



GRAPH-THEORETIC APPROACHES TO PERSONALIZED HEALTH NETWORKS

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DOI: <https://doi.org/10.5281/zenodo.17275073>

Article Received on 19/08/2025

Article Revised on 08/09/2025

Article Accepted on 28/09/2025

ABSTRACT

The emergence of precision health has transformed the landscape of preventive care by emphasizing individualized risk assessment and targeted interventions. This paper explores the application of **graph-theoretic models** to construct and analyze **personalized health networks**, where nodes represent health determinants—such as genetic markers, behavioral traits, environmental exposures, and clinical metrics—and edges encode relationships, dependencies, or influence pathways among them. We propose a framework that leverages **centrality measures, community detection algorithms**, to identify critical health factors, predict disease onset, and optimize intervention strategies. This graph-theoretic perspective not only enhances the predictive power of precision health models but also supports scalable, data-driven strategies for population-level wellness planning. The findings underscore the potential of network science to bridge the gap between individualized care and public health optimization.

KEYWORDS: Precision Health, Graph Theory, Personalized Health Networks, Network Optimization, Health Determinants, Centrality Measures, Community Detection, Alpha, Beta, Gamma Indices.

INTRODUCTION

Precision health aims to deliver proactive, personalized care by integrating diverse data sources—genomic profiles, behavioral patterns, environmental exposures, and clinical records—to predict and prevent disease before symptoms arise. In this context, **graph theory** offers a powerful framework for modeling the complex interdependencies among health determinants, enabling the construction of **personalized health networks** tailored to individual risk profiles.

In these networks, nodes represent health-related variables (e.g., biomarkers, lifestyle factors, comorbidities), while edges capture relationships such as causal influence, correlation, or clinical interaction. To analyze and optimize these networks, we employ a suite of graph-theoretic algorithms

- **Centrality Measures** (e.g., degree, betweenness, closeness): to identify key health factors that exert the most influence on overall wellness.
- **Community Detection Algorithms** (e.g., Louvain method, modularity optimization): to uncover clusters of interrelated health variables that may represent syndromic patterns or intervention targets.
- **Shortest Path and Network Flow Algorithms** (e.g., Dijkstra's algorithm, Ford-Fulkerson): to

model optimal intervention pathways and resource allocation strategies.

- **Alpha, Beta, Gamma Indices:** to quantify network connectivity, redundancy, and robustness, offering insights into the resilience of an individual's health system.

By applying these algorithms to real-world data—such as electronic health records (EHRs), wearable sensor outputs, and genomic annotations—we demonstrate how graph-theoretic models can enhance risk prediction, guide personalized interventions, and support scalable public health planning.

Precision health goes beyond traditional medicine by focusing on *proactive, personalized care*. It aims to:

- **Predict risk** before disease occurs
- **Prevent illness** through targeted interventions
- **Tailor treatments** to individual genetic, environmental, and lifestyle factors

It integrates data from Genomics and biomarkers, Electronic health records (EHRs), Wearables and mobile health apps, Social and environmental determinants of health.

Traditional Medicine vs. Precision Medicine vs. Precision Health.

Aspect	Traditional Medicine	Precision Medicine	Precision Health
Focus	Reactive treatment after symptoms appear	Personalized treatment based on genetic and clinical data	Proactive prevention and wellness based on holistic data
Approach	One-size-fits-all	Tailored therapy for diagnosed conditions	Individualized risk prediction and lifestyle optimization
Data Used	Symptoms, basic diagnostics	Genomics, biomarkers, clinical history	Genomics, behavior, environment, EHRs, wearables
Timing	Post-diagnosis	Post-diagnosis	Pre-diagnosis and continuous monitoring
Goal	Cure or manage disease	Optimize treatment outcomes	Prevent disease and promote long-term health
Graph-Theoretic Role	Not applicable	Limited to molecular interaction networks	Central to modeling personalized health determinants

In **Traditional medicine** treats disease after it occurs, often ignoring individual variability.

In **Precision medicine** customizes treatment but still reacts to disease presence.

In **Precision health**, supported by **graph-theoretic models**, shifts the paradigm by mapping and analyzing the full spectrum of health influences—allowing for **early intervention, targeted prevention, and system-level optimization.**

Centrality Measures in Graph Theory

Centrality measures help identify the most influential or critical nodes in a network. Each measure captures a different notion of "importance"

1. Degree Centrality

Definition: Number of direct connections a node has.

Use: Identifies highly connected nodes.

Example: In social networks, popular individuals with many friends.

2. Betweenness Centrality

Definition: Number of shortest paths that pass through a node.

Use: Detects nodes that act as bridges or bottlenecks.

Example: Key intermediaries in communication networks.

3. Closeness Centrality

Definition: Inverse of the average shortest path from a node to all others.

Use: Finds nodes that can quickly reach others.

Example: Efficient broadcasters in a network.

4. Eigenvector Centrality

Definition: Measures influence based on connections to other influential nodes.

Use: Highlights nodes connected to well-connected peers.

Example: Google's PageRank is a variant of this.

Community Detection Algorithms

Community detection identifies groups of nodes (communities) that are more densely connected internally than with the rest of the network. It's widely used in: Social networks (e.g., friend groups), Biological networks (e.g., protein interactions), Healthcare systems (e.g., patient clusters), Infrastructure planning (e.g., transport zones).

precision health and graph-theoretic modeling, these algorithms can:

- Detect **functional clusters** in health networks.
- Identify **risk communities** in epidemic modeling.
- Optimize **resource allocation** in healthcare systems.

Algorithm	Key Idea	Best For
Louvain	Optimizes modularity using hierarchical clustering	Large-scale networks
Girvan–Newman	Removes edges with high betweenness to reveal communities	Small to medium networks
Label Propagation	Nodes adopt the most frequent label among neighbors iteratively	Fast, scalable detection
Leiden	Improves Louvain with better community quality and faster convergence	High-quality partitions
Kernighan–Lin	Minimizes edge cuts between partitions through iterative swaps	Balanced partitions in small graphs

Shortest Path Algorithms in Precision Health

Shortest path algorithms help optimize **timing, routing, and resource access** in healthcare systems.

Patient Routing: Dijkstra's or A* algorithms can optimize ambulance routes or patient transfers between facilities.

Clinical Decision Support: Algorithms like Bellman-Ford can model diagnostic pathways with varying risk levels or treatment costs.

Genomic Pathways: Floyd-Warshall helps analyze shortest regulatory or signaling paths in molecular interaction networks.

Example

A hospital network can be modeled as a graph where nodes are departments and edges represent transfer pathways. Dijkstra's algorithm finds the fastest route for a patient needing multi-specialty care.

Optimizing Patient Transfer in a Hospital Network

A regional healthcare system consists of **6 hospitals** connected by roads with varying travel times. A patient at **Hospital A** needs urgent care at the **nearest facility**

with ICU availability. we want to find the **shortest travel time** from Hospital A to all other hospitals.

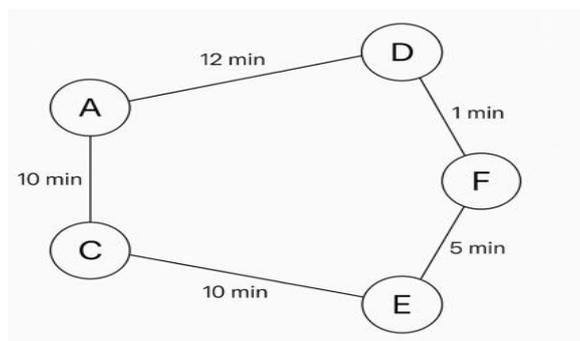
Graph Representation

Each hospital is a **node**, and each road is an **edge** with a weight equal to **travel time in minutes**.

Hospitals: A, B, C, D, E, F

Edges (with weights): A–B: 10 min, A–C: 15 min, B–D: 12 min, C–E: 10 min, D–F: 1 min

E–F: 5 min.



Use **Dijkstra's Algorithm** to find the shortest path from **Hospital A** to all others, especially to **Hospital F**, which has ICU availability.

Solution**Step-by-Step Using Dijkstra's Algorithm**

1. **Initialize distances**
 - Dist [A] = 0
 - All others = ∞
 - Priority queue = {A}
2. **Visit A**
 - Update B: dist [B] = 10
 - Update C: dist [C] = 15
 - Queue = {B, C}
3. **Visit B**
 - Update D: dist [D] = 10 + 12 = 22
 - Queue = {C, D}
4. **Visit C**
 - Update E: dist [E] = 15 + 10 = 25
 - Queue = {D, E}
5. **Visit D**
 - Update F: dist [F] = 22 + 1 = 23
 - Queue = {E, F}
6. **Visit F**
 - Already optimal path found
 - Final shortest path from A to F = **23 minutes**

Outcome

The patient should be transferred via **A → B → D → F**, taking **23 minutes**, which is the shortest route to an ICU-equipped hospital.

Dijkstra's Algorithm, a classic graph-based method for finding the shortest path in a network, plays a vital role in **precision health** by enabling efficient, personalized decision-making across healthcare systems.

Optimizing Patient Transfers

- Identifies the fastest route between healthcare facilities for emergency care or specialized treatment.
- Minimizes delays in critical interventions, improving outcomes.

Personalized Care Pathways

- Models diagnostic or treatment sequences as weighted graphs.
- Helps select the least-risk or least-cost path tailored to individual patient profiles.

Healthcare Resource Routing

- Optimizes distribution of medical supplies, vaccines, or mobile health units.
- Ensures timely access to care in underserved regions.

CONCLUSION

In the evolving landscape of precision health, graph-theoretic models offer more than computational elegance—they provide a **conceptual shift** in how we understand, navigate, and optimize human health. By treating biological systems, care pathways, and resource flows as dynamic networks, we unlock the ability to personalize interventions with mathematical precision.

Dijkstra's algorithm, long celebrated for its efficiency in finding shortest paths, emerges as a **cornerstone** in this paradigm. Whether routing emergency care, decoding protein interaction networks, or tailoring treatment

sequences, it transforms static data into actionable insights. Its simplicity belies its power: in a world of complex health variables, it offers clarity, speed, and adaptability.

We make this approach truly unique is its **fusion of abstraction and empathy**—using graph theory not just to model systems, but to **map individual journeys** through health and disease. Each node becomes a decision point, each edge a possibility, and each path a story of care shaped by data, context, and need.

As we move forward, the challenge is not merely technical but philosophical: to design health networks that are not only efficient but **equitable**, not only optimized but **human-centered**. Graph-theoretic approaches, with Dijkstra's algorithm at their core, are poised to lead this transformation—one personalized path at a time.

REFERENCES

1. Applying Personal Knowledge Graphs to Health by Ola Shirai, Oshani Seneviratne, Deborah L. McGuinness, arXiv: 2104.07587.
2. Graph Theory Approaches to Functional Network Organization in Brain Disorders by Michael N. Hallquist, Frank G. Hillary, MIT Press – Network Neuroscience.
3. A Comprehensive Review of Graph Theory Applications in Network Analysis by D. K. Kothimbire et al. International journal of Mathematics and computer Research.
4. Blondel, V. D., Guillaume, J.-L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2008; (10): P10008.