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Disease Screening Model and Fuzzy Hierarchy Analysis for Frequently Occurred Diseases in Children

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Abstract

Diseases like common cold, influenza, dengue fever, respiratory syncytial virus (RSV), and hand-foot-and-mouth disease (HFMD) are very common in children because they have low immunity and cannot avoid the risk of contracting the disease. In addition, all of these five diseases exhibit similar types of symptoms. Sometimes, it is difficult to identify one disease from the others from those symptoms alone, which may lead to an outbreak. This work was a design and construction of a mathematical model and a fuzzy hierarchical analysis process for assisting in disease screening of common diseases with similar symptoms. Data on observable and self-measured patient symptoms were available in the screening process. The output from the screening process will be the probability of contracting the disease, which can be used in the screening process to isolate patients, reduce the spread of pathogens, and put the patient in the care of specialist expeditiously.

Keywords: FAHP; common cold; influenza; dengue fever; RSV infection; hand-foot-and-mouth disease.

1. Introduction

In general, immune system development in children, from birth to 7 years old, is still not complete. Some children have low immunity. Because of mischievous behaviors of children in this age, they are exposed to both viral and bacterial pathogens, the main causes of many diseases, and leads to easy contraction of infectious diseases. Survey data from the Department of Disease Control in Thailand [1] indicate that outbreaks of colds, influenza, dengue fever, respiratory syncytial virus (RSV), and hand-foot-mouth disease (HFMD) are frequently occurred in children.

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Common cold is a very common disease in both adults and children, especially infants. Infants can catch cold as often as 6 to 8 times a year because children have lower immunity than adults. In particular, children with allergies are at an increased risk of catching a cold, even a chronic cold with complications [1,2,3]. A common cold may manifest in symptoms similar to those manifested by influenza. The difference is that, usually, the most common symptoms of common cold are stuffy nose, runny nose, cough, sneezing, and itchy throat, but rarely high fever and muscle pain.

Influenza is an acute respiratory tract infection. Two types of viruses, Influenza A and B, cause the disease. Influenza viruses infect the lining of the upper respiratory tract and the nose and throat. It can spread to the bronchi and lungs [1,2,3,4]. People contracted with influenza should be treated differently from people contracted with common cold because influenza patients frequently develop more complications. Symptoms are generally more severe and last much longer than common cold. If influenza patients can be identified correctly among patients with common cold, the special care given to these high-risk patients will improve.

Dengue hemorrhagic fever - DHF is a dengue viral infection. Its first outbreak in Thailand was in 1958, which later spread to other countries in tropical Asia. Dengue hemorrhagic fever occurs mainly in children under 15 years old and is generally not fatal. However, some cases are severe and cause an anaphylactic shock that may lead to death [5,6].

Respiratory Syncytial Virus-RSV is a type of virus that causes both upper and lower respiratory tract infection. The disease can infect both children and adults, but most often occurs in infants under 3 years old. RSV can be transmitted through various kinds of body fluids such as mucus, saliva, aerosol from coughing, sneezing, and especially from direct contact. During the first 2 to 4 days of infection, the symptoms are similar to common cold such as mild fever, coughing, sneezing, and runny nose. As the disease progresses, inflammation of the lower airways follows, leading to bronchitis, laryngitis, and pneumonia. Some patients may develop even more severe symptoms. Currently, there is no drug that can destroy RSV directly. In general, treatments are for managing harmful symptoms, such as treatments of antipyretic medication, cough suppressant, and bronchodilator spray as well as “knock on lungs” and suctioning of mucus [7].

Over the past 10 years, in Thailand and other countries in East and Southeast Asia, several widespread outbreaks of hand, foot and mouth disease-HFMD have occurred. Many deaths from neurological complications have been reported. Most of the patients were infants under 5 years old. Although there is no specific treatment for this disease, a correct diagnosis can prompt a proper symptomatic treatment in the early stages of the disease, increasing the survival rate and mitigating severe complications that may result in disability. HFMD is caused by several species of enteroviruses. The disease is often found in infants and children. Most infected people do not have any symptoms or may experience very mild symptoms such as mild fever, headache, nausea, and aches. These symptoms generally appear for 3-5 days and disappear on their own. However, some may develop severe symptoms, depending on the type of the infecting virus [8,9].

Cold, influenza, RSV, dengue and HFMD are common pandemic diseases among children as they usually stay closely together in a large group in schools and shelters. Children in this age are often unable to protect

themselves or avoid germs. The danger of this inability is that some diseases have similar symptoms and are difficult, if not impossible, to identify the right one. Some diseases lead to more serious illness. If not treated in a timely manner, some diseases can cause death, such as dengue fever. The similar nature of the symptoms of those diseases, coupled with no in-depth inquiry and lack of follow-up, may result in misdiagnosis. Advantages of being able to primarily identify the right disease are such as reduction of waiting time to see a doctor and lower requirement on sufficient number of medical personnel and specialists as well as being able to accommodate a higher number of patients. Oftentimes, time constraints in hospital operations affect data integrity and the descriptions of symptoms, leading to misdiagnosis and mismanagement. A primary means for identifying a disease among those with similar symptoms is of utmost value for dealing with these issues. In recent past, there have been not much studies on infectious disease diagnosis that employed fuzzy logic, most of them applied it in the fuzzy rules-based approach. The authors in [10] conducted a multicriteria decision analysis (MCDA) using a weighted linear combination (WLC) to assess dengue risk. The authors in [11] applied fuzzy logic approach for infectious disease diagnosis. The authors in [12] applied decision making and fuzzy sets theory to evaluate the healthcare and medical problems. All of them different from this research as such, we apply a scoring model and fuzzy hierarchy analysis to create disease screening model for frequently occurred diseases in children. The authors were interested in applying the concept of fuzzy hierarchical analysis in the decision-making process and constructing a mathematical model for screening common pediatric respiratory diseases. We expected that the constructed model that would allow physicians to come up with a correct diagnosis faster. In addition, the authors expected that the constructed model would enable faster and more accurate early screening and diagnosis so that treatments can be provided in a timely and well-targeted manner. Patients will recover faster, and the spread of disease will be halted more rapidly. Moreover, if this screening and diagnosis model is developed into computer programs for smart robots, the robots can reduce the burden of many healthcare workers and support less direct contact between workers and patients, preventing further spread of an outbreak.

2. Research objective and scope

The objective of this work was to design and construct a mathematical model for early diagnosis of common pediatric diseases and primary screening of patients who may contract one of those diseases. The scope of this research was to consider a group of five respiratory diseases frequently occurring in children: cold, influenza, RSV, dengue, and hand-foot-and-mouth diseases. Information about each disease and its symptoms were obtained from interviews, symptom data collection, histories of diagnosis and treatment from 4 specialists, and studies referenced in some diagnostic manual textbooks [1:9]. Diagnostic data, expert interviews, relevant research and data from diagnostic manuals, and fuzzy hierarchical analysis processes were considered or applied in the design of the screening and diagnosis model. The key steps of this work were the following.

1) Collecting data on symptoms of common pediatric diseases from diagnostic textbooks and professional diagnosis histories.

2) Organizing the data and use them to define the screening criteria.

3) Applying the Fuzzy Analytics Hierarchy Process (FAHP) to the data pertaining to the level of expertise of each specialist. The results are the weight value of each specialist.

4) Designing a screening and diagnosis model and evaluating it against the patient's symptom data.

5) Importing the patient's symptom data in the checklist marked by the patient and processing them into output of the probability of contracting each disease.

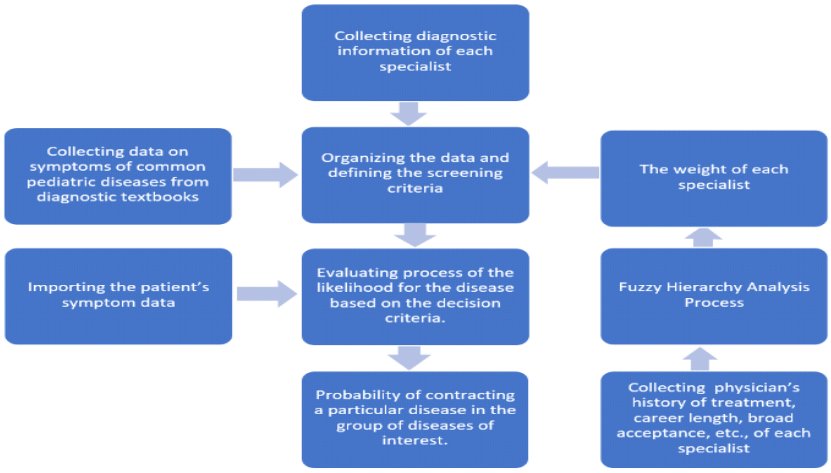

Figure 1: Conceptual framework of screening and diagnosis model.

3. Preliminaries

3.1 Fuzzy Hierarchy Analysis Process

Fuzzy hierarchy analysis process is a mathematical decision-making process capable of making multi-criteria decisions. It has been widely used to solve problems in diverse fields [13:]. Such decision criteria can be either quantitative or qualitative. In a fuzzy hierarchy analysis process, a preference is stored in a pairwise comparison matrix, which is a reciprocal matrix, and it is assigned a numerical value in the range of [0,1]. The meanings of every preference level are shown in Table 1.

Table 1: Meanings of preference levels.

Fuzzy paired interval scale	Definition
0.5	Equally importance
(0.5, 0.6)	Weakly importance
[0.6, 0.7)	Moderately importance
[0.7, 0.8)	Strongly importance
[0.8 ,0.9)	Very strongly importance
[0.9, 1]	Extremely importance

In this section, an additive reciprocal preference relation and its consistency are defined as follows:

Definition 1. Let $X = \{x_1, x_2, x_3, ..., x_n\}$ and $u : X' X \to [0,1]$ be a relation on $X' X$. If $R = \left(r_{ij}\right)_{n}$ which

$r_{ij} = u(x_i, x_j)$, $i \neq j$; $r_{ij} = 0.5$, $i = j$ for all $i, j = 1,...,n$, then R is called a fuzzy comparison matrix.

Definition 2. Let $R = [r_{ij}]_n$ be a fuzzy comparison matrix. Then R is said to be an additive reciprocal matrix if $r_{ij} + r_{ji} = 1$ for all $i, j = 1,...,n$.

Definition 3. Let $R = [r_{ij}]_n$ be a fuzzy-reciprocal matrix. Then matrix R is said to be an additive consistency matrix if there is a weighted vector $W = \langle w_1, w_2, ..., w_n \rangle$ such that $\sum_k^n w_k = 1$ and $r_{ij} = w_i / (w_i + w_j)$ for all $i, j = 1,...,n$.

Let $R = [r_{ij}]_n$ and $A = [a_{ij}]_n$, $a_{ij} = r_{ij} / (1 - r_{ij})$. Note that R is a fuzzy additive-reciprocal matrix if and only if A is a multiplicative reciprocal matrix (i.e., $a_{ij} = 1/a_{ji}$). From Definition 3, R is the additive consistency matrix if A is the multiplicative consistency matrix. As a result, $W = \langle w_1, w_2, ..., w_n \rangle$ is the weight vector of A only if W is the weight vector of R. Therefore, we can calculate the weight vector of the fuzzy additive-reciprocal matrix R by calculating the weight vector of multiplicative consistency matrix A. The procedure for calculating the weight vector of A involves the following definitions and theorems.

Theorem 4. Suppose that $l_1,...,l_n$ are the eigenvalues of A and $l_{\max} = \max_k l_k$. If $l_{\max} = n$, then A is a consistency matrix.

Definition 5. The consistency index (CI) of a comparison matrix A can be expressed as

$$CI = \left| \frac{l_{\max} - n}{n - 1} \right|. \qquad (1)$$

The consistency ratio (CR) of a comparison matrix A can be expressed as

$$CR = \frac{CI}{RI}, \qquad (2)$$

where RI is the Random consistency index. Some values of RI for matrices of different sizes are shown in Table 2.

Table 2: Random consistency index of different-sized matrices.

Matrix size	1	2	3	4	5	6	7	8	9	10
RI	0	0	0.58	0.90	1.12	1.24	1.32	1.41	1.45	1.49

Note: A is a consistency matrix when $CR = 0$. Since it is difficult to construct a consistency matrix for $3' 3$ matrices and larger, it is agreeable to accept a comparison matrix with a CR close to zero, which is called an acceptable consistency matrix. Generally, a comparison matrix is considered an acceptable-consistency matrix when CR does not exceed 10%.

3.2 Calculation of weight vectors and verification of consistent property

Given a fuzzy reciprocal matrix $R = \left[r_{ij} \right]_{n \times n}$, the weight vector of R can be calculated by applying a normalization technique with some additional steps. Let us call it Process (C):

<u>*STEP-C1)*</u> Create a matrix $A = \left[a_{ij} \right]_{n \times n}$, where $a_{ij} = r_{ij} / (1 - r_{ij})$.

<u>*STEP-C2)*</u> Calculate the weight vector $W = \langle w_1, w_2, ..., w_n \rangle$ from the matrix A by the formula below,

$$w_i = \frac{1}{n} \left(\sum_{j=1}^{n} \frac{a_{ij}}{\sum_{k=1}^{n} a_{kj}} \right). \tag{3}$$

<u>*STEP-C3)*</u> Calculate the consistency index, CI, from the formula $CI = \left| \frac{l_{\max} - n}{n - 1} \right|$ when

$$l_{\max} = \sum_{k=1}^{n} \left(w_k \sum_{k=1}^{n} a_{ik} \right). \tag{4}$$

<u>*STEP-C4)*</u> Calculate the consistency ratio CR as the formula (2).

If the consistency ratio CR is less than or equal to 10%, R is accepted as an acceptable consistency matrix. On the other hand, if CR is higher than 10%, R is rejected as an acceptable fuzzy consistency matrix.

4. Model of the Screening Process

In this work, a model of primary disease screening process was constructed by applying fuzzy hierarchy analysis process. The screening process involves the following steps. Let us call it Process (S).

<u>*STEP-S1)*</u> Determine the disease group to be screened.

Assume that $D = \{D_1, ..., D_m\}$ represents the group of m diseases. In this work, the disease group that occurred most frequently in children was selected for the reasons mentioned above.

<u>*STEP-S2)*</u> Collect all symptoms of diseases from diagnosis textbooks, interviews and history of diagnosis from

specialists.

Suppose $E = \{E_1, ..., E_n\}$ represents the set of n physicians who specialize in the diagnosis and treatment of group D. Define

$$c_k = \begin{cases} 1, \text{ if the symptom } k^{th} \text{ is presented} \\ 0, \text{otherwise} \end{cases}, \quad (5)$$

to be the symptom index k of each disease.

STEP-S3) Organize the information on symptoms of each disease and the diagnosis information from a medical professional.

STEP-S4) Evaluate the level of each physician's expertise. (In practice, this may be assessed based on the physician's history of treatment, career length, broad acceptance, etc. The evaluation can even be based on using a secret expert assessment strategy). In this work, the expertise level was evaluated based on the career lengths of every participating physician, which were readily accessible to the authors.

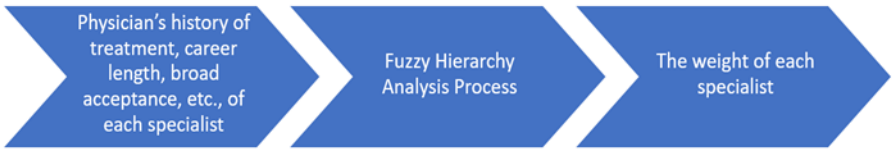

Figure 2: Expertise Assessment Process.

STEP-S5) Create a pairwise comparison matrix to compare each physician's expertise from the data obtained from STEP-S4).

Based on the information in STEP-S4), construct a reciprocal fuzzy matrix R, which is a comparison matrix of each expert $E_i, i = 1, ..., n$. The value of r_{ij} is in accordance with Table 1.

STEP-S6) Calculate the weight of each medical professional from a comparison matrix of expertise using a fuzzy hierarchical analysis process.

Let $W = \langle w_1, w_2, ..., w_n \rangle$ be a weight vector, and w_i, $i = 1, ..., n$ represents the weight of the expert $E_i, i = 1, ..., n$.

STEP-S7) Design decision criteria for disease screening process.

STEP-S8) Import patient data by checking the symptom list.

Practically, this may include other risk factors contributing to the disease, such as contact or close proximity to the sick or people living in an epidemic area, etc. Imported patient symptoms or considered risk factors (D_{input}) were recorded. Each recorded symptom was accompanied with an index c_k that indicated the presence or absence of the symptom.

STEP-S9) Evaluate the likelihood of the disease based on the decision criteria, weight of expertise, and input from step 8). The results are the probability of contracting the disease.

5. Numerical Example

In this section, we present an example of screening and diagnosis model for five diseases that occur frequently in children: common cold, influenza, RSV, HFMD, and Dengue. Diagnostic data obtained from interviews with four medical professionals and from the diagnostic manual were used to create the model. We demonstrate the process for calculating the probability of each disease by importing a patient's hypothetical data. Let us call it Process (S).

STEP-S1) We determine the disease group that occurs frequently in children.

For this example, let $D = \{D_1,...,D_5\}$,where D_1 represents common cold , D_2 represents influenza , D_3 represents RSV, D_4 represents HFMD, and D_5 represents dengue.

STEP-S2) Collect all symptoms of the diseases from diagnosis textbooks, interviews, and history of diagnosis from specialists.

In the set of specialists, $E = \{E_1, E_2, E_3, E_4\}$, E_1, E_2 , E_3 and E_4 represented the four specialists, and $c_k, k = 1,...,18$ represented the k^{th} symptom (see Table 3). Each specialist, E_1, E_2 , E_3 and E_4 , examined the patient's symptoms by oral interview and assigned a value of 0 or 1 to each c_k , where 0 indicated the absence of the symptom, while 1 indicated its presence. The values assigned to every c_k , $k = 1,...,18$, by every physician are tabulated in Table 4.

STEP-S3) Organize information on symptoms of each disease and diagnosis information from a medical professional. Information on the symptoms of every disease and the opinions of every specialist on each symptom are tabulated in Table 3 and 4. All information and calculations were stored and processed by Microsoft Excel computer program.

Table 3: Symptoms and assigned symbols**.**

Symbol	Symptom	Symbol	Symptom
c_1	Nasal symptoms such as stuffy, runny or mucus nose	c_{10}	Fatigue
c_2	Have a fever of less than 38 degrees or no fever	c_{11}	Severe and noisy coughing
c_3	Coughing or sneezing	c_{12}	Wheezing, difficulty in breathing
c_4	Sore throat	c_{13}	Clear bumps on the tongue, gums, cheeks, palms and soles of the feet.
c_5	A high fever with a temperature of 38 degrees or higher	c_{14}	Anorexic
c_6	Headache	c_{15}	Vomiting
c_7	Body aches	c_{16}	Red spots or bruises on the body
c_8	Pain in the eye socket area	c_{17}	Nose bleed
c_9	Noisy breathing	c_{18}	Scurvy

Table 4: Diagnosis of each disease by each medical professional.

E_k	D_k	c_1	c_2	c_3	c_4	c_5	c_6	c_7	c_8	c_9	c_{10}	c_{11}	c_{12}	c_{13}	c_{14}	c_{15}	c_{16}	c_{17}	c_{18}
E_1	D_1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	D_2	1	0	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0
	D_3	1	1	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0
	D_4	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
	D_5	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1
E_2	D_1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	D_2	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0
	D_3	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
	D_4	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
	D_5	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	1	1	1
E_3	D_1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	D_2	0	0	0	0	1	1	1	0	0	1	1	0	0	0	0	0	0	0
	D_3	1	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0
	D_4	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
	D_5	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	1	1	1
E_4	D_1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	D_2	1	0	0	1	1	1	1	0	0	1	1	0	0	0	0	0	0	0
	D_3	0	1	1	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0
	D_4	0	1	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0
	D_5	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	1	0	0

STEP-S4) Evaluate each medical professional's expertise. (In practice, this may be assessed based on the history of treatment, qualification, life, research results, broad acceptance, etc., or by using a secret expert assessment strategy).

This work evaluated the level of expertise of the specialists (pediatricians) from the length of their career. However, in a typical usage scenario, the level of expertise can be determined from the specialist's treatment history or level of satisfaction toward the treatment or any other reasonable metrics. In this work, the levels of expertise from pairwise comparison were assigned a numerical value in the range of $[0,1]$.The significance of the numerical value of this level is as described in Table 1, and the levels of expertise from pairwise comparison of the four specialists are listed in Table 5.

STEP-S5) Create a pairwise comparison matrix to compare each physician's expertise from the data obtained from step 4).

Based on the information in STEP-S4), a reciprocal fuzzy matrix R which is the comparison matrix of each physician $E_i, i = 1,...,4$ is constructed. The value of a constructed r_{ij} depended on the preference level listed in Table 1. The levels of expertise from pairwise fuzzy comparison are shown in Table 5.

Table 5: Comparison matrix of the physician's expertise by career length.

E_k	E_1	E_2	E_3	E_4	w_k
E_1	0.500	0.750	0.375	0.330	0.200
E_2	0.250	0.500	0.167	0.143	0.067
E_3	0.625	0.833	0.500	0.450	0.333
E_4	0.670	0.857	0.550	0.500	0.400
		CI		0.0000149	
		RI		0.9000000	
		CR		0.0000166<0.1	

STEP-S6) Calculate the weight for each specialist from the comparison matrix of expertise using a fuzzy hierarchical analysis process, following Process (C). The weights for every specialist are shown in the last column of Table 5 (the column with green background).

STEP-S7) Design decision criteria for disease screening process.

From the primary diagnosis information shown in Table 4 and let $D_j, j = 1,...,5$, represents a piece of diagnosis information, calculate the values of every parameter used in the screening criteria by the CK steps below.

CK-1) Construct c_k^{new} for each c_k, $k = 1,...,18$,

$$c_k^{new} = c_k \prime \; n_{c_k}, \tag{6}$$

where n_{c_k} is the number of physicians whose opinion was that c_k was an important symptom of that disease.

CK-2) Calculate the weight for each symptom $c_k, k = 1,...,18$ and express $SC_k^{D_j}$ as

$$SC_k^{D_j} = \sum_{l=1}^{4} w_l c_k^{new} . \quad (7)$$

CK-3) Normalize $SC_k^{D_j}$, $k = 1,...,18$, to $NSC_k^{D_j}$ that is used in the calculation of the probability of contracting D_j.

$$NSC_k^{D_j} = \frac{SC_k^{D_j}}{\sum_{k=1}^{18} SC_k^{D_j}} \quad (8)$$

Note: An example of c_k^{new}, $SC_k^{D_1}$, $NSC_k^{D_1}$ calculation for disease D_1 are shown in Table 6, while $c_k^{new}, SC_k^{D_j}$, $NSC_k^{D_j}$ for every disease are shown in Table 8.

Table 6: Example of c_k^{new} calculation for disease D_1 (for convenience c_k^{new} is represented by c_k).

D_k	E_k	w_k	c_1	c_2	c_3	c_4	c_5	c_6	c_7	c_8	c_9	c_{10}	c_{11}	c_{12}	c_{13}	c_{14}	c_{15}	c_{16}	c_{17}	c_{18}
D_1	E_1	0.200	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_2	0.067	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_3	0.333	4	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_4	0.400	4	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	$\sum SC_k^{D_1}$ =10.932	$SC_k^{D_1}$	4	4	0.733	0.733	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	$\sum NSC_k^{D_1}$ =1	$NSC_k^{D_1}$	0.366	0.366	0.134	0.134	0	0	0	0	0	0	0	0	0	0	0	0	0	0

STEP-S8) Import patient data (D_{input}) according to their symptoms in the symptom checklist (Table 3).

Example of checklist of patient's symptoms (D_{input}) and assigned score values of index c_k, say c_k^{input}, are shown in Table 7.

Table 7: Example of checklist of patient's symptoms (D_{input}) and assigned score values of index c_k .

	Symptom	c_1	c_2	c_3	c_4	c_5	c_6	c_7	c_8	c_9	c_{10}	c_{11}	c_{12}	c_{13}	c_{14}	c_{15}	c_{16}	c_{17}	c_{18}
D_{input}	Check list	1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0

<u>*STEP-S9)*</u> Evaluate the likelihood of the disease ($Prob(D_j)$) based on the decision criteria ($NSC_k^{D_j}$).

From the weights obtained in *STEP-S8)*, calculate the probability of contracting the disease D_j, $Prob(D_j)$, by the formula below,

$$Prob^{D_j} = \sum_{k=1}^{18} \left(c_k^{input} \cdot NSC_k^{D_j} \right). \qquad (9)$$

The calculated values of $Prob(D_j)$, $j = 1,...,5$ and the probability of contracting a particular disease in this group of diseases for the imported patient data D_{input} are listed in Table 8.

Table 8: Example of calculation of screening criteria and $c_l^{new}, l = 1,...,18$, of disease D_j, $j = 1,...,5$; yellow fill rows list the weight of every criterion (symptom), $c_l, l = 1,...,18$, for calculating the probability of contracting a certain D_j. (For convenience c_k^{new} is represented by c_k).

	E_k	w_k	c_1	c_2	c_3	c_4	c_5	c_6	c_7	c_8	c_9	c_{10}	c_{11}	c_{12}	c_{13}	c_{14}	c_{15}	c_{16}	c_{17}	c_{18}
D_1	E_1	0.200	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_2	0.067	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_3	0.333	4	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_4	0.400	4	4	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	$SC_k^{D_1}$	10.932	4	4	0.733	0.733	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	NSC_i	1	0.366	0.366	0.134	0.134	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	D_{input}		1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0
	Prob	0.634	0.366	0	0.134	0.134	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_1	0.200	2	0	1	0	4	3	4	1	0	0	0	0	0	0	0	0	0	0
	E_2	0.067	0	0	0	2	4	0	4	0	0	0	0	0	0	0	0	0	0	0

	E_3	0.333	0	0	0	0	4	3	4	0	0	2	2	0	0	0	0	0	0	0
D_2	E_4	0.400	2	0	0	2	4	3	4	0	0	2	2	0	0	0	0	0	0	0
	$SC_k^{D_1}$	12.332	1.200	0	0	0	4	0	4	0.200	0	1.466	1.466	0	0	0	0	0	0	0
	NSC_i	1	0.097	0	0	0	0.324	0	0.324	0.016	0	0.119	0.199	0	0	0	0	0	0	0
	D_{input}		1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0
	Prob	0.864	0.097	0	0	0	0.324	0	0.324	0	0	0.119	0	0	0	0	0	0	0	0
	E_1	0.200	2	3	0	0	0	0	0	0	3	0	3	4	0	0	0	0	0	0
	E_2	0.067	0	3	0	0	0	0	0	0	0	0	3	4	0	0	0	0	0	0
	E_3	0.333	2	0	0	0	0	0	0	0	3	0	3	4	0	0	0	0	0	0
D_3	E_4	0.400	0	3	1	1	0	0	0	0	3	0	0	4	0	0	0	0	0	0
	$SC_k^{D_3}$	13.264	1.066	2.799	0.400	0.400	0	0	0	0	2.799	0	1.800	4.000	0	0	0	0	0	0
	NSC_i	1	0.080	0.211	0.030	0.030	0	0	0	0	0.211	0	0.136	0.302	0	0	0	0	0	0
	D_{input}		1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0
	Prob	0.140	0.080	0	0.030	0.030	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	E_1	0.200	0	4	0	0	0	0	0	0	0	0	0	0	4	3	0	0	0	0
	E_2	0.067	0	4	0	0	0	0	0	0	0	0	0	0	4	3	0	0	0	0
	E_3	0.333	0	4	0	0	0	0	0	0	0	0	0	0	4	0	1	0	0	0
D_4	E_4	0.400	0	4	0	0	0	0	0	0	0	1	0	0	4	3	0	0	0	0
	$SC_k^{D_4}$	10.734	0	4	0	0	0	0	0	0	0	0.400	0	0	4	2.001	0.333	0	0	0
	$NSC_k^{D_4}$	1	0	0.373	0	0	0	0	0	0	0	0.037	0	0	0.373	0.186	0.031	0	0	0
	D_{inpu}		1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0
	Prob	0.037	0	0	0	0	0	0	0	0	0	0.037	0	0	0	0	0	0	0	0
	E_1	0.200	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	4	3	3
	E_2	0.067	0	0	0	0	4	3	2	2	0	0	0	0	0	0	0	4	3	3
	E_3	0.333	0	0	0	0	4	3	0	0	0	0	0	0	0	0	1	4	3	3

D_5	E_4	0.400	0	0	0	0	4	3	2	2	0	0	0	0	0	0	0	4	0	0
	SC_k^D	16.201	0	0	0	0	4.000	2.400	0.934	0.934	0	0	0	0	0	0	0.333	4.000	1.800	1.800
	$NSC_k^{D_5}$	1	0	0	0	0	0.247	0.148	0.058	0.058	0	0	0	0	0	0	0.021	0.247	0.111	0.111
	D_{input}		1	0	1	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0
	Prob	0.435	0	0	0	0	0.247	0.148	0.058	0	0	0	0	0	0	0	0	0	0	0

Importing the symptom of a patient from the checklist of observable or measurable symptoms, shown in Table 6, led to the outcomes tabulated in Table 9 which indicated that the patient had an 86.4% probability of contracting influenza and 63.4 % probability of contracting common cold. With this indication, a primary action should be to isolate the patient from any communities to curb the spread of the disease and to provide patient with proper medical care immediately.

Table 9: Output of the approach showing the probability of contracting a particular disease in the group of the diseases.

Symbol	Disease	Probability (%)
D_1	Cold	63.4
D_2	Influenza	86.4
D_3	RSV	14.0
D_4	Hand, foot and mouth disease	3.7
D_5	Dengue	43.5

5. Application (Application program)

The screening model was constructed into a mobile application for the patient or the caregiver to use. It could also be developed into a piece of software for nursing robots to primarily screen the disease, reducing the risk of the disease spreading to the healthcare team. The mobile application design process is shown in Figure 3.

Figure 3: Step of Mobile application design process.

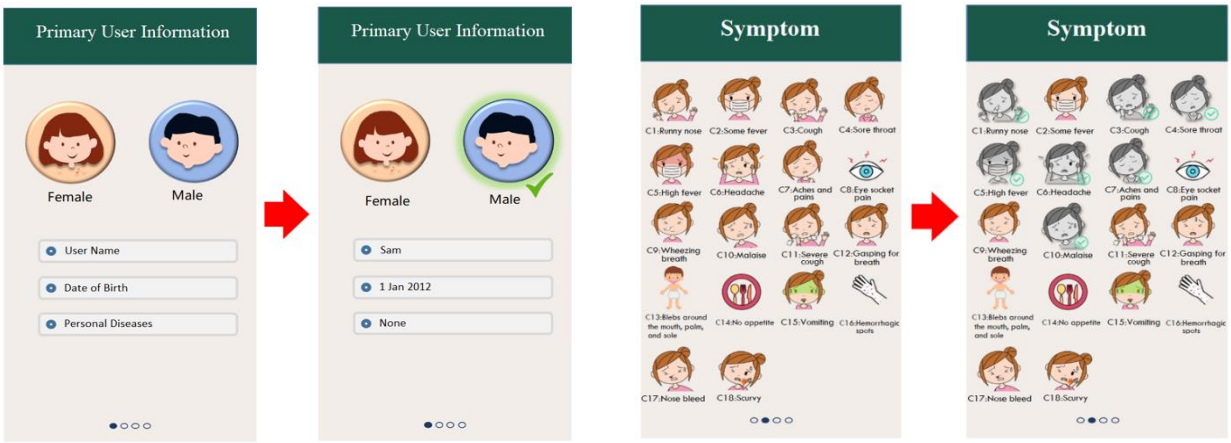

Figure 3: Step of Mobile application design process.

(4a): Screen showing Monitor primary data input page (4b): Symptom checklist

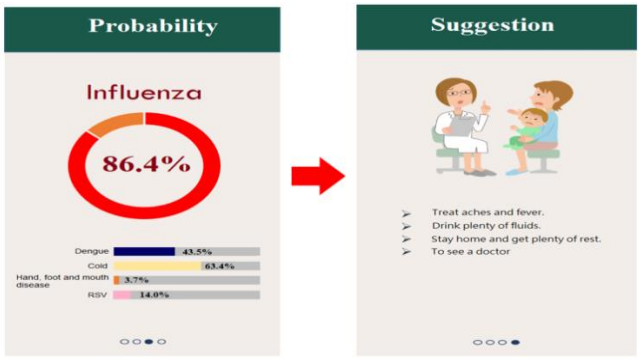

Figure 4: Prototype infographic of a mobile application for the patient or the caregiver.

(4c): (left) A monitor screen showing the output page of the probability of contracting common cold, influenza, RSV, HFMD, and dengue;(right) A monitor screen showing the suggestions and primary care for the patient.

6. Conclusion

This study constructed the screening model for primary diagnosis of a disease in a group of common, similar-symptom respiratory tract diseases from observable or measurable external symptoms, based on fuzzy hierarchical analysis. The disease group consisted of five diseases: common cold, influenza, respiratory syncytial virus (RSV), hand-foot-and-mouth disease (HFMD)**,** and dengue. The screening model was designed as a mobile phone application that the patient and the caretaker could use easily by themselves so that the patient would get proper and timely primary care and the disease would not be transmitted to communities and spread out. The physicians can use the data collected by the application as primary data for the final diagnosis, reducing medical examination time. However, the accuracy of the screening model depends on medical professionals' expertise and the number of medical professionals. The model is just a simple initiative model. There are model limitations that may affect the accuracy of the model's prediction results such as the number of specialists and physician expertise. In addition to the factors mentioned in the research, other factors affect the risk of getting sick such as, environmental health factors, close contact with patients, and certain behaviors that contribute to

infection. etc. Moreover, we can apply the knowledge of machine learning and data analysis to analyze the diagnosis history of physicians for each disease. The results of analysis data can be used as a knowledge base for improving and developing more accurate models. The authors hoped that this idea would be well-accepted and developed further into new software for nursing robots to screen and primarily diagnose the disease, which, on top of the mentioned benefits, would reduce the health care team workload, and more importantly, would reduce the need for direct contact between the patient and the health care team, thus reducing the risk of health care team contracting a disease from patients.

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