Development and Evaluation of a Personalized Health Knowledge Graph Using Graph Algorithms: A Case Study on Diabetes Management Recommendations

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Abstract—The challenge of providing real-time, personalized, and interpretable healthcare recommendations for chronic conditions like Type 2 Diabetes Mellitus (T2DM) is compounded by fragmented patient data and the limitations of traditional analytical methods. To address this, we developed a comprehensive Personalized Health Knowledge Graph (PHKG) that models complex relationships among clinical metrics, demographic information, and lifestyle factors. This study evaluates a multi-layered analytical framework using three distinct graph algorithms: Personalized PageRank (PPR) for fine-grained relevance retrieval, Node2Vec for structural representation learning and community detection, and Graph Attention Networks (GATs) for generating attention-weighted embeddings crucial for predictive reasoning. Implemented as an automated, end-to-end pipeline, the system integrates patient data, processes graph insights, and culminates in tailored health advice generated by the Gemini 2.5 Flash model via Natural Language Generation (NLG). Our evaluation confirms that this hybrid graph-based approach effectively addresses the cold-start problem and enhances analytical precision. PPR successfully identified highly relevant health episodes, Node2Vec facilitated the discovery of coherent patient cohorts based on latent behavioral patterns, and the GAT-derived embeddings demonstrated improved separation for downstream classification tasks. The integration of these graph-derived insights with an NLG model successfully delivers contextually appropriate, traceable, and personalized recommendations, establishing a foundation for advanced, highly interpretable personalized digital health coaching.

Keywords—Diabetes Management, Graph Algorithms, Health Informatics, Knowledge Graphs, Personalized Recommendations.

I. INTRODUCTION

Graph-based analysis is increasingly vital in healthcare, offering a robust method to model complex relationships within patient data, thereby enhancing decision-making and personalized care. According to Abu-Salih et al. [1], Knowledge Graphs (KGs) enable the integration of diverse health information, such as clinical metrics and lifestyle factors, supporting applications from drug repurposing to chronic disease management. In the context of Diabetes Management, which affects millions globally and incurs significant costs which estimated at USD 600 million annually in Malaysia alone [2], graph-based approaches provide a scalable solution to improve patient outcomes and reduce healthcare burdens. Studies highlight that Personalized Healthcare Knowledge Graphs (PHKGs), tailored to individual patient profiles, enhance physician decision-making and digital coaching, making them a cornerstone for modern healthcare innovations [3].

A. Problem Statement

Despite these advancements, personalizing recommendations and detecting patient groups remain challenging due to the fragmented nature of health data and the lack of real-time, actionable insights. Traditional systems, including smartphone applications and wearable devices, often fail to deliver tailored interventions, leading to poor patient adherence and suboptimal management of T2DM [4][5]. While PHKGs hold promise, their ability to translate complex data into understandable, personalized guidance remains underexplored, particularly in addressing cold-start problems with limited patient data. Moreover, identifying meaningful patient cohorts

for targeted interventions is hindered by the absence of comparative analyses of graph algorithms, necessitating deeper investigation into clustering and similarity detection methods.

B. Motivation

In the context of Personalized Healthcare Knowledge Graphs (PHKGs) for T2DM management, selecting graph algorithms that can effectively model both local patient-level relationships and global population structures is critical. To this end, Personalized PageRank (PPR), Node2Vec, and Graph Attention Networks (GATs) were chosen to represent three complementary analytical paradigms, graph propagation, representation learning, and neural inference.

PPR is particularly suited for this study as it computes patient-specific importance scores through random walks with restart, allowing relevance propagation from a seed node (patient) across interconnected entities such as activities, meals, and clinical features. This enables fine-grained personalization and similarity retrieval even under sparse data conditions, addressing cold-start challenges in individualized recommendations.

Node2Vec extends this analysis by learning structural embeddings through biased random walks that balance homophily and structural equivalence, allowing the model to capture both lifestyle similarity and cross-pattern behaviours among diabetic patients. These embeddings facilitate downstream clustering and community detection, crucial for identifying patient subgroups with shared risk factors or adherence patterns.

Finally, GATs were integrated to leverage deep learning-based attention mechanisms that adaptively weight node neighbourhoods during message passing, enhancing the model's ability to perform patient classification and outcome prediction with interpretability.

Together, these algorithms form a multi-layered analytical framework capable of bridging personalization, structural discovery, and predictive intelligence, thereby aligning tightly with the project's goal of advancing data-driven, individualized healthcare insights.

C. Research Objectives

The objectives of this study are to develop and implement a Personalized Health Knowledge Graph (PHKG) that integrates diabetes-related clinical data, demographic information, and lifestyle factors to support individualized analysis and insight generation.

This research aims to evaluate and compare the effectiveness of three graph-based algorithms in extracting personalized health insights from the PHKG. In addition, a functional prototype will be developed to translate these graph-derived insights into tailored healthcare recommendations through Natural Language Generation (NLG) techniques.

Overall, the study seeks to demonstrate how the integration of PHKGs, graph-based analytics, and NLG models can enhance the personalization, interpretability, and effectiveness of healthcare interventions for diabetes management. The project is planned to be completed within six months, comprising PHKG construction (one month), graph algorithm evaluation (two months), prototype development (two months), and system validation (one month).

II. LITERURE REVIEW

Recent advances in health informatics demonstrate increasing interest in integrating machine learning, graph-based modelling, and knowledge representation to support personalised healthcare analytics. Prior studies have explored various approaches to structuring and interpreting complex health data, although their goals, data modalities, and evaluation protocols differ substantially from the requirements of LLM-driven health information systems.

Several works have focused on modelling health conditions using molecular-level biological data. For instance, recent research in the Journal of Biomedical Semantics analysed disease states using high-dimensional gene expression profiles, leveraging molecular signatures to classify patient conditions. While this contributes to precision medicine from a biological perspective, the methods rely on gene-expression vectors that are fundamentally different from the demographic, behavioural, lifestyle, and statistical data used in our system. Moreover, these models are optimized for deterministic prediction tasks rather than contextualised, semantically grounded responses to user queries, limiting their applicability to conversational or LLM-integrated health systems.

Beyond molecular datasets, personalised health knowledge graphs (PHKGs) have been explored as a mechanism for patient-specific modelling. A notable example is the Personalized Diabetes Management Digital Twin framework presented in the Journal of Personalized Medicine (2024), which constructs a PHKG for each patient using HL7-standardised clinical data. Their system supports real-time glucose prediction, insulin optimisation, and lifestyle adjustments within a clinical decision-making workflow. Although this demonstrates the feasibility of PHKGs for personalised health insights, the focus is strongly tied to clinical environments, HL7 integrations, and treatment optimisation for diabetes management, constraints that differ from our objective of building a scalable, population-level health inquiry system that can function independently of clinical protocols.

Other graph-based approaches emphasise predictive modelling through patient similarity structures. AdaMedGraph (Lian et al., 2023), for example, proposes an ensemble of weak Graph Neural Networks (GNNs) applied to automatically constructed patient-similarity graphs for disease progression prediction. While this method shows how graph topology can enhance predictive performance, its graph structure is homogeneous (patients only) and oriented toward clinical classification tasks. It does not extend to multi-entity representations, lifestyle-behaviour relationships, or explainable reasoning pathways, capabilities essential for transparent, interpretable recommendations in a conversational health information system.

Collectively, these studies highlight important directions in graph-based healthcare analytics but also reveal several gaps relative to the needs of an LLM-integrated, community-oriented health information platform. First, prior works relying on gene-

expression or structured numerical vectors cannot be directly adapted to LLM evaluation, which requires assessment of semantic correctness, contextual appropriateness, and hallucination control rather than purely numerical prediction accuracy. Second, while PHKG-based systems demonstrate the value of structured knowledge graphs, existing implementations either depend on clinical standards (e.g., HL7) or focus on medical treatment pathways, limiting their scalability for general-purpose health inquiry support. Third, graph-based predictive systems such as AdaMedGraph do not incorporate behavioural data, lifestyle patterns, or multi-entity reasoning, nor do they support explainability mechanisms suitable for delivering transparent guidance to end-users.

In contrast, our work builds a multi-entity personalised health knowledge graph (PHKG) integrating demographic, lifestyle, behavioural, and statistical health indicators specific to Sarawak's population context. We implement a fully automated, real-time pipeline that constructs the PHKG, applies multiple graph algorithms, including Personalized PageRank, Node2Vec embeddings with community detection, and Graph Attention Networks, and supports retrieval, similarity search, and classification in a unified framework. Finally, our system bridges graph-based insights with natural language generation, providing interpretable, traceable health explanations grounded in graph pathways, addressing key challenges of LLM safety, hallucination mitigation, and contextual accuracy.

III. METHODS

A. Dataset

The dataset used in this study was a real dataset that captures realistic clinical and lifestyle information for diabetic patients. The overall database was designed with eight tables to support both analytical and system-related functions. However, only three core tables, which are users, patients and health_data were utilized as the primary dataset for the construction and evaluation of the personalized health knowledge graph.

A summary of the number of records in each core dataset table is presented in TABLE I, while TABLE II outlines the key attributes and their purposes.

TABLE I. SUMMARY OF CORE DATASET USED FOR THE KNOWLEDGE GRAPH CONSTRUCTION

Table Name	Purpose	No. of Records
users	System users (1 admin & 4 doctors)	5
patients	Patient demographic and relational data	20
health_data	Clinical and lifestyle parameter	95

TABLE II. ATTRIBUTES AND DESCRIPTIONS OF THE CORE DATASET TABLES

Table Name	Key Attributes	Descriptions
users	user_id, username, email, password_hash, role, photo, created_at, last_login, status, phone_number specialist	System users and their access infomation
patients	patient_id, doctor_id, full_name, age, gender, created_at, status	Stores patient demographic information and doctor relationships
health_data	data_id, patient_id, timestamp, cgm_level, blood_pressure, heart_rate, cholesterol, insulin_intake, food_intake, activity_level, weight, hb1ac, is_synced	Contains patients' physiological and lifestyle data used for graph analysis.

The remaining tables including patient_summaries, graph_insights, graph_update, recommendation, and system_log were implemented to support system functionalities such as algorithm output storage, reporting and logging, which stores system-generated results.

B. Data Pre-processing

Before integration into the system, several pre-processing steps were applied to ensure data completeness, consistency and analytical readiness. The dataset was obtained from real patient records, the entries were inspected to confirm that values followed clinically reasonable ranges and aligned with typical patterns observed in diabetic patient profiles. Missing or incomplete fields were replaced with reasonable default values to prevent data sparsity.

Numerical features including HbA1c, cholesterol and CGM level, were standardized to ensure uniform scale and facilitate fair comparison across patient records. The blood_pressure attribute was kept in the "systolic/diastolic" format to preserve clinical interpretability, while activity_level and food_intake was normalized into structured text categories such as "Gym workout 45 minutes" and "Milo, Butter Cake".

Categorical variables such as gender and status, were encoded numerically for computational processing. Date and time fields like created_at and timestamp were formatted to a consistent YYYY-MM-DD HH:MM:SS standard to align with MySQL's datetime structure.

Each record was checked for logical consistency. For example, ensuring that doctor_id values in the patients table corresponded to existing entries in the users table and that patient_id values were properly referenced in the health_data table. These steps ensured referential integrity and data reliability prior to graph construction.

Fig. 1. Database schema

C. Feature Engineering

Feature engineering was applied to extract and transform key attributes from the Health Data table into meaningful variables suitable for graph-based analysis. The selected features including HbA1c level, glucose level, activity level and food intake were chosen for their relevance in representing both

clinical and lifestyle aspects of diabetes management. These transformed features enable the knowledge graph to visually highlight relationships between patient conditions and behavioural patterns, while also ensuring consistency with the database used for generating recommendations.

1) HbA1c Level (mmol/mol): The HbA1c value represents the average blood glucose concentration over approximately three months and was used as a key indicator of long-term glycemic control. In this study, HbA1c values were expressed in mmol/mol according to IFCC (International Federation of Clinical Chemistry) standards.

To facilitate interpretation, the values were categorized into three clinical ranges:

- Normal: < 39 mmol/mol
- Pre-diabetes: 39–46 mmol/mol
- Diabetes: ≥ 48 mmol/mol

This categorization enables observation of patients' glycemic status within the knowledge graph, supporting the identification of high-risk individuals.

2) Glucose Level: The CGM (Continuous Glucose Monitoring) level represents each patient's blood glucose concentration at specific timestamps. To maintain consistency across all records, the values were standardized prior to analysis. Glucose readings were categorized into three clinical ranges for clearer interpretation:

- Normal: < 7.0 mmol/L
- Pre-diabetes: 7.0–10.0 mmol/L
- Diabetes: > 10.0 mmol/L

These categorized values allowed for temporal trend analysis and were later incorporated into Cypher queries to visualize glucose variation among patients within the knowledge graph.

3) Activity Level: The activity_level attribute contained descriptive text such as "Gym workout 45 minutes" or "Light walking 30 minutes." These entries were retained in their original textual form to preserve contextual meaning for interpretation. Through Cypher queries, the recorded activities were later correlated with other health indicators such as glucose and HbA1c levels, allowing identification of lifestyle patterns that may influence diabetic stability and metabolic control.

4) Food Intakel: The food_intake attribute recorded patients' daily meals, such as "Salmon with quinoa" or "Fried rice and egg." These entries were preserved as textual data to maintain dietary context. During graph-based analysis, food intake records were linked with corresponding glucose readings taken within the same day to explore potential associations between meal types and blood glucose fluctuations. This feature provided insight into how specific dietary habits could influence glycemic variation and supported the recommendation generation process in the system.

These engineered features were represented as nodes and relationships within the personalized health knowledge graph, forming the foundation for graph algorithm analysis and the generation of personalized health insights.
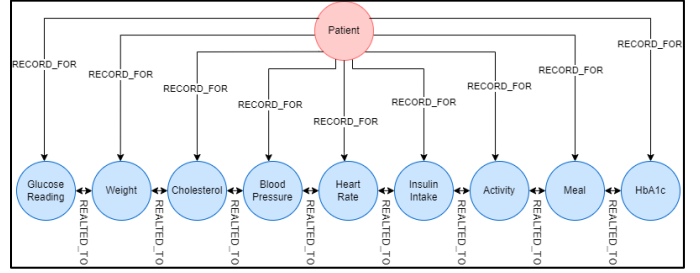
D. Graph Schema

Fig. 2. Graph data schema designed for representing patient health records

Fig. *2* shows the graph data schema designed for representing patient health records. Each Patient node serves as the central entity connected to various health-related parameters including Glucose Reading, Weight, Cholesterol, Blood Pressure, Heart Rate, Insulin Intake, Activity, Meal, and HbA1c. Three relationships are shown below.
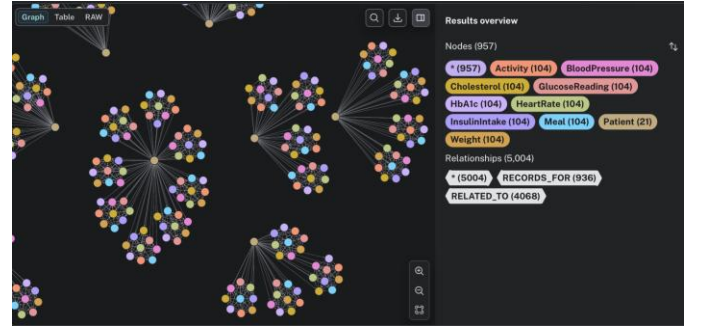
1) RECORD_FOR: Connects Patient to each health-related node, indicating that the respective health data belongs to or was recorded for that patient.

2) RELATED_TO: Represents relationships or correlations between different health parameters with the same data_id. This relationship captures potential dependencies and trends across various health measurements.

3) SIMILAR: Artificially constructed in the experiment test to evaluate and visualize the behavior of embedding-based patient similarity within the graph environment. This design enables testing model interpretability, verifying whether embedding-based similarity forms coherent patient communities, and validating the Node2Vec model's ability to capture latent health behavior patterns.

E. Graph Algorithms

1) Personalized PageRank (PPR):

Personalized PageRank (PPR) is an adaptation of the traditional PageRank algorithm that prioritizes specific nodes by directing random jumps to a designated seed node or subset of nodes, making it highly effective for personalized network analysis [6]. Unlike standard PageRank, which requires extensive iterations to converge on large graphs, PPR biases the random walk toward a single seed node, typically using a default damping factor to control the probability of random jumps [6]. This approach is particularly valuable in health data graphs, where it can identify influential nodes, such as patients

with significant health metric connections, for applications like anomaly detection or patient prioritization [6]. In the implemented system, PPR focuses on a single seed node to assess node importance, aligning with its use in targeted analyses. However, its computational complexity can hinder real-time applications, often necessitating efficient approximations to improve performance [6]. Unlike the global PageRank formulation, which distributes importance uniformly across the entire graph, PPR introduces a personalization vector that biases random walks toward selected nodes of interest. This approach allows the algorithm to compute localized node importance scores, thereby supporting fine-grained, patient-centric analysis in healthcare graphs such as the Personalized Health Knowledge Graph (PHKG).

In this study, the PPR algorithm was implemented using the NetworkX library's pagerank function, configured to utilize the framework's default damping factor of 0.85. The damping factor determines the probability that the random walk continues following the graph structure rather than restarting at the seed node, thus balancing global and local information propagation. The personalization vector was defined such that all nodes were initialized with a weight of zero, except for the target node, which was assigned a weight of one. This setup ensures that the random walk process consistently restarts from a specific patient or data record, allowing the algorithm to calculate patient-specific influence scores within the health graph.

The seed node, representing an individual patient's record, serves as the focal point of the random walk process. By propagating through edges connecting clinical and lifestyle parameters—such as glucose levels, activities, and meals—PPR identifies which nodes are most strongly associated with that patient's health patterns. Nodes that receive higher PPR scores are interpreted as being more influential or contextually related to the seed node within the PHKG, effectively ranking entities by their personalized relevance.

No additional hyperparameters were explicitly modified beyond the default configuration to maintain computational stability and interpretability. When a subset of nodes was specified through the filter_nodes parameter, the algorithm selectively returned relevance scores for those nodes only, thereby optimizing performance for targeted analyses. The resulting PPR scores were subsequently stored in the Neo4j and MySQL databases, where they support downstream applications such as personalized recommendation generation, similarity-based node ranking, and anomaly detection.

This personalized propagation framework provides a computationally efficient method for quantifying contextual importance in patient-centered health graphs, enabling localized insights that contribute to improved interpretability and precision in diabetes management.

2) Node2Vec:

Node2Vec is a self-supervised learning framework that generates low-dimensional embeddings for graph nodes by leveraging biased random walks to capture both local and global network structures [7]. Unlike supervised methods requiring labeled data, Node2Vec produces versatile embeddings that support tasks such as clustering, classification, and similarity analysis, making it suitable for health data networks where relationships between patients or health metrics need to be explored [7]. In the current implementation, Node2Vec uses a walk length of 10 and an embedding dimension of 128 to balance computational efficiency with structural representation, enabling the identification of similar entities, such as patients with comparable health profiles [7]. Studies have demonstrated Node2Vec's ability to outperform simpler methods like DeepWalk in capturing complex relationships, particularly in domains like biological networks, due to its flexible sampling strategy [7]. Unlike traditional graph embedding methods, Node2Vec introduces a biased random walk strategy that flexibly balances homophily (similar nodes connected closely) and structural equivalence (nodes with similar roles in different regions of the graph). This balance allows Node2Vec to produce richer representations that preserve the nuanced relational patterns inherent in healthcare data.

In this study, Node2Vec was employed to generate latent feature representations for each node in the Personalized Health Knowledge Graph (PHKG), enabling similarity analysis and clustering of patient-related entities. The implementation utilized the Node2Vec module from the NetworkX and Gensim libraries, configured with a walk length of 10, 100 walks per node, and an embedding dimension of 128. These parameters were selected to ensure an optimal trade-off between representational depth and computational efficiency. The shorter walk length emphasizes the preservation of local connectivity patterns—such as correlations among health metrics within a single patient—while the high number of walks enhances the diversity of traversed paths, ensuring robust learning of the global graph structure.

The random walks generated from the Neo4j-derived PHKG were processed by a Word2Vec model using the Skip-Gram architecture to learn context-based representations of nodes. Each node was thereby embedded as a 128-dimensional vector, where the proximity between vectors reflects the structural and semantic similarity of the corresponding health data points. These embeddings were later utilized for downstream analytical tasks, including patient similarity detection, community discovery, and visual clustering of health parameters in the graph database. When required, only embeddings for a filtered subset of nodes were extracted, optimizing computational performance.

This embedding-based approach enables the PHKG to support personalized insights by identifying nodes that share comparable clinical or lifestyle patterns, such as similar HbA1c trends or correlated activity behaviors. Consequently, Node2Vec plays a critical role in bridging raw graph connectivity with actionable similarity-driven intelligence for diabetes management.

3) Graph Attention Networks (GATs):

Graph Attention Networks (GATs) are advanced neural architectures designed for graph-structured data, employing self-attention mechanisms to dynamically weight the contributions of neighboring nodes [8]. Unlike traditional graph

convolutional networks that rely on uniform neighbor aggregation, GATs prioritize relevant connections, making them highly effective for irregular domains like health data networks [8]. In the implemented system, GATs generate 128-dimensional embeddings without supervised training, focusing on pre-trained representations for downstream tasks like node classification or clustering [8]. This approach excels in modeling complex relationships, such as those between health metrics and patient profiles, and supports generalization to unseen graphs, as demonstrated in benchmarks like citation and biological networks [8]. GATs' ability to handle variable-sized inputs and focus on significant neighbors positions them as a powerful tool for predictive and analytical tasks in graph-based health applications.

In this study, the GAT model was implemented using the PyTorch Geometric framework. The network architecture consists of two attention layers designed to balance representational richness and computational efficiency. The first layer (gat1) applies a graph attention convolution with 64 output channels and two attention heads, followed by an Exponential Linear Unit (ELU) activation function to introduce non-linearity. The second layer (gat2) aggregates the outputs from the preceding layer into a 128-dimensional embedding space using a single attention head with concat=False, ensuring the results are combined through averaging rather than concatenation. A dropout rate of 0.2 was applied to both layers to mitigate overfitting and enhance generalization stability across different graph structures.

Each node in the PHKG was initialized with a one-hot encoded identity vector, forming an identity matrix that served as the input feature matrix (x). This encoding allowed the model to distinguish nodes uniquely even in the absence of pre-defined node attributes. The graph's structural connectivity was defined by an edge index tensor (edge_index), representing bidirectional relationships between nodes derived from Neo4j. The network was executed in evaluation mode (model.eval()) without training, as the objective was to generate attention-weighted node embeddings for unsupervised analysis rather than perform supervised classification or prediction. Consequently, the model did not employ an optimizer, backpropagation, or iterative training loop. Instead, it produced embeddings through a single forward propagation pass, resulting in a 128-dimensional latent vector representation for each node.

Since the model was utilized purely for representation learning, no explicit loss function was applied. The embeddings generated were subsequently exported to both the MySQL and Neo4j databases to support downstream analytical tasks, including patient similarity detection, clustering, and visualization within the PHKG. This streamlined implementation effectively balances interpretability and computational efficiency, enabling scalable integration of GAT-based embedding generation within personalized healthcare systems.

F. System Architecture and Implementation

The system was developed as an automated end-to-end pipeline that connects patient health data to knowledge-graph reasoning, algorithmic analysis, and final recommendation generation. When a doctor adds a patient's health information, the data is first stored in MySQL and then synchronised to Neo4j when the doctor clicks the upload button. This updated data is incorporated directly into the Personalized Health Knowledge Graph (PHKG), which forms the foundation for all downstream analytics. Once the PHKG is refreshed, the system automatically triggers a series of graph algorithms including Personalized PageRank (PPR), Node2Vec and Graph Attention Networks (GAT), which are executed using Python and PyTorch Geometric. These algorithms generate node embeddings which are written back into Neo4j and stored in structured insight tables.

To support the recommendation logic, each algorithm contributes a specific type of analytical output:

- PPR generates personalised relevance scores for a patient's record, which are then used to identify similar patients for tailored recommendations.
- Node2Vec produces embeddings used for similarity measurement and clustering
- GAT generates high-dimensional representations for predictive reasoning.

All algorithm outputs flow into an insight layer that consolidates nearest neighbours, cluster memberships, similarity relationships, and explanatory episode patterns for each patient. A backend process retrieves each patient's health data along with these graph-derived insights and constructs a prompt that combines the data, analytical patterns, and example outputs. This prompt is sent to the Gemini 2.5 Flash model, which generates concise, easy-to-understand, personalized health recommendations. The recommendations are then automatically saved into the recommendation table in the database. This fully automated workflow ensures that every patient receives advice tailored to their medical condition, which can be accessed through the system's web application.
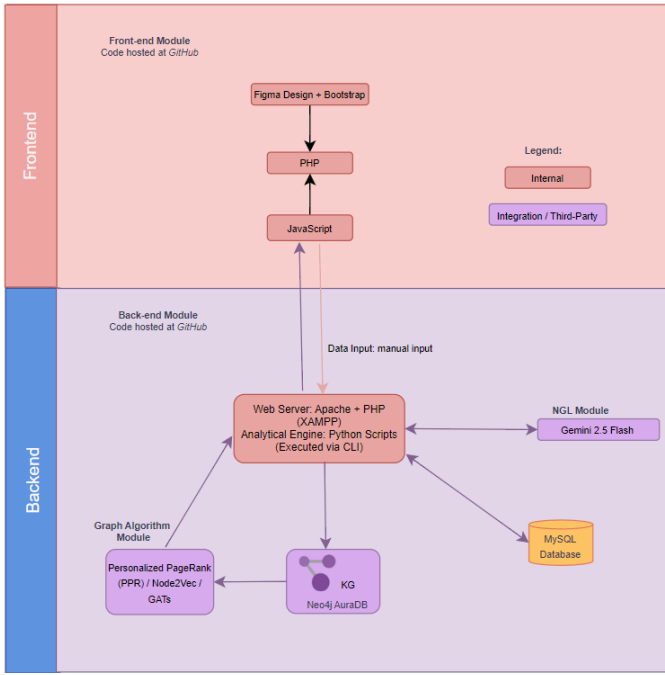
Fig. 3: Architecture diagram of the execution flow

Data flows seamlessly through these components, starting from patient data entry, moving through graph construction and automated algorithm execution and culminating in human-readable, personalized recommendations. This design ensures continuous integration of data updates, graph-based reasoning, machine-learning outputs and insight delivery to the user.

G. Experiment Setup and Configuration

Headings, or heads, are organizational devices that guide the reader through your paper. There are two types: component heads and text heads.

1. Step 0: Graph Structure Exploration

This step aimed to confirm that all nodes and relationships were correctly formed in the Neo4j graph database. The purpose was to ensure that the projected subgraph contained the correct entities and properties for subsequent analysis. The Cypher query "CALL db.schema.visualization();" was executed to visualize the schema, revealing the expected node labels and relationship types including RECORDS_FOR and RELATED_TO. The RECORDS_FOR links connected health nodes to their corresponding patient nodes, while RELATED_TO linked health nodes within the same data ID to enable correlation analysis and enhance interpretation of graph insights.

2. Step 1: Add Simple Patient Features (for Algorithms)

This step aimed to enrich each Patient node with key numeric attributes to support machine learning algorithms such as Node2Vec and Graph Attention Networks (GATs). The purpose was to enable these algorithms to capture clinical similarity between patients by integrating features like the latest

HbA1c value, weekly exercise frequency, and average glucose spike rate. These attributes were derived from the available health data and computed through Cypher queries to ensure each Patient node contained consistent, latest clinical information for analysis. The Patient nodes were updated accordingly using queries that aggregated the most recent health measurements and converted descriptive records into average numerical frequencies. The resulting graph displayed a set of enriched patient nodes containing standardized and comparable numeric features, forming the foundation for similarity detection and model evaluation in subsequent steps.

3. Step 2: Extract Episodes (Meal → Spike) for Explanations

The objective of this step was to identify meal records that occurred within three hours before each instance of high glucose level. A Cypher query was executed to retrieve Meal nodes connected to Patient nodes through the RECORDS_FOR relationship, filtered by timestamps where glucose readings exceeded 10 mmol/L. The output displayed meals recorded on the same day as the glucose spike, providing clear links between dietary intake and elevated glucose levels. This helped form human-readable explanations for better interpretation of patient data.

4. Step 3: Verification of Graph Embedding Integration

This step aimed to validate that externally generated embeddings and scores including Node2Vec, GAT and PPR were correctly written back into Neo4j, ensuring their successful integration for further analysis and visualization. A Cypher query was executed to verify that the node2vec_embedding, gat_embedding, and ppr_score properties were correctly stored in the GlucoseReading nodes. The embeddings and scores were generated externally through a Python pipeline (run_algorithms.py) and imported back into Neo4j as permanent node attributes. This approach bypassed the need for in-memory GDS projections while preserving the same analytical functionality for downstream insight generation.

5. Step 4A – Personalized PageRank (PPR): Find Top Related Patients to a Seed

The objective of this step was to rank patients based on their connectivity relevance to a selected seed patient. Personalized PageRank (PPR) scores were used as a measure of similarity through the graph's paths, which can serve as features for downstream tasks such as identifying patients with similar risk profiles. A Python script was implemented to fetch embeddings from Neo4j for the seed patient and all other patients. Cosine similarity was computed between the seed patient's embeddings and those of other patients and an average similarity score was calculated for each patient. The patients were then ranked by similarity, producing a top-N list of the most related patients. This approach allows patient relationships to be captured in a way that reflects the graph structure, rather than relying solely on raw clinical values.

6. Step 4B – Node2Vec: Learn Patient Embeddings

The objective of this step was to generate node embeddings that capture the underlying structure and connectivity patterns within the patient graph. The purpose was to enable downstream analytical tasks such as patient similarity comparison, clustering and classification. A Cypher query was executed to calculate the cosine similarity between the Node2Vec embeddings of a seed patient and other patients in the graph. Each Patient node already contained a node2vec_embedding property generated from the external Python pipeline. The query aggregated these similarity values across all corresponding records per patient to identify those with the most similar embedding patterns. These embeddings were later utilized for clustering through K-Means and other comparative analyses.

7. Step 5 – Detect Communities

The objective of this step was to group patients into distinct cohorts based on similarities in their learned graph embeddings. The purpose was to enable cohort-level analysis, which allows the comparison of health outcomes and behavioural trends across different patient groups. A K-Means clustering algorithm was executed externally in Python using the exported patient embeddings from Neo4j. Each embedding vector represented the patient's relational and structural context within the graph. The algorithm assigned each patient to one of five clusters, generating a CSV file containing the patient IDs and their corresponding cluster labels. The clustering results were then imported back into Neo4j using a Cypher query, where each Patient node was updated with its assigned cluster property. This step facilitated the visualization and interpretation of patient communities directly within the graph database.

8. Step 6 – Export Graph for GATs (PyTorch Geometric)

The objective of this step was to prepare the graph data, including node features, edge lists and labels to train a Graph Attention Network (GAT) for node-level prediction tasks, such as identifying patients at high risk of a spike event. The purpose was to leverage deep learning to capture complex structural and relational patterns within the patient graph. In this step, a custom Python function was implemented to generate node embeddings using a GAT. The graph was first converted into a NetworkX object, from which an edge index and a mapping from node IDs to consecutive indices were created. Each node was represented using an identity matrix as the feature vector, ensuring unique representation for every node. A GAT model with 128 output channels was then applied via PyTorch Geometric, generating 128-dimensional embeddings for each node. These embeddings capture the structural context and relationships of each node and can be exported for downstream analysis or predictive modelling.

9. Step 7 – Shortest Paths for Human-Readable Explanations

The objective of this step was to generate concise, human-readable narratives that illustrate relationships in the patient graph such as Patient → Meal → Glucose Spike. This enhances interpretability and provides explanations that complement model outputs. A Python was executed in Neo4j to retrieve shortest paths for a given patient, filtering for glucose readings above 10 mmol/L. For each high reading, the query matched the corresponding meal and returned a structured path displaying the patient ID, meal description and glucose level. The output provides a direct visualization of the patient's data in an intuitive format, helping clinicians or analysts understand how patient activities relate to glucose spikes.

10. Step 8 – Build Insight JSON (per patient)

The objective of this step was to consolidate relevant patient information into a single, structured JSON object for each patient. This includes top neighbors identified via Personalized PageRank (PPR) or Node2Vec embeddings, community or cluster membership, key labels and human-readable explanations. Cypher queries were executed in Neo4j to compute the top five Node2Vec-based neighbors per patient and create SIMILAR relationships with corresponding similarity scores. Recent glucose spike episodes were collected for each patient and community IDs were assigned based on similarity paths with high-confidence scores. Finally, the data was bundled into a JSON record per patient, capturing their neighbors, community, clinical status (such as high spikes and latest HbA1c) and recent glucose episodes. This structured format provides a clean, ready-to-use dataset for downstream tasks like recommendation generation, visualization or reporting.

IV. EXPERIMENT TEST RESULT

TABLE III. PERFORMANCE COMPARISON AND CLINICAL INTERPRETATION OF GRAPH ALGORITHMS ACROSS TWO

Graph Algorithms	Key Findings (from Dataset 1 & 2)	Interpretation
Personalized PageRank (PPR)	• Dataset 1: High precision (Precision@5 = 1.0), nDCG@5 = 0.94 • Dataset 2: Moderate Precision (0.20), Recall (0.33) due to small graph size Found 1 out of 3 clinically similar patients	PPR accurately identifies patients with closely matching diabetes profiles, showing perfect precision and high-ranking quality. It's fast and simple, suitable for similarity searches, but it may miss patients who are clinically similar but indirectly connected (if the trained graph size is small). Overall, this algorithm is suitable for interpretable analysis.
Node2Vec	• Dataset 1: Moderate precision (0.51), recall (0.21); Purity of clusters up to 0.81 • Dataset 2: Higher Precision (0.40) and Recall (0.67); Found 2 out of 3 clinically similar patients	Node2Vec retrieved some clinically similar patients but missed many others (Precision = 0.60, Recall = 0.23), showing it can capture general health pattern similarity but lacks accuracy for precise clinical matching. However, Node2Vec learns hidden and indirect relationships between patients. It performs better than PPR by combining local and global patterns in the network. Making

Graph Algorithms	Key Findings (from Dataset 1 & 2)	Interpretation
		it best for finding clinically similar patients and pattern discovery in medical data.
Louvain Clustering (based on Node2Vec Embeddings)	• Dataset 1: Moderate purity (0.56 – 0.81), weak separation (Silhouette ≈ 0) • Dataset 2: - Community 0: Purity = 1.00, Silhouette = 0.71 - Community 1: Purity = 0.80, Silhouette = 0.40	The Louvain clustering results for Dataset 1 reveal that Communities 0, 2, and 4 have relatively high purity ($\geqslant$0.74), suggesting patients in these groups share similar glucose spike patterns, while Community 1 is more mixed ($\approx$ 0.56). The slightly negative Silhouette scores ($\sim$−0.01) indicate weak separation between clusters. For Dataset 2, Louvain forms clearer communities, with Community 0 showing perfect homogeneity and Community 1 moderately mixed, demonstrating effective separation between high-risk and normal-risk patients. Overall, both datasets support the conclusion that the Louvain method can identify clinically meaningful patient groupings based on glucose patterns, though Dataset 1 exhibits weaker separation while Dataset 2 achieves stronger community distinction.
Graph Attention Network (GAT)	• Dataset 1: Accuracy = 0.50 Precision = 0.50 Recall = 1.00 F1 = 0.67 ROC-AUC = 0.50 • Dataset 2: Perfect Recall (1.0) but low Precision (0.5) – detects all high-risk cases with some false positives	GAT detected all high-risk patients (recall = 1.0) but misclassified some normal ones. It focuses on not missing risky cases, making it useful for early risk warning systems. Future improvement can raise precision and balance.
Shortest Path Explanations (Graph Queries)	• Paths like Patient → Meal → GlucoseReading → Activity clarify causal relationships between behaviors and spikes.	Provides explainable reasoning behind model predictions. Enhances trust, interpretability, and patient understanding by connecting behavior patterns to medical outcomes.

V. RESULTS & DISCUSSIONS

This section presents the performance of the implemented graph algorithms including Personalized PageRank (PPR), Node2Vec, Louvain clustering, and Graph Attention Networks (GAT), as well as their effectiveness in producing personalised recommendations for diabetes management. Results are reported for two datasets: a simulated dataset of 20 patients and a real medical dataset. The discussion connects algorithm performance to the quality, reliability, and interpretability of the final recommendations produced by the system.

A. System Output Overview

The system developed in this study follows a structured, end-to-end pipeline that mirrors the experimental workflows commonly applied in graph-based health analytics research. The process begins with patient data ingestion, where individual health profiles are uploaded and transformed into a multi-relational health knowledge graph capturing relationships among patients and their health data. Graph embeddings are then generated to represent both direct and indirect health patterns within the data. Each graph algorithm of Personalized PageRank, Node2Vec, and Graph Attention Networks, produces its own analytical perspective, ranging from similarity rankings and neighbourhood discovery to community detection and risk identification. Finally, an NLG component synthesizes these algorithm-specific outputs into personalised health recommendations, ensuring that the insights produced are contextualised, interpretable, and actionable. This unified pipeline enables systematic comparison of algorithm performance and provides a consistent basis for evaluating how graph-derived insights contribute to personalised diabetes management guidance.

Each algorithm provides a different perspective of patient understanding, resulting in unique recommendation styles:

- PPR → interpretable, ranking-based personalised risk factors
- Node2Vec → similarity-based lifestyle patterns and behavioural insights
- GAT → high-risk patient warnings and early alerts
- Louvain → cluster-based community patterns and collective risk profiles (verify effectiveness of Node2vec/GAT on forming meaningful patient communities)
- Graph queries → explanation paths (why a spike occurred)

TABLE IV.   EXPECTED PERSONALISED RECOMMENDATION APPROACH

Trigger	Algorithm Used	Output to user
New glucose spike detected	PPR	" Your recent patterns are similar to 3 other patients who improved through diet moderation."
Weekly trend analysis	Node2Vec + Louvain	"You belong to the 'high-carb morning' group — try reducing carbohydrate intake before lunch."
Continuous monitoring	GAT	"Spike risk level: High — check with your clinician if readings remain above 15 mmol/L."
Explanation layer	Shortest Path	" Your spike yesterday followed a meal containing fried noodles."

This diversity strengthens the overall recommendation pipeline, ensuring that different patient characteristics are captured.

B. Algorithm Performance and Interpretation

TABLE V. ALGORITHM PERFORMANCE METRICS AND USE CASES FOR PERSONALIZED DIABETES RECOMMENDATIONS

Graph Algorithms	Use Cases in Personalised Recommendation
Personalized PageRank (PPR) Dataset 1: • Precision@5 = 1.0 • nDCG@5 = 0.94 Dataset 2: • Precision = 0.20 • Recall = 0.33	Use Case 1→ "Peer Comparison for Diabetes Management" PPR is effective for interpretable, relevance-based patient similarity, particularly when used on reasonably connected graphs. It can quickly identify patients with the most similar clinical history and glucose trends, providing actionable insights for both patients and doctors. By analyzing direct connections in the patient graph, doctors can see which strategies were effective for similar patients and patients to receive personalized guidance based on proven approaches. Clinical illustration: "Patients with similar HbA1c levels successfully stabilized glucose spikes by splitting meals into smaller portions and incorporating post-meal walks."
Node2Vec Dataset 1: •Precision = 0.51 •Recall = 0.21 •Cluster purity up to 0.81 Dataset 2: •Precision = 0.40 •Recall = 0.67 • Retrieved 2 of 3 clinically similar patients	Use Case 1 → "Cluster-Based Recommendations" Node2Vec forms clusters of patients with similar overall health profiles, combining pattern discovery with actionable insights. By analyzing indirect and hidden relationships, it can suggest trends and interventions observed in the cluster. Doctors can use these insights to guide their recommendations, and patients receive tailored advice: Clinical illustration: "Patients in your group improved glucose control by adjusting meal timing, maintaining consistent sleep schedules, and adopting other lifestyle adjustments." Use Case 2 → "Hidden Metabolic Relationship Discovery for Clinical Decision Support" From the doctor/clinician dashboard, Node2Vec is capable in highlighting patients with similar hidden metabolic patterns, linking HbA1c, postprandial glucose 2h, fasting insulin, and triglyceride levels. When reviewing a complex case, the doctor can view a "Similar Patients" panel showing two clinically comparable profiles that Node2Vec discovered through indirect graph relationships. Clinical illustration: "Two patients with matching HbA1c and insulin fluctuation patterns achieved better glucose stability after adjusting rapid-acting insulin timing and moderating dinner carbohydrates." The dashboard presents evidence-based peer comparisons, revealing how similar patients responded to different interventions. This allows doctors to quickly identify effective, personalized treatment adjustments without manually analyzing large datasets.
Louvain Clustering (based on Node2Vec Embeddings) Dataset 1: • Purity = 0.56–0.81 • Silhouette $\approx$ 0 Dataset 2: • Community 0: Purity = 1.00, Silhouette = 0.71 • Community 1: Purity = 0.80, Silhouette = 0.40	Use Case 1 → "Community Wellness Programs" Assigns patients to digital support groups. A clinician dashboard flags clusters like "Low Activity–High Spike" for targeted education sessions. Use Case 2 → "Risk-Stratified Monitoring and Intervention" Louvain clustering groups patients into two distinct communities, one with perfect homogeneity of high-risk profiles and another with mixed but stable patients. The system automatically adjusts follow-up intensity based on community assignment. Clinical illustration: "Patients in the high-risk community are prioritized and receive targeted lifestyle alerts, while those in the stable community continue with routine self-monitoring." The Louvain Clustering algorithm can be implemented through a risk-stratified monitoring feature in the doctor dashboard. Patients are automatically grouped into high-risk and stable communities, visualized using color-coded indicators. The dashboard summarizes key metrics such as HbA1c and glucose variability for each group, enabling quick comparison. Doctors can then prioritize high-risk patients with targeted alerts or closer monitoring, while stable patients continue routine self-management. This transforms Louvain clustering results into an actionable, data-driven tool for proactive and efficient patient care.
Graph Attention Network (GAT) Dataset 1: • Accuracy = 0.50 • Precision = 0.50 • Recall = 1.00 • F1 = 0.67 • ROC-AUC = 0.50 Dataset 2: • Recall = 1.00, Precision = 0.50	Use Case 1 → "Personalized Health Alerts" GAT analyzes patient health data and the network of patient relationships to predict individuals at high risk of glucose spikes, combining node features with graph structure for precise risk assessment. By identifying which patients are likely to experience spikes, the system provides actionable, personalized recommendations. Doctors can use these insights to prioritize interventions and monitor high-risk patients, while patients receive tailored guidance to manage their glucose levels effectively: Clinical illustration: "Based on your profile and similar patient patterns, monitoring post-meal glucose, adjusting meal portions, and incorporating light activity after meals can help reduce spikes." Use Case 2 → "Early Risk Surveillance and Preventive Triage" GAT continuously analyzes patient records to detect emerging high-risk patterns, ensuring that no critical cases are overlooked. When all high-risk patients are identified—even with some false positives—the system generates proactive guidance to encourage early self-management. Clinical illustration: "Your recent health data indicates a possible rise in risk. Consider monitoring your post-meal glucose more closely and maintaining consistent meal and activity routines."

Graph Algorithms	Use Cases in Personalised Recommendation
Shortest Path Explanations (Graph Queries)	Use Case 1→ "Why Did My Glucose Spike?" Shortest Path analysis provides clear, explainable reasoning behind glucose spike predictions by tracing the sequence of patient behaviors leading to the outcome. This enhances trust and interpretability for both clinicians and patients. Doctors can use these insights to understand which behaviors contributed to spikes and advise interventions, while patients gain a clear understanding of cause-and-effect in their daily habits: Clinical illustration: "Your glucose rose to 17.2 mmol/L within 2 hours after eating fried noodles, highlighting the impact of meal composition on glucose levels." Use Case 2→ "Behavior-to-Outcome Pattern Discovery" The system analyzes shortest paths across multiple patients to uncover recurring sequences of behaviors that precede glucose instability. Instead of focusing on a single event, it aggregates explanations to reveal common risk patterns. Clinical illustration: "Across similar patients, late-night meals followed by low activity were frequently linked to higher glucose spikes."

C. Discussion

The findings demonstrate that each graph algorithm contributes uniquely to personalised diabetes management:

TABLE VI. ALGORITHM PERFORMANCE METRICS AND USE CASES FOR PERSONALIZED DIABETES RECOMMENDATIONS

Algorithm	Strength	Role In Recommendation
PPR	High precision, interpretable ranking	High-confidence advice, key risk factors
Node2Vec	Captures indirect/similarity patterns	Lifestyle-based insights, peer comparison
Louvain	Community separation	Population-level risk profiling
GAT	Detects all high-risk patients	Early warning and safety alerts
Graph Queries	Explainable reasoning	Transparent and patient-friendly explanations

Together, these components form a robust multi-perspective recommendation system, offering:

- precision (PPR)
- pattern discovery (Node2Vec)
- community behaviour (Louvain)
- safety alerts (GAT)
- causal/direct explanations (graph paths)

This ensures recommendations are clinically meaningful, personalised, explainable, and trustworthy, meeting the goal of improving the usefulness and reliability expected by your supervisor.

VI. CONCLUSION

This project successfully developed and evaluated a Personalized Health Knowledge Graph (PHKG) utilizing a multi-layered analytical framework to advance data-driven and interpretable personalized healthcare for diabetes management. By integrating diverse patient data—including clinical, demographic, and lifestyle factors, and subjecting it to rigorous analysis using Personalized PageRank (PPR), Node2Vec, and Graph Attention Networks (GATs), we demonstrated a pipeline from raw health data to actionable, personalized recommendations generated by a Natural Language Generation (NLG) model.

The comparative analysis affirmed that each graph algorithm provides unique, complementary insights: PPR excelled at personalized relevance retrieval, Node2Vec generated powerful structural embeddings for community detection and similarity analysis, and GATs provided attention-weighted representations crucial for predictive reasoning. The functional prototype successfully translated these graph-derived insights into tailored, explainable health advice, addressing key challenges related to fragmented data and the need for transparent interventions.

Overall, this work demonstrates a clear step toward interpretable, data-driven, and clinically aligned personalized healthcare, laying the foundation for future expansion in scalability, validation, generalization, and real-world patient engagement.

VII. FUTURE WORK

To fully realize the potential of the Personalized Health Knowledge Graph and the analytical framework developed, future work should focus on the following four strategic directions:

1. Scaling to Longitudinal, Multi-Source Data

The current system was built on a limited dataset for proof-of-concept. Future work must focus on scaling the PHKG to integrate longitudinal data from hundreds or thousands of patients, incorporating time-series information to model disease progression and treatment efficacy over extended periods. This expansion should also include integration of multi-source data, such as electronic health records (EHRs), genomic data, and real-time streaming data from wearable devices. Scaling the PHKG will necessitate the optimization of graph construction and algorithm execution for distributed computing environments.

2. Clinical Validation With Healthcare Providers

While the current work demonstrates technical feasibility and insight generation, its clinical utility requires rigorous validation. Future research must involve collaboration with healthcare providers (doctors, dietitians, and nurses) to implement the system in a real-world clinical setting. This involves conducting pilot studies to evaluate the system's impact on key patient outcomes, such as HbA1c reduction, medication adherence, and patient self-efficacy. Feedback from clinicians is vital to ensure the recommendations are medically sound, practical, and seamlessly integrated into existing clinical workflows.

3. Generalization to Other Chronic Conditions

The current PHKG is specifically tailored for Type 2 Diabetes Mellitus (T2DM) management. A critical next step is to generalize the PHKG schema and analytical framework to other chronic conditions, such as hypertension, cardiovascular disease, or mental health disorders. This involves adapting the node and relationship types to capture the specific pathology and risk factors of new conditions. Generalization will prove the framework's versatility and potential to serve as a unified platform for multi-morbidity management.

4. Patient-Facing Mobile Interface

The current prototype focuses on the backend system and recommendation generation for healthcare providers. To maximize patient engagement and adherence, future development should include the creation of a patient-facing mobile interface. This application would allow patients to directly input lifestyle data, view their personalized PHKG insights, receive real-time recommendations, and track their progress. Integrating features like conversational AI (leveraging the existing NLG component) and personalized feedback loops will be essential for creating an engaging and effective digital health coaching tool.

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