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# Effective Management of Conflict in Learning the Traditional Medicine-Based Medical Ontology

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**Abstract**– In this article, we focus on conflict management when learning traditional medicine. The traditional medicine is involved in almost all diseases that man can encounter using natural products from plant, mineral, animal. The aim is to lay a solid diagnosis in order to implement an effective treatment and minimize the risk of physical and social imbalance of patients. We particularly analyze the different techniques on the basis of visual semantic ontology in order to avoid similar indexing or conflict of a concept (dosages, therapeutic effects). We also analyze the influence of the consideration of the different parts of a query.

**Keywords**– Conflict, Traditional Medicine, Visual Ontology and Learning

## I. INTRODUCTION

TRADITIONAL medicine is the set of traditional knowledge based on the use of medicinal plants [1]. Since this medicine uses the traditional method, it is to better ensure the health using a technique based on visual ontology. Indeed, Ontologies are techniques that are used to define knowledge and are essential in the representation and use of data. An ontology is seen in the Artificial Intelligence (AI) as an explicit specification of a conceptualization. It consists of a set of semantic relations. In Computer Vision (CV) conceptualizations are composed of visual scenes (features, objects, relationships between objects) or events based on ontologies of a specific domain [2]. They are used in the medical field [3]. Generally, the purpose of using ontologies is to enable a dialogue, a cooperation between the system and the users in order not to handle disparately, the information on the computer. This is an excellent way of learning suited to a broad range of users of computers. The networking of computers has greatly facilitated this learning by new practitioners [4]. Indeed, computer science is involved in all areas of human activity especially in the field of education [5]. Since the 70s, many researches on improving the education system have been proposed [6]. Thus from the Programmed Teaching (PT) to Computer Aided Learning (CAL), this research has given rise to Learning Intelligently

Assisted by Computer (LIAC). With the introduction of Artificial Intelligence techniques, these LIAC gave birth to Computer Environment for Human Learning (CEHL) commonly known as Intelligent Systems Tutorials (ITS) in North American or English speaking backgrounds, introducing the concept of partnership between man and machine [6]. The main objective of this research is to improve the interaction between the user and the computer so that these exchanges are as natural as possible. This technological evolution on learning, allowed to propose educational applications typologies, often called Pedagogical Applications of Computer (PAC) [7]. Thus it is important that learners are able to use new technologies to improve patient health. It turns out that this new technology has shortcomings in its application in the sense that, identifying and finding the treatment of a disease with traditional medicine is very complex. This complexity is a source of conflict. What we mean by conflict is when a finite set of symptoms provided by a practitioner identifies several diseases instead of one. To avoid possible cases of conflict and facilitate learning by learners we implement a methodology based on the visual ontology of traditional medicine. This methodology will allow us to resolve cases of conflicts noted above. We begin by making a state of the art on medical ontologies. Then, a brief presentation of a case of conflict. Finally, the modeling approach proposed in this article will be conducted followed by a conclusion.

## II. RELATED WORK

In literature, ontologies have been the subject of many researches. These researches focus on various subjects including the learning of medicine that primarily interests us. Thus, KOUAME Appoh and others [11] propose the ontoMETRAD. It is a system based on visual ontology of traditional medicine that includes a variety of traditional knowledge relevant to a given disease. However, as to SEIBOGA, MEDITRA and MedTrad systems [12], [13], they ironically identify medicinal plants and then find their healing powers. Similarly they capitalize the African ancestral knowledge of herbal medicine and storage of knowledge

about diseases. The SADMEDTra [14] system, rests on intelligent agents and ontologies to diagnose and treat diseases and offers traditional healers, a better understanding of their treatments. Indeed, the author presenting this system seeks to understand the structure of knowledge, the evolution of this knowledge and the relationships between them. However, these systems do not provide learning techniques to new learners.

Alice Hermann and others [15] develop a device called TELEOS (Technology Enhanced Learning Environment for Orthopaedic Surgery). This device is part of the research on the development of ILE. It is also a transmission and knowledge acquiring environment "Vertebroplasty and ilio-sacral screw" also adopted in [16], [17].

As for Pierre Tchounikine [18], he mentions that the ILE are IT environments that align the interaction of human and artificial agents. To this end, he stipulates that the ILE provide access to training resources, and aim to follow and accompany learning. ITS systems (The Intelligent Tutoring Systems) of Renaudie [19] and Diag-K of Amina BAGHLI [5], pass judgment on the actions and responses of the learner. On this, they propose explanations based on ontological knowledge so that detected errors no more occur. For that they get their own representation of the problem to solve and are able to evaluate whether the aim of the exercise is reached or not.

Alice Hermann and others [15] present the UTILIS method (Updating Through Interaction in Logical Information Systems). It is a method to help creating new objects. UTILIS seeks similar objects to the new object by applying relaxation rules in its description.

Through all existing work presented above we can say that some of the cited authors give an explanation of the ontological structure of traditional medicine. But without deepening the learning mechanism of traditional medicine and others have spoken of learning in general; without mentioning the learning of traditional medicine through the visual ontology. Similarly few authors mention the problem of conflict management in traditional medicine. Our job will be to detect collision between diseases, realizing a learning algorithm to treat the symptoms.

### III. NEW LEARNING APPROACH BASED ON VISUAL ONTOLOGY

#### A) Approach

To solve the problem of conflict in traditional medicine, two cases of diseases (disease\_Z and disease\_P) were used (see picture of visual ontology below). The graph used in this example contains medicine, disease, medicinal plants and clinical signs semantically related to XML and RDF format. An RDF file is used to describe web resources to facilitate the automatic processing and interoperability of information.

Through this ontology, few data were obtained (see table below). These data are for indicative purpose. They do not refer to diseases. These are illnesses highlighted for illustration purpose. Here, a learner makes a request composed of some clinical signs presented with their percentages (see the following Table 1). The system returns

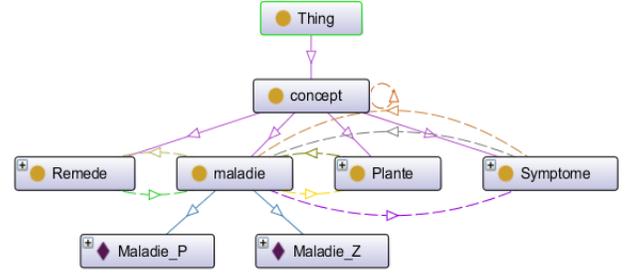


Fig. 1: Visual ontology of traditional medicine

Table 1: Overview of cases of conflict

Disease_Z	%	Disease_P	%
Headache	5%	Headache	5%
Fever	5%	Fever	5%
?	0%	Diarrhea	100%
Vomiting	100%	?	0%

two (2) diseases namely  $Z$  and  $P$ . Indeed, the system encountered in this specific case a conflict situation.

In order to identify the right disease, additional clinical signs will be subject to the application. Next section presents this modeling approach.

#### B) Modeling

##### 1) Assumptions of the problem

Let's consider  $S = (s_j = (t_j, v_j))_{j \in J}$  as all known symptoms of our learning base. Indeed, the learning base allows the construction of decision-making process with short response times for the realization of applications with high real-time constraints. Each symptom  $s_j$  is characterized by  $t_j$  a string that describes it and  $v_j$  a parameter that describes the importance of the symptom. This value is set by the user of the system according to a grading scale defined when setting up the system. We assume that this set is finite. Either  $|S| = \text{card}(S) = n$ . Either  $M = (M_r)_{r \in I}$  with  $I$  a finite set and  $\text{card}(I) = t$ . Each disease  $M_r$  is defined by a set of  $n$  symptoms. We define our learning basis from  $m$  samples representing the characteristic parameters (the probabilities of occurrence of the symptoms) of different diseases. So we have to consider the following matrices:

We will define the onset of symptoms matrix

$$X = \begin{pmatrix} (x_1)^T \\ (x_2)^T \\ \vdots \\ (x_m)^T \end{pmatrix},$$

In which  $x_i = (x_{ij}/1 \leq j \leq n)$  are vectors  $\in M_{n,1}(R)$ . Each  $x_{ij}$  is the probability of observation of the symptom  $s_j$  in the disease  $M_i$ . We define the matrix  $Y = (y_{ij})_{1 \leq i \leq m, 1 \leq j \leq n}$  in which each  $y_{ij}$  represents the degree of importance (according to a given classification scale from 1 to 5 for very low, low, medium, high, very high) symptom for the disease  $M_i$ .  $y_{ij} = 0$  if a symptom  $s_j$  is not part of the symptoms of disease  $M_i$ .

We also define the matrix  $Z = \begin{pmatrix} z_1 \\ z_2 \\ \vdots \\ z_m \end{pmatrix}$ ,

Wherein each  $z_i$  is an integer assigned to the disease characterized by the vector  $(x_m)^T$ . The system receives as input a subset  $\Lambda$  of all parts  $P(S)$  composed of a finite number of symptoms. Let's consider  $q = \text{card}(\Lambda) \leq \text{card}(S)$ . For our works we are going to put  $q \geq 3$ .

There is a conflict when the result of the output of our algorithm applied to the entire  $S$  identifies several diseases. To enable effective diagnosis, we can't allow such conflicts. We then propose our two-step algorithm to avoid potential conflicts. The proposed algorithm is in two steps:

- Detection of conflict
- Conflict Resolution

*i) Detection of the conflict*

From our training set let's define the binary matrix  $R = (R_{ij})_{1 \leq i \leq t, 1 \leq j \leq n}$  in which  $R_{ij} = 1$  if the symptom  $s_j$  is a symptom of disease  $M_i$ . 0 if it is not a symptom of that disease. In other words  $R_{ij} = 1$  if and only if there are indices  $p \in \{1, 2, \dots, m\}$  and  $f \in \{1, 2, \dots, n\}$  such that  $x_{pf} \neq 0$  and  $z_p = M_i$ . To detect the conflict, we seek to determine the cardinality of the set  $\xi = \{r \in I \mid \sum (R_{rj}, 1 \leq j \leq n) = q\}$ . These cases can occur:

- $\text{card}(\xi) = 0$ . In this case all the symptoms given do not match any disease. This corresponds to a case of aberration. Either the database does not contain this disease and that database is to be completed, or there is an inconsistency in the symptoms and it is impossible that such symptoms describe a disease. This case is not part of our area of study.
- $\text{card}(\xi) = 1$ . In this case the entered symptoms describe a single disease. There is no conflict; the index of the disease gives us the corresponding disease
- $\text{card}(\xi) > 1$ . We detected a conflict. We are then launching the conflict management process.

*ii) Conflict Management*

This step contains two phases. A phase of "treatment of missing data". The name of this phase is borrowed from the statistics that in this phase estimate from the collected data and data from the base a set of the most likely values to classify the data. Furthermore, we assume in the treatment phase of missing data that symptoms selected and the missing symptoms are mutually independent. This phase is followed by the classification phase of our symptoms from the K-means algorithm.

Let's consider  $\psi = i \in \{1, 2, 3, \dots, m\}$  such as  $z_i \in \xi$ . Let's modify the  $Y$  matrices by adding in the last line the values of symptoms  $s_j$  of  $S$ . Also, let's add in the last line of the matrix t the zero vector.

*2) Handling missing data*

The goal is to move from a space of  $q$  dimension to a space of larger size in order to fill a linear classifier. This binder is based on regression methods combined with a descending gradient algorithm. We can then indicate the value of these data with minimum error by the least squares method. The theoretical model consists of a family of functions  $f(x; \theta)$  of one or more dummy variables  $x$ , indexed by a family of unknown parameters. The least squares method is used to select among these functions, the one that best reproduces the experimental data. The method consists of the function  $f(x, \theta)$  construction which minimizes the sum of squared deviations of measures of the  $f(x; \theta)$  predictions. If, for example, we have  $N$  variables with  $i = 1, 2, 3, \dots, N$ , the parameters  $\theta$  "optimal" in the sense of the least squares method are those which minimize the amount

$$S(\theta) = \sum_{i=1}^N (y_i - f(x_i; \theta))^2 = \sum_{i=1}^N r_i^2(\theta)$$

Let's for that determine the following sets:  
 $\Upsilon$  All the symptoms of diseases of the learning base, whose index  $i$  is in  $Z$  and for which  $x_{ij} \neq 0$  and not belonging to  $S$ . Let's set  $\Omega = S \cup \Upsilon$  in which the symptoms are arranged in ascending order of their indices  $j$ . Given  $\Phi$  the largest of these indices. And  $\Upsilon = \Phi$ . We turn to the classification stage.

Given  $\Upsilon \neq \Phi$ . So we will seek to complete the missing data. Let's define the matrix

$$M = (m_{ij}) = \begin{cases} 1 & \text{si } i \in \psi, 1 \leq j \leq n \text{ et } x_{ij} \neq 0 \\ 1 & \text{si } i=m+1 \text{ et } \text{si } v_j \neq 0 \\ 0 & \text{sinon} \end{cases}$$

2 cases are then possible:

If  $\sum_{j=1}^n R_{\Phi j} = q$ , we move to the classification.

If  $\sum_{j=1}^n R_{\Phi j} > q$ , we need to handle missing data.

The following Table 2 illustrates the situation in which we are: the variable  $s_3, s_6$  et  $s_{11}$  represent the input parameters of our system. These variables are the only common to the

Table 2: Example of y matrix representing the degree of importance of symptoms in diseases of our learning base

	S <sub>1</sub>	S <sub>2</sub>	S <sub>3</sub>	S <sub>4</sub>	S <sub>5</sub>	S <sub>6</sub>	S <sub>7</sub>	S <sub>8</sub>	S <sub>9</sub>	S <sub>10</sub>	S <sub>11</sub>	S <sub>12</sub>	S <sub>13</sub>	S <sub>14</sub>	S <sub>15</sub>	S <sub>16</sub>
z <sup>(1)</sup>	2	2	1	0	1	0	2	0	3	4	0	2	1.5	5	0	0
z <sup>(2)</sup>	1.5	0	2	0	2.5	5	0	2	0	0	1	0	2.5	0	0	0
⋮																
z <sup>(10)</sup>	0	0	3	0	3	4	0	1	0	0	5	0	3.5	0	0	0
⋮																
z <sup>(25)</sup>	2.5	0	3.5	0	3.5	4	0	1.5	0	0	2.5	0	0	0	0	0
⋮																
z <sup>(50)</sup>	2	0	2	0	5	5	0	2	0	0	3	0	3	0	0	0
⋮																
?	?	0	3	0	?	4	0	?	0	0	2.5	0	?	0	0	0

diseases  $z_1, z_2, z_{10}, z_{25}$  and  $z_{50}$ , so we are in the presence of a conflict because  $\{s_3, s_6, s_{11}\}$  identify several diseases in our learning database (cf. Paragraph on conflict detection).  $\Upsilon = \{s_1, s_5, s_8, s_{13}\}$ . The disease  $z_2$  has the largest number of symptoms, so  $\Phi = 13$ . The last line of this table represents the values of the symptoms entered by the user, and we intend to predict from the known values of the learning base, missing values illustrated by question marks.

We will use the principle of linear regression with adjustment to better approximate the missing values. This will allow us to minimize the square error of the approximation made on the observed data. Missing data will be given by  $Y_{m+1j} = (\theta_j)^T X_{m+1}$  for  $j$  such as  $1 < j < \Phi$ . For that we will determine the optimal parameters  $\theta$  family and the vector  $X_{m+1}$  that minimizes the solution of the equation.

$$J(x_{m+1}, \theta_1, \theta_2, \dots, \theta_\phi) = 1/2 \sum_{(i,j):m_{ij}=1} ((\theta_j)^T x_i - y_{ij})^2 + \gamma/2 \sum_{k=1}^n (x_{m+1k})^2 + \gamma/2 \sum_{j=1}^{\phi} \sum_{k=1}^n (\theta_{jk})^2$$

For any  $i$  in  $M_1$  the algorithm is:

1 Initialization  $x_{m+1}, \theta_1, \theta_2, \dots, \theta_m$  by small random values

2 Minimization of function  $J(x_{m+1}, \theta_1, \theta_2, \dots, \theta_\phi)$

For  $j = 1, 2, 3, \dots, \phi$  and  $i = 1, 2, 3, \dots, m_z$

$$x_{m+1k} = x_{m+1k} - \alpha (\sum_{j:m_{ij}=1} ((\theta_j)^T x_i - y_{ij}) \theta_{kj} + \gamma x_{m+1k})$$

$$\theta_{kj} = \theta_{kj} - \alpha (\sum_{i:m_{ij}=1} ((\theta_j)^T x_i - y_{ij}) x_{ik} + \gamma \theta_{kj})$$

3 For  $j = 1, 2, 3, \dots, \phi$  such that  $y_{ij}$  is not defined, we set

$$y_{ij} = (\theta_j)^T x_i \text{ is the scalar product of vectors } \theta_j \text{ and } x_i$$

Note: The parameters are chosen very small. Typically values of 0.03 or 0.01. As for the parameter lambda, he was chosen typically between  $\frac{1}{10}$  and  $\frac{1}{5}$

3) Classification of the new data

From our learning base, we must determine to which class our new vector belongs to, that is to say determine  $z_{m+1}$ . To do this using the k-means algorithms, we will determine the centroids of classes and compare the distance between the

centroids  $C_k$  of our vector  $X_{m+1}$ . That is to determine the index  $k$  of  $M_1$  minimizing the distance  $d(X_{m+1}, C_k)$  with distance  $d$  taken as Euclidean distance. Specifically we aim to resolve  $\text{argmin}_{k \in M_1} d(x^{(1)}, C_{g(k)})$ . Where  $g(k)$  is the function with  $k$  element of  $M_1$  assigns a number between 1 and  $k$  in ascending order and  $g(i_s) = K$

The algorithm is the following:

- 
- 1 Rearrange by ascending order the elements and assign index and between
  - 2 Determine the k-means algorithm centroids Solve
- 

#### IV. CONCLUSION

In this study, we were interested in the resolution of conflicts arising from the learning of traditional medicine by users. To achieve our goals in the first instance, we reviewed the existing work of our predecessors in the field. As a contribution we have proposed a new approach to learning traditional medicine based on a visual ontology of said area. This ontology has allowed us to optimize the learning mechanism.

We aim, in addition, to extend the learning process several attractions for the same user and therefore to a higher number of symptoms, and to assess the impact on the size of the training data the one hand, and on the other hand search performance.

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