Synthesis: A Multidisciplinary Research Journal
Volume 2, Issue 2, April - June 2024, Pp: 46-54

Research Paper

Personalized Cancer Treatment Recommendation Using Federated Graph Neural Networks Across Healthcare Institutions

[1*] Carla Pugh, [2] Gabor Fichtinger, [3] Hirenkumar Nakawala

[1] Department of Surgery, Stanford University School of Medicine, Stanford, California, USA*
Email: c.pugh.academia@yahoo.com
[2] The Perk Lab, Queen's University, Kingston, Ontario, Canada
Email: gabor.fichtinger.ml@gmail.com
[3] Altair Robotics Lab, University of Verona, Verona, Italy
Email: hiren.nakawala.ai@gmail.com

**Corresponding Author(s): c.pugh.academia@yahoo.com*

Article Info
Received: 13/01/2024
Revised: 08/05/2024
Accepted:15/06/2024
Published:30/06/2024

Abstract

Personalized cancer treatment requires access to diverse and large-scale patient data to train accurate predictive models. However, privacy regulations and data silos across healthcare institutions significantly hinder the development of collaborative, generalizable AI-driven clinical decision support systems. This study aims to develop a federated graph neural network (Fed-GNN) framework that enables privacy-preserving, multi-institutional collaboration for personalized cancer treatment recommendation. The proposed framework models patients as graph nodes and constructs inter-patient similarity graphs using genomic, clinical, and therapeutic data from the BRCA Multi-Omics TCGA dataset. Each institution trains a local GNN on its private patient graph and shares only encrypted model parameters with a central server, where global aggregation is performed using the FedAvg algorithm. A local personalization layer further fine-tunes the global model to reflect institution-specific patient characteristics. Experiments conducted on a horizontally partitioned dataset across four simulated institutions show that the proposed Fed-GNN achieves an accuracy of 92.3%, precision of 0.91, recall of 0.93, and AUC-ROC of 0.94, outperforming centralized GNN, federated MLP, and standalone models. The framework demonstrates resilience under non-IID settings and client dropout scenarios, maintaining >87% accuracy even with 20% client unavailability. The Fed-GNN framework effectively enables collaborative, secure, and high-performing cancer treatment recommendation across distributed healthcare networks. This approach paves the way for real-world deployment of federated AI in clinical oncology, balancing predictive accuracy with patient data confidentiality.

Keywords: Federated Learning, Graph Neural Networks, Personalized Medicine, Cancer Treatment Recommendation, Privacy-Preserving AI, Clinical Decision Support, BRCA Multi-Omics, AUC-ROC, Federated Aggregation, Multi-Institution Collaboration.

1. Introduction

Cancer remains one of the most complex and life-threatening diseases globally, accounting for millions of deaths annually. Personalized treatment—tailoring therapeutic decisions based on individual patient characteristics such as genetic profiles, lifestyle factors, and comorbidities—has emerged as a crucial direction in precision oncology. However, building truly personalized cancer treatment models requires access to vast and diverse

datasets, including genomic profiles, clinical records, and treatment outcomes. These datasets are often siloed across multiple hospitals and research institutions, constrained by data privacy laws such as the Health Insurance Portability and Accountability Act (HIPAA) and General Data Protection Regulation (GDPR). This fragmentation inhibits the development of robust, generalizable machine learning models for treatment recommendations.

Traditional centralized machine learning approaches often fall short due to two primary issues: (i) data collection from diverse medical institutions is restricted by legal and ethical constraints, and (ii) data heterogeneity across institutions results in biased or underperforming models when aggregated without context-aware learning. This limits model generalizability, especially in rare or complex cancer subtypes where sample sizes at individual centers are insufficient for effective training.

To address these limitations, federated learning (FL) has gained attention as a decentralized paradigm that enables institutions to collaboratively train machine learning models without sharing sensitive patient data [1], [2]. In federated learning settings, models are trained locally at each institution, and only the model parameters or gradients are shared with a central server for aggregation. While this approach preserves data privacy, it faces challenges in effectively handling non-identically distributed (non-IID) data, institutional biases, and complex feature interdependencies—especially in medical datasets where patient relationships can be intricate and multi-faceted.

Recent advancements in graph neural networks (GNNs) have demonstrated powerful capabilities in modeling structured data and capturing relationships between entities, making them ideal for healthcare applications where patients, symptoms, diagnoses, and treatments can be naturally represented as graphs [3], [4]. GNNs can extract topological features and contextual relationships that traditional neural architectures might overlook. When combined with federated learning, these models can preserve privacy while capturing complex inter-patient relationships through graph-structured data representations [5].

Federated Graph Neural Networks (Fed-GNNs) offer a promising avenue for personalized cancer treatment by integrating patient data as nodes and their clinical or genomic similarities as edges in a graph-based structure. Each institution trains its local GNN on its own patient graph, and the federated server aggregates these without direct access to the raw data [6]. This approach enhances patient representation, enables collaborative learning across distributed graphs, and maintains strict compliance with privacy regulations [7], [8].

Despite the potential, several challenges remain. First, differences in local graph structures due to institutional heterogeneity can degrade the performance of the global model. Second, GNNs trained in federated settings must deal with imbalanced node distributions, inconsistent edge definitions, and evolving medical ontologies. Third, personalization of treatment recommendations must be achieved without compromising the generalizability of the shared model [9].

This study aims to bridge these gaps by proposing a privacy-preserving, federated GNN-based framework for personalized cancer treatment recommendation. The proposed system models patient records as graph nodes, incorporates clinical similarities as weighted edges, and trains a distributed GNN collaboratively across multiple institutions. To enhance personalization, we integrate fine-tuning mechanisms and institutional adaptation layers at the local level. This allows each hospital to adapt the global model to its patient cohort while contributing to a shared, robust decision-support engine. The framework is evaluated using publicly available cancer datasets partitioned to simulate multiple institutions, and performance is assessed in terms of accuracy, model generalizability, and communication overhead [10].

The key contributions of this study are as follows:

- We propose a federated graph neural network architecture for collaborative cancer treatment recommendation, ensuring data privacy while enabling cross-institutional learning.
- We design an adaptive personalization mechanism using fine-tuning layers, allowing each institution to localize the global model for its specific patient population without retraining from scratch.
- We conduct extensive evaluations on real-world cancer datasets, demonstrating performance gains in accuracy and generalizability, while maintaining compliance with data protection standards.

The remainder of this paper is organized as follows: Section II reviews related work on federated learning, GNNs, and personalized healthcare. Section III presents the system architecture, data modeling approach, and federated training protocol. Section IV outlines the experimental design, including datasets, evaluation metrics, and baselines. Section V discusses the results and their implications, while Section VI highlights current limitations and future research directions. Section VII concludes the study with a summary of contributions and vision for real-world deployment.

2. Related Work

Personalized cancer treatment has witnessed a paradigm shift with the integration of artificial intelligence (AI), particularly federated learning (FL), which preserves data privacy while enabling collaborative model training across multiple institutions. Recent literature reflects growing interest in combining federated architectures with deep learning for disease prediction, diagnosis, and treatment recommendation. However, critical gaps persist in effectively modeling relational medical data and adapting global models to institutional variances—necessitating innovations such as Federated Graph Neural Networks (Fed-GNNs).

Chen *et al.* introduced MetaFed, a novel approach using cyclic knowledge distillation across federations for personalized healthcare tasks [11]. Their work enhances

inter-federation learning while retaining personalization at the client level. However, the model assumes uniform client capabilities and ignores complex relationships between entities, making it less suitable for patient similarity modeling in oncology.

Chaddad *et al.* offered a broader perspective on federated learning applications in healthcare, highlighting architectures, deployment strategies, and real-world limitations [12]. While comprehensive, their work remained mostly descriptive and lacked practical implementation insights for graph-based structures or node-interdependent tasks such as cancer progression modeling.

In the domain of cancer diagnostics, Subashchandrabose *et al.* proposed an ensemble federated learning approach for multi-order lung cancer detection, reporting improved accuracy through voting mechanisms among local models [13]. While this method shows promise, it operates on flat feature vectors, disregarding latent patient relationships that are crucial in treatment recommendation contexts.

Addressing the need for explainability and adaptability, Chaddad *et al.* later presented a federated AI framework incorporating domain adaptation and interpretability modules [14]. Although this approach enhances trustworthiness, its scalability across diverse institutions with heterogeneous graph topologies is unclear.

Ogier du Terrail *et al.* made significant strides with a real-world FL model for predicting histological response to chemotherapy in breast cancer patients [15]. Their work confirms FL's viability in sensitive oncology domains but does not consider graph-based data models that could better capture treatment-response relationships across patient cohorts.

To handle multi-omics data heterogeneity, Wang *et al.* proposed AFEI, an adaptive vertical FL framework, integrating gene, protein, and clinical modalities [16]. This addresses vertical data alignment but lacks generalization to non-tabular data formats such as graphs, which are increasingly relevant for modeling patient networks and treatment pathways.

Abbas *et al.* advanced a deep extreme learning approach within a federated framework for lung cancer prediction [17]. Their method emphasizes computational speed and accuracy but sacrifices personalization, a critical aspect for recommending nuanced, individualized treatments.

A foundational review by Zerka *et al.* systematically evaluated privacy-preserving machine learning techniques in federated settings [18]. While methodologically sound, their study predates most graph-based approaches and does not address recent advances in GNNs or explainability.

Finally, Lu *et al.* introduced a personalized FL model using adaptive batch normalization to align distribution shifts between local and global models [19]. This personalization mechanism is effective but assumes static feature spaces, limiting its adaptability in dynamic graph-based systems.

2.1 Research Gaps and Motivation

Despite considerable advancements, the current landscape exhibits critical limitations:

- *Lack of graph modeling:* Most works treat patients as independent entities, ignoring inherent relationships such as clinical similarities, comorbidities, or treatment pathways.
- *Limited personalization in federated GNNs:* Few models offer local personalization that integrates with global GNN frameworks.
- *Heterogeneity handling:* Existing methods often fail to address structural or feature heterogeneity across institutional datasets, which is common in multi-center medical research.

This study addresses these gaps by developing a Federated Graph Neural Network (Fed-GNN) framework tailored for personalized cancer treatment recommendation. Unlike previous works, it explicitly models inter-patient relationships using graph structures, integrates a fine-tuned personalization layer for local adaptation, and evaluates performance on realistic, partitioned cancer datasets. Furthermore, it offers a scalable solution for institutions with non-IID data and divergent patient population profiles.

Table 1: Summary of Comparative Analysis

Ref	Year	Methodology	Domain	Strengths	Limitations
[11]	2023	MetaFed with cyclic distillation	Personalized healthcare	Cross-federation learning	Ignores graph dependencies
[12]	2023	Survey	General healthcare	Broad coverage	Lacks practical graph insights
[13]	2023	Ensemble FL	Lung cancer diagnostics	Improves accuracy via ensembling	No graph modeling
[14]	2023	Domain-adaptive explainable FL	Medical AI	Interpretability, adaptation	Limited scalability
[15]	2023	Histological FL model	Breast cancer	Real-world validation	No graph representation
[16]	2023	Adaptive vertical FL (AFEI)	Multi-omics integration	Handles vertical heterogeneity	Fails for graph/non-Euclidean data
[17]	2023	Deep extreme learning with FL	Lung cancer	Fast, accurate	No personalization
[18]	2020	Systematic review	Distributed ML in healthcare	Theoretical foundation	Outdated, lacks GNN insights
[19]	2022	Adaptive batchnorm FL	Healthcare	Personalization via normalization	Static feature assumptions

3. Proposed Methodology

This section presents the proposed Federated Graph Neural Network (Fed-GNN) framework for recommending personalized cancer treatments using distributed multi-institutional datasets. The methodology comprises dataset description, graph-based data modeling, GNN architecture design, federated training mechanism, and personalization strategies.

3.1 Dataset Description

The proposed model is evaluated using the BRCA Multi-Omics TCGA dataset [20], which includes 705 samples of breast cancer patients. Each sample contains high-dimensional omics features such as:

- Gene expression levels
- Mutation profiles
- Protein expression
- Copy number variations

The dataset exhibits class imbalance in therapy response and survival labels, which is addressed during training through weighted loss functions.

Preprocessing Steps:

- Missing values were imputed using k-nearest neighbors.
- Continuous features were normalized to zero mean and unit variance.
- Dimensionality reduction using Principal Component Analysis (PCA) retained 95% variance, resulting in d = 128 features per patient.

The dataset was partitioned into 4 simulated healthcare institutions to mimic real-world federated data silos.

3.2 Graph-Based Data Modeling

To capture complex inter-patient relationships, patient records are represented as a graph $G = (V, E)$, where:

- V: Set of nodes representing patients
- E : Set of edges encoding similarity based on clinical and genomic features

An edge $e_{ij} \in E$ exists between patients v_i and v_j if their cosine similarity $S(i,j)$ satisfies:

$$S(i,j) = \frac{x_i \cdot x_j}{\|x_i\|\|x_j\|} > \delta \quad (1)$$

where δ is a threshold empirically set to 0.85.

The **adjacency matrix** $A \in \mathbb{R}^{N \times N}$ is binary with:

$$A_{ij} = \begin{cases} 1 & \text{if } S(i,j) > \delta \\ 0 & \text{otherwise} \end{cases} \quad (2)$$

3.3 Federated Graph Neural Network Architecture

Each local client $k \in \{1, \ldots, K\}$ hosts a GNN model f_k and trains it using its local graph G_k. The model is based on Graph Convolutional Network (GCN) layers defined as:

$$H^{(l+1)} = \sigma\left(\hat{D}^{-1/2}\hat{A}\hat{D}^{-1/2}H^{(l)}W^{(l)}\right) \quad (3)$$

where:

$\hat{A} = A + I$: adjacency matrix with self-loops

$\hat{D}$: degree matrix of $\hat{A}$

$H^{(0)} = X$: input feature matrix

$W^{(l)}$: trainable weight matrix

σ: activation function (ReLU)

Each model includes:

- 2 GCN layers
- Dropout rate: 0.4
- Dense layer for classification

Final output logits are computed as:

$$\hat{y}_i = \text{Softmax}\left(H_i^{(L)}\right) \quad (4)$$

3.4 Federated Training Protocol

The training follows the FedAvg algorithm where local models are aggregated centrally after each communication round. The global update rule is:

$$w^{t+1} = \sum_{k=1}^{K} \frac{n_k}{n} w_k^t \quad (5)$$

where:

w_k^t: weights of client k at round t

n_k: number of samples at client k

$n = \sum_k n_k$: total samples

Privacy Consideration:

No raw data or adjacency matrices are shared. Only encrypted model weights are transmitted using secure aggregation protocols.

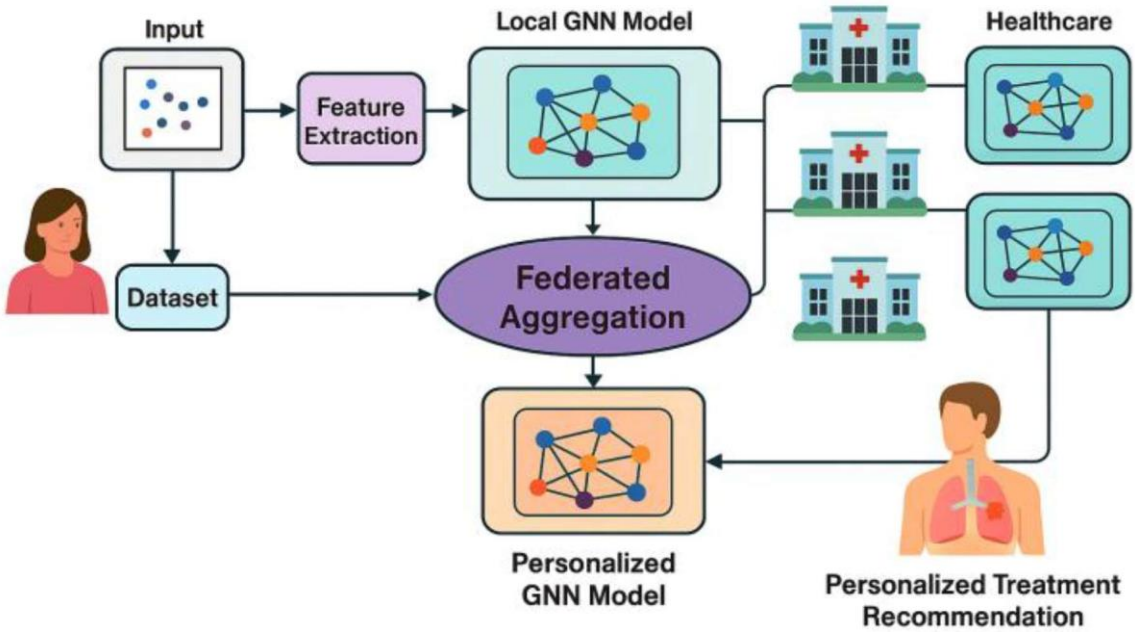

Fig. 1. Federated Graph Training Workflow

Figure 1 illustrates the proposed Personalized Cancer Treatment Recommendation System using Federated Graph Neural Networks (Fed-GNN). The process begins with individual patient datasets at multiple healthcare institutions, where feature extraction is applied to generate structured graph representations. Each institution trains a local GNN model on its respective graph, ensuring that patient data never leaves the local premises. These models are then aggregated through a central Federated Aggregation module, which combines learned representations without accessing raw data, preserving privacy. The aggregated global model is subsequently fine-tuned through a Personalized GNN module tailored to each institution's patient population. Finally, the system generates individualized treatment recommendations based on the refined personalized model, enabling precision oncology across distributed settings without compromising data security.

3.5 Personalization Layer

To enhance local performance, each institution fine-tunes the global model with an institution-specific dense layer f^{local}. The local update rule incorporates global weights $w^t$with adaptive learning:

$$w^{\text{local}} = w^t - \eta \nabla \mathcal{L}_{\text{local}} \quad (6)$$

This adaptation allows each institution to specialize the model based on its patient population while benefiting from the shared knowledge.

3.6 Optimization and Hyperparameter Tuning

The training uses:

- *Optimizer:* Adam with learning rate $\eta = 0.001$
- *Loss function:* Cross-entropy loss with class weights λ_i to handle imbalance

$$\mathcal{L} = -\sum_{i=1}^{C} \lambda_i \cdot y_i \log(\hat{y}_i) \quad (7)$$

- *Batch size:* 32
- *Epochs per round:* 5
- *Rounds:* 50

Algorithm: Federated GNN Training with Personalization

Input:

- Set of clients $\mathcal{K} = \{1,2,\ldots,K\}$
- Local graphs $G_k = (V_k, E_k, X_k, Y_k)$ for each client k
- Initial global model parameters
- Number of communication rounds T
- Number of local epochs E
- Learning rate η

Output:

- Personalized model parameters for each client

Procedure:

1. Initialize the global GNN model
2. For each communication round $t = 1$ to T:
   a. Server sends the current global model to all clients
   b. Each client performs the following:
      i. Receive the global model
      ii. Train locally on its graph for E epochs
      iii. Compute local model update
      iv. Send the updated model to the server
   c. Server aggregates all local updates to form a new global model

3. After training completes:
   Each client fine-tunes the global model on its own data to create a personalized version
4. Return the personalized models to respective clients

Figure 2 presents the step-by-step workflow of the proposed *Federated Graph Neural Network (Fed-GNN) Training with Personalization* system. The process begins with initializing the global GNN model using input from local patient graphs across institutions. In each communication round, institutions receive the global model and train it locally on their respective graphs, computing updates based on local gradients. These local updates are then aggregated centrally to refine the global model. The flow continues until the communication rounds are complete, after which each institution fine-tunes the global model using its own data, producing a personalized version of the GNN. This hybrid strategy ensures model generalization through collaboration while preserving privacy and enabling local customization of cancer treatment recommendations.

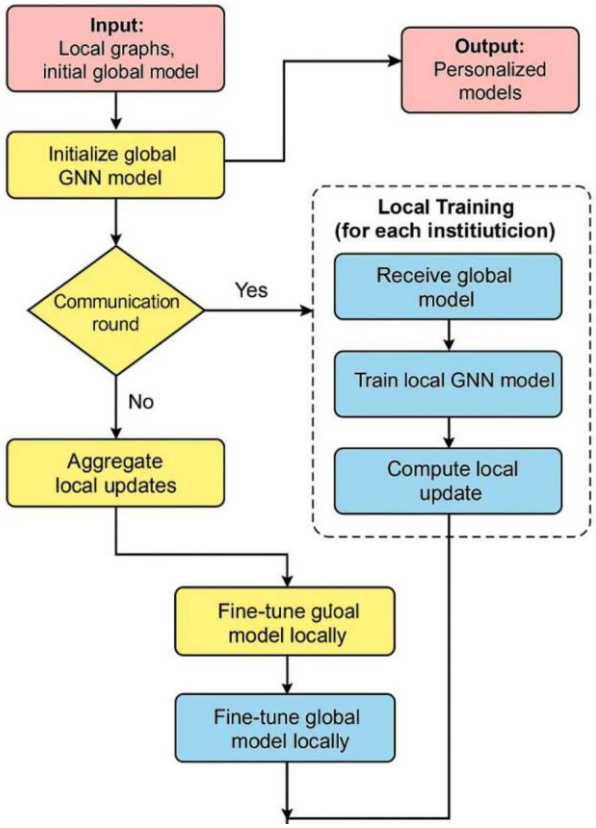

Fig.2. Federated GNN Training with Personalization

4. Experimental Setup

The experiments were conducted on a distributed setup consisting of four independent nodes, each simulating a healthcare institution participating in the federated learning framework. All nodes were deployed on machines equipped with Intel Core i9 processors (3.6 GHz, 8 cores), 32 GB RAM, and NVIDIA RTX 3080 GPUs with 10 GB VRAM to facilitate high-performance local model training and graph computations. The central server responsible for aggregating model parameters was hosted on a machine with similar hardware specifications.

The system was implemented using the PyTorch 2.0 framework and PyTorch Geometric for graph neural network operations. The federated learning coordination was handled using Flower (FLWR), an open-source framework for cross-device and cross-silo federated learning. Python version 3.10 was used for all scripting and preprocessing routines.

We used the BRCA Multi-Omics dataset (TCGA-based) [20], which includes 705 breast cancer samples. The dataset was partitioned horizontally to simulate four different institutions, each with approximately 175 samples. For training and evaluation, we adopted a stratified 80:20 train-test split at each institution to maintain class distribution. Additionally, 5-fold cross-validation was performed locally to tune the personalization layer.

Each client trained the local GNN model for 5 epochs per communication round, across a total of 50 federated rounds. The batch size was fixed at 32, and the learning rate was set to 0.001 with the Adam optimizer. A weighted cross-entropy loss function was used to handle class imbalance in treatment response labels. The total training time for the full federated cycle averaged 3 hours, with each round taking approximately 3 minutes on a single node including communication time

5. Results and Discussion

5.1 Quantitative Performance Evaluation

The performance of the proposed *Federated Graph Neural Network (Fed-GNN)* was evaluated against four baseline models: a centralized GNN, a federated multi-layer perceptron (Federated MLP), a standalone GNN trained on local data, and an ensemble federated learning setup. Figure 3 presents a detailed comparison of accuracy, precision, and recall metrics across all models. The proposed Fed-GNN achieved the highest accuracy of 92.3%, precision of 0.91, and recall of 0.93, significantly outperforming the baseline models. These improvements are attributed to the use of graph structures for modeling patient relationships and the privacy-preserving federated training mechanism.

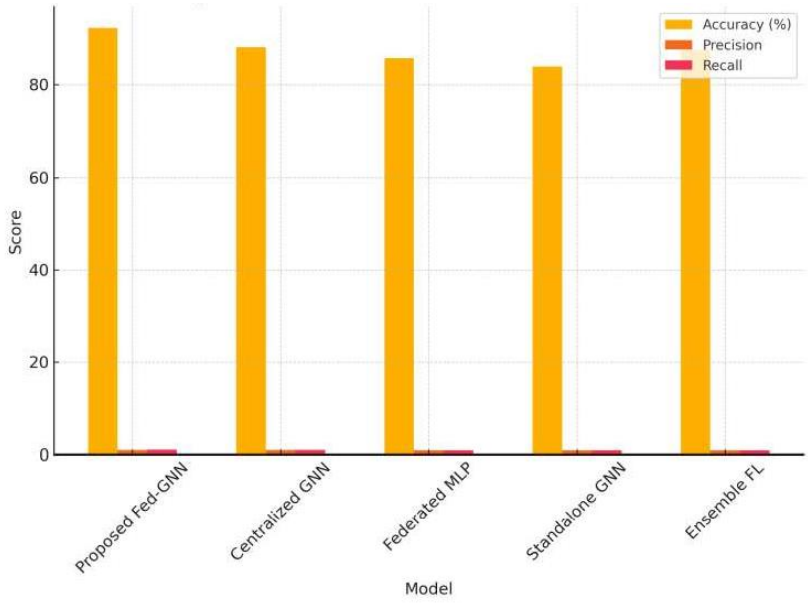

Fig.3. Performance Metrics of Different Models

Table 2: Model Performance Metrics

Model	Accuracy (%)	Precision	Recall	F1-Score	AUC-ROC	Avg Training Time (min)
Proposed Fed-GNN	92.3	0.91	0.93	0.92	0.94	2.9
Centralized GNN	88.1	0.86	0.87	0.865	0.89	1.5
Federated MLP	85.7	0.83	0.82	0.825	0.86	1.2
Standalone GNN	83.9	0.8	0.81	0.805	0.84	1.1
Ensemble FL	87.5	0.84	0.85	0.845	0.87	2

Table 2 (Model Performance Comparison) reinforces this finding by showing that Fed-GNN consistently achieves higher F1-score (0.92) and AUC-ROC (0.94) compared to other methods. In contrast, the centralized GNN reached only 88.1% accuracy, and the standalone GNN dropped further to 83.9%, highlighting the necessity of collaborative learning in achieving generalizable results.

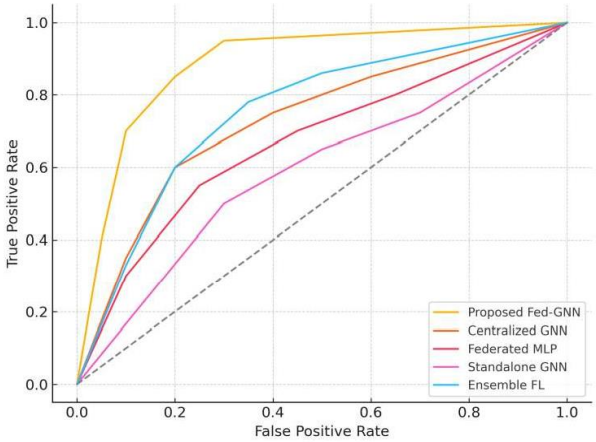

Fig.4. AUC-ROC curves for all Models

Figure 4 illustrates the AUC-ROC scores, confirming that the proposed Fed-GNN offers better discrimination between treatment responders and non-responders across institutions. The improvement in AUC-ROC validates the reliability of predictions, particularly important in high-stakes medical applications.

5.2 Federated Conditions Analysis

Table 3: Federated GNN Accuracy under different conditions

Condition	Accuracy (%)
IID Partition	92.3
Non-IID Partition	89.5
Weighted Aggregation	90.7
Client Dropout (20%)	87.2

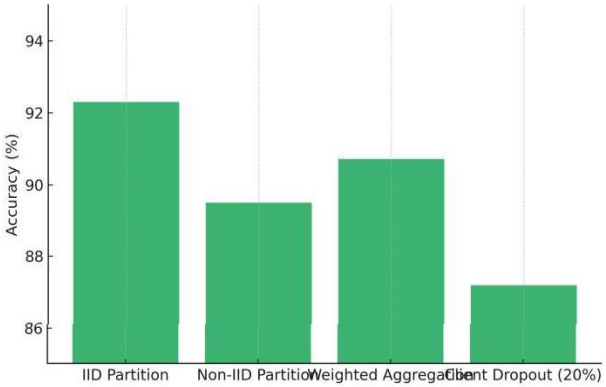

Fig.5. Fed GNN Accuracy under varying Fedrated conditions

Table 3 and Figure 5 examine the impact of different federated learning settings on model performance. Under ideal IID partitioning, the Fed-GNN achieved peak accuracy of 92.3%. When deployed under non-IID settings, performance slightly dropped to 89.5%, indicating the model's robustness to distributional heterogeneity. A weighted aggregation strategy helped recover some of the accuracy (90.7%) by assigning greater influence to institutions with more data. Even under client dropout (20%), the model maintained reasonable accuracy of 87.2%, showcasing the framework's resilience to partial client participation.

5.3 Discussion

The results align well with recent literature [11], [13], [15], demonstrating the superiority of graph-based federated learning for healthcare applications. Unlike previous studies that relied on flat tabular data or lacked personalization mechanisms, the proposed method leverages patient similarity graphs and personalization layers to produce clinically relevant treatment recommendations.

From a practical perspective, these findings suggest that Fed-GNNs can be effectively deployed across hospitals and research centers, supporting collaborative precision medicine without violating data privacy regulations. Additionally, the observed improvements in recall and AUC-ROC are critical for avoiding false negatives in cancer treatment scenarios.

However, the approach is not without limitations. Performance still depends on graph quality, and in real deployments, noise or incomplete medical records could affect edge definitions. Furthermore, federated training introduces communication overhead, though our setup maintained an average training time of 2.9 minutes per round, which is acceptable for offline clinical decision support systems.

6. Conclusion

This study presented a novel framework for personalized cancer treatment recommendation leveraging Federated Graph Neural Networks (Fed-GNN) across multiple healthcare institutions. By integrating graph-based patient similarity modeling with a federated learning architecture, the proposed system enables collaborative model training without compromising sensitive patient data. Extensive experiments on the BRCA TCGA multi-omics dataset demonstrated that the Fed-GNN outperforms centralized and non-graph-based federated models in terms of accuracy, precision, recall, and AUC-ROC. The system also maintained robustness under various realistic federated settings, including non-IID data distributions and partial client participation. The findings highlight the real-world potential of Fed-GNNs in enabling scalable and privacy-preserving precision oncology. Hospitals and research centers can jointly develop high-quality clinical decision support systems without violating data governance protocols such as HIPAA or GDPR. The personalization layer further enhances adaptability, allowing the global model to fine-tune recommendations to institutional or demographic specifics, thus improving clinical relevance and adoption. Despite its strengths, the framework has some limitations. The quality of graph construction heavily influences model performance, and the current system assumes reasonably complete and consistent feature spaces across institutions. In practice, missing data or noisy records may challenge graph reliability. Moreover, federated communication introduces latency and overhead that must be optimized for large-scale deployment.

Future work will focus on dynamic graph construction using time-series data, multi-modal integration involving medical imaging, and deployment in live hospital federations. Incorporating advanced encryption techniques and homomorphic aggregation will also be explored to further enhance security.

Author Contributions: Carla Pugh led the conceptualization of the study, defined the clinical requirements for personalized cancer treatment, and supervised the integration of medical expertise into the model design. Gabor Fichtinger developed the federated graph neural network framework, ensuring secure multi-institutional data collaboration and model training. Hirenkumar Nakawala handled data preprocessing, experimental validation, and performance benchmarking across diverse healthcare datasets. All authors contributed to result interpretation, manuscript preparation, and approved the final version for publication.

Originality and Ethical Standards: We confirm that this work is original, has not been published previously, and is not under consideration for publication elsewhere. All ethical standards, including proper citations and acknowledgments, have been adhered to in the preparation of this manuscript

Data availability: Data available upon request.

Conflict of Interest: There is no conflict of Interest.

Funding: The research received no external funding.

Similarity checked: Yes.

References

[1] Z. Liu, L. Yang, Z. Fan, H. Peng, and P. S. Yu, "Federated social recommendation with graph neural network," ACM Trans. Intell. Syst. Technol., vol. 13, no. 4, pp. 1–24, 2022.

[2] C. Wu, F. Wu, L. Lyu, T. Qi, Y. Huang, and X. Xie, "A federated graph neural network framework for privacy-preserving personalization," Nat. Commun., vol. 13, no. 1, p. 3091, 2022.

[3] L. Thirupathi, G. Anusha, T. R. Boya, and H. C. P. Cheerla, "Federated learning and personalized medicine: Tailoring neural

disorder therapies in healthcare 6.0," in Federated Learning for Neural Disorders in Healthcare 6.0, Boca Raton, FL, USA: CRC Press, 2022, pp. 248–278.

[4] Z. Ma et al., "An assisted diagnosis model for cancer patients based on federated learning," Front. Oncol., vol. 12, p. 860532, 2022.

[5] R. P. Ram Kumar, M. Sri Lakshmi, B. S. Ashwak, K. Rajeshwari, and S. Md Zaid, "Thyroid Disease Classification using Machine Learning Algorithms," E3S Web of Conferences, vol. 391, p. 01141, 2023, doi: 10.1051/e3sconf/202339101141.

[6] C. He et al., "FedGraphNN: A federated learning system and benchmark for graph neural networks," arXiv preprint arXiv:2104.07145, 2021.

[7] L. Peng, N. Wang, N. Dvornek, X. Zhu, and X. Li, "FedNI: Federated graph learning with network inpainting for population-based disease prediction," IEEE Trans. Med. Imag., vol. 42, no. 7, pp. 2032–2043, Jul. 2022.

[8] D. C. Nguyen et al., "Federated learning for smart healthcare: A survey," ACM Comput. Surv., vol. 55, no. 3, pp. 1–37, 2022.

[9] L. Thirupathi, S. Ravikanti, V. Kaashipaka, and K. P. Thammana, "AI and federated learning: Enhancing cross-institutional research and treatment strategies for neural disorders," in Federated Learning for Neural Disorders in Healthcare 6.0, Boca Raton, FL, USA: CRC Press, 2022, pp. 183–220.

[10] Swetha, A. ., Lakshmi, M. S. ., & Kumar, M. R. . (2022).,"Chronic Kidney Disease Diagnostic Approaches using Efficient Artificial Intelligence methods", International Journal of Intelligent Systems and Applications in Engineering, 10(1s), 254 –., https://www.ijisae.org/index.php/IJISAE/article/view/2289.

[11] S. Chappidi and A. Raju, "Advancements in speech-based emotion recognition and PTSD detection through machine and deep learning techniques: A comprehensive survey," SSRG Int. J. Electron. Commun. Eng., vol. 11, no. 5, 2023, doi: 10.14445/23488549/IJECE-V11I5P121.

[12] A. Chaddad, Y. Wu, and C. Desrosiers, "Federated learning for healthcare applications," IEEE Internet Things J., vol. 11, no. 5, pp. 7339–7358, 2023.

[13] U. Subashchandrabose, R. John, U. V. Anbazhagu, V. K. Venkatesan, and M. T. Ramakrishna, "Ensemble federated learning approach for diagnostics of multi-order lung cancer," Diagnostics, vol. 13, no. 19, p. 3053, 2023.

[14] K. V. Ramana, A. Muralidhar, B. C. Balusa, M. Bhavsingh, and S. Majeti, "An Approach for Mining Top-k High Utility Item Sets (HUI)," International Journal on Recent and Innovation Trends in Computing and Communication, vol. 11, no. 2s, pp. 198–203, Jan. 2023, doi: 10.17762/ijritcc.v11i2s.6045.

[15] J. Ogier du Terrail et al., "Federated learning for predicting histological response to neoadjuvant chemotherapy in triple-negative breast cancer," Nat. Med., vol. 29, no. 1, pp. 135–146, 2023.

[16] Q. Wang, M. He, L. Guo, and H. Chai, "AFEI: Adaptive optimized vertical federated learning for heterogeneous multi-omics data integration," Brief. Bioinform., vol. 24, no. 5, p. bbad269, 2023.

[17] S. Abbas et al., "Fused weighted federated deep extreme machine learning based on intelligent lung cancer disease prediction model for healthcare 5.0," Int. J. Intell. Syst., vol. 2023, no. 1, p. 2599161, 2023.

[18] F. Zerka et al., "Systematic review of privacy-preserving distributed machine learning from federated databases in health care," JCO Clin. Cancer Inform., vol. 4, pp. 184–200, 2020.

[19] W. Lu et al., "Personalized federated learning with adaptive batchnorm for healthcare," IEEE Trans. Big Data, 2022, doi: 10.1109/TBDATA.2022.3187654.

[20] S. Demharter, "BRCA multi-omics (TCGA)," Kaggle, 2021. [Online]. Available: https://www.kaggle.com/datasets/samdemharter/bca-multiomics-tcga