. This meticulously curated collection of records is systematically managed through a PostgreSQL database, formatted as SQL tables for efficient data handling. Time within the database is uniquely indicated by offsets, rendering the admission times of patients as negative values, thereby facilitating researchers in accurately tracking post-admission event timings. The utilization of this database mandates a formal application process, alongside the completion of a confidentiality training pertaining to patient information and the execution of a data use agreement, subsequently granting free access to the database for research purposes.

1) Data Preprocessing

The prediction target of this article is Acute Kidney Injury[25,26] (AKI), based on the universal definition of AKI proposed by the Kidney Disease Improving Global Outcomes (KDIGO)[27], as shown in Table 1.

Table 1 Disease criteria for acute kidney injury.

AKI Stage	Criteria for Assessment
Stage 1	（1）It is 1.5-1.9 times the SCr concentration reference value （2）Increased by more than0.3 mg/dl (26.4 μmol/l)
Stage 2	It is 2.0-2.9 times the Scr concentration reference value
Stage 3	（1）3 times the SCr concentration reference value （2）Increase over 4.0 mg/dl (354 μmol/l)

Among the indicators, the patient's Serum Creatinine (SCr) monitoring indicator can be used to judge and measure the outbreak or degree of AKI. When representing the label value of AKI in patients, the most recent historical data value measured before admission is taken as the baseline value for serum creatinine. If no measurement was made before admission, the value measured at the time of admission is defined as the baseline value.

To meet the data structure requirements of machine learning, this paper adopts the following data preprocessing strategies:

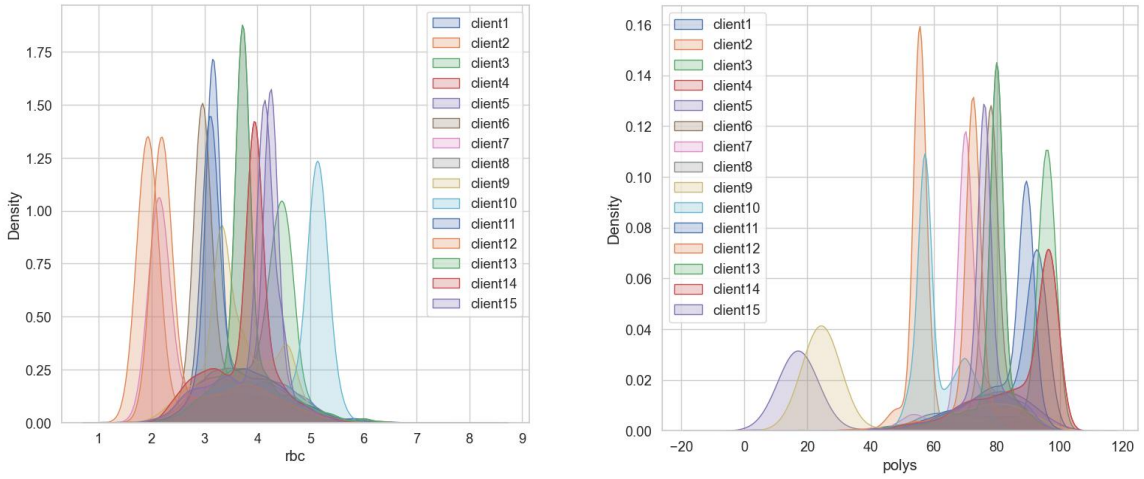
For patient records with AKI occurrences, it is necessary to ensure that the prediction point is set before the onset of AKI. In this study, the prediction point is established 48 hours (2 days) prior to the AKI onset; only records occurring before this prediction point are collected. For patients without AKI, the prediction node is set to 48 hours (2 days) before the last SCr measurement. Consequently, the feature set formed from data within 48 hours prior to the prediction node can be used to predict whether a patient will develop AKI 48 hours in advance.

For discrete data, one-hot encoding is employed for processing. For features with temporal information and multiple record values within the prediction time window, this paper selects the data closest to the prediction point as the feature value. Features with a missing rate higher than 0.1% are deleted, retaining only those with a lower missing rate for disease prediction or risk factor identification. Finally, expert knowledge is utilized for feature selection.

2) Description of data statistics

To best align with the real-world scenario of dispersed and highly heterogeneous hospital data, this study categorizes the eICU[28] data by hospital and excludes those with too few samples. Subsequently, all hospitals are divided into quartiles based on the size of their sample populations, selecting 5 hospitals from each of the 25%, 50%, and 75% percentiles, totaling 15 hospitals. These hospitals serve as the 15 clients and exhibit significant differences in both the number of patients and the proportion of AKI cases, better reflecting the performance of the algorithm in scenarios with data diversity.

To further illustrate the data distribution differences among these 15 clients, we evaluated the distribution of six features across these clients. These six features are diastolic blood pressure, systolic blood pressure, age, red blood cells, partial pressure of oxygen, and polymorphonuclear leukocytes. Figure 2 displays the distribution of these features.From the graph, it is evident that these 15 clients not only vary in sample size but also exhibit significant differences in the distribution of data features, effectively representing real-world medical scenarios. Subsequent research will be conducted based on these 15 clients, with the data from each client divided into a training set and a test set at a ratio of 7:3.



(**a**) (**b**)

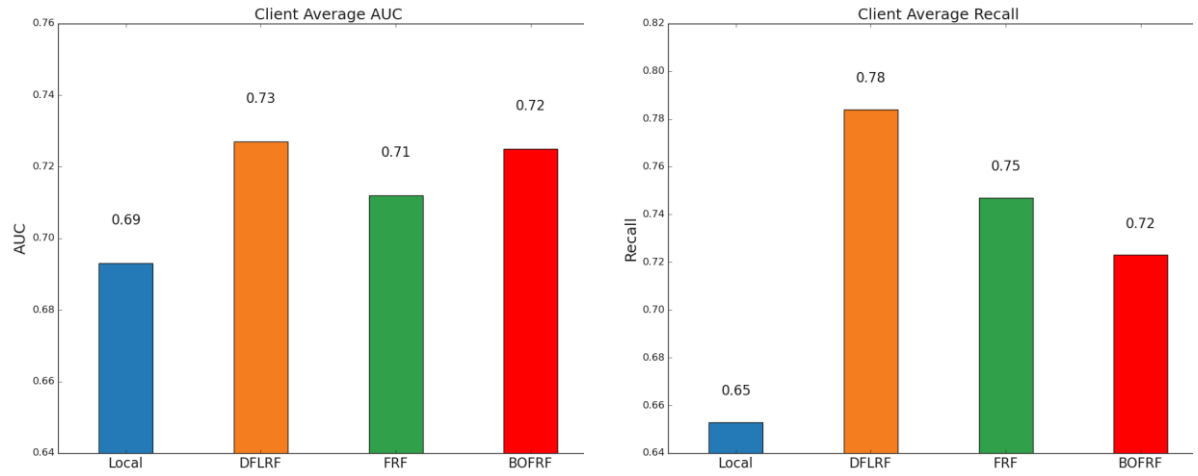
Figure 2 Differences in feature distributions across different client data

(**a**) Distribution of Red Blood Cell ; (**b**) Distribution of Polymorphonuclear leukocyte.

B. 4.2 Experimental Results and Analysis

1) Predictive performance

To illustrate the effectiveness of the proposed DFLRF algorithm we compare its performance with that of the local model and existing horizontal federated random forest algorithms (FRF[29], BOFRF[30]), as well as the global model across all clients, as depicted in Figures 3.



(**a**) (**b**)

Figure 3 (a)Comparison of average model AUC of different methods.(b)Comparison of average model Recall of different methods.

Analysis of the charts reveals that, on average, the AUC performance of the DFLRF algorithm model is the highest at 0.727. This demonstrates an approximate 4% improvement over the Local model across all clients, a 1.5% increase compared to the FRF model, and slightly better performance than the BOFRF model, which averages 0.725, as detailed in Table 2. Regarding Recall performance averaged across clients, the DFLRF algorithm model demonstrates a significant improvement compared to other models. It exceeds a 13% increase over the Local model, nearly a 4% improvement over the FRF model, and a 6% increase over the BOFRF model, as shown in Table 3. This validates the effectiveness of the proposed DFLRF algorithm in this study.

Table 2 Comparison of model AUC in every client of different methods.

Client	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	Avg
Local	0.714	0.634	0.661	0.712	0.851	0.826	0.710	0.749	0.697	0.691	0.601	0.551	0.730	0.668	0.603	0.693
DFLRF	0.713	0.663	0.700	0.709	0.866	0.856	0.788	0.784	0.688	0.657	0.702	0.645	0.728	0.722	0.681	0.727
FRF	0.707	0.662	0.683	0.644	0.833	0.827	0.749	0.768	0.724	0.688	0.709	0.660	0.728	0.689	0.614	0.712
BOFRF	0.680	0.666	0.685	0.702	0.891	0.875	0.760	0.784	0.718	0.660	0.686	0.622	0.760	0.709	0.675	0.725

Table 3 Comparison of model Recall in every client of different methods.

Client	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	Av-erage
Local	0.735	0.488	0.548	0.692	0.737	0.669	0.756	0.598	0.667	0.736	0.796	0.316	0.507	0.837	0.706	0.653
DFLRF	0.743	0.693	0.731	0.813	0.737	0.806	0.872	0.821	0.882	0.793	0.796	0.825	0.648	0.857	0.735	0.784
FRF	0.640	0.646	0.548	0.935	0.699	0.734	0.936	0.857	0.824	0.770	0.816	0.614	0.549	0.816	0.824	0.747
BOFRF	0.691	0.606	0.473	0.944	0.821	0.815	0.872	0.661	0.549	0.724	0.959	0.772	0.606	0.816	0.529	0.723

2) Interpertability Analysis

In machine learning modeling, the interpretability of a model can be analyzed in the following aspects:

(1) Which features are considered most important by the model

(2) How each feature influences the final prediction outcome for a specific record

In tree models, owing to their unique structure, models can capture interactions between features in the data and quantify each feature's contribution to the model's prediction. Most importantly, tree models are relatively straightforward to explain. The tree structure can be naturally visualized, and the prediction result for an individual instance can be represented as follows: if a certain feature exceeds/falls below a split point, the prediction will be

y1 rather than y2. The federated tree model algorithm proposed in this study offers better model interpretability compared to other federated algorithms, such as deep neural networks and MLPs. With other federated algorithms, interpreting the model, such as identifying important features or visualizing it, is challenging. Next, we will elucidate the federated random forest algorithm DFLRF model by incorporating experiments, particularly the model employed in predicting whether hospitalized patients across different clients will develop AKI.

To elucidate the performance enhancement of the federated random forest DFLRF algorithm model, we selected the local random forest models of clients 11, 12, and 15, which exhibited significant improvements, for comparative analysis. Initially, we compared the top 10 important features of the models for clients 11, 12, and 15 with those of the federated model. Subsequently, we visualized the models to explore how features influence the prediction results. Table 4 displays the top 10 important features of the models for various clients.

Table 4 Top 10 Important Features of Different Models.

Rank	Client 11	Client 12	Client 15	Federated Model
1	hypertension	coronary_artery_disease	pulmonary_disease	hct
2	diabetes	hypertension	peep	coronary_artery_disease
3	heart_disease	pulmonary_disease	bedside_glucose	pulmonary_disease
4	pulmonary_disease	cancer	mpv	ptt
5	coronary_artery_disease	diabetes	phosphate	bicarbonate
6	stroke	heartrate	mch	basos
7	rbc	race0	st2	fibrinogen
8	o2_sat	bun	etCo2	pao2
9	race5	respiration	polys	platelets1000
10	atrial_fibrillation	basos	atrial_fibrillation	insulin

The table illustrates significant variations in the important features between different clients and the federated model. Through analyzing the important features of different clients and the global federated model, along with assessing the impact of these features on prediction results, we can augment the weight of important differential features or conduct tree pruning operations to adjust the local model. This process enhances the performance of the local model.

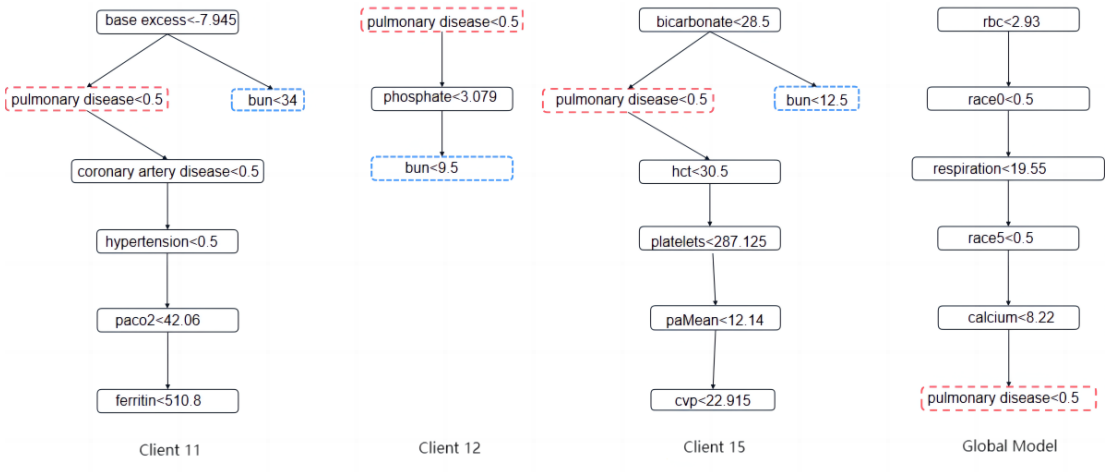
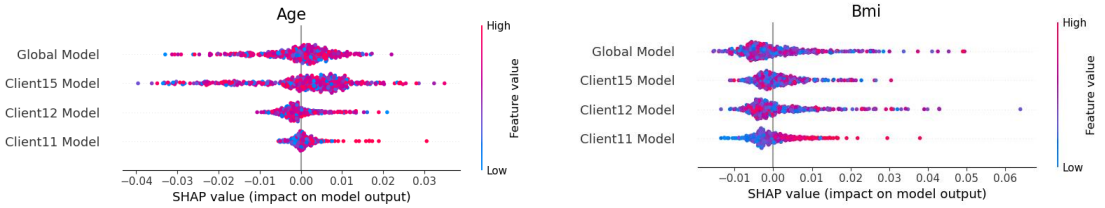


Figure 4 Branching Structures of Different Model Trees

To provide further interpretation of the differences among models, we use SHAP[31]to quantitatively explain and analyze the impact of important features on classification and visualized a portion of the structure of the first tree in the random forest model and analyzed the positions of the same features in tree nodes across different models, as depicted in Figure 4. For the discrete feature "pulmonary disease" (indicated by the red dashed box in the figure), the depths in the random forest models for clients 11, 12, and 15 are 2, 1, and 2 respectively, while in the federated random forest model, it is at the sixth level. Additionally, there are notable differences in the division values of nodes for continuous features. For example, consider the feature "bun" (indicated by the blue dashed box). The division values at the feature nodes are <34, <9.5, and <12.5 for clients 11, 12, and 15 respectively. However, this feature does not appear in the federated random forest model.



(**a**) (**b**)

Figure 5 (a)SHAP Values of Age in Different Models. (b)SHAP Values of Bmi in Different Models.

Subsequent to analyzing the impact of features on the model, this study calculated the SHAP values for the same feature across each model, as depicted in Figure 5a and 5b for the features age and BMI. The figure illustrates that the contribution of the age feature varies among different clients, yet its correlation remains consistent. Conversely, the BMI feature displays different correlations across models. For instance, in the model for client 15, as the BMI value increases, it demonstrates a negative correlation, whereas in the global federated model, it shows a positive correlation.

V CONCLUSIONS

In this paper , we propose DFLRF, a highly interpretable multi data center joint modeling algorithm. This method can be applied not only to disease prediction modeling on EHR, which is the focus of this study, but also to joint modeling across data silos that focus on the interpretability of other algorithms such as biomedical and financial fields. During the federated training phase, each client utilizes bootstrap sampling techniques with replacement to ensure that the decision tree models obtained by each client in each federated round are different. During the Random Forest update phase, each client evaluates and integrates all tree models from the current round using tree model and loss transmission strategy. It selects the optimal trees to join the Random Forest based on a loss matrix. To evaluate the effectiveness of this method, federated experiments were conducted using data from 15 hospitals in the eICU database. The results indicate that compared to baseline algorithms, the DFLRF algorithm effectively enhances AUC and Recall, balancing model complexity and performance while ensuring data security. This contributes to the interpretability and adaptability of federated learning.

However, our method also has some shortcomings. For example,the decision tree selected in each round of federated learning is the one with the lowest average loss across all clients, which is considered to have the best generalization performance. Yet, this approach may not perform well in some personalized federated scenarios.We will continue to discuss this issue in-depth in our future work.

Data Availability Statement: The data presented in this study are available on https://eicu-crd.mit.edu/about/eicu/
Conflicts of Interest: The authors declare no conflict of interest.

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