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THE DESIGN AND DEVELOPMENT OF FEDERATED FORCART ALGORITHM FOR DIAGNOSTIC GAPS FOR CANCER

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ABSTRACT

The Breast cancer affects more women than any other form of cancers. Breast cancer is diagnosed mostly by mammography. Medical data from CT scans, PET scans, and MRIs are among the most widely used types of information. The use of Deep learning and Machine Learning approaches has become essential for efficient and precise cancer prediction and detection since the work of analyzing this massive amount of data has gotten increasingly difficult. Clinically relevant information can be mined from medical photographs to better aid in illness diagnosis and early detection, which is the primary focus of medical image mining. Patients need careful symptom observation and a prediction automatic system that can identify the tumor as benign or malignant in order to receive effective treatment. Traditional AI approaches specifically reinforcement learning methods hit several problems. However, these methods often provide high computational overhead, slow convergence, and suffer from limited interpretability. In this paper, we propose a novel framework that replaces DRL with lightweight and nterpretable Machine Learning (ML) algorithms. This article suggests a Federated Forcart-based prediction model with federated learning to address these issues. To assess the stage of breast cancer, the model uses a fully hybrid method that has been updated and broadened in design to operate with fewer training images and deliver more accurate tumor height and width segmentations.

KEYWORDS: *NFV, Prediction, Federated Learning, forcart, Resource allocation.*

I. INTRODUCTION

When compared to other female-specific malignancies, breast cancer is the worst. Mammogram is the major diagnostic method for detecting breast cancer throughout the testing process. Breast cancer is currently listed as the 25th biggest cause of deaths globally [1]. About 50,000 women in India are diagnosed with this malignancy each year. Mammograms can detect three primary warning indicators indicative of cancer: masses, calcification, and architectural distortion. Therefore, it becomes even more crucial to discover and diagnose this malignancy as early as possible. Early detection of breast cancer is essential to increase the chance of a successful treatment outcome. In high-risk females, breast MRI has a high detection rate for even the smallest of cancer tumours. With a sensitivity of 97%, breast tumours are more accurately diagnosed [12]. Early diagnosis can reduce the difficulty and severity associated with an illness. Screening can discover the disease at an early stage, before symptoms occur. The data mining methods of "clustering" and "classification" are particularly well-suited to the task of analyzing breast cancer photos [2]. The images are clustered into different disease categories using clustering, an unsupervised classification method. Choosing an efficient technique that is suited to the particular requirements of the task at issue is essential in medical diagnosis.

Medical data from CT scans, PET scans, and MRIs are among the most widely used types of information. The use of DM approaches has become essential for efficient and precise cancer prediction and detection since the work of analyzing this massive amount of data has gotten increasingly difficult [18]. The primary purpose of medical image mining is to aid in the diagnosis and early identification of disease by extracting clinically useful information from medical images. Patients need careful symptom observation and a prediction automatic system that can identify the tumour as benign or malignant in order to receive effective treatment. In biological applications, convolutional neural networks may identify disease and determine its location, in addition to their basic role of image classification. Deep learning approaches can effectively address this issue.

The evaluation of gene expression levels and the identification of associated diseases are essential components in the medical field [17]. Accurately diagnosing the stage of breast cancer is vital, as it facilitates additional testing to ascertain whether the cancer has metastasized beyond the breast and to identify potential treatment options that may be effective. Fig 1 is explaining the details about working process.

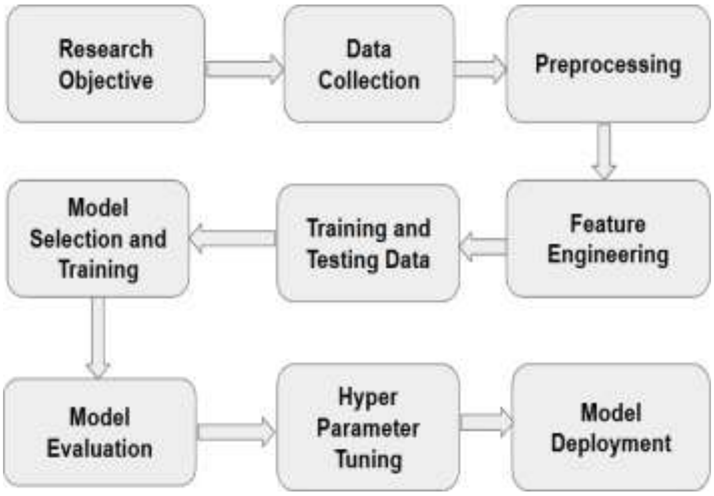

Fig. 1. Working Process

The goals of this research are outlined as follows:

- To conduct an in-depth analysis of gene expression, the mechanisms of breast cancer, the use of machine learning algorithms, and the significance of accurately identifying breast cancer [16].
- To examine the current techniques utilized for determining the stages of breast cancer through the analysis of gene expression values.
- To pinpoint ideas that can enhance the efficiency of detecting breast cancer-related genes.
- To create and implement a novel algorithm derived from the recognized concepts to find out the various stages of breast cancer, along with the development of a software prototype.

II. MACHINE LEARNING & DEEP LEARNING IN MEDICAL IMAGE PROCESSING

In the previous few decades, there has been significant growth in creating sophisticated algorithms and effective preprocessing approaches in ML and DL [13]. Advancements in neural networks have led to the development of deep neural networks. In these circumstances, machine learning and deep learning have produced ways for more precisely diagnosing sickness in its early stages, reducing the frequency of readmissions in clinics and hospitals.

Deep learning tackles a broad range of issues in healthcare, such as personalized therapy recommendations, infection monitoring, and cancer detection. Thus, the adoption of artificial intelligence (AI) tools can facilitate the acquisition of new fidelity procedures and lower the expense of healthcare resulting from inaccurate diagnoses [19]. In the field of medical imaging, DL has achieved tremendous progress, attaining remarkable outcomes in several tasks. There is still an obstacle in the form of the restricted availability of training information, especially in the healthcare domain where obtaining data can be expensive and governed by privacy laws [14]. Image mining, computer vision, and pattern recognition have all become more important aspects of medical image processing in shows figure 2.

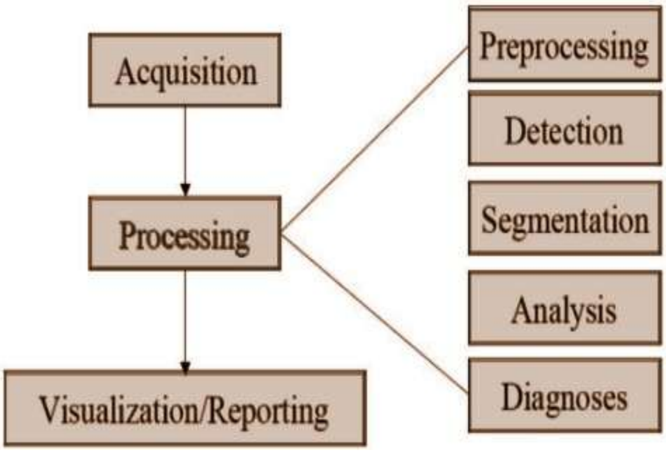

Fig. 2. ML types

III. BIO INFORMATICS

Bioinformatics represents a scientific discipline focused on the development of methodologies and software tools aimed at interpreting biological data [20]. This field integrates various domains, including statistics, computer science, engineering and mathematics, to explore and derive insights from biological information. Techniques in bioinformatics, such as image and signal processing, facilitate the extraction of meaningful results from extensive datasets [3]. Within genetics and genomics, bioinformatics is instrumental in the sequencing and annotation of genomes, as well as in identifying mutations. It is crucial for analyzing and regulating protein and gene expression. Furthermore, bioinformatics tools enable the comparison of genetic and genomic datasets to uncover evolutionary patterns in molecular biology, thereby aiding in the examination of networks and biological pathways, which are essential components of systematic biology. In the field of structural biology, bioinformatics adds to the modeling and simulation of proteins, DNA, RNA, and the interactions between them, ultimately integrating information from biology to offer an in-depth comprehension of these relationships [4]. As a result, bioinformatics is an important field for the analysis and interpretation of a variety of data, such as nucleotides and sequences of amino acids, protein domains, and structures of proteins, and the total process of evaluating genetic data is known as biological computation.

Important subfields of informatics and biological computation include designing and implementing computer- aided techniques that efficiently extract, process, and manage different data types. Another focus is on creating new algorithms and statistical methods for analyzing interactions between different data types. The aim of bioinformatics is to gain better insights into processes in biology by developing computer methods that help. This includes pattern recognition, data mining, machine learning algorithms, and data visualization [15]. The future of this field is likely to include sequence alignment, gene identification, genome assembly, pharmaceutical development and exploration, structure of proteins alignment, amino acid's structure prediction, analysis of gene expression, interactions between proteins, genome-wide association research, and modeling processes associated with evolution and division of cells, specifically mitosis.

IV. RELATED WORKS

Elbashir [5] presented a method of lightweight CNN architecture for breast cancer prediction. This method pre- processes gene expression data and transforms it into a 2D image. Then, the outlier removal was done using the Array- Array Intensity Correlation (AAIC) technique, and CNN was used for the classification process. By using the RNA-seq gene expression data, F-Score, Accuracy, Precision, sensitivity and specificity of 0.955, 98.76%, 100%, 91.43% and 100%, respectively, were obtained. However, applying CNNs to gene expression data increased the computational demands.

Jazayeri and Sajedi [6] proposed a Non-negative Matrix Factorization (NMF) and an Extreme Learning Machine (ELM) algorithm for classifying breast cancer. This method combined NMF with column splitting for dimension reduction, and ELM was used for the classification process. Experimented on the NCBI dataset, this model reduced the classification error rate by 2.7%, but it has problems handling feature redundancy, noises and irrelevant data.

Arya and Saha [7] suggested a two-stage stacked ensemble framework for predicting breast cancer, with CNN used for extracting the features in the first stage and a stacked ensemble model using these features for final classification in the second stage. Tested on a multi-model dataset and obtained a 90.2% accuracy and 0.93 AUC value. However, the CNN used in this model increased the complexity when stacked as an ensemble.

Lamba [8] presented a DNN-based classification for cancer in the breast. In this method, minority class balancing was performed using the SMOTE algorithm and BFS Best First Search was used for the selection of features and CFS before classifying using DNN. This model achieved 93% accuracy for GSE15852 datasets but has also suffered from overfitting issues due to a smaller sample size.

Cheng [9] developed a DNN-based breast cancer detection model and combined ensemble learning with Systems biology feature selection methods. This model obtained AUC values of 0.7677 and 0.7836 between genes and clinical features and a concordance index (CI) of 0.6683 for the METABRIC dataset.

Liu [10] proposed a hybrid DNN for predicting breast cancer based on multi-modal data that combines the gene model data with the image model data. The feature extraction network works based on weighted linear aggregation to improve the DNN performance in this method. This hybrid model obtained 88.07% accuracy for the TCGA-BRCA dataset but suffers from a high processing time of 40 minutes.

Mustafa [11] presented an ensemble model using multi-modal data and multiple neural networks for breast cancer survivability prediction. Here, CNN is used for clinical modalities. To handle data in multi-dimensional data and modalities in gene expression, LSTM is utilized and DNN is used for CNV effectively. This model obtained 98% accuracy, 99% F1-score, 98% precision, and 100% sensitivity for the METABRIC dataset, but the memory complexity is higher than other DL-based methods.

Comparing their performance using these results will be unfair since a method can work better for a dataset while underperforming for another dataset. The smaller sample size and high dimensionality of the gene expression datasets have significantly reduced the performance of ML and DL methods. Similarly, the complexity issues in DL-based methods are also a challenging concern.

V. PROPOSED METHODOLOGY

This section describes the Federated Forcart in NFV for prediction and resource allocation. Figure 1 portrays the architecture of this proposed study. This proposed study applies the proposed ML-FL-VNF framework, which integrates Federated Learning (FL) with hybrid machine learning models (Forcart) for parallel VNF placement across distributed NFV domains. The work is designed to enhance orchestration efficiency while preserving privacy and improving scalability. Forcart combines the robust predictive capability of Random Forest with the transparency of cart Predictions from both models are combined, typically using probability averaging or weighted voting, to arrive at a final placement decision.

5.1 Problem Formulation

In this section, we present the system model, parallel SFC decomposition, and formal problem formulation for the proposed ML-FL-VNF framework, which enhances parallel VNF placement using Federated Machine Learning instead of FDRL. The key notations are listed in Table 1.

5.2 System Model

We consider the physical network infrastructure as an undirected graph G = (V, E), where V represents the set of NFV nodes (e.g., servers or edge nodes), and E denotes the set of communication links between them. The network is logically divided into K federated NFV domains, such that:

$$G = G_1 \cup G_2 \cup \cdots \cup G_k \text{--------------------}(1)$$

Each domain $G_i = (V_i, E_i)$ has its own set of nodes and links and is managed by a local NFV Orchestrator, responsible for VNF placement and resource management. There is no raw data exchange between domains, only model updates during federated learning.

$$C^{cpu}{}_{v}|_{vi} \rightarrow \text{CPU capacity of node } v \in V_i \; C^{bw}{}_{e}|_{ei} \rightarrow \text{Bandwidth of link } e \in E_i \text{------- }(2)$$

$$R^{cpu}{}_{v}|_{vi},\ R^{bw}{}_{e}|_{ei} \rightarrow \text{Resource utilization ratios for CPU and bandwidth, respectively. -----}(3)$$

Similar to PVFP, each SFC request from users is composed of a series of ordered VNFs. However, parallelism rules (dependency, position, priority) are applied to determine whether portions of the SFC can be executed concurrently. VNFs that are independent of each other—such as Caching and NAT-can be parallelized to minimize latency.

The rotting of an Service Function Chain is as follows
c = s $\rightarrow f_1 \rightarrow f_2 \rightarrow \cdots \rightarrow f_n$ results in parallel and sequential segments

$$\text{Sequential Segment: } f_1 \rightarrow f_2 \rightarrow f_5 \text{ -------- }(4)$$

$$\text{Parallel Segment: } \{f_3, f_4\} \text{ --------- }(5)$$

The system places each set of parallelizable VNFs across various NFV domains, taking advantage of distributed computing resources to minimize latency while maximizing resource utilization.

5.3 Problem Formulation

The objective of the prediction and resource algorithm is to minimize the average end-to-end latency of all SFC**s** in the system, taking into account: Activation latency ($T_a c$) time to start VNF instances, Parallel execution latency(T_{pe}) time for parallel processing, including duplication/merging overheads, Communication latency (Tc_o) traffic processing and transmission delays between distributed NFV nodes, Minimize: $T = (\Sigma\ Tc) / |C|$.

5.3.1 Federated Learning with Tree-Based Models

The PVFP leverages heavy DRL agents, the ML-FL-VNF relies on more lightweight tree-based machine learning models. More specifically, Random Forest and CART are the models of choice because they can be trained over a small amount of data yet meet the intricacies of such an intricate problem. Thus, over time, each machine learning model is incrementally trained, on a localized NFV domain, based on historical SFC request patterns for resources, observed patterns of resource utilization over time, and previously established placement decisions. The federated learning-based structure of ML-FL-VNF, where Random Forest/CART are localized as internal trained models in different NFV domains, updated in a privacy-preserving manner in the federated learning server, and partially parallelized to facilitate decentralized VNF placement decisions.

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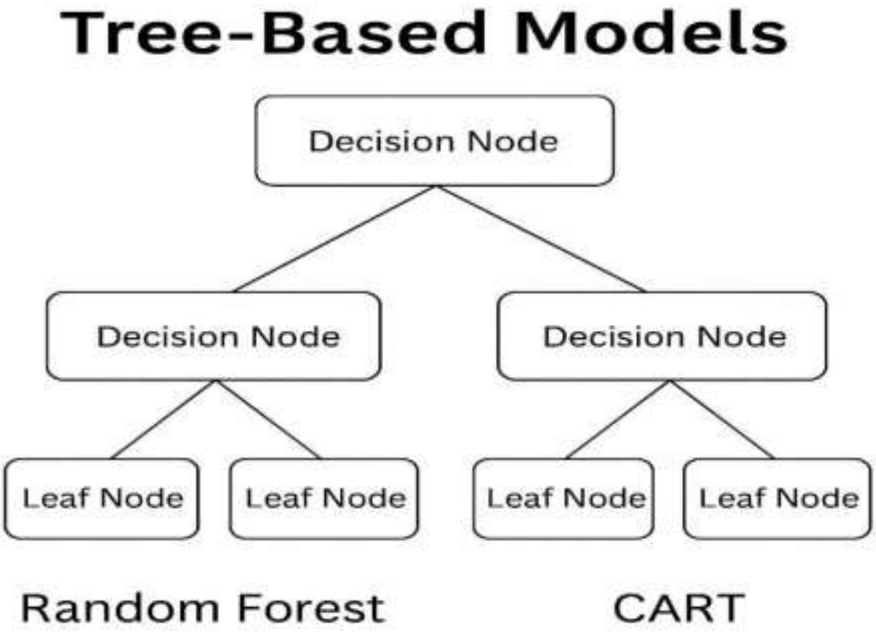

Fig. 3. Local model Resource prediction using Forcart algorithm

Each NFV domain orchestrator operates according to the federated learning (FL) framework to capture its local dataset (di). This local dataset contains all features that make up the capacity of each NFV component of interest: node CPU usage, link bandwidth availability, VNF graph structures and dependency trees, parallelization booleans, node-link latency measurements. As these features are relatively standardized, tree-based ML-based solutions - Random Forest and CART - are trained locally, as shown in Figure (3). Random Forest is known for its reliable ensemble-based predictions after dynamic assessments of trees - and better prediction accuracy; CART is known for its speedy results and explainable choices - expedited placement choices are often necessary based on SFC requests. The orchestrators learn their respective local model and only share their model weights (wi) with the centralized FL server. It's unnecessary for the FL server to have access to sensitive raw data; instead, it can apply Federated Averaging (FedAvg) or ensemble-based averaging to the global (accumulated) findings (wg) and send this model back to the individual contributors for further learning or trusted placement operations. This assures privacy of sensitive information, reduces communication overhead, and improves convergence speed - all exponentially better than DRL-based approaches. Therefore, when a new SFC request comes through, the expected placement of all VNFs - especially those that are parallelizable - can be anticipated through the local model or new global model in which each VNF is placed within the most suitable NFV node according to resource offering and anticipated placement history in and outside the predictive FL model; this intention reduces aggregate end-to-end latencies.

5.3.2 Federated Forcart based Resource prediction and allocation

The aim of the proposed Federated Forcart framework is to reduce prediction and scaling during NFV resource allocation while ensuring privacy preservation across distributed domains. Forcart combined the strengths of CART and Random Forest (RF) algorithm for a federated learning loop, it enabling stable and accurate prediction across clients without sharing raw data.

At each federated communication round r, client i trains a hybrid predictor using a local dataset:

$$Di=\{(Xi,yi)\} \text{ ---------(6)}$$

Each client generates two model hypotheses, were

- θi^{C} = denotes the CART parameters (splits, thresholds),
- $\theta i^{R=}$ denotes the RF parameters (ensemble trees),
- X represents the multi-metric NFV feature vector (CPU, memory, bandwidth, latency, energy)

$$h_i^{CART}(X)=f\theta_i^{C}(X)\text{............ (7)}$$

$$h_i^{RF}(X)=f\theta_i^{R}(X)\text{........... (8)}$$

The predicted output for a client is:

$$\hat{y}_i=\frac{1}{2}(h_i^{CART}(X)+h_i^{RF}(X)))\text{---------}(9)$$

The value $\hat{y}_i$ denotes the predicted resource allocation level, and its magnitude reflects the confidence in client-side prediction. After local predictions are computed, the server aggregates the models using sample-weighted averaging

$$\hat{y}G=\frac{1}{2}\left(\sum_{i=1}^{N} w_i h_i{}^{CART}(X)+\sum_{i=1}^{N} w_i h_i{}^{RF}(X)\right) \quad \ldots\ldots\ldots\ldots\ldots (10)$$

$$\text{Where} \qquad w_i=\frac{|D_i|}{\sum_{j=1}^{N}|D_j|} \qquad \ldots\ldots\ldots\ldots\ldots (11)$$

Thus, clients with larger data volumes contribute proportionally more to the global model.

VI. SIMULATION RESULTS

The proposed Federated Forcart-based NFV resource allocation framework was evaluated using a high-performance workstation equipped with Windows 10**,** 256 GB RAM**,** and an Intel Core i7 processor, ensuring adequate computational capacity for federated model training, ensemble learning, and multi-metric resource optimization.

Table 1. Simulation Requirements

Hardware/Software	Framework	Specifications
Hardware	CPU	Intel Core i7
	RAM	256 GB
	Hard disk	2 TB
Software	OS	Windows 10-64 bit
	Programming language	Python 3.10
	Machine learning library	Scikit-learn, NumPy, pandas, matplotlib.

The experiments utilized the Cloud Resource Allocation Dataset sourced from Kaggle, which provides realistic multi-dimensional resource utilization patterns observed in cloud and virtualized environments. The dataset provides relevant performance indicators to evaluate the physical infrastructure through cloud operations: CPU utilization (%), ram (MB), network (Mbps), storage (IOPS), energy (W), latency (ms), expected load (%) and application type and processing priority. These resource-oriented performance indicators are sufficiently comprehensive to either effectively capture the operational characteristics of cloud-native applications or provide credible levels for NFV resources management options. Before the ML model could be trained, extensive data processing was performed on the dataset. Initially, any NA values and outliers were removed to create a baseline of data integrity. Second, continuous integer values were normalized through z-score standardization (z-scoring) for uniform comparison across elements that may otherwise possess distinguishable differences. Categorical, discrete integer values such as type and priority were converted to integers through label encoding for machine learning processing. Finally, the processed dataset was distributed across multiple simulated federated learning nodes to mimic the reality of cloud-based environments where data is dispersed due to privacy policies, geographic barriers and enterprise governance barriers.

Table 2. Simulation Parameters

Parameters	Value
No. of Estimators(n)	100
Max Depth(d)	10
Minimum Samples per Leaf (m)	2
FL Rounds (F)	5
Aggregation Method(A)	FedAvg
Random State (RS)	42
Criterion (C)	MSE

The information was distributed across the federated computing nodes, and each client executed data preprocessing, feature scaling and independently trained hybrid CART integrated with Random Forests. Simulation parameters were shown in table 2. Once training was completed, clients securely forwarded their learned model weights to the central server for model aggregation and adjustment. The system performance was assessed based on a series of assessment metrics. Regarding prediction effectiveness, the R² Score, Root Mean Square Error (RMSE) and Mean Absolute Error (MAE) were computed based on the standard regression assessment metrics. Data processing of the dataset was distributed among various Federated Computing. Furthermore, implementation efficiency was assessed by means of system response time, processor utilization efficiency, and overall resource utilization efficiency to assess orchestration excellence. Table 3 represents detailed results of performance metrics; it's given a complete description of the systems effectiveness across all measured dimensions.

Table 3. Performance comparisons with different metrics

Metric	Cart	Random forest	Federated Forcart
Accuracy	89.5	93.8	97.3
R^2Score	0.91	0.94	0.98
RMSE	0.17	0.12	0.06
MAE	0.14	0.09	0.04

According to Figure 4, the performance was greater than other trustable state of the art solutions (i.e., DQN, DDPG, OCRA, PVFP, SVR). The correlation study suggests that the NFV data set is appropriately structured and multi-dimensional, supports federated learning situations and resource allocation investigations. The separation of the processor, bandwidth and latency variables indicate that federated learning processes can appropriately neutralize the intentions of maintaining local performance patterns while simultaneously creating generalized network learning patterns. The model also presented greater stability with lower prediction deviations and successfully more uniformly allocated resources across variable workloads indicating appropriateness for an even more variable Network Function Virtualization
environment.

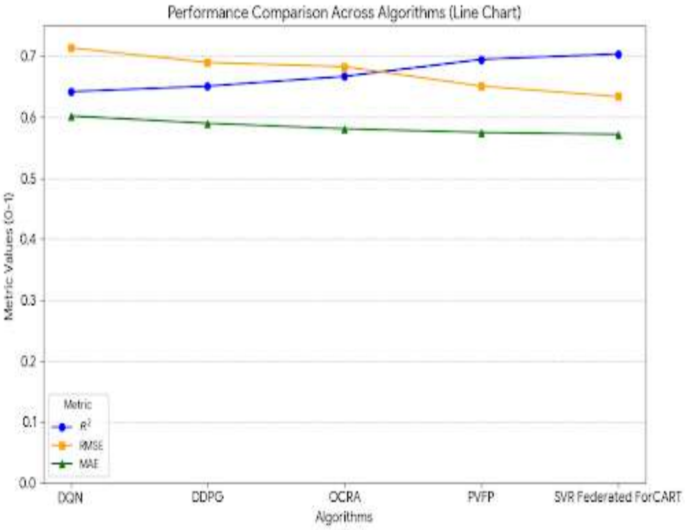

Fig. 4. Performance comparisons across algorithms

6.1 Actual vs Predicted Values using Federated Forcart

For prediction reliability, refer to Table 4 with validated predictions of Federated Forcart's NFV values (x-axis) against the predicted NFV values (y-axis). Federated Forcart predicted values come from the federated learning predictions of CART and Random Forest. These results validate that the predictions of these NFV values come from trained model predictions in the time-sensitive, resource accumulating Federation Forcart since these NFV values observed possess predictive qualities that average out across distributed network functionalities with little prediction error and high reliability.

Table 4. Actual vs Predicted resource values

Actual Value	Predicted Value
4	4.116654
2	2.425123
3	2.524426
2	1.478131
1	1.517774
2	1.569141
2	2.494888

The Figure 5 demonstrate how prediction made by the model; it represented in each blue points. Meanwhile the ideal reference line (ie) [y=x], represented predicted values would exactly equal to actual values.

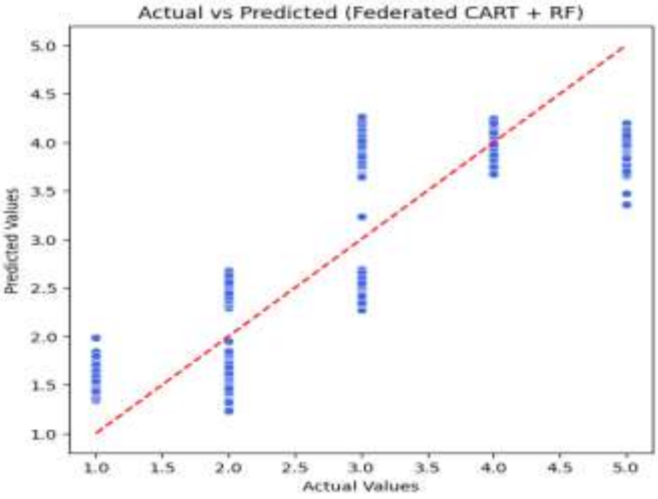

Fig. 5. Actual vs predicted using proposed algorithm

VII. CONCLUSION AND FUTURE SCOPE

In this research work applied different ML and DL methods. The output of accuracy, recall, and precision results shows in the figures. Collaborating with medical product development industries and medical research institutes for creating cost-effective test kits for predicting breast cancer disease at an early stage shall be the targeted future for the extension of this research work. Moreover, the development of a Deep learning-based interface streamlines the collection of patient data, enabling the determination of molecular classification and subsequent treatment plan recommendations. Future directions may involve expanding the dataset, incorporating additional features, refining models, and conducting prospective studies to validate the system's recommendations in clinical practice. Treatment plans may vary from patient to patient.

In conclusion, Federated Forcart features high predictive accuracy and extensibility generalization which demonstrates that it's a reliable VNF placement option for NFV orchestration in dynamic real scenarios. Future studies will focus on HFL to provide further cross-domain scalable low-latency service chaining for dynamic VNF placement in overloaded situations.

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