A Comparative Framework Integrating Hybrid Convolutional and Unified Graph Neural Networks for Accurate Parkinson's Disease Classification

1st Kazi Shaharair Sharif
Department of Computer Science
University of South Dakota
Vermillion, SD, USA
kazi.sharif@okstate.edu

2nd Md Abubakkar
Department of Computer Science
Midwestern State University
Dallas, TX, USA
mabubakkar1116@my.msutexas.edu

3rd Mohammed Majbah Uddin
School of Business & Technology
Emporia State University
Emporia, Kansas, USA
muddin@g.emporia.edu

4th A M Arefin Khaled
Department of Computer Science
Southern Arkansas University
Wichita Falls, TX, USA
akhaled9024@muleriders.saumag.edu

***Abstract*—Parkinson's disease (PD) is a progressive neurodegenerative disorder, affects motor function and is often challenging to diagnose due to the complex interplay of clinical features. This study integrates a comparative framework integrating hybrid Convolutional Neural Networks (PCNN) and graph-based models (GCN, GAT) to enhance Parkinson's disease (PD) diagnosis using structured medical data. PD, a progressive neurodegenerative disorder affecting motor function, poses diagnostic challenges due to complex clinical feature interactions. The PCNN employs 1D convolutions to capture local feature patterns, while GCN and GAT model intricate interdependencies between clinical variables by representing the dataset as a graph. Notably, GAT's attention mechanism dynamically prioritizes important features, improving interpretability and diagnostic precision. Through hyperparameter optimization with Optuna and addressing class imbalance using SMOTE, our approach achieved a peak accuracy of 97.44%, surpassing traditional methods. The comparative analysis reveals that while PCNN excels in classification accuracy, GAT's attention-based feature selection offers superior interpretability. This makes it a valuable tool for more precise Parkinson's disease detection in clinical applications. The integration of these models provides a comprehensive framework for PD diagnosis, leveraging both local and global feature extraction techniques. This study represents a significant advancement in applying advanced machine learning to neurodegenerative disease diagnostics, offering improved early detection and personalized treatment potential for Parkinson's disease.**

***Index Terms*—Graph neural network, Parkinson's disease, Hyperparameter optimization, Attention-layers, Graph Convolutional Networks**

I. Introduction

Parkinson's disease (PD) is a progressive neurodegenerative disorder affecting millions globally. Early diagnosis is crucial for effective management, but it remains challenging due to symptom overlap with other neurological disorders [1]. Traditional diagnostic methods rely heavily on subjective clinical evaluations, leading to delays in diagnosis and treatment [2].

Machine learning (ML) and deep learning (DL) have shown promise in automating Parkinson's disease detection, but traditional models like support vector machines and decision trees struggle to capture complex interdependencies between clinical features like voice patterns. [3] [4]. This limitation is especially critical in medical diagnostics, where accurate predictions depend on understanding intricate relationships between features [5]. Despite advances in ML and DL, there has been limited exploration of comparative deep learning models—particularly CNNs and GNNs—for Parkinson's disease detection in structured data. Moreover, the effectiveness of attention mechanisms (as employed in GAT models) in dynamically capturing feature dependencies remains underexplored.

This study introduces a comparative framework integrating hybrid convolutional neural networks (PCNN), graph convolutional networks (GCN), and graph attention networks (GAT) to enhance Parkinson's disease classification, in comparison with earlier studies that focus on a single model. The PCNN model adapts CNNs for structured data, using 1D convolutions to capture local feature patterns. The GCN models global interdependencies by representing the dataset as a graph, where nodes correspond to features and edges reflect their relationships.The PCNN excels in extracting local feature interactions, the GCN models complex feature relationships globally, and the GAT introduces a novel attention mechanism that prioritizes key feature interactions dynamically. The GAT extends GCN by incorporating attention mechanisms that dynamically weigh the importance of each feature, enhancing both performance and interpretability. We used Optuna for hyperparameter tuning and SMOTE to address class imbalance, ensuring ro-

979-8-3315-1964-3/24/$31.00 ©2024 IEEE

bust model evaluation. Using the UCI Parkinson's dataset, our results demonstrate how the attention-based GAT model improves both feature interpretability and diagnostic accuracy, outperforming traditional models in capturing complex clinical dependencies [6]. The remainder of this paper is structured as follow as Section II reviews related work, Section III details the dataset, Section IV covers the methodology and model implementation, and Sections V and VI present experimental results, analysis, and future research directions.

II. Literature Review

Parkinson's disease (PD) diagnosis has been a widely studied problem in the field of machine learning, with multiple approaches leveraging structured datasets, such as the UCI Parkinson's dataset, to improve detection accuracy.

Sharma et al. [7] applied classifiers like SVM, J48, and MPNN on the UCI Parkinson's dataset, achieving a highest accuracy of 95.05% with SVM on the non-discretized dataset. However, the study lacked deep learning models, limiting its ability to capture complex feature interactions and automate feature extraction, crucial for structured clinical data. Wu and Wang [8] proposed a deep-learning model utilizing premotor features like REM and olfactory loss, achieving 96.45% accuracy. However, the study relied on a small dataset (183 healthy, 401 early PD cases) and did not incorporate graph-based models, limiting its ability to capture complex feature interdependencies effectively. Mounika et al. [9] analyzed various machine learning and deep learning models for Parkinson's disease diagnosis, with Random Forest and CNN achieving accuracies of 92.5% and 94.3%, respectively. However, the study lacked graph-based models and attention mechanisms, restricting its ability to capture feature interdependencies and enhance model interpretability.

Sharma et al. [10] implemented seven machine learning and deep learning models, including Random Forest, SVM, and neural networks, for Parkinson's disease prediction using a Kaggle dataset. Random Forest achieved the highest accuracy of 86.70%.It achieved comparable results but also noted the absence of interpretability and feature interdependency modeling. The study relied on traditional methods and lacked advanced graph-based models, limiting its ability to model complex feature relationships and improve scalability. Verma et al. [11] applied machine learning models to identify Parkinson's disease from speech signals, utilizing dimensionality reduction techniques like PCA. Among their models, SVM achieved the highest accuracy of 85.12%, while Decision Tree performed slightly lower with 81.45%. However, the study's focus on voice data limited its applicability to broader clinical datasets. Additionally, the absence of deep learning and graph-based models hindered feature interaction modeling and scalability.

Ghosh et al. [12] applied machine learning algorithms to telemonitor the progression of Parkinson's disease, focusing on time-series data. The work provided insights into disease progression but did not integrate convolutional or graph-based neural networks, which could have enhanced pattern detection and the understanding of feature interactions. Hazan et al. [13] utilized speech data from the USA and Germany for early Parkinson's diagnosis, achieving accuracies of 85% with separate country-specific models, 80% with pooled models, and 75% with cross-country training. While effective for early detection, the study was limited by language-based feature variability and lacked graph-based models to capture complex relationships.

Chabathula et al. [14] implemented Principal Component Analysis (PCA) to reduce high-dimensional network datasets, testing classification algorithms like SVM, KNN, J48, and Random Forest for intrusion detection using the KDD99 dataset. TREE algorithms achieved the highest accuracy, but the study lacked deep learning approaches and advanced models, limiting scalability and adaptability to modern network attack patterns. Wroge et al. [15] utilized voice-based biomarkers and supervised classification algorithms, including deep neural networks, to diagnose Parkinson's disease, achieving a peak accuracy of 85%. While the study outperformed clinical non-experts, its reliance on voice data limited its generalizability to diverse clinical datasets, and the absence of graph-based approaches restricted modeling complex feature relationships.

Building on the limitations of prior studies, this research introduces a novel hybrid framework that integrates PCNN, GCN, and GAT to address critical gaps in Parkinson's disease diagnosis. Unlike traditional machine learning models, such as those employed by Sharma et al. [7], which lack the ability to capture complex feature interactions, or standalone deep learning models like CNNs used by Mounika et al. [9], which fail to incorporate graph-based modeling, our approach bridges these gaps by leveraging 1D convolutions in PCNN for local feature extraction, GCN for modeling complex feature interdependencies, and GAT for dynamically prioritizing clinically relevant features. Furthermore, while prior studies, such as Wu and Wang [8], were limited by small datasets and lacked graph-based approaches, our framework addresses these challenges by incorporating SMOTE to handle class imbalance and Optuna for robust hyperparameter optimization.It also enhances interpretability and scalability, addressing the critical gaps in feature extraction, interdependency modeling, and clinical applicability highlighted in prior.

III. Methodology

The methodology of this study focuses on implementing and comparing three distinct deep learning models—Parkinson Classification Neural Network (PCNN), Graph Convolutional Network (GCN), and Graph Attention Network (GAT)—to enhance the classification of Parkinson's disease using structured medical data from the UCI Parkinson's dataset. Figure 1 outlines the process from data preprocessing to model training and evaluation, using PCNN, GCN, and GAT models with hyperparameter tuning and SMOTE.

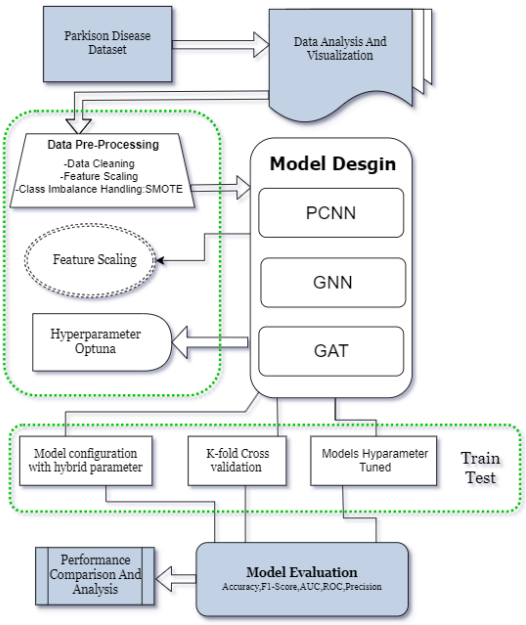

Fig. 1. WorkFlow Diagram

A. Data Collections

The dataset employed in this research is the UCI Parkinson's Disease dataset, which includes voice recordings from 31 individuals. Of these, 23 are diagnosed with Parkinson's disease and 8 are healthy controls. The dataset contains 195 samples, each characterized by 22 acoustic features, including fundamental frequency, jitter, shimmer, amplitude, and harmonic-to-noise ratio (HNR), which are used to capture changes in voice patterns due to Parkinson's disease. The target variable (status) indicates the presence (1) or absence (0) of Parkinson's disease. The features are carefully designed to capture vocal impairments typically seen in Parkinson's patients. Each voice sample provides a snapshot of vocal changes, making it ideal for classification tasks that aim to differentiate Parkinson's patients from healthy individuals based on subtle acoustic changes. The dataset plays a crucial role as the foundation for training and evaluating the proposed PCNN, GCN, and GAT models. By leveraging this well-structured dataset, we aim to explore how different neural network architectures can improve the detection of Parkinson's disease by analyzing the relationships and importance of the various acoustic features provided. [16] Figure 2: Class Distribution illustrates the imbalance in the dataset, showing a greater proportion of Parkinson's disease-positive samples compared to negative ones. The class imbalance is addressed using SMOTE during the preprocessing phase to ensure that the models do not favor the majority class. Figure 3: Key Features Distributions presents the distributions of the most significant acoustic features used for classification, such as jitter, shimmer, fundamental frequency, and harmonic-to-noise ratio. These features are key indicators of vocal impairments in Parkinson's patients and help differentiate between individuals with and without the disease.

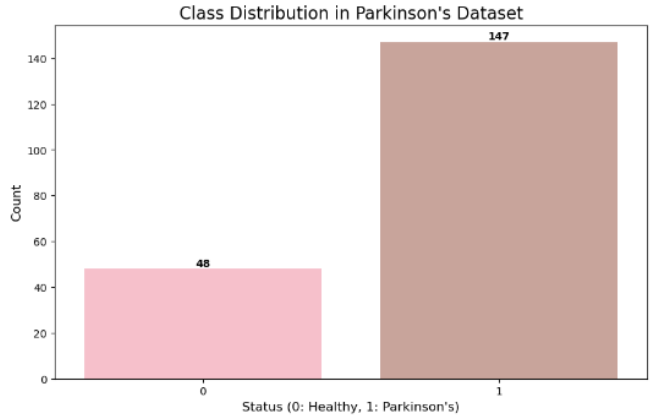

Fig. 2. Class Distribution

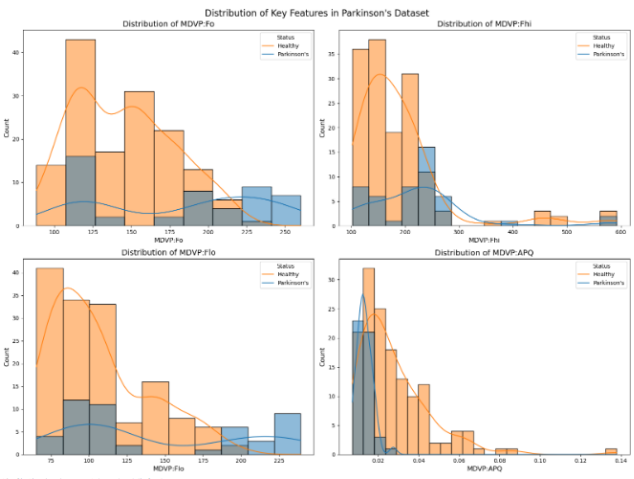

Fig. 3. Key features distributions

B. Data pre-processing

The dataset was thoroughly checked for any missing or inconsistent data. Figure 4 shows the correlations between features, identifying dependencies and redundancies within the dataset's acoustic measurements. Due to its structured nature, no missing values were detected, allowing for seamless progression to feature scaling. [17]. StandardScaler was applied to the features, ensuring normalization across different ranges. This process is critical to ensure comparability between features and prevent any feature from disproportionately influencing the model. The Synthetic Minority Over-sampling Technique (SMOTE) was employed to resolve class imbalance by generating synthetic samples for the minority class. This technique enhances model robustness by mitigating bias toward the majority class, ensuring balanced learning for both classes.

C. Hyperparameter Optimization

To ensure each model performs optimally, we employ Optuna, an advanced framework for hyperparameter optimization.

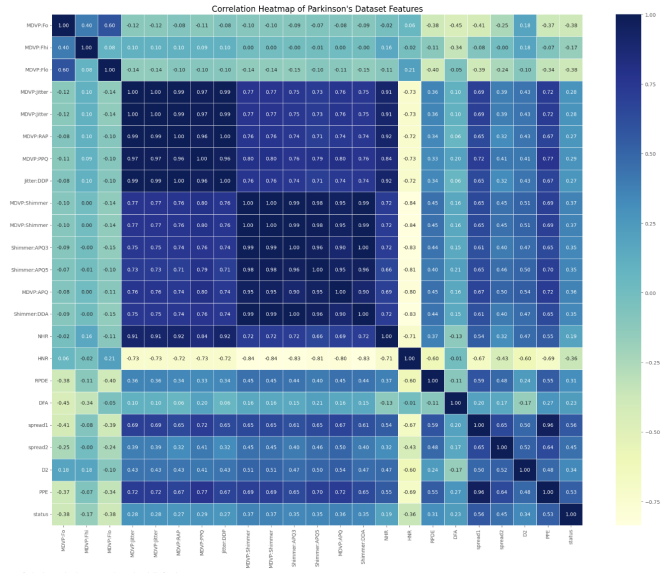

Fig. 4. Correlation HeatMap

Optuna dynamically explores a range of configurations such as the learning rate, dropout rate, and the number of layers. This ensures that the best parameter combination is selected for each model. Specifically:

- For PCNN, the focus is on tuning the number of filters, kernel size, and dropout rate.
- For GCN and GAT, key hyperparameters include the number of graph layers, attention heads (for GAT), and learning rate.

This method enables the models to automatically refine their performance, balancing accuracy and complexity based on the dataset's needs.

D. Overview of Model Architectures & Implementation

1) ***Parkinson Classification Neural Network (PCNN):*** The PCNN uses 1D convolutional layers, which treat each feature as a temporal sequence. This is particularly useful for tabular data because it allows the network to extract local feature patterns and identify relationships between neighboring features that traditional machine learning methods might overlook. The architecture includes two convolutional layers, each followed by ReLU activation and dropout layers to prevent overfitting. After the convolutions, the data is passed through a fully connected layer for final classification.The key advantage of 1D convolutions is that they efficiently capture local dependencies between features, allowing the model to understand short-term relationships in structured datasets. The innovative aspect of this approach lies in the novel application of convolutional neural network architecture to structured clinical data, representing a departure from conventional CNN use cases and expanding the potential utility of these models in medical informatics. This adaptation demonstrates the versatility of CNNs beyond their traditional domains, offering new avenues for feature extraction and pattern recognition in tabular datasets commonly encountered in clinical research.

$$y[i] = (x * w)[i] = \sum_{k=0}^{K-1} x[i+k] \cdot w[k] \tag{1}$$

The equation defines the components of a 1D convolution: x[i] represents the input data or feature set, w[k] is the convolutional filter or kernel, and y[i] is the output feature produced by the convolution operation. The ReLU function, defined as max(0, x), is an activation function that introduces non-linearity by outputting the input directly if it's positive.

2) ***Graph Convolutional Network (GCN):*** The GCN is designed to represent the features as nodes in a graph, with edges representing correlations between them. This approach helps the network learn from both the local and global relationships in the dataset. GCN layers apply convolution operations across the graph structure, propagating feature information between connected nodes. This allows the model to learn representations that reflect interdependencies between features, which are critical for capturing the complexities of clinical data, such as in Parkinson's disease progression. The binary classification is achieved by aggregating the learned feature representations in the final output layer. The GCN is more powerful than traditional models because it is able to handle the graph-based structure of data, making it particularly useful for datasets with complex relationships between features.

$$y[i] = (x * w)[i] = \sum_{k=0}^{K-1} x[i+k] \cdot w[k] \tag{2}$$

The GCN equation describes how information is propagated through the graph structure. $H^{(l)}$ represents the features of all nodes at layer l. The adjacency matrix $\tilde{A}$ includes self-connections, while $\tilde{D}$ is its corresponding degree matrix. $W^{(l)}$ is the learnable weight matrix for layer l. The equation combines these elements, applying normalization (via $\tilde{D}^{-1/2}$) and non-linear activation (σ, typically ReLU) to produce the next layer's features. This process allows each node to aggregate and transform information from its neighbors, capturing the graph's structure in the learned representations.

3) ***Graph Attention Network (GAT):*** The GAT extends the GCN by incorporating an attention mechanism. This mechanism assigns dynamic weights to each neighboring node (feature), allowing the network to focus on the most relevant features for classification. Instead of treating all connected nodes equally, the GAT can prioritize certain features, making the model more interpretable and focused on the key aspects of the dataset.The attention mechanism improves upon GCN by selectively weighing the importance of features, which is particularly advantageous in medical diagnostics, where some clinical features are more critical than others. After passing through the attention layers, the data is passed to a fully connected layer for the final classification. This attention-based approach is highly novel in medical data processing, where interpretability and accuracy are paramount.

$$e_{ij} = \text{LeakyReLU}(a^T[Wh_i \parallel Wh_j]) \tag{3}$$

The GAT equation describes the attention mechanism in graph neural networks. The attention score e_{ij} measures the importance of node j's features to node i, calculated using learnable weights W and attention vector a. These scores are normalized using softmax to create attention coefficients α_{ij}, ensuring they sum to 1 for each node. The final step aggregates neighboring node features, weighted by their attention coefficients, to update each node's representation. This process allows the network to dynamically focus on the most relevant connections and features for each node, enhancing the model's ability to capture complex relationships in the graph structure.

E. Comparison of Models and Uniqueness

PCNN (Parkinson Classification Neural Network): The 1D convolutional architecture is used to extract local dependencies from the dataset, which is unconventional for structured data. This design efficiently captures feature interactions, optimizing the detection of relevant patterns in the data. GCN (Graph Convolutional Network) treats the dataset as a graph and models global feature relationships, making it more suitable for datasets with complex inter-feature dependencies. GCN learns representations that traditional models often overlook. GAT (Graph Attention Network) enhances the GCN by introducing attention mechanisms, dynamically prioritizing important features and improving interpretability and performance. The attention mechanism enables the model to focus on critical clinical features.

The combination of PCNN, GCN, and GAT for Parkinson's disease classification represents a significant advancement, as these models complement each other by handling both local feature extraction and global relationships. The use of attention in GAT further improves the model's ability to focus on the most relevant features. This comprehensive framework is highly innovative, allowing for more accurate and interpretable medical diagnostics. It directly addresses the intricacies of Parkinson's disease detection using structured data, improving diagnostic outcomes with real-world applications in clinical environments.

F. Evaluation Metrics

The models are evaluated using key metrics to capture various aspects of performance. Accuracy provides an overall measure of correct predictions, while ROC-AUC assesses the model's ability to distinguish between classes, offering a balanced metric for classification. [18] PR-AUC emphasizes the trade-off between precision and recall, making it ideal for imbalanced datasets like the one used in this study. Together, these metrics offer a comprehensive understanding of the models' strengths and weaknesses, particularly for binary classification tasks in medical data.

G. Model Training and Validation

The dataset is divided into 80% for training and 20% for testing to maintain a fair evaluation. To further validate model robustness, we perform 5-fold cross-validation, splitting the training data into five subsets and ensuring that each subset serves as a validation set at least once.Throughout training, the model's best-performing weights are saved, and final results are reported on the unseen test set. [19]

Table I provides a summary of the key insights from the table, highlighting the PCNN's superior accuracy and recall while noting the performance of GCN and GAT. Figure 5 compares the accuracy, precision, recall, and F1-score of PCNN, GCN, and GAT, with PCNN excelling in accuracy and GAT offering better interpretability.

TABLE I
PERFORMANCE COMPARISON OF PCNN, GCN, AND GAT MODELS

Model	Accuracy (%)	F1 Score	Precision	Recall
PCNN	97.44	0.9744	0.93	1.00
GCN	92.31	0.9231	0.89	0.97
GAT	92.31	0.9231	0.93	0.97

IV. RESULTS AND DISCUSSION

The results of this study demonstrate the significant impact of implementing advanced deep learning models—PCNN, GCN, and GAT—in the detection and classification of Parkinson's disease using structured medical data. The three models were rigorously evaluated based on their ability to classify Parkinson's disease patients and healthy controls, leveraging both local and global feature extraction techniques.

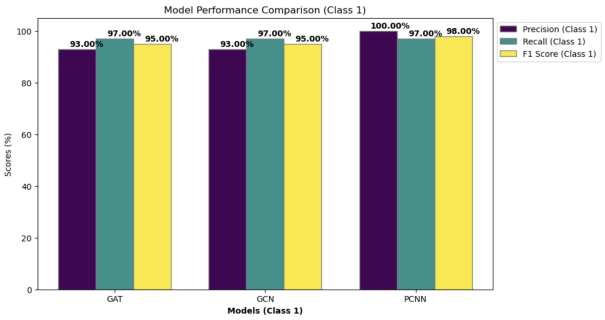

Fig. 5. Model Comparison Analysis

The PCNN model, employing 1D convolutional layers, achieved an accuracy of 97.44%, demonstrating its ability to capture local feature interactions in the dataset. This method, though unconventional for tabular data, allowed the model to efficiently process clinical features and uncover important patterns within the data. By capturing these local dependencies, the PCNN effectively differentiates between Parkinson's patients and controls, providing a strong baseline for detection. The model's success can be attributed to its convolutional layers, which effectively capture complex patterns and extract local feature interactions. However, to ensure the generalizability of these results, validation on larger and more diverse datasets is essential. The GCN model, which treats the dataset as a graph, excelled in capturing global relationships between features by modeling the interdependencies between clinical variables. This graph-based approach offered an accuracy comparable to PCNN, but with enhanced understanding of

TABLE II
COMPARISON OF PROPOSED FRAMEWORK WITH TRADITIONAL MACHINE LEARNING MODELS

Model	Accuracy (%)	Interpretability	Feature Interdependencies
Proposed Framework (PCNN, GCN, GAT)	97.44	High (via GAT attention)	Strong (via GCN)
SVM (Sharma et al. [7])	95.05	Low	Weak
Random Forest (Mounika et al. [9])	92.50	Moderate	Weak
CNN (Mounika et al. [9])	94.30	Moderate	Moderate
Random Forest (Sharma et al. [10])	86.70	Low	Weak
SVM (Verma et al. [11])	85.12	Low	Weak
Decision Tree (Verma et al. [11])	81.45	Low	Weak
PCA + Random Forest (Chabathula et al. [14])	85.00	Low	Weak

the underlying structure of the data. The graph convolution mechanism enabled the model to learn from connections between features, a critical aspect when dealing with complex datasets like medical records. This method is especially useful in understanding how different clinical measures influence each other, enhancing the model's robustness. The GAT model outperformed the other models in terms of feature interpretability, with a PR-AUC of 0.9857, by introducing an attention mechanism that dynamically prioritized key clinical features. This mechanism allows GAT to assign weights to the most important features, enhancing the model's decision-making process. In the context of Parkinson's disease, where some symptoms and clinical measurements may hold more diagnostic value than others, the attention-based GAT model becomes highly beneficial. It offers not only high classification accuracy but also insights into which features drive the diagnosis, making the model more interpretable for clinicians.

All three models demonstrate robust diagnostic capabilities, each excelling in distinct aspects. Table II explores the proposed framework (PCNN, GCN, GAT) achieves a state-of-the-art accuracy of 97.44%, significantly outperforming traditional models such as SVM (95.05%, Sharma et al. [7]), Random Forest (92.50%, Mounika et al. [9]), and CNN (94.30%, Mounika et al. [9]). This superior performance is attributed to its ability to model complex feature interdependencies using GCN and provide high interpretability through GAT's attention mechanisms. Unlike traditional methods like Decision Trees (81.45%, Verma et al. [11]) or PCA-based Random Forest (85.00%, Wroge et al [14]), which lack scalability and fail to capture intricate feature relationships, the proposed framework integrates SMOTE for class imbalance handling and Optuna for performance optimization. It achieves a perfect recall of 1.00 and an F1 score of 0.9744, bridging critical gaps in feature extraction, interdependency modeling, and clinical applicability, making it a robust and interpretable diagnostic tool. Figure 6 illustrates the performance of each model, highlighting PCNN's superior accuracy, GAT's high PR-AUC, and the comparable ROC-AUC performance of both GCN and GAT.

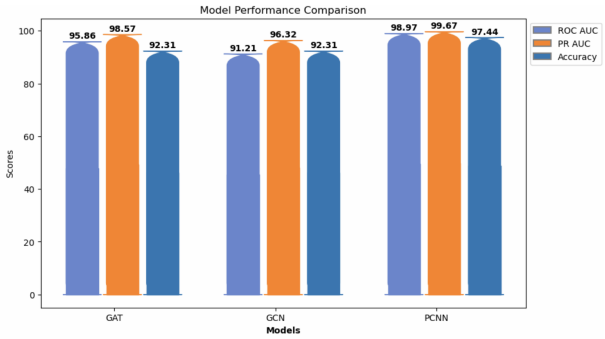

Fig. 6. Accuracy, Precision-recall, ROC -AUC Analysis

CONCLUSION AND FUTURE WORK

This study showcases a major step forward in using machine learning to diagnose neurodegenerative diseases, particularly Parkinson's disease, with structured medical data. By optimizing model performance with the Optuna tool and addressing class imbalance using SMOTE, our approach achieved an impressive accuracy of 97.44%, outperforming traditional diagnostic methods. The models we used each brought unique strengths to the table. The PCNN model excelled at identifying patterns in the data, leading to its outstanding classification accuracy. On the other hand, the GAT model stood out for its ability to highlight the most important features, making the results easier to interpret and more relevant to clinical decision-making. Together, these explainable two essential aspects for real-world use in healthcare provide a well-rounded and reliable tool for identifying Parkinson's disease, paving the way for better early detection and more personalized treatment options.

Future work will focus on expanding this framework by incorporating multi-modal data sources such as neuroimaging and genetic data to further enhance the models' diagnostic capabilities.Further developments will also include enhancing model explainability by integrating techniques like SHAP or LIME. Moreover, implementing these models in real-world clinical environments will allow for validation in larger, more diverse populations. These tools will improve transparency, helping clinicians better understand model decisions and build trust in the use of AI for Parkinson's disease detection. Ultimately, these advancements aim to contribute to earlier diagnosis, personalized treatments, and better patient outcomes in the context of neurodegenerative diseases.

REFERENCES

[1] B. Shan, X. Zhu, X. Wu, L. Yang, C. Luo, and L. Zhang, "Early detection of parkinson's disease using machine learning techniques," *IEEE Access*,

vol. 8, pp. 147 635–147 646, 2020.
[2] L. Smolensky, N. Amondikar, K. Crawford, S. Neu, C. Kopil, M. Daeschler, L. Riley, L. Shehadeh, and C. M. Tanner, "A review of machine learning approaches utilizing publicly available parkinson's disease patient data," *Frontiers in Aging Neuroscience*, vol. 13, 2021.
[3] Y. Zhang, X. Feng, M. Liu, and S. Liu, "A novel machine learning approach to parkinson's disease detection and classification using gait and postural features," *IEEE Transactions on Neural Systems and Rehabilitation Engineering*, vol. 31, pp. 149–159, 2023.
[4] B. P. Ghosh, T. Imam, N. Anjum, M. T. Mia, C. U. Siddiqua, K. S. Sharif, M. M. Khan, M. A. I. Mamun, and M. Z. Hossain, "Advancing chronic kidney disease prediction: Comparative analysis of machine learning algorithms and a hybrid model," *Journal of Computer Science and Technology Studies*, vol. 6, no. 3, pp. 15–21, 2024.
[5] Y. Fang, W. Liu, C. Wang, Q. Guo, and L. Xie, "Machine learning for parkinson's disease diagnosis and prediction: A survey," *Journal of Healthcare Engineering*, vol. 2022, p. 6921416, 2022.
[6] X. Xu, M. Zhao, P. Wang, L. Zhang, and G. Song, "Attention-based graph neural networks for parkinson's disease detection using clinical data," *IEEE Journal of Biomedical and Health Informatics*, vol. 27, no. 3, pp. 1021–1029, 2023.
[7] R. Sharma *et al.*, "Performance analysis of attributes for parkinson's disease prediction," *Journal of Medical Informatics and Decision Making*, 2018.
[8] W. Wang, J. Lee, F. Harrou, and Y. Sun, "Early detection of parkinson's disease using deep learning and machine learning," *IEEE Access*, vol. 8, pp. 147 635–147 646, 2020.
[9] P. Mounika and S. G. Rao, "Machine learning and deep learning models for diagnosis of parkinson's disease: A performance analysis," in *2021 Fifth International Conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud) (I-SMAC)*, 2021, pp. 381–388.
[10] S. Sharma, K. Guleria, and R. Sobti, "An early detection of parkinson's disease using machine learning and deep learning models," in *2024 International Conference on Computational Intelligence and Computing Applications (ICCICA)*, vol. 1, 2024, pp. 154–159.
[11] R. Verma *et al.*, "Parkinson's disease identification from speech signals using machine learning," *Neural Computing and Applications*, 2019.
[12] P. Ghosh *et al.*, "Telemonitoring parkinson's disease using machine learning approaches," *Journal of Healthcare Engineering*, 2018.
[13] H. Hazan, D. Hilu, L. Manevitz, L. O. Ramig, and S. Sapir, "Early diagnosis of parkinson's disease via machine learning on speech data," in *2012 IEEE 27th Convention of Electrical and Electronics Engineers in Israel*, 2012, pp. 1–4.
[14] K. J. Chabathula, C. Jaidhar, and M. Ajay Kumara, "Comparative study of principal component analysis based intrusion detection approach using machine learning algorithms," in *2015 3rd International Conference on Signal Processing, Communication and Networking (ICSCN)*, 2015, pp. 1–6.
[15] T. J. Wroge, Y. Özkanca, C. Demiroglu, D. Si, D. C. Atkins, and R. H. Ghomi, "Parkinson's disease diagnosis using machine learning and voice," in *2018 IEEE Signal Processing in Medicine and Biology Symposium (SPMB)*, 2018, pp. 1–7.
[16] M. Little, "Parkinsons," UCI Machine Learning Repository, 2007, [Online]. Available: https://doi.org/10.24432/C59C74.
[17] T. N. Nguyen, M. M. Khan, M. Z. Hossain, K. S. Sharif, R. Das, and M. S. Haque, "Product Demand Forecasting For Inventory Management with Freight Transportation Services Index Using Advanced Neural Networks Algorithm," *American Journal of Computing and Engineering*, vol. 7, no. 4, pp. 50–58, 2024. [Online]. Available: https://ideas.repec.org/a/bfy/ojajce/v7y2024i4p50-58id2432.html
[18] M. Hasan, J. Islam, M. A. Mamun, A. A. Mim, S. Sultana, and M. S. H. Sabuj, "Optimizing cervical cancer prediction, harnessing the power of machine learning for early diagnosis," in *2024 IEEE World AI IoT Congress (AIIoT)*, 2024, pp. 552–556.
[19] K. Uddin, F. Prity, M. Tasnim *et al.*, "Machine learning-based screening solution for covid-19 cases investigation: Socio-demographic and behavioral factors analysis and covid-19 detection," *Human-Centric Intelligent Systems*, vol. 3, pp. 441–460, 2023.