A Comprehensive Review of Privacy-Preserving Machine Learning Techniques for Heart Disease Prediction

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Abstract:

Heart disease is perpetually among the top-ranked causes for deaths worldwide, thus making its early and accurate prediction a matter of paramount importance. Thanks to the digitization of the medical knowledge base, ML models have shown a great promise in the analysis of complex clinical datasets to enable effective diagnosis. Nevertheless, the centralized nature of traditional ML approaches engenders some serious concerns regarding patient privacy, regulatory compliance, and data interoperability. This review systematically discusses the privacy-preserving paradigms, particularly FL, that support the collaborative building of models without access to raw patient data. We assess the performance of algorithms such as Support Vector Machines, XGBoost, and hybrid ensemble models in federated settings and study their impacts on varied healthcare datasets. Advanced modeling and optimization techniques are proposed to circumvent class imbalance, overfitting, and heterogeneity in distributed settings. Also reviewed are cryptographic techniques, differential privacy, and secure aggregation, which are key in protecting sensitive information. This paper tries to provide a holistic picture of the trends, challenges, and future directions of privacy-aware ML for heart disease prediction.

Keywords: *Heart Disease Prediction, Federated Learning, Privacy-Preserving AI, Support Vector Machine, XGBoost, Medical Data Security*

I. INTRODUCTION

Cardiovascular diseases still remain among the major causes of death, with millions dying each year. The earlier the diagnosis and intervention, the better the prospects for patients and fewer financial burdens on healthcare systems [1]. Thus, with the digitization of medical records and health data proliferating between institutions, there appears to be much untapped potential for the development of enhanced computational models for heart disease prediction. However, this data is often distributed across different hospitals and research centers, and barriers exist regarding data sharing, privacy, and interoperability [2]. In regular centralized machine learning approaches, raw data must be transmitted; but this is impossible because of regulatory and ethical issues. Federated learning and privacy-preserving data mining approaches appear to be potential solution avenues to overcome these obstacles [3]. This work is aimed at the development of an efficient heart disease prediction model from distributed media. Fig.1shows Heart Disease Prediction

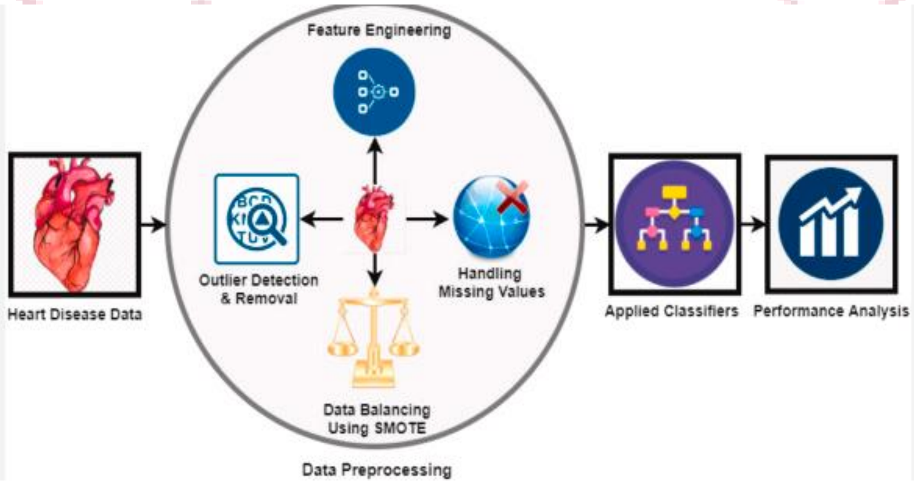

Fig.1: Heart Disease Prediction [3]

Cardiovascular illnesses rank first in terms of causing death, claiming nearly 17.9 million deaths yearly, which constitutes about 32% of all deaths worldwide, according to WHO. Heart diseases, including coronary artery disease [4], arrhythmias, and heart failure, are the most common among CVDs and are largely responsible for the socio-economic burden. Upward trends of heart-related ailments have been attributed to sedentary lifestyles, unhealthy food habits, obesity, diabetes, and smoking, especially in low- and middle-income countries [5]. On top of that comes the silent onset of early symptoms in most cases, making diagnosis at a very early stage almost impossible until symptoms are severe. Hence, the need for mechanisms that will help in cantilevering the disease early and an accurate prediction of the disease. Combining digital technologies with health—which include Electronic Health Records (EHR)—has become an ultimate answer to the realization of data-driven healthcare [6]. Machine learning has further entered this scene to train-medical data with high dimensions and uncover latent patterns in either clinical or ECG features or demographics using algorithms like Support Vector Machines (SVM), Decision Trees, Neural Transfer, and XGBoost. Thereby stratifying risks of patients, enabling preventive care, and facilitating personalised treatment choices when the choice is there on. But the course of success for machine learning in healthcare depends largely on access to large and diverse datasets, which are all too often split apart across multiple institutions [7].

Whilst the advantages are theoretically there, challenges abound for the centralized learning frameworks in medicine, mainly because patient data is so sensitive and heavily protected by privacy laws. Centralizing datasets from several different institutions increases the chances for data breach and identity theft and could raise even higher legal and ethical concerns [8]. The stigma around confidentiality often makes it very difficult for either patient groups or providers to proceed with sharing data, thereby posing the greatest challenge to assembling comprehensive training data sets. Apart from these, strict regulations such as the Health Insurance Portability and Accountability Act (HIPAA) in the U.S. and the General Data Protection Regulation (GDPR) [9] in the EU lay down stringent restrictions on how medical data can be shared and processes, particularly across borders. These hurdles therefore, impede the linking of data from multiple sources to aircraft training for accurate, and generalized ML models. On top of this, the technical inconveniences stare back: centralized solutions for model training often suffer from issues of scalability, latencies, and heavy infrastructure costs. Furthermore, the difference present between patient data structure and quality among various institutions stigmatizes integration even more [10]. In contrast, the traditional setting of data accumulation within a central repository for training has been somewhat identified as a risky and rather inefficient alternative in the case of healthcare settings.

With these issues, FL has developed into one such transformative stage, making it ideally suited to the healthcare industry. FL allows various medical institutions to train machine learning models collaboratively without having to share the dirty data. Instead, the institutions (clients) train locally on the private datasets and share only the learned parameters, such as weights or gradients, with the central server for aggregation. This decentralized setup complies with data protection laws and serves to minimize the risk associated with privacy issues [11] The aggregated global model is then sent back to the institutions for further local training, fostering an iterative and privacy-compliant learning process. FL really shines when it comes to settings such as heart disease prediction, where data lies in different healthcare centers, and patients differ based on demographics and clinical profiles. By enabling secure, distributed training, FL ensures model generalizability and performance while remaining compliant with HIPAA and GDPR. Therefore, FL is not only a technical innovation but also a practical and scalable ethical solution to developing robust predictive models in modern healthcare landscapes.

With FL securing distributed training, generalizability, and the performance of AI models, it guarantees the health information privacy act (HIPAA) and the General Data Protection Regulation (GDPR). In fact, this keeps FL from being seen merely as a technical innovation and situates it as a real-world, scalable, and morally appropriate solution to build powerful predictive models in modern healthcare ecosystems. In this light, the present review provides a comprehensive discussion on recent machine learning-based approaches for predicting heart diseases, analyzing their methodology, datasets, performance criteria, and key limitations-laying the foundation for the incorporation of privacy-preserving technologies like FL into clinical use [12].

II. LITERATURE REVIEW

Chintan M. Bhatt et al. [1] (2023) performed K-modes clustering with Huang initialization and used four algorithms, namely Random Forest, Decision Tree, MLP, and XGBoost, on a Kaggle dataset consisting of 70,000 instances. Results of GridSearchCV on hyperparameter tuning showed MLP to be better than its counterparts, with classification accuracy reported at 87.28% and AUC scores reaching 0.95. Nevertheless, issues of generalizability arise owing to the size and nature of the dataset.

ALLE HARSHA VARDHAN et al. [2] (2023) proposed a hybrid ensemble classifier which combined strong and weak learners, utilizing a large training and validation dataset to improve prediction accuracy for heart conditions. The ensemble outperformed single classifiers such as Random Forest, Decision Tree, SVM, Naive Bayes, and Logistic Regression. However, the study does not mention any limitations of the model or its generalizability to datasets that are diverse.

Zeinab Noroozi et al. [3] (2023) have located and examined a set of sixteen feature selection methods and seven ML algorithms using the Cleveland Heart Disease dataset. The performance of J48 improved greatly through feature selection, but the accuracy for MLP and Random Forest deteriorated. The best accuracy observed was 85.5%, attained by SVM-CFS, Information Gain, and the like. This leads to a number of issues, especially because of the small size of the dataset restricting use of the models for actual clinical applications.

Nadikatla Chandrasekhar et al. [4] (2023) implemented six algorithms: Random Forest, KNN, Logistic Regression, Naïve Bayes, Gradient Boosting, and AdaBoost on Cleveland and IEEE Dataport datasets. Their ensemble-based approach using soft voting yielded better performance with an accuracy of 93.44% on Cleveland and 95% on IEEE Dataport. This, however, puts into question the applicability in real-life clinical settings due to dependence on curated datasets.

Qadri et al. [5] (2023) proposed a new method of feature engineering, Principal Component Heart Failure (PCHF), and tested it under nine machine learning algorithms. The Decision Tree model, in particular, managed to give 100% accuracy, showing its real potential. This method, however, may suffer from overfitting as it was tested on a dataset that is rather small or too specific.

Biswas et al. [6] (2023) attempted to perform feature selection by Chi-Square, ANOVA, and Mutual Information methods, using six classifiers. Random Forest combined with the mutual information subset SF3 gave the best result of 94.51% accuracy and AURC of 94.95. However, this also limited the generalization of the model across other diverse populations because of its dependency on a particular healthcare dataset.

K. Arumugam et al. [7] (2023) worked on diabetic-specialized heart disease prediction employing Decision Tree, Naive Bayes, and SVM classifications, wherein the Decision Tree performed slightly better than others. However, the study stands constrained due to the limited availability of complete datasets specific to diabetic patients.

Ahmed A. H. Alkurdi et al. [8] (2023) built the entire preprocessing pipeline for normalization, SMOTE, and feature selection with the UCI Heart Disease dataset. They evaluated Decision Trees, Random Forest, SVM, and k-NN classifiers, all highly capable of metrics such as accuracy and ROC AUC. The biggest disadvantage is that it has become overly dependent on SMOTE and thus, might be an introduction for synthetic bias.

Mr. J. A. Jevin et al. [9] (2023) proposed a distributed association rule mining framework utilizing intelligent agents across different medical data sites under privacy constraints. Under stringent privacy considerations, the framework enabled the efficient discovery of global rules with very low communication. The drawback, however, is that coordination of agents becomes rather difficult in heterogeneous and dynamic environments.

K-modes clustering and machine-learning models like Random Forest, Decision Tree, MLP, and XGBoost were applied by Mukesh Kumar Saini et al. [10] (2023) on a Kaggle Dataset of 70,000 samples to GRIDSEARCHCV for tuning of parameters. MLP reported accuracy of 87.28% with good AUC scores though dependence on a single dataset undermines the utility of the model in the real world.

M. H. Fadly et al. [15] (2023) applied SVM, AdaBoost, and hybrid SVM-AdaBoost models on the UCI Cardiac Disease dataset based on the CRISP-DM methodology. The hybrid technique obtained 90% accuracy, which was better than what SVM and AdaBoost achieved individually. Nevertheless, there was not any external validation, so the method cannot be generalized to broader clinical environments.

S. Yuda Prasetyo et al. [16] (2023) analyzed SVM, Naive Bayes, Decision Tree, and Random Forest algorithms on the Heart Failure Prediction dataset. Random Forest (91.85%) and SVM (90.76%) showed promising results, thereby justifying their use for heart disease risk prediction. Nonetheless, the study requires further tuning and validation on a larger dataset.

H. V. R. Bindela et al. [17] (2023) applied SVM with an RBF kernel and K-means clustering on the UCI Cardiac Disease dataset. SVM scored 91.85% accuracy, while K-means was able to segregate some subgroups with an accuracy of 84%. The primary drawback is the manual setting of the number of clusters, which decreases consistency and scalability.

[Six ML models, namely Logistic Regression, SVM, Decision Tree, Bagging, XGBoost, and LightGBM, were assessed for the prediction of myocardial disease by J. Miah et al. 18] (2023). XGBoost scored first with 92.72% accuracy. The lack of external data testing curbed the robustness of the model.

Anudeepa Gon et al. [19] (2023) examined whether Neural Networks, Logistic Regression, SVM, Random Forest, Naive Bayes, AdaBoost, and XGBoost yield improvements when applied to clinical and demographic features. Hence, different versions of the system could attain great accuracy, thus promoting early detection through feature importance insights. On the other hand, applicability to new populations now depends on the quality and scope of the training data.

V. R. Burugadda et al. [20] (2023) worked with Logistic Regression, Decision Tree, Random Forest, SVM, and ANN methods and predicted heart failure readmissions using EHR data. The models helped identify the patients at a high risk of readmissions to better plan their interventions. Limitations include some lack of interpretability and the underrepresenting of some socioeconomic variables.

In 2024, S. NagaMallik Raj et al. [21] designed a web application thatIntegrated XGB-Classifier and gradient boosting are applied on UCI Heart Disease dataset. With an accuracy of 85% and 93%, the system offers reliable risk predictions, allowing the users to evaluate the risk adequately. However, the existing prediction model does not consider the time-based features and may be overfitting; therefore, restricting its wider applicability.

In 2024, Sarah A. Alzakari et al. [22] integrated an IoT-system with XGBoost and Bi-LSTM models for remote monitoring of cardiac diseases with the real-time and electronic clinical data. This framework produces 99.4% accurate prediction with the best temporal forecast, but privacy issues and challenges in deploying it on a large scale come up as major obstacles.

J. Shanker Mishra et al. [23] (2024) took advantage of XGBoost, Bi-LSTM, and ResNet for cardiac datasets and MRI imaging to achieve an enhanced diagnostic accuracy of up to 99.4%. The Deep learning inclusion in the system increased the capability for enhancing feature representation while still requiring solutions for model interpretability and annotated data.

H. F. El-Sofany et al. (2024) [24] theoretically used feature selection (Chi-square, ANOVA, Mutual Information), combined with ten ML models, including XGBoost and the SVM, on the UCI dataset. With the SF-2, XGBoost attained an accuracy of 97.57% and an AUC of 98% according to SHAP interpretation. Still, clinical validation is lacking, and this brings the synthetic data bias into question.

Class imbalance was tackled by Adedayo Ogunpola et al. [25] (2024) through optimizations of XGBoost, CNN, Random Forest, and various other classifiers on the UCI dataset. XGBoost topped the leaderboards with 98.50% accuracy and 98.71% F1 score. While the results are quite good, one wonders whether the said results will generalize induced because the tuning was done in a specific dataset.

Table 1: Based on Machine Learning Techniques

Ref (Author, Year)	Technique Used	Dataset Used	Key Findings	Results	Limitations
[1] Chintan M. Bhatt et al., 2023	K-modes clustering with Huang initialization + RF, DT, MLP, XGB	Kaggle dataset (70,000 instances)	GridSearchCV tuning improves classification. MLP outperforms others.	MLP: 87.28% accuracy; AUC up to 0.95	Limited generalizability due to dataset size and composition
[2] ALLE HARSHA VARDHAN et al., 2023	Hybrid Ensemble Classifier integrating weak and strong learners	Large training and validation datasets	Ensemble model outperforms individual models in predicting heart conditions	Ensemble > RF, DT, SVM, NB, LR in accuracy	Not specified; possibly generalizability not discussed
[3] Zeinab Noroozi et al., 2023	16 Feature Selection Methods + 7 ML algorithms	Cleveland Heart Disease Dataset	Feature selection boosts J48 performance but reduces MLP and RF	Accuracy up to 85.5% with SVM-CFS, Info Gain	Small dataset, limited real-world applicability
[4] Nadikatla Chandrasekhar et al., 2023	RF, KNN, LR, NB, GB, AdaBoost + Soft Voting Ensemble	Cleveland & IEEE Dataport datasets	Ensemble outperforms individual models	Soft Voting: 93.44% (Cleveland),	Dependency on curated datasets

				95% (IEEE Dataport)	
[5] A. M. Qadri et al., 2023	PCHF feature engineering + 9 ML algorithms	Health data (dataset unspecified)	DT achieves perfect classification; PCHF improves detection	DT: 100% accuracy	Overfitting due to small or specific dataset
[6] Niloy Biswas et al., 2023	Chi-Square, ANOVA, Mutual Info + 6 ML classifiers	Not specified (healthcare dataset)	RF with mutual info features (SF3) performs best	RF: 94.51% accuracy, 94.95 AURC	Dataset dependency limits broad generalization
[7] K. Arumugam et al., 2023	Decision Tree, Naive Bayes, SVM	Diabetes-specific heart disease dataset	DT performs best in diabetic heart disease prediction	DT > SVM, NB (accuracy not specified)	Limited diabetic-specific data
[8] Ahmed A. H. Alkurdi et al., 2023	DT, RF, SVM, k-NN + Preprocessing (SMOTE, Normalization, Feature Selection)	UCI Heart Disease Dataset	Robust preprocessing pipeline enhances model performance	High scores across all metrics (Accuracy, Precision, ROC AUC)	Overuse of SMOTE may cause synthetic bias
[9] Mr. J. A. Jevin et al., 2023	Distributed Association Rule Mining using Multi-Agent System	Distributed medical data (privacy constraints)	Localized computation enables privacy-preserving rule mining	Efficient rule discovery with minimal communication	Complexity in agent coordination in dynamic networks
[10] Mukesh Kumar Saini et al., 2023	K-modes clustering + RF, DT, MLP, XGB + GridSearchCV	Kaggle (70,000 instances)	MLP achieves highest accuracy; strong AUC values for all	MLP: 87.28% accuracy, AUC up to 0.95	Single dataset limits cross-scenario applicability
[15] M. H. Fadly et al. (2023)	SVM, AdaBoost, Hybrid (SVM-AdaBoost)	UCI Cardiac Disease Dataset	Hybrid model offers best performance using CRISP-DM methodology	Hybrid: **90%**, SVM & AdaBoost: **86.67%**	No external validation; limits generalizability
[16] S. Yuda Prasetyo et al. (2023)	SVM, Naive Bayes, Decision Tree, Random Forest	Heart Failure Prediction Dataset	RF and SVM showed strong accuracy for heart disease risk prediction	RF: **91.85%**, SVM: **90.76%**	Needs further tuning and testing on larger datasets
[17] H. V. R. Bindela et al. (2023)	SVM (RBF), K-means Clustering	UCI Cardiac Disease Dataset	High SVM accuracy; K-means finds hidden subgroups	SVM: **91.85%**, K-means: **84%**	Manual cluster selection limits consistency
[18] J. Miah et al. (2023)	LR, SVM, DT, Bagging, XGBoost, LightGBM	Not UCI Cardiac Disease Dataset	XGBoost outperformed others in myocardial illness prediction	XGBoost: **92.72%**, LightGBM: **90.60%**	No external validation reduces robustness
[19] Anudeepa Gon et al. (2023)	Neural Networks, LR, SVM, RF, NB, AdaBoost, XGBoost	Clinical & Demographic Data	High accuracy; feature importance helps in early detection	High accuracy (not quantified)	Real-world applicability depends on dataset quality

[20] V. R. Burugadda et al. (2023)	LR, DT, RF, SVM, ANN	Electronic Health Records (EHR)	ML models help identify high-risk heart failure readmission patients	Evaluated via accuracy, precision, recall, F1	Gaps in interpretability and fairness due to unbalanced features
[21] S. NagaMallik Raj et al. (2024)	XGB-Classifier, Gradient Boosting	UCI Heart Disease Dataset	Web app enables early diagnosis and risk prediction	XGB: **85%**, GB: **93%**	Excludes time-based feature; possible overfitting
[22] Sarah A. Alzakari et al. (2024)	IoT + XGBoost + Bi-LSTM	ECD + Real-time Data	Remote monitoring with Bi-LSTM yields excellent temporal prediction	**Accuracy: 99.4%**	Privacy and IoT deployment challenges
[23] J. Shanker Mishra et al. (2024)	XGBoost, Bi-LSTM, ResNet	Cardiac Data + MRI Images	Combines imaging and structured data; deep learning boosts accuracy	Accuracy: **up to 99.4%**	Needs annotated data; interpretability concerns
[24] H. F. El-Sofany et al. (2024)	FS (Chi2, ANOVA, MI) + 10 ML Models incl. XGBoost, SVM, RF	UCI Cardiac Disease Dataset	XGBoost with SF-2 subset gave top accuracy; SHAP for explainability	Accuracy: **97.57%**, AUC: **98%**	Lacks clinical validation; synthetic data may bias results
[25] Adedayo Ogunpola et al. (2024)	XGBoost, CNN, RF, + 4 others	UCI Cardiac Disease Dataset	Tackles class imbalance; XGBoost achieved best overall metrics	Accuracy: **98.50%**, F1: **98.71%**	Limited generalizability beyond tuned dataset

III. MACHINE LEARNING TECHNIQUES FOR HEART DISEASE PREDICTION

Supervised algorithms for learning are also applied to train medical-labeled datasets for heart disease prediction. They detect concealed patterns in data sets on patients to predict health outcomes. The models are useful for risk stratification, timely diagnosis, and individual treatment so that healthcare actions can be carried out earlier [13].

a) Support Vector Machines (SVM)

SVMs for heart disease classification try to find optimal hyperplanes in high-dimensional spaces. They do well with binary classification and work best with small-scale data that are well structured. The flipside to SVMs is parameter selection since if parameters are selected wrongly, the classifier becomes almost useless; they also are not great with medical data often fraught with noise and sometimes with an imbalance of classes [14].

b) Decision Trees and Random Forests

Decision Trees provide interpretable, rule-based classifications. Random Forests as ensemble methods aim at increasing accuracy via combining multiple decision trees [15]. They can handle missing values and large feature sets considering plenty of technicalities, which makes them fit for clinical datasets. Still, if not trained properly, they risk overfitting the model.

c) Neural Networks and Deep Learning

As Neural Networks and Deep Learning models such as CNNs and LSTMs learn complicated, non-linear associations in huge datasets, they suit very well image-based or sequential cardiac data. While offering massive precision, they demand a lot of data, computational power, and all-in-all can't offer an alternative in terms of explainability [16] for medical application.

d) Gradient Boosting (XGBoost, LightGBM)

Feature engineering transforms raw data into features acceptable for modeling, whereas feature selection refers to techniques used to select features that are most relevant for model training. Chi-square, ANOVA, and Mutual Information methods are good examples that reduce dimensionality [17], thereby giving better accuracy and avoiding overfitting. However, if the wrong parameters get selected, important clinical variables might be omitted, thus decreasing model robustness.

A. Ensemble and Hybrid Models

Ensemble classification models increase the performance and robustness of the model by combining outputs from different classifiers [18]. Ensemble methods employ bagging, boosting, and stacking techniques. Hybrid models possess the ability to integrate different algorithm strengths (e.g. SVM-AdaBoost) and can generalize better. They, however, often demand huge computational resources and may suffer from interpretability issues [19].

B. Limitations of Current Approaches

Some existing ML models for predicting heart diseases use data that are mostly very small or imbalanced, or worse, biased, thereby limiting their ability to generalize. In addition, the environmental setting of data collection is centralized, proving to be a big issue in maintaining privacy. Models thus can also be sometimes not so interpretable, and real-time usability is also low [20]. Technicalities of being in overfitting, cost of training, and regulations also work against deployment on large scale in clinical practices.

IV. COMPARATIVE ANALYSIS OF EXISTING ML APPROACHES

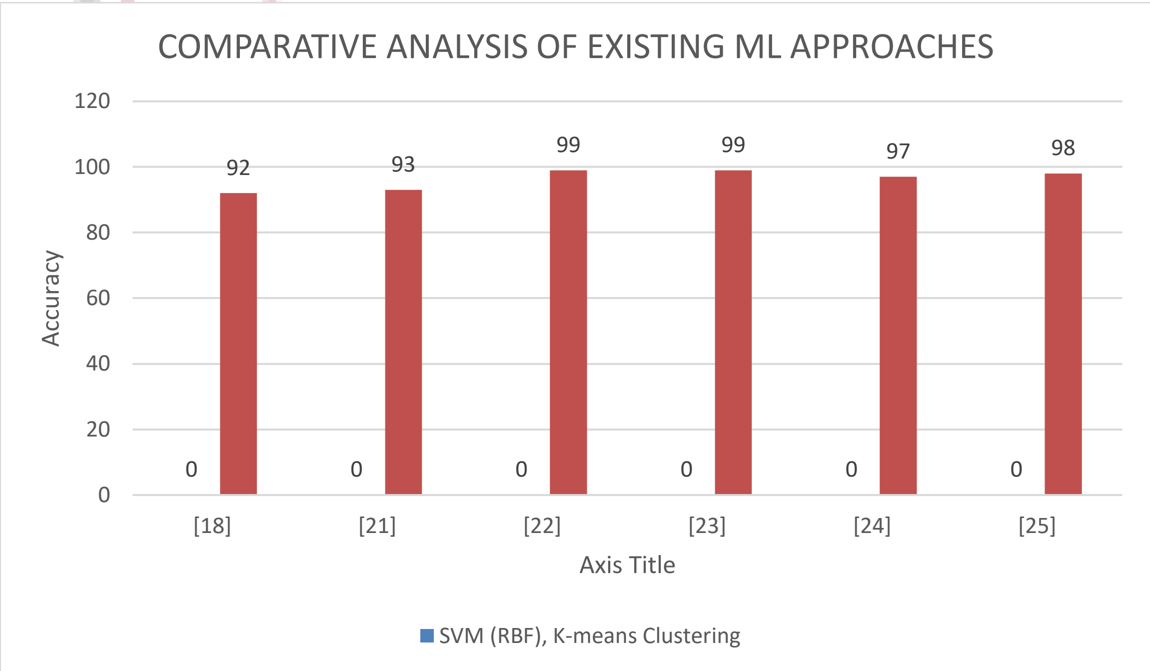

Fig .2: COMPARATIVE ANALYSIS OF EXISTING ML APPROACHES

The bar graph titled "Comparative Analysis of Existing ML Approaches" is a performance comparison of various machine-learning models for the prediction of heart diseases made reference to in [18], [21], [22], [23], [24], and [25]. The y-axis shows values for accuracy (up to 100), while the x-axis gives corresponding reference numbers.

Red-colored bars denote the accuracies (%) of different advanced ML methods except for SVM(RBF) and K-means Clustering, as in the legend. The blue bars for SVM(RBF) and K-means Clustering stand firm at 0% throughout, suggesting that either these methods were not employed, or their performance was not reported in these studies in particular.

Among the models evaluated, studies [22] and [23] exhibit the highest accuracy at 99%, followed closely by [25] with 98% and then [24] at 97%. Study [21] completes the fifth position with 93%, and finally, Study [18] bears the least rating with 92% of accuracy, respectively, showing that there is clear precedence for recent or hybrid deep learning-based methods (e.g., Bi-LSTM, CNN, and XGBoost ensembles) over traditional ones.

The chart also marks the increasing dominance of contemporary ensemble and deep learning models for heart disease prediction, while implying their remained limited or no usage of SVM (RBF) or K-means amongst these particular ones.

VII. CONCLUSION

The review attests to a transformation that came about when privacy-preserving machine learning methods were applied toward heart disease prediction. Simply put, as healthcare data increases with sensitivity, conventional centralized methods are rendered obsolete by privacy concerns, legal liabilities, and lack of interoperability. As a result, Federated Learning is now being hailed as a revolutionary alternative paradigm that supports decentralized training among different institutions without compromising data confidentiality. The inclusion of algorithms such as SVM and XGBoost in the Federated Learning framework has so far yielded promising results in terms of both predictive performance and regulatory compliance. Besides that, differential privacy, homomorphic encryption, and secure model aggregation methods create an additional layer of defense against data leakage through adversarial attacks. Another concern is imbalance between classes in data sets, which can be dealt with and generalized well by adopting a more advanced approach to local modeling, for there is often a trade-off in enhancing applicability. Despite existing problems like data heterogeneity, communication overheads, and delayed convergence, federated approaches offer a scalable, ethical, and efficient solution for healthcare systems of the 21st century. Therefore, continued investigations, mainly on navigating the harmony of federated model updates and incorporating explainability, will eventually pay off in Capitalizing Privacy-Aware AI in Clinical Settings.

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