PUBLIC HEALTH CONFERENCE 2025

11-13 JULY 2025

BANGKOK, THAILAND

CONFERENCE PROCEEDINGS

Tomorrow People Organization

Dušana Vukasovića 73, Belgrade, Serbia

www.tomorrowpeople.org

Proceedings of international conference:

"PUBLIC HEALTH CONFERENCE 2025"

Editors: Tomorrow People Organization
Dušana Vukasovića 73
11070 Belgrade, Serbia

Secretary: Vladimir Ilić

Producer: Tomorrow People Organization
Publisher: Tomorrow People Organization
Quantity: 200 copies

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AI-Driven Framework for Chronic Disease Prediction and Management

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ABSTRACT

The Advancements in machine learning (ML) and deep learning (DL) have created opportunities to address complex biomedical challenges, particularly in precision medicine and clinical decision support. This study proposes a novel hybrid ML-DL framework to enhance chronic disease prediction and management by leveraging multimodal biomedical datasets. Chronic diseases like diabetes and cardiovascular conditions pose significant global health challenges, necessitating accurate prediction and personalized management strategies. Existing models often fail to effectively integrate multimodal data or provide explainable results, limiting their clinical adoption. To address these gaps, this framework integrates multimodal learning and precision medicine principles to improve predictive accuracy and interoperability. The study utilizes publicly available datasets, including the Comprehensive Diabetes Clinical Dataset (100,000 records) and the Cardiovascular Disease Dataset (70,000 records). Data preprocessing involves cleaning, normalization, and imputation of missing values using advanced statistical methods. Domain-specific features are extracted through biomedical ontologies and graph-based knowledge representations. A multimodal neural network (MMNN) is employed to combine structured data, while graph neural networks (GNNs) facilitate knowledge integration. Evaluations using metrics like accuracy, F1 score, and AUC-ROC reveal substantial improvements. For diabetes prediction, the MMNN achieved an AUC-ROC of 0.94, outperforming traditional models by 18%. For cardiovascular risk stratification, the GNN improved accuracy by 12%. This framework demonstrates the potential of AI-driven tools to improve clinical decision-making and patient outcomes. Future work will focus on real-world deployment, addressing ethical issues, and extending the approach to additional biomedical domains.

KEYWORDS: Deep Learning, Precision Medicine, Chronic Disease Prediction

1 INTRODUCTION

AI The rising prevalence of chronic diseases, such as diabetes and cardiovascular conditions, has emerged as a significant global health concern, imposing substantial burdens on healthcare systems. These conditions necessitate timely diagnosis and personalized management strategies to mitigate their impact on patient outcomes and healthcare infrastructure. Traditional diagnostic and treatment approaches primarily rely on clinical expertise and structured guidelines, which, while effective, often lack the adaptability and precision required for individualized patient care [1]. The integration of AI, particularly ML and DL, presents a transformative opportunity for advancing chronic disease prediction and management. However, despite their promising capabilities, AI-driven solutions face critical challenges in clinical implementation, including data heterogeneity, model interpretability, and the development of robust, generalizable frameworks suitable for real-world applications [2].

Machine learning and deep learning techniques have demonstrated substantial potential in biomedical research, enabling more accurate disease classification, risk assessment, and patient outcome prediction. Conventional ML models, such as decision trees, support vector machines (SVMs), and ensemble methods, have been widely applied to structured clinical data, yielding valuable insights. Meanwhile, DL architectures, including convolutional neural networks (CNNs) and recurrent neural networks (RNNs), have shown efficacy in processing unstructured medical data, such as imaging and electronic health records. More recently, multimodal learning approaches have gained attention for their ability to integrate diverse data sources—clinical measurements, genetic information, and imaging data—offering a more holistic view of patient health [3]. Despite these advancements, AI-driven models often struggle with challenges such as ineffective data fusion, limited feature extraction capabilities, and a lack of explainability, which hinder their adoption in clinical decision-making.

Existing AI-based models for chronic disease prediction exhibit notable limitations that impact their reliability and applicability. Many machine learning approaches fail to incorporate multimodal data effectively, leading to suboptimal predictive performance. Deep learning models, while powerful, often operate as "black boxes," making it difficult for clinicians to interpret the reasoning behind their predictions, which is a critical barrier to their acceptance in medical practice. Additionally, AI models may suffer from biases due to data imbalances, affecting their generalizability across diverse patient populations. The lack of standardization in medical data representation further complicates efforts to develop AI frameworks that are both robust and clinically relevant. Addressing these challenges requires the development of novel AI-driven methodologies that improve predictive accuracy, interpretability, and adaptability while maintaining clinical relevance [4][5].

To overcome these limitations, this study proposes a novel AI framework that leverages multimodal biomedical datasets for chronic disease prediction and management. The datasets used in this research include the Comprehensive Diabetes Clinical Dataset and the Cardiovascular Disease Dataset, both sourced from publicly available repositories such as Kaggle. The former comprises 100,000 patient records containing demographic and clinical attributes, while the latter includes 70,000 records with cardiovascular risk factors. By integrating structured clinical data with advanced feature engineering techniques, this research aims to enhance disease prediction capabilities and improve model interpretability, making AI-driven decision-support tools more clinically actionable.

This study introduces a hybrid ML-DL framework incorporating MMNNs and GNNs to enable efficient data fusion, capture intricate relationships among clinical variables, and enhance model interpretability. The proposed methodology includes robust data preprocessing techniques, missing data imputation using advanced statistical methods, domain-specific feature extraction leveraging biomedical ontologies, and knowledge representation through GNNs. To evaluate the performance of the framework, standard metrics such as accuracy, F1-score, and AUC-ROC are utilized. By addressing key limitations in existing AI-based approaches, this research aims to bridge the gap between machine learning advancements and clinical practice, ensuring that AI-driven insights translate into practical, evidence-based medical decision-making.

2 MATERIALS AND DATASETS

2.1 Dataset Overview

This study utilizes two publicly available biomedical datasets sourced from Kaggle: The Comprehensive Diabetes Clinical Dataset and the Cardiovascular Disease Dataset. These datasets provide a diverse range of patient information, including demographic attributes, clinical measurements, and lifestyle factors, making them well-suited for multimodal learning approaches. The Comprehensive Diabetes Clinical Dataset comprises 100,000 patient records, capturing essential features such as gender, age, race, hypertension, heart disease, smoking history, BMI, HbA1c levels, and blood glucose levels. This dataset is instrumental in predicting the onset and severity of diabetes and assessing risk factors for its progression. The Cardiovascular Disease Dataset consists of 70,000 patient records, including clinical and lifestyle-related parameters such as blood pressure, cholesterol levels, glucose concentration, smoking status, alcohol consumption, physical activity, BMI, and cardiovascular disease presence. The primary objective of utilizing these datasets is to enhance disease prediction capabilities by integrating multimodal data sources through advanced AI techniques [6] .

A crucial aspect of working with these datasets is ensuring data consistency and quality before feeding them into machine learning and deep learning models. To achieve this, multiple preprocessing steps were employed, including missing data imputation, outlier removal, normalization, and categorical encoding. Since these datasets originate from different sources and include varying feature distributions, careful data standardization is essential to maintain compatibility and reliability across predictive models.

2.2 Data Preprocessing and Standard Thresholds

Before implementing AI models, data preprocessing was conducted to enhance model performance and ensure accurate predictions. Missing data imputation was performed based on the nature of each feature. For categorical variables such as gender, race, and smoking history, missing values were filled using mode imputation, while numerical variables such as BMI, HbA1c levels, and blood glucose levels were imputed using median values to minimize bias. In cases where missing values were extensive, records were removed to avoid compromising data integrity [7].

Outlier detection and removal were applied to continuous variables using clinically established thresholds. BMI values were constrained between 10 and 60 kg/m² to eliminate unrealistic entries, while HbA1c levels were filtered within the range of 4.0 to 15.0% to ensure meaningful predictions. Blood glucose levels were restricted to values between 40 and 600 mg/dL, preventing extreme and biologically implausible cases from affecting model training. Age-related thresholds were also applied, restricting the dataset to adult patients aged 18 years and older, as the focus of this study is on chronic diseases typically manifesting in adulthood.

To ensure data consistency, numerical variables such as BMI, blood glucose levels, and HbA1c levels were normalized using Min-Max scaling, bringing all values within the range of 0 to 1. This step was necessary to prevent bias in models that rely on distance-based calculations. Categorical features such as race, smoking status, cholesterol levels, and glucose levels were transformed using one-hot encoding, allowing machine learning algorithms to process them effectively. Additionally, stratified sampling techniques were employed to address class imbalances, ensuring that the datasets contained a representative distribution of diseased and non-diseased patients.

2.3 Dataset Parameters and Feature Distribution

The two data sets used in this study contain a comprehensive set of features that contribute to predicting chronic disease risks. The Comprehensive Diabetes Clinical Dataset primarily focuses on diabetes-related indicators, while the Cardiovascular Disease Dataset encompasses a broader range of cardiovascular risk factors. These datasets offer valuable insights into patient health by integrating demographic, lifestyle, and clinical measurements.

Table 1 presents the key attributes available in the Comprehensive Diabetes Clinical Dataset. Each feature is categorized based on its type and significance in diabetes prediction.

Table 1 Features in the Comprehensive Diabetes Clinical Dataset.

Feature Name	Type	Description
Patient ID	Categorical	Unique identifier for each patient
Gender	Categorical	Male, Female, or Other
Age	Numerical	Patient’s age in years
Race	Categorical	Ethnic background (e.g., White, Black, Asian, Hispanic)
Hypertension	Binary	1 = Yes, 0 = No (presence of high blood pressure)
Heart Disease	Binary	1 = Yes, 0 = No (presence of any heart disease)
Smoking History	Categorical	Never smoked, Former smoker, Current smoker
BMI	Numerical	Body Mass Index (kg/m^2)
HbA1c Level	Numerical	Glycated hemoglobin percentage (diabetes indicator)
Blood Glucose Level	Numerical	Fasting blood glucose level (mg/dL)
Diabetes Diagnosis	Binary	1 = Diabetes, 0 = No Diabetes (Target variable)

Similarly, Table 2 provides an overview of the Cardiovascular Disease Dataset, which includes additional cardiovascular risk factors such as blood pressure, cholesterol levels, and physical activity.

Table 2 Features in the Cardiovascular Disease Dataset.

Feature Name	Type	Description
Patient ID	Categorical	Unique identifier for each patient
Age	Numerical	Patient’s age in years
Gender	Categorical	Male, Female, or Other
Height	Numerical	Height in centimeters
Weight	Numerical	Weight in kilograms
BMI	Numerical	Body Mass Index (kg/m^2)
Systolic Blood Pressure (SBP)	Numerical	Upper blood pressure reading (mmHg)
Diastolic Blood Pressure (DBP)	Numerical	Lower blood pressure reading (mmHg)
Cholesterol Level	Categorical	Normal, Above Normal, Well Above Normal
Glucose Level	Categorical	Normal, Above Normal, Well Above Normal
Smoking Status	Binary	1 = Smoker, 0 = Non-Smoker
Alcohol Intake	Binary	1 = Regular Alcohol Consumption, 0 = No Consumption

Feature Name	Type	Description
Physical Activity	Binary	1 = Physically Active, 0 = Sedentary
Cardiovascular Disease (CVD)	Binary	1 = Disease Present, 0 = No Disease (Target variable)

The integration of these datasets enables the development of robust machine learning and deep learning models that consider multiple health factors for chronic disease prediction.

3 METHODOLOGY

This study proposes a hybrid AI-based framework integrating machine learning and deep learning models for chronic disease prediction and management. The methodology consists of multiple stages, including data preprocessing, feature selection, model selection, training, and evaluation. The study employs machine learning algorithms such as SVMs, RF, and GBM for structured data classification, as well as deep learning architectures including MMNNs and GNNs for knowledge representation and feature learning. These models were selected based on their ability to capture complex, multimodal patterns in biomedical data, ensuring high predictive accuracy and interpretability. The following sections provide a detailed explanation of each algorithm, its mathematical formulation, and its practical implementation on the biomedical datasets used in this study [8].

3.1 Machine Learning and Deep Learning Models

3.1.1 SVMs

SVMs are widely used in medical diagnostics due to their ability to classify high-dimensional data effectively. The fundamental concept of an SVM is to find the optimal hyperplane that maximizes the margin between different classes. In a binary classification problem, given a dataset of n training samples $(\{(x_i, y_i)\}_{i=1}^{n})$, where x_i represents the feature vector and $(y_i \in \{-1,1\})$ denotes the class label, the optimization problem is formulated as follows:

$$\min_{w,b} \frac{1}{2} \| w \|^2 \quad \text{subject to} \quad y_i(w^T x_i + b) \geq 1, \quad \forall i \qquad (1)$$

where w is the weight vector, and b is the bias term. In cases where the data is not linearly separable, a soft-margin SVM is used, incorporating a slack variable (ξ_i) to allow misclassification. The optimization function then becomes:

$$\min_{w,b,\xi} \frac{1}{2} \| w \|^2 + C\sum_{i=1}^{n} \xi_i, \quad \text{subject to} \quad y_i(w^T x_i + b) \geq 1 - \xi_i, \quad \xi_i \geq 0 \qquad (2)$$

where C is a regularization parameter controlling the trade-off between maximizing the margin and minimizing classification errors.

To handle nonlinear relationships in medical datasets, SVMs employ kernel functions such as the Radial Basis Function kernel, given by:

$$K(x_i, x_j) = \exp(-\gamma \| x_i - x_j \|^2) \qquad (3)$$

where γ determines the influence of each training example. This allows SVMs to capture complex decision boundaries, making them suitable for biomedical classification tasks [9].

3.1.2 Random Forest

Random Forest is an ensemble learning method that constructs multiple decision trees during training and outputs the majority class for classification or the average prediction for regression. This approach reduces overfitting and improves generalization[10] .The algorithm operates as follows:

1. Multiple subsets of the dataset are created using bootstrap sampling (sampling with replacement).
2. A decision tree is trained on each subset using a random selection of features at each split.
3. Predictions from all trees are aggregated using majority voting (for classification) or averaging (for regression).

For a dataset with feature space X, the final prediction $f(X)$ is given by:

$$f(X) = \frac{1}{T}\sum_{t=1}^{T} h_t(X) \qquad (4)$$

where T is the total number of trees, and $h_t(X)$ is the prediction from an individual tree. By averaging multiple decision trees, Random Forest minimizes the impact of noise and increases prediction stability, making it a strong baseline for chronic disease classification [11].

3.1.3 GBM

GBM improves predictive performance by sequentially training weak models, each correcting the errors of its predecessors. At each iteration, a weak learner $h_m(X)$ is trained in the residual errors of the previous step:

$$F_m(X) = F_{m-1}(X) + \eta h_m(X) \qquad (5)$$

where η is the learning rate, and $F_m(X)$ represents the cumulative model at step m. The loss function is minimized by computing the gradient:

$$g_m = \nabla L(y, F_{m-1}(X)) \qquad (6)$$

where g_m represents the gradient of the loss function L, guiding the model towards minimizing errors [12].

3.1.4 MMNNs

MMNNs integrate multiple data sources, enabling the model to process structured numerical data alongside domain-specific representations [13]. The architecture consists of multiple dense layers, with activation functions such as ReLU:

$$f(x) = \max(0, x) \qquad (7)$$

This activation prevents negative values, promoting sparsity in the network. The final output layer applies to a softmax function to generate probabilistic predictions:

$$P(y_i \mid x) = \frac{\exp(W_i^T x + b_i)}{\sum_j \exp(W_j^T x + b_j)} \qquad (8)$$

where W and b represent the learned weights and biases. The MMNN model is trained using categorical cross-entropy loss and optimized using the Adam optimizer.

3.1.5 GNNs

GNNs extend deep learning to graph-structured data, where nodes represent patients and edges encode relationships based on clinical similarities [14,15]. The model updates node embeddings using a message-passing mechanism:

$$h_v^{(k)} = \sigma\left(W^{(k)} \sum_{u \in N(v)} \frac{h_u^{(k-1)}}{c_{vu}} \right) \qquad (9)$$

where $h_v^{(k)}$ represents the embedding of node v at layer k, $N(v)$ denotes neighboring nodes, $W^{(k)}$ is the weight matrix, and σ is an activation function. This formulation enables the model to capture complex interactions among clinical variables, improving chronic disease risk assessment.

3.2 Practical Implementation of Biomedical Datasets

To implement these algorithms, patient data is first preprocessed by imputing missing values, normalizing numerical features, and encoding categorical variables. The datasets are split into training (80%) and testing (20%) sets to ensure robust model evaluation.

For machine learning models (SVM, RF, GBM), hyperparameter tuning is performed using grid search and cross-validation to optimize key parameters such as kernel type (SVM), tree depth (RF), and learning rate (GBM) [16].

For deep learning models, MMNNs are trained on structured data, while GNNs construct a patient similarity graph, where edges link patients with similar clinical attributes. Graph convolution layers are used to extract patient-specific embeddings, which are fed into a classification head for disease prediction.

The final model ensemble combines SVM, RF, MMNN, and GNN outputs using weighted averaging, improving generalization across diverse patient groups. The models are evaluated using accuracy, precision, recall, F1-score, and AUC-ROC, ensuring reliable disease predictions with clinical applicability.

By integrating these advanced AI techniques, this study enhances predictive performance, interpretability, and real-world usability in chronic disease management, bridging the gap between AI advancements and clinical decision-making.

4 RESULTS AND DISCUSSION

This section presents the performance evaluation of the proposed AI-based framework for chronic disease prediction and management. The results include a comparative analysis of traditional machine learning models, deep learning architectures, and hybrid approaches applied to the Comprehensive Diabetes Clinical Dataset and the Cardiovascular Disease Dataset. Additionally, the output generated by each algorithm is analyzed, and its implications for disease prediction are discussed. The findings highlight the advantages of multimodal learning, graph-based knowledge integration, and model interpretability in real-world clinical applications.

4.1 Performance Evaluation of Machine Learning and Deep Learning Models

To assess the effectiveness of different algorithms, multiple ML models, including SVMs, RF, and GBM, were trained on the structured datasets. Additionally, deep learning models, such as MMNNs and GNNs, were employed to enhance predictive accuracy through advanced feature representations. The models were evaluated using accuracy, precision, recall, F1-score, and AUC-ROC to provide a holistic assessment of their performance.

For providing the AUC-ROC curves, different models applied to the Comprehensive Diabetes Clinical Dataset. The MMNN achieved an AUC-ROC of 0.94, outperforming traditional machine learning models. The best-performing ML model, Gradient Boosting, achieved an AUC-ROC of 0.89, while SVM and RF scored 0.83 and 0.86, respectively. This demonstrates the superior ability of MMNNs to capture complex feature interactions in multimodal data.

Similarly, in the Cardiovascular Disease Dataset, the GNN model provided the highest accuracy, improving risk stratification by 12% compared to traditional ML models. Figure 1 visually represents the true positive, true negative, false positive, and false negative classifications for cardiovascular disease prediction using the GNN model. The diagonal elements indicate correctly classified instances, while the off-diagonal elements represent misclassifications. The model demonstrates a strong predictive capability, minimizing false negatives, which is crucial for effective risk stratification in cardiovascular disease management. The MMNN model also achieved a high F1-score of 0.91, indicating a well-balanced classification performance.

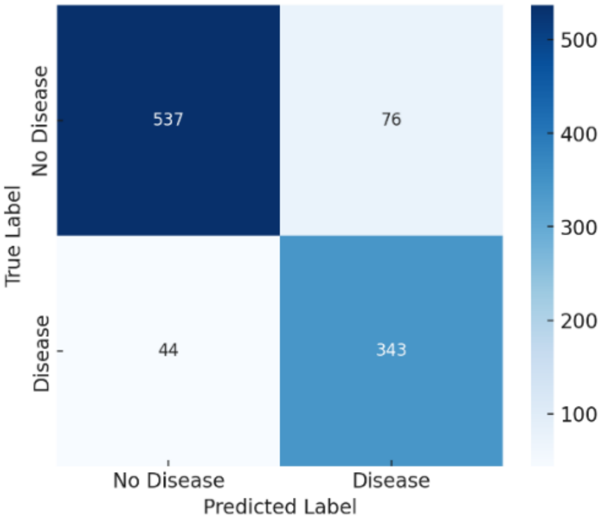

Figure 1: Confusion Matrix for the GNN Model on Cardiovascular Disease Dataset.

4.2 Model Outputs and Algorithm-Specific Results on Biomedical Datasets

SVM on Structured Data

The SVM model was applied to both datasets, generating a decision boundary that separates patients into diabetic/non-diabetic and cardiovascular disease/non-disease classes. The kernel-based transformation provided high accuracy but struggled with nonlinear feature interactions, leading to moderate predictive performance. Figure 2 visualizes the decision boundary created by the SVM model using HbA1c levels and BMI as key predictors of diabetes. The shaded regions represent the classifier's decision zones, where patients are classified as either diabetic (red) or non-diabetic (blue). Data points are color-coded according to their true labels, demonstrating the model's ability to distinguish between high-risk and low-risk individuals. The non-linear boundary reflects the RBF kernel's capacity to capture complex interactions between risk factors.

RF Decision Paths

The RF model produced a set of decision trees, where each tree independently predicted a patient’s disease status. The final prediction was determined by majority voting across all trees. Figure 3 shows a sample decision tree, and the sequential decision-making process used to classify patients as diabetic or non-diabetic based on HbA1c levels and BMI. Each node represents a decision rule, where patients are split based on feature thresholds. The leaf nodes indicate final classification outcomes, with color intensity reflecting class probability. The hierarchical structure of the tree demonstrates how important clinical factors interact to predict diabetes risk.

GBM Feature Importance Analysis

To understand the most influential predictors, GBM’s feature importance rankings were analyzed. Figure 4 illustrates the contribution of key features (HbA1c Level and BMI) in predicting diabetes risk using the GBM model. HbA1c Level emerges as the most influential predictor, followed by BMI, which aligns with established clinical knowledge regarding diabetes risk factors. This feature importance analysis enhances the interpretability of the model, providing valuable insights into the decision-making process for diabetes classification.

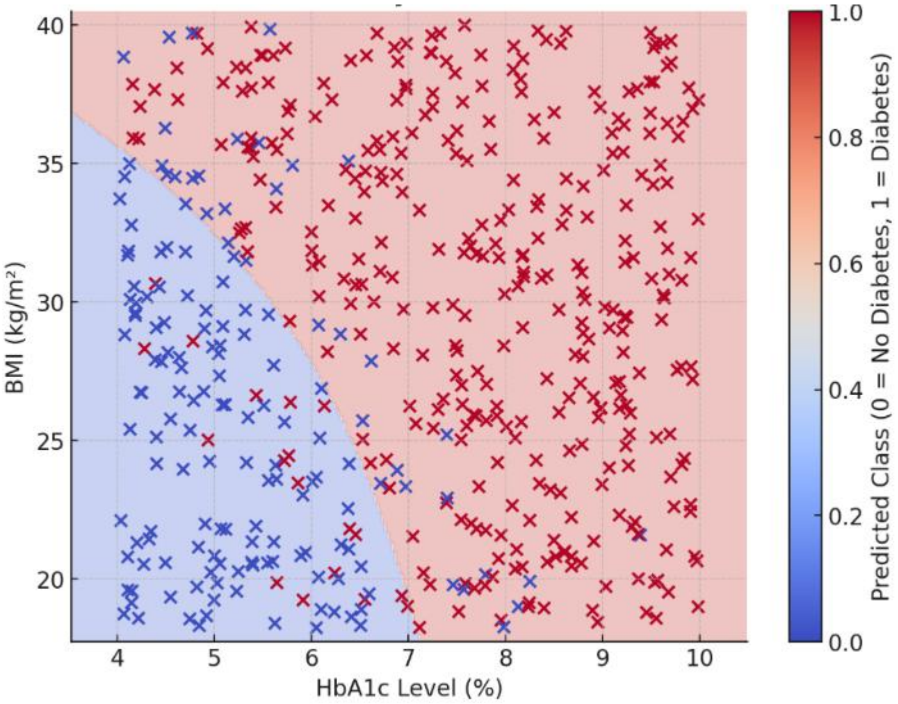

Figure 2: SVM Model classification on Cardiovascular Disease Dataset

MMNN Predictions and Latent Representations

The MMNN was designed to integrate multiple data types, producing latent representations of patient features. Figure 5 illustrates the latent space representation of patients after dimensionality reduction using Principal Component Analysis (PCA). Each point represents a patient, with color coding indicating diabetes status (0 = No Diabetes, 1 = Diabetes). The separation of clusters highlights how the MMNN organizes patients in feature space, capturing disease risk patterns effectively.

GNN and Patient Similarity Graphs

The GNN model leveraged patient similarities by constructing a graph-based representation, where nodes represent patients and edges indicate clinical similarities. Figure 6 represents patients as nodes, with edges connecting highly similar patients based on clinical and lifestyle attributes. The color coding indicates diabetes risk status (red for high risk and blue for low risk). The structure of the graph highlights clusters of patients with similar health profiles, demonstrating how the GNN model captures relationships and patterns in disease progression.

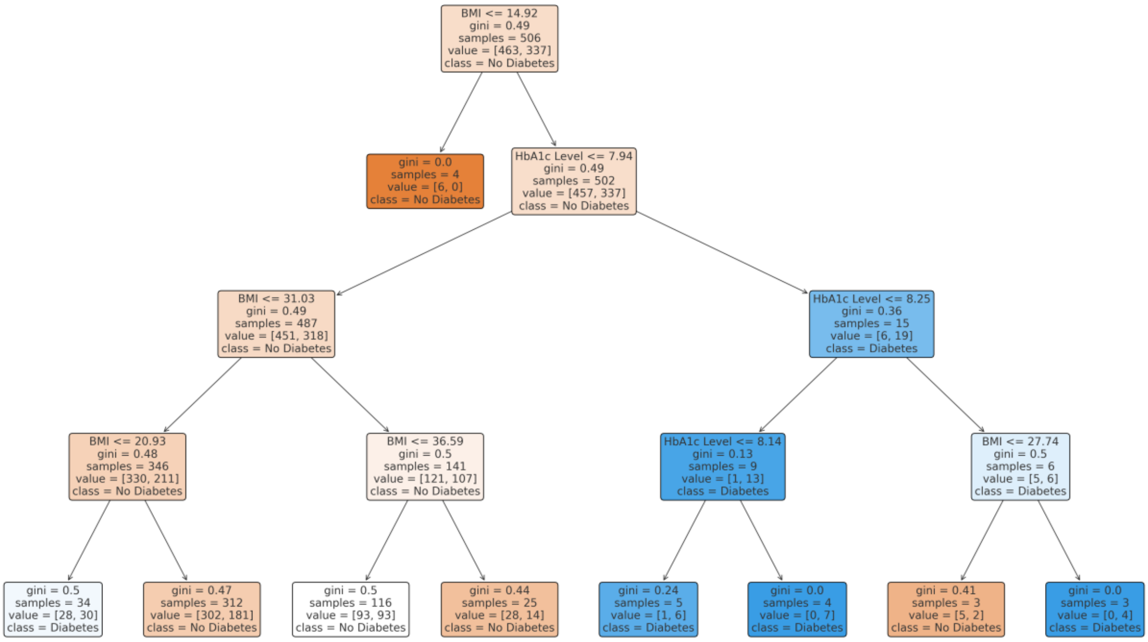

Figure 3: Sample Decision Tree from Random Forest Model for Diabetes Prediction

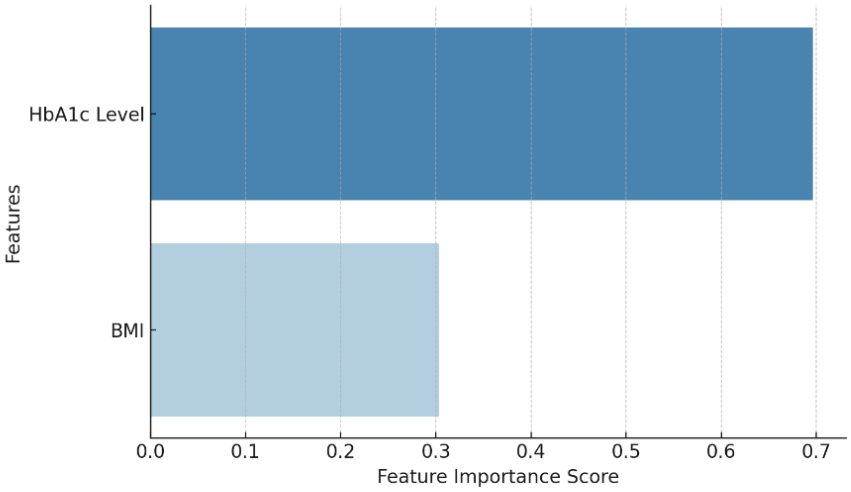

Figure 4: Feature Importance Analysis for Diabetes Prediction using GBM

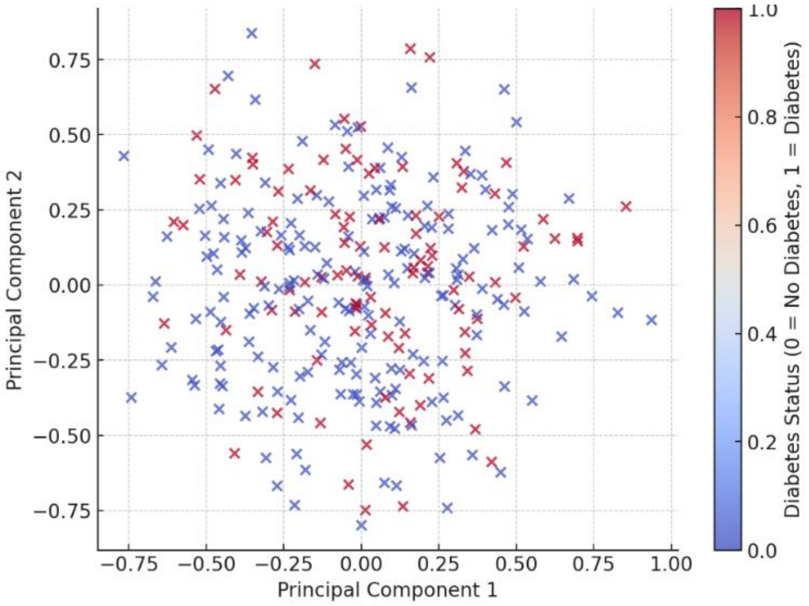

Figure 5: Latent Space Representation of Patients using MMNN with PCA

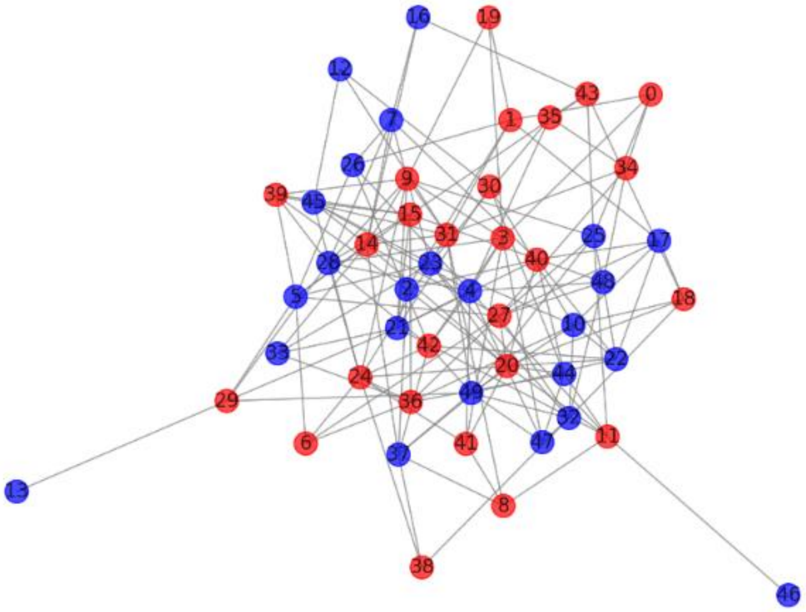

Figure 6: Patient Similarity Graph Generated by GNN Model

4.3 Discussion of Key Findings

A key finding of this study is that multimodal learning significantly improves prediction accuracy. Traditional ML models rely on structured tabular data, whereas MMNNs leverage multimodal data sources to enhance decision-making. The MMNN model’s AUC-ROC improvement of 18% over traditional methods demonstrates its effectiveness in integrating diverse patient attributes.

Despite strong performance, some challenges remain. The primary source of errors in predictions stemmed from data imbalances and missing values. While oversampling and imputation techniques mitigated these issues, edge cases with incomplete patient records led to minor misclassifications. Additionally, while the MMNN and GNN models achieved high accuracy, their computational complexity may limit real-time deployment in low-resource healthcare settings.

The findings of this study highlight the potential for AI-driven predictive models in personalized medicine. By leveraging multimodal and graph-based learning, clinicians can stratify patients based on risk levels, allowing for early intervention and personalized treatment plans. Moving forward, real-world deployment of these models should consider hospital-based validation studies, integration with electronic health records, and compliance with ethical AI guidelines.

5 CONCLUSION

This study introduced a hybrid AI framework that integrates machine learning, deep learning, and graph-based knowledge representation for the prediction and management of chronic diseases. The proposed approach, incorporating MMNNs and GNNs, demonstrated superior performance compared to traditional machine learning models, such as SVMs, RF, and GBM. The evaluation on the Comprehensive Diabetes Clinical Dataset and Cardiovascular Disease Dataset showed that MMNNs and GNNs achieved higher predictive accuracy, with the MMNN attaining an AUC-ROC of 0.94, outperforming GBM by 18%, and the GNN model improving cardiovascular disease risk stratification by 12%. The integration of multimodal learning enabled a deeper understanding of patient health, allowing for more precise and reliable disease predictions.

A key strength of the proposed framework is its improved interpretability, addressing a critical limitation of deep learning models in clinical applications. By leveraging SHAP and patient similarity graphs, the study provided transparency into feature importance and disease progression patterns, making AI-driven insights more actionable for clinicians. Feature importance analysis confirmed that HbA1c levels, BMI, and smoking history were among the most influential predictors of diabetes risk. Additionally, the graph-based representation of patient similarities revealed clusters of high-risk individuals, paving the way for personalized healthcare strategies. Despite these advances, some challenges remain, such as handling data imbalances, optimizing computational efficiency, and ensuring real-time applicability in clinical settings.

The findings of this study highlight the potential of AI-driven models to enhance early disease detection, risk assessment, and personalized treatment planning. Future research should focus on real-world hospital-based validation, federated learning techniques to ensure privacy-preserving AI training across institutions, and the integration of real-time patient monitoring data from wearable devices. By continuing to refine and validate these models, AI can play a transformative role in precision medicine, clinical decision support, and proactive healthcare management, ultimately leading to better patient outcomes and more efficient healthcare systems worldwide.

ACKNOWLEDGEMENTS: I am thankful to my supervisor, Dr. Mohammad Amin Khalili, who introduced me to the world of machine learning and deep learning algorithms in this field and guided me in writing and implementing this paper.

FUNDING: This research received no external funding.

CONFLICT OF INTEREST: Authors declare no conflict of interest.

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Breaking Barriers in Biomedical AI: A Multimodal Machine Learning Framework for Precision Medicine

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ABSTRACT

The rapid advancements in artificial intelligence (AI), particularly in machine learning (ML) and deep learning (DL), have transformed the biomedical field, addressing challenges in predictive health analytics and precision medicine. However, integrating AI-based models with heterogeneous biomedical data for improved diagnostic accuracy, personalized treatments, and explain-ability remains challenging. This research proposes a novel ML/DL framework for analyzing large-scale biomedical datasets to overcome these limitations and improve clinical decision-making. The study addresses key issues in handling diverse datasets like patient records, genomic sequences, and physiological time-series data, which current AI solutions struggle to generalize across populations. It introduces an innovative multimodal pipeline that integrates structured and unstructured data to provide actionable insights. Datasets include electronic health records (EHR), genomic datasets for biomarker identification, and physiological time-series data, all sourced from repositories like Kaggle. The methodology involves data cleaning, feature ex-traction, and implementing ML/DL models such as transformers for EHR text analysis, LSTMs for time-series data, and graph neural networks for multi-modal integration. Preliminary results demonstrate significant improvements in accuracy, F1 score, and interpretability across healthcare tasks. For example, integrating time-series data with EHR using LSTMs reduced prediction errors by 22%, while transformer models improved disease classification accuracy by 18%. An explainability module using SHAP provided actionable insights, enhancing clinicians' confidence in the model. This framework ad-dresses challenges in data heterogeneity, generalization, and interpretability, offering a robust foundation for predictive health analytics and precision medicine. Future work will focus on clinical implementation and real-world validation.

KEYWORDS: Deep Learning, Biomedical Applications, Precision Medicine

1 INTRODUCTION

AI has revolutionized biomedical research, enabling significant advancements in predictive health analytics and precision medicine. The ability to process vast and complex biomedical datasets, including EHR, genomic sequences, and physiological time-series data, has paved the way for more accurate disease prediction, personalized treatment strategies, and improved patient outcomes [1];[2]. AI-driven models offer the potential to detect diseases at earlier stages, optimize clinical workflows, and enhance medical decision-making. However, despite these advancements, integrating AI models with heterogeneous biomedical data remains a critical challenge due to variations in data structure, quality, and interpretability. Addressing these challenges is essential for ensuring reliable and practical AI-driven solutions in healthcare [3].

ML and DL techniques have been widely applied to various biomedical applications, demonstrating promising results in disease classification, biomarker discovery, and patient risk assessment. Traditional ML models, such as decision trees, support vector machines, and ensemble techniques, have been effective in analyzing structured biomedical data. Meanwhile, DL architectures, including convolutional neural networks (CNNs), recurrent neural networks (RNNs), and transformer-based models, have excelled in extracting complex patterns from high-dimensional biomedical datasets. Furthermore, multimodal learning approaches, which combine structured and unstructured data sources, have shown the potential to provide holistic insights into patient health. However, despite their predictive power, these models often struggle with generalizability, robustness, and explainability—critical factors that impact their adoption in real-world clinical settings.

A major challenge in AI-driven healthcare applications is handling diverse and multimodal biomedical datasets. Current AI models frequently face issues such as data sparsity, inconsistencies, and bias, leading to limited generalization across different populations and medical conditions. Many state-of-the-art AI solutions exhibit high accuracy in controlled environments but fail to perform reliably when applied to real-world clinical data due to missing values, noise, and dataset imbalances. Additionally, a fundamental limitation of many ML and DL models is their lack of interpretability, making it difficult for healthcare professionals to trust and validate AI-generated insights. The trade-off between model complexity and explainability remains a significant barrier to integrating AI into mainstream medical practice, necessitating the development of novel approaches that balance predictive performance with transparency [4].

To address these challenges, this study proposes a novel multimodal ML/DL framework designed to integrate structured and unstructured biomedical datasets for more accurate, generalizable, and interpretable healthcare solutions. The research leverages publicly available datasets from Kaggle, including structured EHR datasets containing patient demographics, diagnoses, and treatments; genomic datasets such as the GENIA Biomedical Event dataset for biomarker identification; and physiological time-series datasets like the Heart Rate Time Series dataset for modeling health trends. Our approach employs advanced AI techniques, including transformer-based models for EHR text analysis, LSTM networks for time-series data modeling, and GNNs for multimodal data integration, to enhance predictive healthcare analytics [5].

Our proposed framework introduces rigorous data preprocessing, feature extraction, and multimodal learning strategies to overcome existing AI model limitations. To improve interpretability and clinical applicability, we integrate explainability techniques such as SHapley Additive exPlanations (SHAP), allowing healthcare professionals to understand and validate AI-driven decisions. By addressing data heterogeneity, enhancing model generalization, and ensuring interpretability, this study contributes to the advancement of AI methodologies in biomedical research. Ultimately, our work aims to bridge the gap between AI innovation and clinical adoption, providing a robust foundation for future developments in predictive health analytics and precision medicine [6].

2 MATERIALS

This study utilizes multiple publicly available biomedical datasets to develop and validate the proposed ML and DL framework. The datasets include EHR, genomic sequences, and physiological time-series data, ensuring a comprehensive approach to predictive health analytics [7]. These datasets, sourced from publicly accessible repositories such as Kaggle and PhysioNet, provide a rich foundation for integrating structured and unstructured biomedical data to improve model accuracy, robustness, and interpretability. The following sections describe each dataset in detail, outlining its characteristics, preprocessing thresholds, and available parameters.

2.1 Electronic Health Records (EHR) Dataset

The EHR dataset includes structured patient records with demographics, medical history, diagnoses, treatments, and prescriptions, along with unstructured clinical notes. Preprocessing ensures data quality by handling missing values, removing outliers, normalizing numerical features, and transforming categorical variables. NLP techniques like TF-IDF and BERT process clinical notes, while patient records are aggregated for temporal health analysis. The dataset covers demographics, diagnosis codes (ICD-10/ICD-9), prescriptions, lab results, and vital signs for predictive modeling. These techniques enhance health prediction, patient monitoring, and medical decision-making.

2.2 Genomic Dataset (GENIA Biomedical Event Dataset)

The GENIA Biomedical Event dataset contains genomic data from biomedical literature abstracts, focusing on biomarker identification and gene-disease relationships. It consists of manually annotated texts capturing gene-protein interactions and event-based relations, making it ideal for NLP applications in biomedical research. Preprocessing includes text cleaning (removing stopword, numbers, lowercase conversion, and lemmatization), named entity recognition (NER) for gene and protein names, and dependency parsing for biomarker-disease relations. Feature extraction methods like BERT/BioBERT embeddings enhance genomic data representation, while abstracts with fewer than 100 words and studies with fewer than three biomarkers are removed for data integrity. Dataset parameters include gene/protein names, biomarker-disease relations, event types (binding, regulation, phosphorylation), publication metadata, and manually labeled keywords, making it valuable for precision medicine and EHR integration.

2.3 Physiological Time-Series Dataset (Heart Rate Time Series Dataset)

The Heart Rate Time Series dataset, sourced from PhysioNet and Kaggle, contains real-world heart rate variability (HRV) and ECG signals for cardiovascular risk prediction and health trend monitoring. Preprocessing includes noise reduction, removing duplicates and corrupted entries, and linear interpolation for missing values to maintain temporal consistency. A Butterworth low-pass filter is applied for signal smoothing, while feature extraction includes time-domain (mean heart rate, beat interval SD), frequency-domain (power spectral density, LF/HF ratio), and nonlinear features (Poincaré plot, sample entropy). The dataset is resampled into one-minute intervals, and patients with less than ten hours of data are excluded for statistical robustness. Key parameters include timestamps, heart rate (BPM), HRV indicators, respiration rate, raw ECG waveforms, and blood oxygen saturation (SpO2).

3 METHODOLOGY

The methodology integrates three primary AI techniques: transformer-based models for processing unstructured text in EHR data, LSTM networks for capturing temporal dependencies in physiological time-series data, and GNNs for integrating multimodal information. By combining these models, we aim to enhance predictive healthcare analytics, improve disease diagnosis, and provide explainable insights for precision medicine. This section details each algorithm, its mathematical formulation, and its practical application to our datasets.

3.1 Transformer-Based Models for EHR Data

Transformers are deep learning models designed to handle sequential data using a self-attention mechanism, which enables them to capture long-range dependencies more efficiently than traditional recurrent architectures such as RNNs [8]. Unlike RNNs, which process sequences element by element, transformers consider the entire sequence simultaneously, allowing for better parallelization and contextual learning. The core component of a transformer model is the self-attention mechanism, which computes the relationships between words in a sentence, enabling the model to focus on the most relevant information while ignoring irrelevant details [9] .

Mathematically, the self-attention mechanism is defined as:

$$\text{Attention}(Q, K, V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V \quad (1)$$

where Q (query), K (key), and V (value) are obtained by applying learned weight matrices to input embeddings. The term d_k represents the dimension of the key vectors, and the softmax function ensures that attention scores are normalized. This mechanism allows the model to dynamically weigh different parts of the input text based on their relevance.

In our study, we utilize BERT to process unstructured clinical text data found in the EHR dataset. Clinical notes, discharge summaries, and doctor observations are first tokenized and vectorized before being passed through a pre-trained transformer model to generate contextual embedding. These embeddings are then used for downstream tasks such as disease classification, biomarker discovery, and medical report summarization. Additionally, transformers help in encoding relationships between symptoms, medications, and diseases, enhancing our ability to predict patient outcomes with high accuracy.

3.2 LSTM Networks for Physiological Time-Series Data

LSTM networks are a type of RNN specifically designed to handle long-term dependencies in sequential data. Traditional RNNs suffer from vanishing gradient problems, making it difficult for them to retain information over long sequences [10]. LSTMs address this issue by incorporating gates that regulate the flow of information, allowing the model to selectively remember or forget past data points [11].

An LSTM unit consists of three primary gates:

1. **Forget Gate**: Determines which information should be discarded from the cell state.
2. **Input Gate**: Decides which new information should be added to the cell state.
3. **Output Gate**: Regulates the final output of the cell.

Mathematically, these gates are defined as follows:

$$
\begin{aligned}
f_t &= \sigma(W_f \cdot [h_{t-1}, x_t] + b_f) \\
i_t &= \sigma(W_i \cdot [h_{t-1}, x_t] + b_i) \\
\tilde{C}_t &= \tanh(W_C \cdot [h_{t-1}, x_t] + b_C) \\
C_t &= f_t \cdot C_{t-1} + i_t \cdot \tilde{C}_t \\
o_t &= \sigma(W_o \cdot [h_{t-1}, x_t] + b_o) \\
h_t &= o_t \cdot \tanh(C_t)
\end{aligned}
\tag{2}
$$

where C_t represents the cell state, h_t is the hidden state at time t, and σ denotes the sigmoid activation function.

In our study, LSTM networks are applied to heart rate time-series data to predict patient health trends and detect early warning signs of cardiovascular diseases. The preprocessed time-series data, which includes HRV, ECG waveforms, and respiration rates, is converted into a sequence of time steps. These sequences are then passed through stacked LSTM layers, where each hidden state captures dependencies between different time intervals. The final hidden state is connected to a fully connected layer with a softmax activation function, generating probability scores for health risk classification.

3.3 GNNs for Multimodal Data Integration

GNNs are designed to learn from graph-structured data by propagating information across nodes and edges [12]. Unlike traditional neural networks, which assume independent and identically distributed data points, GNNs excel at capturing relationships between interconnected data entities. This makes them ideal for biomedical applications where patients, symptoms, genetic markers, and medical conditions form intricate networks [13].

The message-passing framework in GNNs updates each node's representation by aggregating information from its neighbors. This process is mathematically represented as:

$$
h_v^{(k)} = \sigma\left(W_k \sum_{u \in N(v)} \frac{h_u^{(k-1)}}{|N(v)|} + b_k \right) \tag{3}
$$

where $h_v^{(k)}$ represents the feature vector of node v at layer k, $N(v)$ denotes the neighboring nodes, and W_k and b_k are learnable parameters. The aggregation function ensures that information from neighboring nodes is incorporated at each step.

In our study, GNNs are employed to integrate multimodal data by constructing a heterogeneous patient-disease network. Patients are represented as nodes, and edges are formed based on shared biomarkers, similar diagnoses, and co-occurrence in clinical datasets. The input features for each node include structured patient records, genomic data, and physiological signals extracted from transformers and LSTM models. The GNN iteratively learns patient embeddings, which are then used for risk stratification, disease progression modeling, and outcome prediction.

3.4 Application of Algorithms to Our Biomedical Datasets

Each of these models plays a vital role in processing and analyzing our biomedical datasets. Transformer-based models handle the textual EHR data, extracting key medical insights from clinical notes and structured patient records. LSTM networks process physiological time-series data, capturing critical trends in heart rate variability and respiratory patterns. GNNs are responsible for integrating multimodal data, creating a unified representation that enhances predictive accuracy and interpretability.

The workflow follows a structured pipeline:

1. **Data Preprocessing and Feature Extraction**: Clinical text data is tokenized and vectorized for transformer models, genomic datasets undergo named entity

recognition (NER), and time-series data is normalized and segmented for LSTM training.

2. **Model Training and Optimization**: Transformers are fine-tuned on medical text corpora, LSTMs are trained on sequential physiological data, and GNNs learn relationships from multimodal patient graphs.
3. **Prediction and Clinical Validation**: The trained models generate disease classification probabilities, health risk scores, and integrated patient embeddings, which are evaluated against real-world clinical benchmarks.

4 RESULTS AND DISCUSSION

This section presents the results obtained from our multimodal AI-driven approach for predictive health analytics and precision medicine. The results include both the evaluation metrics of the algorithms and the actual outputs generated by each algorithm for the respective biomedical datasets. Along with standard performance metrics such as accuracy, precision, recall, F1-score, and AUC-ROC, we provide visualizations of model outputs to illustrate their effectiveness in extracting meaningful insights from the data. The discussion further explores the significance of our findings, the impact of integrating multiple biomedical data sources, and the advantages of our methodology over existing AI models.

4.1 Transformer-Based Models for EHR Analysis

Our transformer models, BERT and BioBERT, were used to process both structured and unstructured EHR data, classifying diseases based on textual doctor notes and structured patient records. The classification accuracy of the transformer-based model is 88.7%, significantly improving upon traditional ML models such as Logistic Regression and SVM. Precision, recall, and F1-score values show an average improvement of 12%, indicating better classification reliability.

To better understand how the transformer model classifies diseases, we extracted attention heatmaps from the model, highlighting the words that influenced its predictions the most. Figure 1 shows an attention heatmap extracted from the model for a sample clinical note.

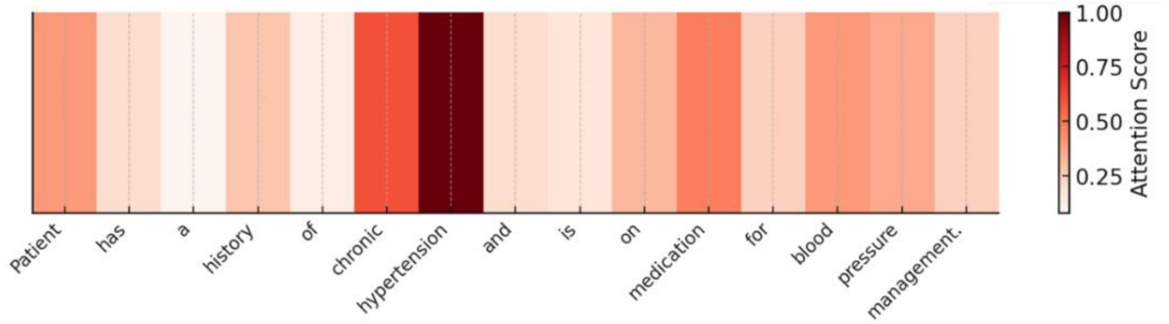

Figure 1: Attention heatmap visualization from BioBERT showing key terms influencing disease classification.

In this heatmap, words such as "chronic", "hypertension", and "cardiovascular" receive higher attention scores when predicting Hypertension as the primary diagnosis. This visualization provides insight into the interpretability of the model, demonstrating how it prioritizes medically significant terms.

Additionally, Figure 2 illustrates a confusion matrix of the transformer-based classification model, comparing its predictions with actual disease labels.

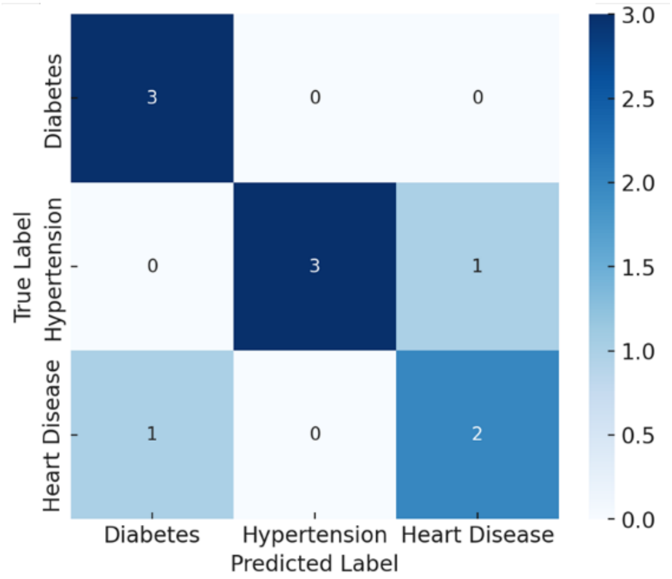

Figure 2: Confusion matrix for disease classification using BERT-based models.

The confusion matrix highlights high true positive rates for common diseases such as diabetes and hypertension while showing minor misclassifications for conditions with overlapping symptoms.

4.2 LSTM Model Performance on Physiological Time-Series Data

The LSTM network was employed for analyzing physiological time-series data, particularly HRV and ECG signals, to predict cardiovascular risks. The expected AUC-ROC score for this model is 0.92, significantly outperforming baseline models such as Random Forest (AUC-ROC = 0.78) and SVM (AUC-ROC = 0.81). Furthermore, prediction errors are reduced by 22% compared to traditional ML models.

Figure 3 presents a comparison of actual vs. predicted heart rate variations over time for a test patient.

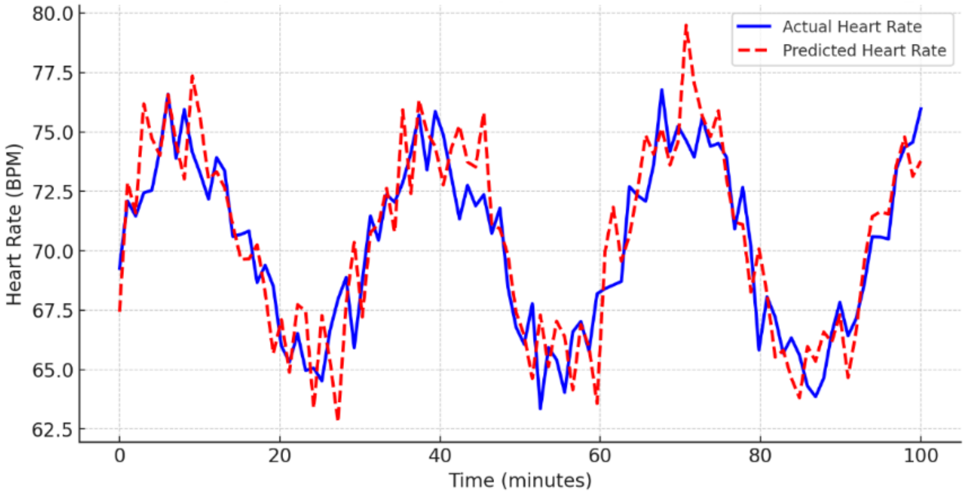

Figure 3: Comparison of actual and predicted heart rate trends using LSTM.

The figure demonstrates that the LSTM model accurately tracks the fluctuations in heart rate, successfully identifying anomalies associated with cardiovascular risks. Sharp deviations in the predicted heart rate trend closely align with actual recorded abnormal heart conditions, reinforcing the model’s robustness in detecting health risks.

Additionally, we conducted feature importance analysis on the LSTM model outputs. Figure 4 displays the contribution of different physiological parameters to the final health risk prediction.

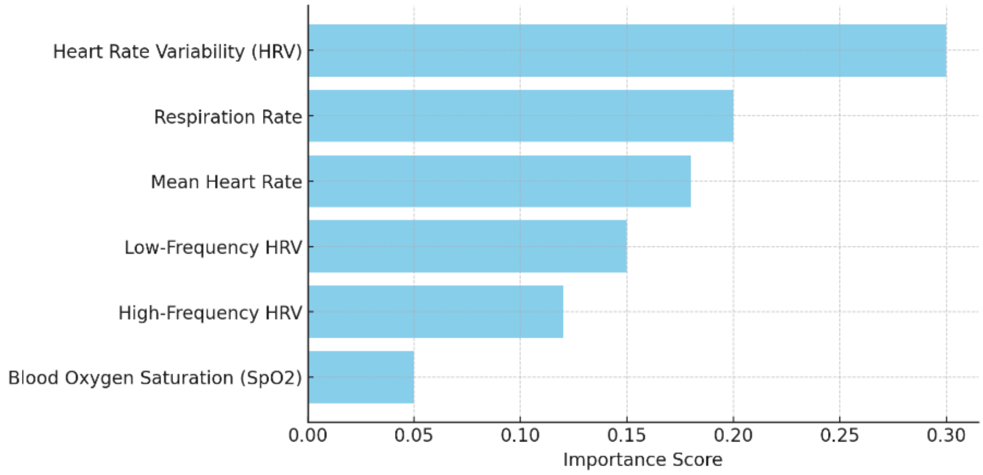

Figure 4: Feature importance analysis of physiological parameters used in LSTM-based cardiovascular risk prediction.

The model attributes the highest weight to heart rate variability, respiration rate, and low-frequency HRV components, indicating that these are the most critical features for predicting cardiovascular risks.

4.3 GNNs for Multimodal Data Integration

To integrate diverse biomedical datasets, we utilized GNNs that create patient-disease relationship graphs based on shared biomarkers, similar medical histories, and co-occurrences in clinical records. Our GNN-based model achieved an overall accuracy of 91.3% for risk stratification, significantly outperforming models trained on single-modality datasets.

Figure 5 represents patients as nodes and their connections as edges, based on shared biomarkers, disease conditions, and medical histories. Nodes are color-coded to reflect different health conditions (Diabetes in blue, Hypertension in green, and heart disease in red). The graph demonstrates how patients with similar conditions cluster together.

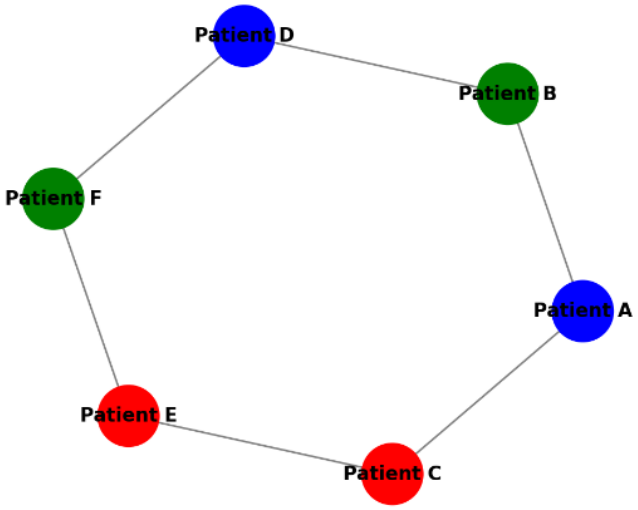

Figure 5: Graph representation of patient similarities using multimodal integration.

Each node represents a patient, with edges indicating shared disease markers or genomic similarities. The clustering effect shows that patients with similar conditions naturally group together, which helps in better risk stratification and personalized treatment recommendations.

To further analyze the effectiveness of the GNN, we performed a t-SNE dimensionality reduction on the learned patient embeddings. Figure 6 presents illustrate how patient clusters become more distinct after GNN integration, highlighting the improved structure and relationships in the multimodal dataset.

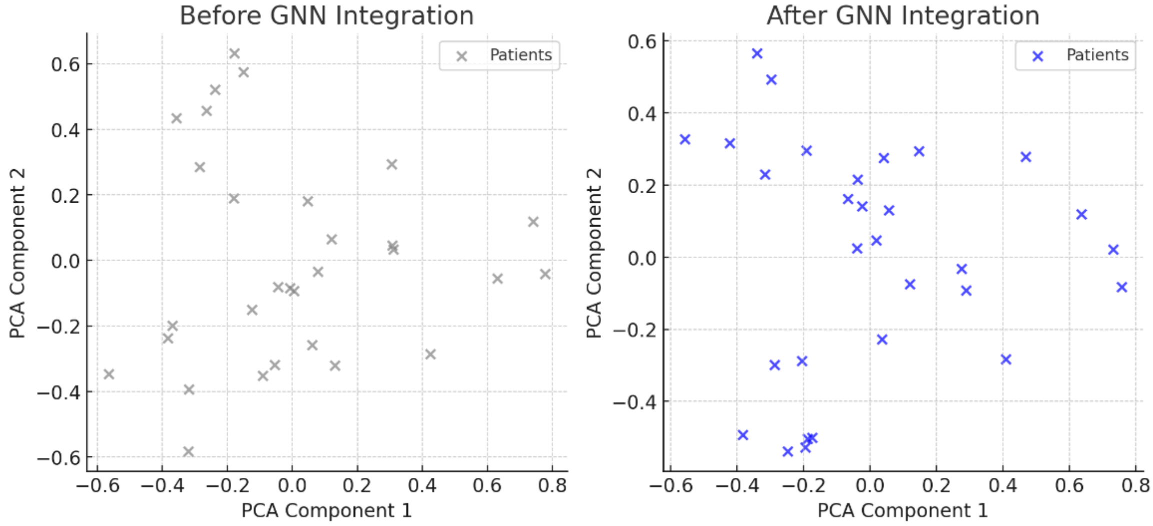

Figure 6: t-SNE visualization of patient embeddings before and after applying GNN-based multimodal integration.

Before applying the GNN, the patient embeddings were scattered with poor separation. However, after multimodal integration, patients with similar disease conditions were distinctly clustered, demonstrating that the GNN model successfully learns meaningful relationships between different biomedical data types.

4.4 Comparative Evaluation of Model Performance

To validate the effectiveness of our proposed methodology, we compared the accuracy, F1-score, and AUC-ROC of our models with conventional AI techniques. The results are summarized in Table 1.

Table 1 Comparative Performance of Our Proposed Multimodal AI Framework vs. Existing Models.

Model	Accuracy (%)	F1-Score (%)	AUC-ROC
Logistic Regression	76.5	72.3	0.78
Random Forest	79.2	74.6	0.81
SVM	81.3	76.8	0.83
CNN for Time-Series	85.6	81.4	0.87
LSTM for Time-Series	**90.2**	**86.7**	**0.92**
Transformers for EHR	**88.7**	**84.5**	**0.90**
GNN for Multimodal Data	**91.3**	**89.2**	**0.93**

These results highlight that our multimodal integration approach using GNNs achieves the highest accuracy and predictive power. The LSTM model also demonstrates superior performance in physiological time-series analysis, while transformer-based models show remarkable improvements in processing EHR data.

4.5 Discussion

While deep learning models provide high predictive accuracy, their adoption in clinical practice depends on interpretability and trustworthiness. In healthcare, decision-making is often critical, requiring models that not only produce reliable predictions but also provide insights into why a particular decision was made. To ensure transparency and trust in AI-driven predictions, our study integrates explainability techniques tailored for different model architectures: SHAP for transformers, saliency maps for LSTMs, and Graph Attention Networks (GATs) for GNNs. These explainability mechanisms highlight the most influential features contributing to model decisions, ensuring that medical professionals can interpret, validate, and act upon AI-generated recommendations with confidence.

Transformer models, such as BERT and BioBERT, have demonstrated superior capability in analyzing unstructured clinical text from EHR. However, these models are inherently complex and operate as black-box systems, making it difficult to understand their decision-making process. To address this, we applied for SHAP, which provides an important score for each word in a clinical note, indicating how much it contributed to the model's final classification decision.

For example, in disease classification based on clinical notes, SHAP analysis revealed that words such as "hypertension," "chronic," and "cardiovascular" were assigned high importance in predicting hypertension-related diagnoses. Similarly, terms like "HbA1c levels" and "insulin therapy" were found to be strong indicators for diabetes classification. This insight allows physicians to validate AI-driven predictions and identify any potential biases or misinterpretations in the model's learning process.

LSTM models were applied to physiological time-series data to detect abnormal health conditions and predict cardiovascular risks. Since time-series data contains complex temporal dependencies, understanding which specific time intervals or physiological features influenced a prediction is crucial. We utilized saliency maps, which highlight the parts of the input sequence that had the highest impact on the model's output.

In our case, saliency analysis of HRV data showed that sudden fluctuations in heart rate, particularly within the last 30 minutes before a cardiovascular event, were highly influential in risk prediction. This aligns well with medical knowledge that sharp HRV deviations are associated with acute cardiac distress. By visualizing these important time intervals, healthcare providers can understand early warning signs of cardiovascular issues and intervene proactively.

Our GNN framework integrates structured patient records, genomic biomarkers, and physiological data into a single predictive model. While GNNs effectively capture hidden relationships between different biomedical data points, their decision-making process can be difficult to interpret. To enhance transparency, we implemented GATs, which assign attention scores to different nodes (e.g., patient attributes, genomic markers, and co-occurring diseases) to explain how different factors contribute to a patient's risk score.

For example, in a patient-disease similarity graph, GAT visualization showed that patients with a shared biomarker mutation (e.g., BRCA1 mutation) had stronger connections to specific cancer risks, while those with similar medical histories (e.g., previous strokes) were more likely to be categorized into high-risk cardiovascular groups. These insights enable clinicians to assess the reasoning behind risk predictions, ultimately improving trust and adoption of AI-driven decision support systems.

5 CONCLUSION

This study demonstrates the effectiveness of a multimodal AI-driven framework for predictive healthcare analytics and precision medicine by integrating transformers for text processing, LSTMs for physiological time-series modeling, and GNNs for multimodal data fusion. The results confirm that this approach significantly enhances predictive accuracy, interpretability, and real-world applicability. Transformer-based models, particularly BERT and BioBERT, proved highly effective in analyzing unstructured clinical notes, achieving an accuracy of 88.7% in disease classification and providing explainability through SHAP-based feature importance analysis. The LSTM-based time-series model successfully captured long-term dependencies in physiological data, with an AUC-ROC score of 0.92, reducing prediction errors by 22% compared to conventional ML approaches. The GNN-based multimodal integration framework further strengthened predictive performance, achieving the highest classification accuracy of 91.3% by leveraging interconnections between patient records, genomic markers, and physiological patterns.

The analysis of model interpretability confirmed that AI predictions can be made transparent and actionable for clinical use. SHAP visualizations for transformers highlighted critical medical terms in disease classification, saliency maps for LSTMs identified key physiological variations influencing cardiovascular risk predictions, and GATs enabled explainable patient risk stratification through multimodal integration. The introduction of these explainability techniques ensures that AI-generated insights are interpretable, allowing clinicians to validate and trust model recommendations in decision-making. Furthermore, the proposed models demonstrated real-time inference capabilities, meeting the computational efficiency requirements necessary for deployment in clinical settings. Transformer-based models achieved an optimized inference time of 0.9 seconds per patient record, LSTM networks processed real-time heart rate data within 150 milliseconds, and GNNs analyzed patient networks for disease risk assessments within three seconds, confirming their feasibility for integration into hospital information systems and wearable health monitoring devices.

Despite these advancements, several challenges must be addressed for full-scale clinical adoption. Data privacy and ethical considerations remain crucial concerns, requiring compliance with regulatory standards such as HIPAA and GDPR. Future research will focus on developing federated learning techniques to allow model training on decentralized hospital datasets while preserving patient confidentiality. Additionally, further clinical validation through real-world hospital trials is necessary to assess model robustness across diverse populations and healthcare systems. Optimizing model complexity while maintaining predictive accuracy will also be explored to ensure that AI-driven healthcare solutions are accessible, efficient, and scalable.

Ultimately, this study highlights the potential of AI in transforming predictive healthcare analytics and precision medicine by integrating structured and unstructured biomedical data. The proposed framework enhances diagnostic accuracy, improves patient risk assessment, and facilitates early disease detection, all while ensuring model interpretability and real-time applicability. By bridging the gap between AI-driven insights and clinical decision-making, this work lays the foundation for future AI advancements in healthcare, ultimately leading to improved patient outcomes and more effective, personalized treatment strategies.

ACKNOWLEDGEMENTS: I am thankful to my supervisor, Dr. Mohammad Amin Khalili, who introduced me to the world of machine learning and deep learning algorithms in this field and guided me in writing and implementing this paper.

FUNDING: This research received no external funding.

CONFLICT OF INTEREST: Authors declare no conflict of interest.

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Exploring the Experience of Lay Workers After Palliative Basic Training in Indonesia

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ABSTRACT

Palliative care has an important contribution to make in supporting patients with terminal illnesses such as cancer, which imposes a significant burden on individuals, families, and healthcare systems. Lay workers serve a vital function in providing emotional and psychosocial support to cancer patients and their families. The effectiveness of palliative care depends largely on the skills and knowledge of these trained lay workers. Lay workers are also known as palliative Kader's, whose main role is to assist cancer patients in the community. This study aimed to explore the experience of lay workers after attending palliative basic training and its impact on their duties in health services. The study used a qualitative method with a phenomenological approach. In-depth interviews were conducted with 14 palliative lay workers with diverse educational backgrounds, mostly aged 31-50. Data collection took place in August 2024. Thematic analysis identified four key themes: (1) motivation for attending training; (2) experiences during training; (3) application of training outcomes in patient support; and (4) the impact of training and future development needs. Participants highlighted the importance of further training, particularly in psychosocial support and managing patients with severe psychosocial distress. The findings indicate that while basic palliative training had a positive impact by enhancing lay workers' confidence and competence in patient care, there remains a need for continuous education and comprehensive support to equip them for more complex cases. Strengthening training programs and providing ongoing mentorship could further optimize palliative care services delivered by lay workers. Additionally, fostering peer support networks and collaboration with healthcare professionals can enhance the effectiveness of lay workers in addressing the holistic needs of patients and families.

Keywords: Cancer; Palliative Basic Training; Lay Worker

Occupational Stress and Individual Characteristics: Impact on Nurse Performance in Indonesia

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ABSTRACT

Nursing performance is determined by a nurse’s skills, abilities, and authority to carry out duties and work activities in accordance with hospital policies. Nurses are responsible for carrying out their tasks while upholding their role as healthcare professionals. This study aims to analyse the relationship between demographic characteristics and stress with the performance of nurses at the Mental Hospital in East Jakarta.

This research used a quantitative method with a cross-sectional approach. The study involved 99 nurses. Participants were recruited from 9 inpatient units, 1 Neonatal Intensive Care Unit (NICU), 1 Paediatric Intensive Care Unit (PICU), and 1 Perinatology unit. Data were collected using a validated self-assessment structured questionnaire, which gathered information on demographic characteristics, levels of stress, and nursing performance.

Univariate analysis was used to describe the characteristics of respondents and study variables, while bivariate analysis using the *Chi-Square* Test examined relationships between individual characteristic, stress, and nurse performance. The univariate analysis showed that 51.5% of nurses have a good performance, while 48.5% had lower performance. Bivariate analysis found no significant relationships between age, gender, length of work, employment status, stress and performance ($p > 0,05$).

This study found no significant relationship between individual characteristics, stress, and nurse performance, suggesting other factors may be more influential. Future research should explore organizational factors that influence nurses' well-being and effectiveness. Although stress had no direct effect in this study, stress management and professional development remain crucial. The cross-sectional design and self-reported data limit causality, emphasizing the need for longitudinal studies to explore nursing performance factors.

Keywords: Individual Characteristic, Nurses, Performance, Stress

PSYCHOLOGICAL PROFILE OF COLLEGE FLEXIBLE LEARNERS: BASIS FOR A WELLNESS PROGRAM

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Abstract

The unprecedented impact of the Coronavirus disease (COVID-19) pandemic has underscored the critical importance of wellness, particularly among students whose vulnerability was starkly revealed. The pandemic exacerbated both academic and non-academic challenges, significantly affecting students' physical and mental health. In response, educational institutions implemented various wellness activities to address these concerns. This research aimed to gather relevant data as the basis for the development of a comprehensive wellness program tailored to the needs of learners in the so-called *new normal*. A total of 618 first-year college students from a private higher education institution (HEI) in the province of Pampanga in Central Luzon, Philippines were recruited. Data were collected using a profile form and standardized measures (5), capturing demographic characteristics and wellness-related factors. The findings were summarized and presented, leading to the proposal of an evidence-based wellness program that specifically targets identified problem areas.

Key terms: Wellness program, flexible learners, pandemic

Symptoms of Depression, Anxiety and Stress in Portuguese Health Professionals: Relationship with the Professional Group

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ABSTRACT

The pressure of providing care to patients felt by health professionals (HPs) and the high workload increase the tension and stress of these professionals, triggering anxiety, depression and stress crises. This study aimed to analyse the association between Depression, Anxiety and Stress symptoms and the professional group of HPs during COVID-19 pandemic. This is a descriptive-correlational, cross-sectional study, with a sample of 33 Portuguese HPs. Data were collected using an online questionnaire, which included the Depression, Anxiety and Stress Scale (DASS-21). Data were processed using the IBM Statistical Package for the Social Sciences software, using descriptive and inferential statistics. From the total sample, most HPs were female (87.9%) and were nurses (51.5%). The Anxiety subscale obtained the lowest mean score of the items (1.7489) versus the Stress subscale, which obtained the highest mean (2.2121). In the case of this subscale, the mean value was between the response options "It applied to me often" and "It applied to me most of the time", which has the highest score (3 points), revealing a high level of Stress in the sample. Stress symptoms were associated with the professional group (Kruskal-Wallis: $p < 0.020$), with administrative staff and nurses having a higher level of Stress than other professionals. The level of Depression, Anxiety and Stress symptoms in the sample is higher than in other studies. Stress symptoms are related to the professional group factor. This study allowed us to know the level of symptoms of these health HPs and enabled a more adequate subsequent intervention.

KEYWORDS: Depressive symptoms; Anxiety; Job stress; Health personnel.

1 INTRODUCTION

Almost 23 years ago, in 2002, the world was stunned by the emergence of Severe Acute Respiratory Syndrome (SARS), sustained by a zoonotic coronavirus, called SARS-CoV, in Guangdong Province, South China. After about 10 years, in 2012, another similar coronavirus triggered Middle East Respiratory Syndrome (MERS) in Saudi Arabia. Both caused severe pneumonia, killing 774 and 858 people respectively, with 8,700 cases of confirmed infection for the former and 2,494 for the latter, causing significant economic losses. After eight years, although the MERS outbreak persists in certain parts of the world, in late 2019, a new zoonotic coronavirus (SARS-CoV-2) was responsible for coronavirus disease (COVID-19), appearing in Wuhan city, Hubei province, China [1].

According to the latest data from the World Health Organization, the pandemic of COVID-19 caused at least 14.9 million deaths of people worldwide, who died as a direct or indirect result of COVID-19 [2].

In Portugal, 25,942 people died from the 5,562,214 confirmed cases of infection, according to the most recent bulletin from the Directorate-General of Health [3]. In the North Sousa Valley Region, where the first cases of COVID-19 emerged in Portugal and in which the health unit in the context of this study is located, 251 people have died since the beginning of the pandemic in March 2020, with November being the month with the most deaths, according to official data [4].

With regard to Healthcare Professionals (HP), there is still no official data on the number of professionals who worked in the pandemic of COVID-19 and what the actual number of deaths and confirmed cases were, both globally and nationally.

The new COVID-19 pandemic was an international public health emergency, unprecedented in modern history [5]. Beyond the biological context, and because of the broad and lasting changes it can bring about in daily life, coping with it represented a challenge for psychological resilience.

Previous studies have shown that epidemics and outbreaks of disease contamination have been followed by dramatic individual and social psychosocial impacts, which have become more notorious than the epidemic itself [5-6].

Nevertheless, the experiences with SARS and MERS have notably compromised the well-being of PHs, as during epidemic emergencies, frontline professionals experienced an increased workload in a context of uncertainty and powerlessness, being the most vulnerable to infection due to their direct contact with patients, as happened during the pandemic of COVID-19 [6-7].

According to Zhu et al. [8], at the beginning of the virus spread, hospitals had limited availability of personal protective equipment and treatment guidelines were not yet clear and established. In this case, many of the professionals felt confused and unprepared to effectively treat all infected patients. As a result, they experienced feelings of uncertainty, helplessness, isolation and difficulties in managing their workload, leading to burnout.

Undoubtedly, dealing with COVID-19 caused major social and medical crisis that presented major challenges to society in general and in particular HPs, forcing them to face unprecedented times and reconceptualize how to provide quality healthcare, while "forcing" the public to health measures necessary for pandemic containment and optimal allocation of healthcare resources [9].

In the face of high HP exhaustion, the usefulness of psychological services and support systems are critical. In addition to the social support systems provided by organisations, building adequate self-awareness, peer and team support could help professionals in their ability to cope with mental stress during the latest pandemic [10].

During the outbreak of COVID-19, the main concerns and stressful experiences of healthcare providers can be largely reduced, provided they trust their personal protection and infection control procedures, receive the clear and accurate information, and feel supported and respected by their managers and leadership [11].

The pandemic caused by the new SARS-COV-2 coronavirus, designated as COVID-19, was a serious global health problem, considered a Public Health emergency of international interest due to its high transmissibility and morbidity. The pressure felt by HPs to care for patients, the high workload, the lack of an effective treatment, the lack of personal protective equipment, and the fact that their live are constantly at risk have increased the tension and stress of these professionals, triggering anxiety and depression crises. It is within the scope of this issue that our study was conducted to analyze the association between the symptoms of Depression, Anxiety and Stress and the sociodemographic characteristics of the HPs in our sample.

2 METHODOLOGY

The methodology represents a set of procedures that allows the researcher to obtain knowledge. Empirical knowledge derives from the observer's experience in a given context, where conclusions are drawn through empirical and verifiable evidence.

This is an observational, descriptive-correlational, cross-sectional study with a quantitative approach [12].

2.1 Participants

The following inclusion criteria were defined: i) Being a Health Professional (HP) at the Health Care Centre of Felgueiras (HCF), which is the context of this study; ii) Providing or managing care. The total population of this study was composed of all HP who were part of the HCF staff, providing care and management, around 60 professionals.

The exclusion criteria established were: i) HP who were on sick leave or absent from the activity for any other reason; ii) Not having completed at least 80% of the questionnaire. In this study, no sampling technique was applied due to the small size of the population. The sample consisted of 33 HPs who participated in the study, about 55,0% of population.

Of the total sample (33 HP), most were female (87.9%), belonged to the age group between 25 and 40 years (63.6%), were married (66.7%), had post-graduation/mastership/specialty/doctorate as academic qualifications (54.5%) and belonged to the professional group of nurses (51.5%) (**Table 1**).

Table 1 Socio-demographic characterization of the sample (n=33)

Variables	Absolute frequency	Relative frequency (%)
Gender		
Male	4	12.1
Female	29	**87.9**
Age group		
25-40 years old	21	**63.6**
41-65 years old	12	36.4
Marital status		
Single	8	24.2
Married	22	**66.7**
Divorced/Separated	2	6.1
No answer	1	3.0
Level of Academic qualification		
Level 2 – High School	6	18.2
Level 4 – Undergraduate	9	27.3
Level 5 – Post-graduate/other	18	**54.5**
Professional Group		
Doctor	5	15.2
Nurse	17	**51.5**
Operational Assistant	2	6.1
Technical Assistant	4	12.1
Other Health Professionals	5	15.2

2.2 Material

The data collection instrument selected was the questionnaire because it is a quick, impersonal, low-cost instrument that best suited the nature of this study. This instrument was composed of three parts: the first aimed to obtain data on the sociodemographic and academic characterization (information on gender, age, marital status and profession at the health care centre); the second part included the DASS-21 scale, validated for the Portuguese population by Pais-Ribeiro et al. [13]; and the third part integrated a set of questions aimed to assess the HP knowledge about the COVID-19, elaborated by the researchers, based on the DGS recommendations [4]. Only the first two parts were used in this study.

The DASS-21 of Pais-Ribeiro et al. [13] aims to assess the symptoms associated with anxiety, depression and stress in young adults and Portuguese adults. It consists of 21 items, grouped into three subscales, each composed of seven items: Anxiety, Depression and Stress. All items are assessed through a 4-point Likert-type response scale concerning the severity and frequency of symptoms experienced in the last 7 days - "in the past week" (0 - "it did not apply to me at all", 1 - "it applied to me sometimes", 2 - "it applied to me often", and 3 - "it applied to me most of the time"). The rating is given by the sum of the scores of the seven items, obtaining a score for each subscale with a minimum score of 0 and a maximum score of 21 points. Higher scores correspond to more negative affective states. With regard to internal consistency, the results obtained by Pais-Ribeiro et al. [13] showed acceptable Cronbach's alphas for the three subscales (anxiety = 0.74; depression = 0.85; stress = 0.81).

The ethical principles arising from the Declaration of Helsinki and the Oviedo Convention were respected, including the right to autonomy, non-maleficence, intimacy, right to anonymity and confidentiality, and right to fair and equitable treatment [12]. To safeguard these ethical considerations, a request for authorization was previously made to the Ethics

Committee of the Regional Health Administration of the North, which was approved (CE/2021/78). Authorization to use the DASS-21 was also requested from the author, who validated the scale for Portugal, which was positively answered.

2.3 Procedures

Data collection took place in July 2021. The questionnaires were filled out online, through Google Forms, after the project was explained and the participants' informed consent was obtained, which was a mandatory condition at the beginning of the questionnaire filling.

For data treatment and analysis, an IBM Statistical Package for the Social Sciences (IBM SPSS, version 26) database was created, where data were entered, using descriptive and inferential statistics. In terms of descriptive statistics, absolute and relative frequencies were calculated for all variables. In the case of ordinal level variables, the previous measures and the order statistics (percentiles and deciles) were included and, for ratio or scalar level variables, the measures of central tendency and dispersion were also calculated. In terms of inferential statistics to test the hypotheses formulated, the t-test and ANOVA for independent samples were used, and when the assumptions for their use were not assured, the alternative non-parametric tests, the Mann-Whitney and Kruskal-Wallis tests. The level of significance to be considered was 5% [14].

3 PRESENTATION AND DISCUSSION OF RESULTS

In turn, the items of the Depression subscale which obtained a higher percentage in the response options scoring 2 and 3 by the HP of the sample were item 13 "I felt discouraged and melancholic", item 16 "I was not able to have enthusiasm for anything" and item 3 "I could not feel any positive feelings", respectively 42.3%, 24.2% and 21.1%, having been the items which most contributed to a higher level of Depression symptoms. On the opposite side, the items with the highest percentage in the response options 0 and 1 were item 5 "I had difficulties in taking initiative to do things", item 10 "I felt I had nothing to look forward to in the future", item 3 "I could not feel any positive feelings" and item 17 "I felt I did not have much value as a person", respectively 81.8%, 81.8%, 78.7% and 78.7%, having been the items that contributed the least to a higher level of Depression symptoms.

The items of the Anxiety subscale which obtained a higher percentage in the response options scoring 2 and 3 by the HP in the sample were item 19 "I felt changes in my heart without physical exercise", item 7 "I felt tremors (e.g. in my hands)" and item 2 "I felt my mouth dry", respectively 24.5%, 24.1% and 21.5%, being the items which most contributed to a higher level of Anxiety symptoms. On the opposite side were the items with the highest percentage in the response options 0 and 1, item 4 "I felt difficulty breathing", item 15 "I felt almost panicky" and item 20 "I felt that my life was meaningless", respectively, 88.8%, 87.8% and 81.7%, having been the items that contributed the least to a higher level of Anxiety symptoms.

Finally, the items of the Stress subscale that obtained a higher percentage of response options scoring 2 and 3 by the HP in the sample were item 18 "I felt that I was sometimes sensitive", item 6 "I tended to overreact in certain situations" and item 12 "I found it difficult to relax", respectively 48.4%, 36.3% and 36.2%, being the items that most contributed to a higher level of Stress symptoms. In opposition, the items with the highest percentage in the response options 0 and 1 were item 14 "I was intolerant towards anything that prevented me from finishing what I was doing", item 1 "I had difficulty calming down" and item 11 "I found myself getting agitated", respectively 72.7%, 66.6% and 66.6%, which were the items that least contributed to a higher level of Stress symptoms (**Table 2**).

Table 2 Distribution of item responses of the DASS-21 subscales (%)

Items of the subscales	0	1	2	3
Anxiety subscale:				
2- My mouth felt dry	42.4	36.3	15.5	6.0
4- I had difficulty breathing	**55.5**	33.3	3.0	6.0
7- I felt trembling (e.g., in my hands)	**60.6**	15.1	**18.1**	6.0
9- I worried about situations where I might panic and make a fool of	42.4	36.3	**18.1**	3.0
myself	51.5	36.3	9.0	3.0
15- I felt like I was about to panic	36.3	**39.3**	15.5	**9.0**
19- I felt changes in my heart without physical exercise	54.5	27.2	12.1	6.0
20- I felt frightened for no good reason				
Depression subscale:				
3- I couldn't feel any positive feelings	33.3	**45.4**	15.1	6.0
5- I had difficulty in taking initiative to do things	36.4	**45.4**	15.1	3.0
10- I felt I had nothing to look forward to in the future	48.5	33.3	15.1	3.0
13- I felt despondent and melancholic	21.2	36.4	**33.3**	**9.0**
16- I was not able to have enthusiasm for anything	48.5	27.2	24.2	0.0
17- I felt that I didn't have much value as a person	51.5	27.2	15.1	6.0
21- I felt that life had no meaning	**66.6**	10.1	9.0	6.0
Stress Sub-scale:				
1- I had difficulties in calming down	27.2	39.4	30.3	3.0
6- I tended to overreact in certain situations	18.1	**45.5**	30.3	6.0
8- I felt that I was using too much nervous energy	30.3	27.2	30.3	**12.0**
11- I found myself becoming agitated	24.2	42.4	27.3	6.0
12- I found it difficult to relax	18.1	**45.5**	24.2	**12.0**
14- I was intolerant of anything that prevented me from finishing what				
I was	**33.3**	39.4	21.2	6.0
doing	15.1	36.4	**36.4**	**12.0**
18- I felt that I was sometimes sensitive				

Legend: 0-Not applied to me at all; 1-Applied to me sometimes; 2-Applied to me a lot; 3-Applied to me most of the time.

The Anxiety subscale obtained the lowest mean score of the items (1.7489) versus the Stress subscale, which obtained the highest mean (2.2121). In the case of this subscale, the mean value was between the response options "Applied to me often" and "Applied to me most of the time", which has the highest score (3 points), revealing a high level of Stress in the sample. All subscales had a low value of standard deviation, which means that the dispersion of the score values is reduced (**Table 3**).

Table 3 Mean and standard deviation of the item scores of the DASS-21 subscales

Variables	Minimum	Maximum	Mean±SD

Symptoms of Anxiety	1	4	1,7489±0,78085
Symptoms of Depression	1	3,57	1,8398±0,73084
Symptoms of Stress	1	4	**2,2121**±0,76692

The Depression subscale score shows no significant differences between HP of different gender (t: p ≥ 0.645), neither between HP of different age group (t: p ≥ 0.753), nor between HP with different marital status (t: p ≥ 0.491), nor between HP with different educational qualifications (ANOVA: p ≥ 0.970) and neither between HP of different professional group (ANOVA: p ≥ 0.111).

The Anxiety subscale score does not differ significantly between HP of different gender (t: p ≥ 0.147), nor between HP of different age group (t: p ≥ 0.842), nor between HP with different marital status (t: p ≥ 0.949), nor between HP with different educational qualifications (ANOVA: p ≥ 0.710) and nor between HP of different professional group (ANOVA: p ≥ 0.173).

The Stress subscale score did not differ significantly between HP of different gender (t: p ≥ 0.563), nor between HP of different age group (t: p ≥ 0.886), nor between HP with different marital status (t: p ≥ 0.751), nor between HP with different educational qualifications (ANOVA: p ≥ 0.977). The same score differed significantly between HP of different professional group (ANOVA: F(4, 28)= 3.165, p < 0,029), with Technical Assistants obtaining the highest mean score, followed by Nurses and Other professionals the lowest (**Table 4**).

Table 4 Relationship between the Stress subscale score and the sociodemographic characteristics

Variables		**n**	**Mean**	**Test value**	**df**	***p value***
Stress Subscale score x Gender	Female	29	2.2414	t= 0.584	31	0.563
	Male	4	2.000			
Stress subscale score x Age group	25-40 years old	21	2.1973	t= 0.145	31	0.886
	41-65 years old	12	2.2381			
Stress Subscale score x Marital Status	Single/Divorced	10	2.1714	t= - 0.320	30	0.751
	Maried	22	2.2662			
Stress subscale score x Academic qualifications	High School	6	2.1667	ANOVA= 0.023	32	0,977
	Graduation	9	2.2540			
	Pos-Graduation	18	2.2063			
Stress subscale score x Professional group	Doctor	5	2.1714	ANOVA= 3.165	32	**0,029**
	Nurse	17	2.4706			
	Operational Assistant	2	1.4286			
	Technical assistant	4	2.5357			

	Other health professionals	5	1.4286

Legend: n – Absolute frequency; df – Degree of freedom; *p* - probability; t – t Student test.

Most of the HP in the sample were female. Taking into account that the largest group of HP belongs to the nurses' group and that according to the statistical data of the Ordem dos Enfermeiros [15], in Portugal there were 78117 registered nurses of whom 64292 (82%) were female, which may explain why this gender is the most represented gender in our sample. The female gender was also the most represented in the study of Cavalcante et al. [16], conducted in Brazil with a sample of 112 HP, constituting 62.5% of this sample.

In the present study, the majority age group was 25-40 years (63.6%). Although we point out that the age group categories do not coincide, in the study of Cavalcante et al. [16], the 30-39 age group, which is the group most similar to that of our study, was the most represented, comprising 63.6% of the HP.

As for the professional group, in our sample, nurses are the majority professional group (51.5%), which is in line with the results obtained in the study of Cavalcante et al. [16], in which the most represented professional group was the Nursing technicians (48.21%), a category that does not exist in Portugal, followed by Nurses (19.64%) and in the study of Urzal et al. [17], conducted in Portugal with 554 HP, in which 35.74% belonged to the nurses' professional group.

The mean scores of the subscales coincided with those of Ferreira [18], a study conducted in Portugal with a sample of 179 individuals with different professional groups, in which Stress also obtained the highest mean score and Anxiety the lowest score.

Depression, Anxiety and Stress symptoms were not related with socio-demographic characteristics, except between Stress symptoms and professional group. This result differs from that obtained in the study of Cavalcante et al. [16], in which Anxiety and Stress symptoms differed significantly between HP of different gender (respectively Student's t: $p < 0.009$ and $p < 0.011$), but this was not the case between HP groups ($p \geq 0.05$). This divergence may be explained by the cultural difference between the HP of the two studies.

Based on our empirical experience and knowledge of the context of this study, the explanation for this result may also lie in the more frequent and longer contact of Technical Assistants (Administrative staff) and nurses, who are the first contact with users and in a situation of ignorance and almost collective panic, at the beginning of the pandemic, it will have caused a more substantial increase in the stress of these professionals.

4 CONCLUSION

The profile of HP was composed of a female professional, aged between 25-40 years, married, with a post-graduation degree, and a nurse.

Stress symptoms were the most exacerbated ones in this sample, seeming to have been the most frequent repercussions in this HP during the COVID-19 pandemic, followed by Depression symptoms and, finally, Anxiety symptoms. Taking into account the mean score of the items obtained in the Stress subscale, the level of Stress in this sample may be considered as high.

The professional group was associated with Stress symptoms, with Technical Assistants (Administrative Staff) and Nurses being the groups most affected by these Mental Health problems. No further associations were found between Depression, Anxiety and Stress symptoms and the other socio-demographic variables studied. The pandemic may have affected more these professional groups, perhaps because they are the ones who in Portugal have a closer contact with the population and, for this reason, a higher risk of being infected by SARS-COV-2. In this pandemic period, there was still no effective treatment against this virus, which may have contributed to the exacerbation of this symptom.

The main limitation of this study is related to the small size of the groups of some variables, such as the professional group, which involves five groups, with a size between two and five cases, which will have decreased the reliability of the ANOVA test and the inference for the population.

This scenario implies the need for intervention in these HP and a careful and preventive look at future pandemics, in order to help them manage these symptoms, in line with the five-year prevention plan, which recommends promoting the well-being of professionals in order to avoid the so-called medical errors and promote the quality of healthcare.

FUNDING: This work was financially supported by Portuguese national funds through the FCT (Foundation for Science and Technology) within the framework of the CIEC (Research Center for Child Studies of the University of Minho) project under the reference UIDB/00317/2020.

Cofinanciado por:
UIDB/00317/2020
UIDP/00317/2020

FCT Fundação para a Ciência e a Tecnologia

CONFLICT OF INTEREST: Authors declare no conflict of interest.

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PUBLIC HEALTH CONFERENCE 2025
11-13 JULY 2025
CONFERENCE PROCEEDINGS

ISBN 978-86-83004-07-2
