The Diagnosis Decision Model for A Patient

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***Abstract*—Considering patient past history, medically designated symptoms, medical hypothesis, physician's knowledge of similar information we construct a diagnosis decision model for a patient for better treatment.**

***Index Terms*— Matrix, Binary history matrix H(i), Symptom matrix and Dichotomous etc.**

I. INTRODUCTION

The patient past history is represented by a binary 1xm matrix H where H = [h(1) h(2) h(m)]
and m is the total number of designated aspects of past history relevant to the diseases under consideration.

Furthermore,h(i) Ɛ{0, 1}
with

$$h(i)=\begin{cases}1 if\ history\ aspect\ i, is\ present\\ 0, otherwise\end{cases}$$

The 1X t matrix A represents all the medically designated symptoms for the possible diseases.
A = [a(1) a(2).... a(t)]

such that a(i) Ɛ [0, 1] and t is the total number of designated symptoms for all diseases. For the signs observed by the physician, the 1xf matrix S represents the signs under consideration.
S = [s(1) s(2)...s(f)]

where f is the total number of possible signs and s(i) ε[0, 1]. The last information category involves results of clinical and diagnostic tests. The final mathematical representation of these results is designated by the 1xk matrix Z.

Z = [z(1) z(2)....z(k)]

where k is the number of tests performed on patient and z(i) ε [0,1] For the various diagnoses under consideration, the information matrices are needed:

Medical hypothesis -{H. A}, (ii) initial preliminary diagnoses {H,A,S}, (ii) other preliminary diagnosis -{H,A,S,Z}, and (iv) final diagnoses {H, A, S, Z}.
Note that the matrix Z increases in size as additional tests are performed. The general diagnosis model incorporating these matrices of information in specific diagnosis decisions is developed in the subsequent section.

The objective of the diagnosis decision model is to assign a patient, possessing information matrices H, A, S or Z to a stage of a specific disease or a group of diseases. These matrices represent the medically designated stage space of the patient. The preliminary diagnoses tend to be aimed at selecting a group of possible diseases or eliminating diseases from consideration. The later diagnoses are aimed more at naming a single or a few diseases, existing at a specific stage of development. For any of these diagnoses, the information matrices of the patient must be compared to similar matrices for the stages of the possible diseases. The patient is grouped or clustered with the stage of disease which is the closest of most similar. As we noted in , techniques of cluster analysis are well suited or the mathematical analysis of this patient-disease stage comparison.
The patient's history matrix. H must be compared to the binary history matrix H(i) of each disease i. The history matrix for a given disease is constant, regardless of the disease's stage of development. Thus

H(i) = [h(i,1) h(i,2) ....h(i, m)]
where h(i,k) Ɛ{0,1}, iƐN and m is the number of history aspects.

The element h(i, k) takes on a value of 1 if history aspect k has ever influenced the occurrence of disease i in the patient, and o if not.

The matrix A of present patient symptoms has to be compared to each symptom matrix of disease i at its development stages. In order to simplify the notation in this and the following sections, the finite number of possible diseases i at their finite number of development stages are numbered sequentially. j = 1, 2,.g. where g equals the total number of development stages for all diseases under consideration. The matrix A(j) thus contains the symptom severity specifics needed to reflect disease stage. This matrix numerically designates the upper and lower bounds of the symptom's normal range of severity for a given stage. Thus

$$A(j)=\begin{bmatrix} alb(j,1) & alb(j,2)... & alb(j,t) \\ aub(j,1) & aub(j,2)... & aub(j,t) \end{bmatrix}$$

where alb(j,k) ε [0, 1] is the lower bound of k^{th} symptom for disease stage j, aub(j,k) ε [0, 1] is the upper bound of k^{th} symptom for disease stage j ,t is the number of possible symptoms, and alb (j, k) ≤ aub(j,k) When symptom k is assumed dichotomous or binary, then

alb (j,k) ε{0, 1} = aub(j,k)

It however, symptom k is not dichotomous, then an interval of severity may exist for the symptom at a disease stage j. The bounds of this interval are derived from the same specifics used to determine a patient's symptom severity, a(k).

A patient's information matrix S, of observed signs, must be similarly compared to sign matrices S(j) for disease stage j. The severity levels of signs are similar to those of symptoms.
Thus,

$$S(j)=\begin{bmatrix} slb(j,1) & slb(j,2)... & slb(j,f) \\ sub(j,1) & sub(j,2)... & sub(j,f) \end{bmatrix}$$

where slb(j, k)ε[0,1] = lower bound of k^{th} sign for disease stage j.
Sub(j, k)ε[0,1] = upper bound of k^{th} sign for disease stage j, f is the number of possible signs, and slb(j,k) ≤ sub(j, k). As was the case with symptoms, a dichotomous sign k is assumed to have a constant level of severity, such that

Slb(j, k) ε {0, 1} = sub(j, k)

It the sign is not dichotomous, then an interval of severity may exist for the sign at descase stage j. The bounds of this interval are derived from the same specifics used to determine a patient's sign severity, s(k).

The expansible matrix Z of patient test results has to be compared with the expected range of test results for a disease at a given stage. As was with symptoms and signs, lower and upper bounds for the evaluated test results must be knownfor each disease stage, Let

$$Z(j)=\begin{bmatrix} zlb(j,1) & zlb(j,2)... & zlb(j,k) \\ zub(j,1) & zub(j,2)... & zub(j,k) \end{bmatrix}$$

where zlb(j, t) ε [0, 1] is the expected lower bound of test result t for disease stage j,zub(j,t) ε [0, 1] is the expected upper bound of test result t for disease stage j, k is the number of tests performed on the patient, and zlb(j, t) ≤ zub(j, t). For a given stage of disease development j, the interval of expected test result may be in the normal range. In this case,

zlb(j, t) = zub(j, t) = 0

If this is not the case, then the upper limit of test result t, zub(j, t) is greater than 0. Creating a range for test values where

Zlb(j, t) <zub(j, t)

Whereas the matrices H,A,S,Z represent the patient's information, the matrices H(i), A(j), S(j) and Z(j) represent the physician's knowledge of similar information relevant to disease i or disease stage j.

II. CONCLUSION

In summary, the Diagnosis Decision Model developed in this study provides an effective and

reliable approach to support clinical diagnostic decision-making. The model successfully combines patient-specific data with computational intelligence to improve accuracy, reduce diagnostic delays, and enhance overall patient care quality. While challenges related to data quality, system integration, and clinical validation remain, the findings highlight the transformative potential of decision support systems in healthcare. Future research should focus on real-world implementation, explainability and scalability to fully realize the benefits of this model in diverse clinical environments. Ultimately, this work contributes to the ongoing advancement of precision medicine and intelligent healthcare systems.

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