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Research Paper

Mathematical Modelling of Diagnostic Systems using Soft Graph Theory

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ABSTRACT: *Medical diagnosis is a complex decision-making process often clouded by uncertainty arising from incomplete information, overlapping symptomatology, and parameter-dependent variability. Traditional crisp mathematical models, including classical graphs and matrices, fall short in capturing this inherent vagueness. This paper presents a com- prehensive mathematical framework that leverages soft graphs and soft matrices for robust medical diagnosis. We extend soft set theory to model disease-symptom networks through parameterised adjacency relations. A novel weighted soft matrix decision algorithm is proposed and rigorously analysed. The proposed model offers a mathematical foundation for developing transparent and uncertainty-aware AI-based clinical decision support systems.*

KEYWORDS: *Soft graphs, Soft matrices, Decision-making, Healthcare AI, Uncertainty modelling, Algorithm design.*

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I. INTRODUCTION

Medical diagnosis is fundamentally a multi-criteria decision-making process conducted under conditions of uncertainty. Physicians synthesize information from various sources—patient history, physical examinations, laboratory tests, and imaging-to arrive at a conclusion. This process is complicated by the fact that many diseases share overlapping symptom structures (e.g., fever, headache, and fatigue are common to influenza, malaria, and dengue), and the manifestation of symptoms can vary based on patient-specific parameters like age, immunity, and disease stage [7].

Classical diagnostic models often rely on Boolean logic or crisp set theory, where a symptom is either present or absent. This binary representation is inadequate for modelling the graded or parameter-dependent nature of medical knowledge. To address such complexities, several mathematical frameworks have been proposed, including fuzzy sets [5], rough sets [6], and probabilistic models. While powerful, these methods often require predefined membership functions or probability distributions, which can be challenging to ascertain in practice.

Soft set theory, introduced by Molodtsov[1], offers an alternative and more general approach to uncertainty modelling. Its primary advantage lies in being free from the inadequacies of membership functions, making it purely parameterized and highly adaptable. Building on this foundation, researchers like Maji et al. [2] developed soft set operations, and Cagman and Enginoğlu [3] introduced soft matrices for computational efficiency. Graph-based models, such as Bayesian networks, have been used in medical diagnosis, but the exploration of soft graphs [4] in this domain remains nascent.

The theoretical foundations of soft set theory have been rigorously established through investigations into basic operations and relations. Sezgin and Atagün [15] systematically defined union, intersection, and complement operations, while Babitha and Sunil [9] introduced soft set relations and functions, providing the algebraic basis for structured representations like the soft bipartite graph employed in our framework. Addressing practical applicability, Chen et al. [10] developed parameterization reduction techniques to eliminate redundant parameters without compromising decision-making capability, a crucial consideration for managing complex medical datasets.

Building on these foundations, researchers have extended soft sets through hybrid models and computational algorithms. Feng et al. [11] combined soft sets with fuzzy and rough sets, while Jiang et al. [12] introduced interval-valued intuitionistic fuzzy soft sets for capturing higher-order uncertainty. For decision-making, Alkhazaleh and Salleh [8] proposed soft expert sets to aggregate multiple expert opinions, and Xiao et al. [16] demonstrated fuzzy soft sets in forecasting applications. In medical diagnosis specifically, Liu et al. [13] applied fuzzy soft sets with parameterized symptoms, and Maiti and Roy [14] provided a comprehensive review identifying research gaps. Our work addresses these gaps by introducing a soft graph-based framework with weighted matrices and rigorous theoretical guarantees, advancing beyond existing models that lack such structured representations and formal proofs of stability and resilience.

The concept of a soft set, as defined by Molodtsov [1], provides a parameterized family of subsets over a universal set.

Definition 1.1 (Soft Set [1]). Let U be an initial universe of objects and E be a set of parameters. A pair (F, E) is called a soft set over U if and only if F is a mapping given by $F: E \to \mathcal{P}(U)$, where $\mathcal{P}(U)$ denotes the power set of U. In other words, a soft set is a parameterized family of subsets of U. For a specific parameter $e \in E, F(e)$ is considered the set of e-approximate elements of the soft set.

Definition 1.2 (Soft Graph [4]). Let $G^* = (V, E)$ be a crisp (classical) graph, where V is the set of vertices and $E \subseteq V \times V$ is the set of edges. Let $A \subseteq E_{\text{param}}$ be a set of parameters. A soft graph $\tilde{G} = (F_V, F_E, A)$ consists of

1. A soft set (F_V, A) over V, i.e., $F_V: A \to \mathcal{P}(V)$.
2. A soft set (F_E, A) over E, i.e., $F_E: A \to \mathcal{P}(E)$.

such that for each parameter $a \in A$, the graph $G_a = (F_V(a), F_E(a))$ is a subgraph of G^*.

Definition 1.3 (Soft Matrix [3]). Let (F, A) be a soft set over a finite universe $U = \{u_1, u_2, \ldots, u_m\}$ and a finite parameter set $A = \{e_1, e_2, \ldots, e_n\}$. The soft set can be represented by an $m \times n$ matrix $M = [m_{ij}]$, where

$$m_{ij} = \begin{cases} 1 & \text{if } u_i \in F(e_j), \\ 0 & \text{otherwise .} \end{cases}$$

We introduce new theoretical results, including theorems on ranking invariance under weight scaling, diagnostic consistency, and the impact of noise. An extended numerical case study with five diseases and five symptoms is provided to demonstrate computational feasibility and effectiveness. Furthermore, a Python implementation of the algorithm is presented to bridge the gap between theoretical constructs and practical application.

2. RESULT & DISCUSSION

In this section, we establish the mathematical foundations of our diagnostic framework. We begin by formally defining the components of the model.

Definition 2.1 (Soft Matrix of Model). Let $\mathcal{D} = \{d_1, d_2, \ldots, d_m\}$ be a finite set of diseases and $\mathcal{S} = \{s_1, s_2, \ldots, s_n\}$ be a finite set of symptoms. A soft matrix M is an $m \times n$ matrix defined as $M = [m_{ij}]_{m \times n}$, where $m_{ij} \in [0,1] \subset \mathbb{R}$ represents the degree of association between disease d_i and symptom s_j. A value of $m_{ij} = 0$ indicates no association, while $m_{ij} = 1$ indicates a strong, pathogenic association.

Definition 2.2. A weight vector W is an n-dimensional vector defined as $W = (w_1, w_2, \ldots, w_n)^T \in [0,1]^n$, such that $\sum_{j=1}^{n} w_j = 1$ where w_j quantifies the clinical importance or diagnostic significance of symptom s_j.

Definition 2.3. A patient symptom vector P is an n-dimensional vector defined as $P = (p_1, p_2, \dots, p_n)^T \in [0,1]^n$ where p_j represents the observed presence or severity of symptom s_j in a specific patient, with $p_j = 0$ indicating absence and $p_j = 1$ indicating maximum severity.

Definition 2.4. For a given soft matrix M, weight vector W, and patient vector P, the diagnostic score for disease d_i is a function

$$\Phi: \{1, \dots, m\} \times \mathbb{R}^{m \times n} \times \mathbb{R}^n \times \mathbb{R}^n \to \mathbb{R} \text{ defined as } \Phi(i; M, W, P) = \sum_{j=1}^{n} w_j \cdot m_{ij} \cdot p_j$$

For notational convenience, when the context is clear, we denote $\Phi(i; M, W, P)$ simply as Score (d_i).

We now adapt the general concepts of soft graphs and soft matrices to model the medical diagnosis problem. Let us define the fundamental components of our diagnostic model as follows.

Let $\mathcal{D} = \{d_1, d_2, \dots, d_m\}$ be a finite set of diseases under consideration, $\mathcal{S} = \{s_1, s_2, \dots, s_n\}$ be a finite set of symptoms and $\mathcal{P} = \{p_1, p_2, \dots, p_k\}$ be the set of parameters that provide context or modify the relationship between diseases and symptoms. This could include severity (mild, acute), duration (acute, chronic), demographics (child, adult, elderly), or test results (positive, negative).

We construct a soft bipartite graph $\bar{G} = (\mathcal{D} \cup \mathcal{S}, F, \mathcal{P})$ with the vertex set is the union of diseases and symptoms, $\mathcal{D} \cup \mathcal{S}$ and for each parameter $p \in \mathcal{P}$, we define a mapping $F(p) = E_p$, where $E_p \subseteq \mathcal{D} \times \mathcal{S}$ is the set of edges for that parameter. An edge $(d_i, s_j) \in E_p$ exists if, under the parameter p, the disease d_i is known to cause symptom s_j. For a fixed parameter, we obtain a crisp bipartite graph. By considering all parameters, we get a parameterized family of graphs, i.e., a soft graph. We now establish several theoretical properties of the proposed scoring model.

Theorem 2.5. If the weight vector W is scaled by a positive constant α, the relative ranking of diseases remains invariant.

Proof. Let the original weight vector be $W = [w_1, \dots, w_n]$ and the scaled vector be $W' = \alpha W = [\alpha w_1, \dots, \alpha w_n]$, where $\alpha > 0$. The score for disease d_i under the scaled weights, for a fixed patient vector P, is

$$\text{Score}'(d_i) = \sum_{j=1}^{n} (\alpha w_j) \cdot m_{ij} \cdot P[j] = \alpha \sum_{j=1}^{n} w_j \cdot m_{ij} \cdot P[j] = \alpha \cdot \text{Score}(d_i).$$

Consider two diseases d_a and d_b. If $\text{Score}(d_a) \geq \text{Score}(d_b)$, then multiplying both sides by $\alpha > 0$ preserves the inequality

$$\alpha \cdot \text{Score}(d_a) \geq \alpha \cdot \text{Score}(d_b) \Longrightarrow \text{Score}'(d_a) \geq \text{Score}'(d_b).$$

Thus, the order of diseases is unchanged.

Theorem 2.6. If two diseases d_a and d_b have identical association profiles with respect to all symptoms (i.e., their corresponding rows in the soft matrix M are identical), then for any patient symptom vector P and any weight vector W, they will receive identical diagnostic scores.

Proof. Let the rows for diseases d_a and d_b be identical, meaning $m_{aj} = m_{bj}$ for all $j = 1, \dots, n$. Then their scores are

$$\text{Score}(d_a) = \sum_{j=1}^{n} w_j \cdot m_{aj} \cdot P[j], \text{Score}(d_b) = \sum_{j=1}^{n} w_j \cdot m_{bj} \cdot P[j].$$

Since $m_{aj} = m_{bj}$ for every j, the two summations are term-by-term equal. Therefore,

$$\text{Score}(d_a) = \text{Score}(d_b).$$

Theorem 2.7. The diagnostic score for a disease d_i is monotonic nondecreasing with respect to the presence of any symptom s_j with which it has a positive association ($m_{ij} > 0$).

Proof. The score function $\text{Score}(d_i) = \sum_{k=1}^{n} w_k m_{ik} P[k]$ is a linear function of each $P[j]$. The partial derivative with respect to $P[j]$ is

$$\frac{\partial \text{Score}(d_i)}{\partial P[j]} = w_j m_{ij}.$$

Since $w_j \geq 0$ and $m_{ij} \geq 0$, the derivative is non-negative. If $m_{ij} > 0$ and $w_j > 0$, the derivative is strictly positive, meaning an increase in the patient's symptom value $P[j]$ leads to an increase in the score for disease d_i.

Theorem 2.8. Let the observed patient symptom vector be $P = P_{\text{true}} + \epsilon$, where ϵ is a zero-mean random noise vector with independent components, each having variance σ_j^2. The expected diagnostic score for a disease d_i is unaffected by the noise, i.e., $\mathbb{E}[\text{Score}(d_i)] = \text{Scoree}_{\text{true}}(d_i)$.

Proof. The score for disease d_i is a linear combination of the symptom values

$$\text{Score}(d_i) = \sum_{j=1}^{n} w_j m_{ij} P[j] = \sum_{j=1}^{n} w_j m_{ij} (P_{\text{true}}[j] + \epsilon_j).$$

Taking the expectation, and using the linearity of expectation and the fact that $\mathbb{E}[\epsilon_j] = 0$

$$\mathbb{E}[\text{Score}(d_i)] = \sum_{j=1}^{n} w_j m_{ij} (\mathbb{E}[P_{\text{true}}[j]] + \mathbb{E}[\epsilon_j]) = \sum_{j=1}^{n} w_j m_{ij} P_{\text{true}}[j] = \text{Score}_{\text{true}}(d_i).$$

This shows the scoring function is an unbiased estimator of the true score in the presence of zero-mean noise.

2.1 DECISION ALGORITHM

Based on the mathematical framework, we propose a systematic algorithm for medical diagnosis. The algorithm takes as input the patient's symptom presentation and outputs a ranked list of probable diseases.

Algorithm 1 Weighted Soft Matrix Decision Algorithm for Medical Diagnosis

Input: Soft matrix $M_{m \times n}$ of disease-symptom associations, where $M[i][j]$ is the association score for disease d_i and symptom s_j.

Input: Weight vector $W_{1 \times n}$ representing the clinical importance of each symptom.

Input: Patient symptom vector $P_{1 \times n}$, where $P[j] \in [0,1]$ indicates the presence/severity of symptom s_j in the patient.

Output: A ranked list of diseases based on their likelihood.

```
procedure Diagnose( M, W, P )
    Initialize an empty list Scores of length m.
    for each disease d_i from i=1 to m do
        total_score ←0
        for each symptom s_j from j=1 to n do
            total_score ←total_score +w_j x M[i][j] x P[j]
        end for
        Scores[i] ← total_score
    end for
    RankedList ← Sort diseases in descending order of Scores.
    return RankedList
end procedure
```

Note: In Algorithm 1, the patient symptom vector P modulates the theoretical association $M[i][j]$. If a patient does not have a symptom s_j (i.e., $P[j] = 0$), its contribution to the score becomes zero, even if the association is strong.

2.2 NUMERICAL EXAMPLE

To demonstrate the application of our framework, we consider a scenario with five diseases and five symptoms.

Diseases $(\mathcal{D}) = \{d_1($ Viral Fever $), d_2$ (Malaria), d_3 (Typhoid), d_4 (Dengue), d_5 (COVID-19).$\}$

Symptoms $(\mathcal{S}) = \{s_1($ Fever $), s_2$ (Headache), s_3 (Fatigue), s_4 (Cough), s_5 (Rash/Loss of Taste).$\}$

Then we construct the soft matrix M constructed based on medical knowledge. Here, entries represent the strength of association on a scale of 0 to 1, where 0 means no association and 1 means a very strong, characteristic association.

$$M = \begin{pmatrix} d_1 \rightarrow \\ d_2 \rightarrow \\ d_3 \rightarrow \\ d_4 \rightarrow \\ d_5 \rightarrow \end{pmatrix} \begin{pmatrix} s_1 & s_2 & s_3 & s_4 & s_5 \\ 0.9 & 0.8 & 0.7 & 0.8 & 0.2 \\ 1.0 & 0.9 & 0.6 & 0.1 & 0.0 \\ 0.9 & 0.6 & 0.5 & 0.3 & 0.3 \\ 1.0 & 0.8 & 0.8 & 0.2 & 0.6 \\ 0.8 & 0.5 & 0.6 & 0.9 & 0.7 \end{pmatrix}$$

The weight vector reflects the diagnostic importance of each symptom.

For this example, we define

$$W = (0.25, 0.15, 0.15, 0.20, 0.25)$$

Fever and Loss of Taste/Rash are given higher weight due to their specificity in some diseases (e.g., rash in dengue, loss of taste in COVID-19).

Consider a patient, Mr. X, presenting with the following symptoms (quantified on a scale of 0 to 1)

$$P = (1.0, 0.8, 0.9, 0.1, 0.7)$$

He has high fever, significant headache and fatigue, a mild cough, and has developed a rash.

We apply Algorithm 1. The scores are calculated as

$$\text{Score}(d_i) = \sum_{j=1}^{5} w_j \cdot M[i][j] \cdot P[j]$$

$$\begin{aligned} \text{Score}\,(d_1) &= 0.25 * 0.9 * 1.0 + 0.15 * 0.8 * 0.8 + 0.15 * 0.7 * 0.9 \\ &\quad + 0.20 * 0.8 * 0.1 + 0.25 * 0.2 * 0.7 \\ &= 0.225 + 0.096 + 0.0945 + 0.016 + 0.035 = 0.4665 \\ \text{Score}(d_2) &= 0.25 * 1.0 * 1.0 + 0.15 * 0.9 * 0.8 + 0.15 * 0.6 * 0.9 \\ &\quad + 0.20 * 0.1 * 0.1 + 0.25 * 0.0 * 0.7 \\ &= 0.25 + 0.108 + 0.081 + 0.002 + 0 = 0.4410 \\ \text{Score}(d_3) &= 0.25 * 0.9 * 1.0 + 0.15 * 0.6 * 0.8 + 0.15 * 0.5 * 0.9 \\ &\quad + 0.20 * 0.3 * 0.1 + 0.25 * 0.3 * 0.7 \\ &= 0.225 + 0.072 + 0.0675 + 0.006 + 0.0525 = 0.4230 \\ \text{Score}(d_4) &= 0.25 * 1.0 * 1.0 + 0.15 * 0.8 * 0.8 + 0.15 * 0.8 * 0.9 \\ &\quad + 0.20 * 0.2 * 0.1 + 0.25 * 0.6 * 0.7 \\ &= 0.25 + 0.096 + 0.108 + 0.004 + 0.105 = 0.5630 \\ \text{Score}(d_5) &= 0.25 * 0.8 * 1.0 + 0.15 * 0.5 * 0.8 + 0.15 * 0.6 * 0.9 \\ &\quad + 0.20 * 0.9 * 0.1 + 0.25 * 0.7 * 0.7 \\ &= 0.20 + 0.06 + 0.081 + 0.018 + 0.1225 = 0.4815 \end{aligned}$$

The final scores are:

$$d_4 > d_5 > d_1 > d_2 > d_3$$

$$0.5630 > 0.4815 > 0.4665 > 0.4410 > 0.4230.$$

i.e.

Dengue > COVID-19 > Viral Fever > Malaria > Typhoid.

The algorithm suggests **Dengue** as the most probable diagnosis, followed by COVID-19. This aligns well with the patient's symptoms, particularly the presence of high fever and a rash, which are strong indicators for Dengue in our matrix. The result demonstrates how the weighted model effectively combines multiple symptom clues to produce a nuanced ranking.

2.3 PYTHON IMPLEMENTATION

To demonstrate computational feasibility, we provide a Python implementation of Algorithm. This code reproduces the case study and can be easily adapted for other datasets.

Python Code:

```
import numpy as np
def soft_matrix_diagnosis(M, W, P):
    """
    Performs diagnosis using the weighted soft matrix algorithm.
    Args-
    M (np.ndarray)- Disease-symptom association matrix (m x n).
    W (np.ndarray)- Symptom weight vector (n,).
    P (np.ndarray)- Patient symptom vector (n,).
    Returns-
    list of tuples: Sorted list of (disease_index, score) in descending order.
    """
    m, n = M.shape
    scores = np.zeros(m)
    for i in range(m):
        # Calculate weighted sum: sum_j (W_j * M_ij * P_j)
         scores[i] = np.sum(W * M[i, :] * P)
        # Get sorted indices in descending order
        sorted_indices = np.argsort(scores)[::-1]
        # Return as list of tuples (index, score)
        return [(idx, scores[idx]) for idx in sorted_indices]
    # --- Data from Case Study ---
    diseases = ["Viral Fever", "Malaria", "Typhoid", "Dengue", "COVID-19"]
    symptoms = ["Fever", "Headache", "Fatigue", "Cough", "Rash/LossTaste"]
    # Soft Matrix M (5 diseases x 5 symptoms)
    M = np.array([
    [0.9, 0.8, 0.7, 0.8, 0.2],  # Viral Fever
    [1.0, 0.9, 0.6, 0.1, 0.0],  # Malaria
    [0.9, 0.6, 0.5, 0.3, 0.3],  # Typhoid
    [1.0, 0.8, 0.8, 0.2, 0.6],  # Dengue
    [0.8, 0.5, 0.6, 0.9, 0.7]   # COVID-19
    ])
    # Weight Vector W
    W = np.array([0.25, 0.15, 0.15, 0.20, 0.25])
    # Patient Symptom Vector P
    P = np.array([1.0, 0.8, 0.9, 0.1, 0.7])
    # --- Perform Diagnosis ---
    print("--- Input Data ---")
    print(f"Diseases: {diseases}")
    print(f"Symptoms: {symptoms}")
    print(f"Weight Vector W: {W}")
    print(f"Patient Vector P: {P}")
    print("\n--- Diagnosis Results ---")
    result = soft_matrix_diagnosis(M, W, P)
    for rank, (disease_idx, score) in enumerate(result):
        print(f"{rank+1}. {diseases[disease_idx]}: {score:.4f}")
    print("\n--- Stability Test (Scaling Weights by 2) ---")
    W_scaled = 2 * W
    result_scaled = soft_matrix_diagnosis(M, W_scaled, P)
    for rank, (disease_idx, score) in enumerate(result_scaled):
        print(f"{rank+1}. {diseases[disease_idx]}: {score:.4f} (Scaled) vs
         {result[rank][1]:.4f} (Original)")
    print("Note: Scores are scaled, but ranking order is preserved.")
```

2.4 Output

Running the provided Python script produces the following output:

--- Diagnosis Results ---
1. Dengue: 0.5630
2. COVID-19: 0.4815
3. Viral Fever: 0.4665
4. Malaria: 0.4410
5. Typhoid: 0.4230

This output matches our manual calculations, confirming the correctness of the implementation.

III. CONCLUSION

This paper has developed a comprehensive and rigorous mathematical framework for medical diagnosis using soft graphs and soft matrices. By extending soft set theory to model disease-symptom networks, we have provided a powerful tool for handling the inherent uncertainty of clinical decision-making. The proposed weighted decision algorithm is theoretically grounded, with new theorems proving its stability, consistency, sensitivity, and noise resilience. The extended numerical case study and the accompanying Python implementation demonstrate its computational feasibility and practical applicability. The model's low complexity and interpretability make it an ideal candidate for integration into next-generation AI-based clinical decision support systems, telemedicine platforms, and resource-constrained healthcare settings. This work lays a strong mathematical foundation for future research, including the development of soft graph neural networks and extensive clinical validation.

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