

An Advanced Decision Support System for Medical Diagnosis

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Abstract: This paper presents a clinical diagnosis support system which combines the advantages of Dempster-Shafer theory with Bayesian networks in order to simulate the uncertain medical reasoning. We propose a hierarchical structure using Dempster-Shafer at the upper level for evaluating more general hypothesis (disease groups) and Bayesian networks at the lower level for a more accurate analysis of specific diseases.

1. INTRODUCTION

In many areas, such as medical diagnosis, the main characteristic of information is uncertainty. Most of the human disease states are not sufficiently well understood. Medicine uses empirical knowledge about superficial associations between symptoms and diseases. Also, many data, symptoms, or diagnosis test results can be affected by incompleteness, subjectivity, and inaccuracy. The uncertainty can stem from the inability to evaluate the degree of truth of a hypothesis due to unreliable and incomplete information, or inconsistent knowledge.

The reasoning process in this unreliable and uncertain environment must be based on the main operators of intelligence - grouping (G), focusing attention (F), and combinatorial search (S).

The problem of diagnosis can be largely defined as the process of identifying a set of hypotheses that model completely the problem domain and finding that one hypothesis having the highest odds of matching the real state of the world. As was stated in the previous section, this process is usually empirical involving several cognitive strategies repeated in an iterative manner. In the attempt to build a system which follows as closely as possible the human reasoning pattern, we have tried to emulate such cognitive strategies as generalizing, focusing, and discriminating among hypotheses.

Generalizing and focusing imply that reasoning takes place at different levels of abstraction. An experienced physician begins to form hypotheses based on the most significant symptoms, and an initial physical examination and the patients past medical history. This is the first stage we considered, corresponding to the upper level of abstraction, where hypotheses have a generic meaning and refer to groups of diseases. This level is characterized by loosely connected diagnostic hypotheses which makes the discrimination among them easier. Then, in the context of these initial hypotheses, the clinician proceeds to the acquisition

of evidence in order to make a distinction between the groups of diseases and choose the most probable one. Once a group has been chosen, the reasoning process goes more in depth looking at the hypotheses within that particular group, at a lower level of abstraction. The hypotheses in this second stage of evaluation are more specific, and more strongly connected through the evidence they share. The clinical data is integrated with test results to estimate the likelihood of each diagnostic hypothesis.

In the attempt to develop a system which models the multi-stage process of medical diagnosis as well as the domain dependencies, we consider a hybrid hierarchical solution, which combines the Dempster-Shafer formalism with the Bayesian network approach in a two-level reasoning scheme.

The BN formalism is a popular choice for the development of medical applications, thanks to its close relation to causal models and its natural way of representing uncertainties when dealing with diagnosis, treatment selection, planning, and prognosis in medicine. However, a representation of the medical problem domain can result in large probability models which require great computational efforts and are not always tractable. There are numerous studies which tackle this problem using various approximate algorithms, such as the solution presented in Wemmenhove et al. [2007].

This paper presents a novel solution to the complexity problem, which is intrinsic to the hybrid architecture itself, by the layered mechanism of inference and the structured representation of knowledge. A partitioning of the problem domain is achieved by the use of granular computing concepts, such that the original diagnosis problem is decomposed into sub-problems of more manageable complexity and solved by a suitable combination of heuristic (Dempster-Shafer) and probabilistic (Bayesian networks) methods.

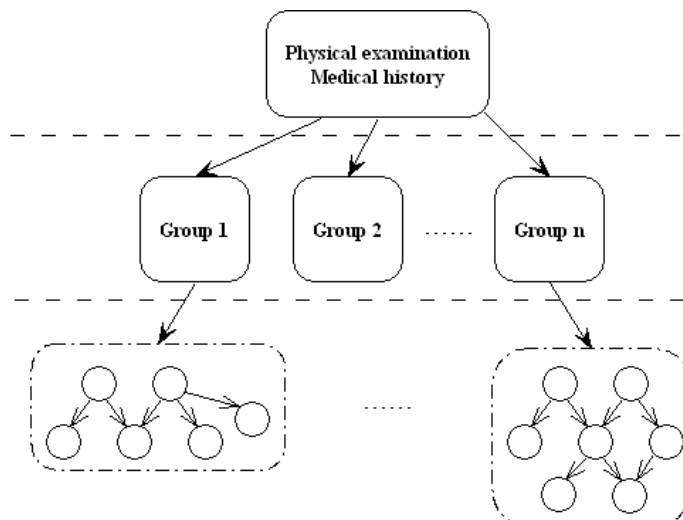


Fig. 1. Knowledge architecture

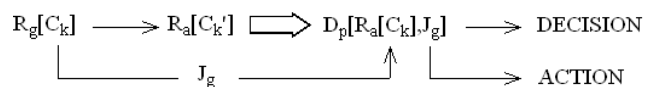
The paper is structured as follows: section 2 presents a granular knowledge architecture chosen so that the knowledge representation is coherent with the two levels of abstraction in the reasoning process. The structure and attributes of this system are described in more detail in Section 3. Section 4 describes a medical application exemplifying all aspects stated in the previous section. Finally, section 5 includes a brief evaluation of the solution proposed and a few concluding remarks on further issues to be solved.

2. MEDICAL KNOWLEDGE STRUCTURE

The medical knowledge architecture, according to the two-level reasoning model is presented in Fig. 1.

The hypotheses grouping idea has emerged in the attempt for the different levels of abstraction in the reasoning process to be reflected in a corresponding, layered knowledge representation of the problem domain. Grouping allows narrowing the search-space of primary hypotheses to manageable dimensions by identifying the strongest similarity patterns among manifestations (symptoms).

To build the model we have used a bottom-up approach, starting from the finest granulation of data (Yao [2004]) (all symptoms and hypotheses) and generalizing up to a coarser granulation (groups of hypotheses) through offline procedures of clustering. If we introduce a representation of knowledge for Grouping and Focusing attention as a $R_g[C_k]$ and $R_a[C_k]$ it is possible to define a Decision-making process as:



A cost function, J_g , was introduced in the above reasoning chain to obtain an optimum decision by a search procedure. The operators G , F , S , are applied to different knowledge categories C_k , and define an optimum decision

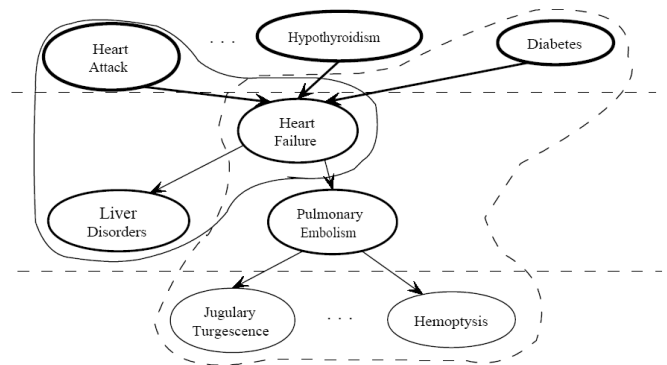


Fig. 2. Example of causal interrelations among hypotheses by selection based on J_g value. Therefore, different procedures can be used to implement the G , F , S operators on the different levels of abstraction.

We examined two clustering methods, hierarchical (Dandrade [1978]), (Salvador and Chan [2004]) and Fuzzy CMeans (FCM) clustering (Albayrak and Amasyali [2003]), which we consider more appropriate for medical diagnosis. The first executes a sharp classification in which each object is either assigned to a class or not, but permits the choice of the degree of generality according to medical experience. The latter can be considered closer to the medical reasoning as it allows objects to belong to several classes at the same time, but with different degrees of membership.

Each group will be defined at the bottom level (lowest level of abstraction) by a causal (Bayesian) network. Considering that the interrelations among the variables of the network are causal, from the medical point of view we obtain several types of variables: diagnostic hypotheses which represent primary causes, diagnostic hypotheses corresponding to profound pathological manifestations or complications of the primary hypotheses, as well as symptoms/signs/relevant tests. A diagnostic hypothesis may have multiple causes, while also affecting several organs (see Fig. 2).

3. DIAGNOSIS SUPPORT SYSTEM STRUCTURE

As presented in Fig. 3, the structure of the Decision Support System (DSS) for medical diagnosis (Dumitrache [2007]) is hierarchical organized and includes a Dempster-Shafer inference module and a Bayesian inference module.

3.1 Dempster-Shafer Module

The Bayesian approach has regained the attention of the AI research community, being considered most appropriate to simulate uncertain reasoning. However, it requires a large amount of probabilistic data, not merely for each piece of evidence, but also for the interrelationship of the evidences with diseases, which is difficult to obtain not only statistically, but also subjectively. As the level of generality increases, the estimation of probabilistic data becomes more and more difficult. This is the main reason why we have chosen the Dempster-Shafer formalism

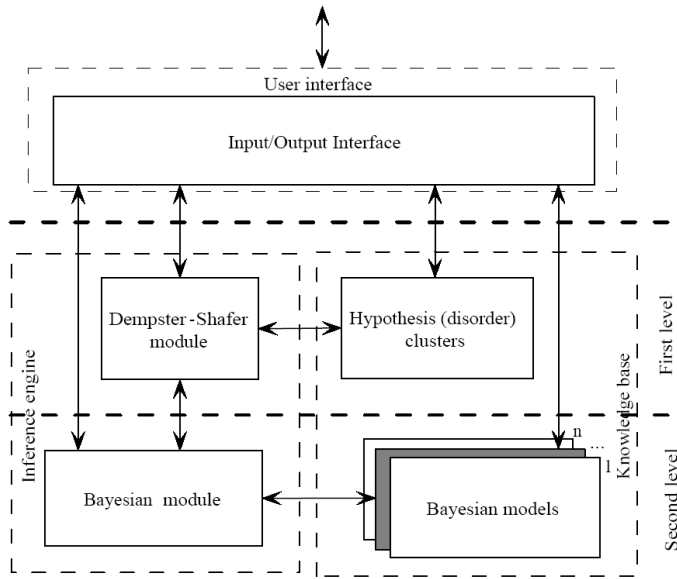


Fig. 3. DSS Structure

(Shafer [1976]) for the assessment and combining of belief at level 1 (high generality - multiple clusters of elementary hypotheses), and also because at this level of generality the clusters can be considered independent.

Another advantage of the Dempster-Shafer theory is that it permits the allocation of belief not only to singleton, but also to subsets of hypothesis (Dumitrache [1998]).

The belief module contains two components: a static component, which contains apriori belief, implemented by a belief list, and a dynamic component for belief combination induced by several pieces of evidence. An example of the structure of the belief list is given in 1. Belief management, the Dempsters rule of combination: $m_{12}(A) = \sum_{X \cap Y = A} m_1(X)m_2(Y)$ was implemented using an algorithm based on the first Mobius transform (Kennes and Smets [1990]).

$$[(e_1, G_1, 0.3); \dots (e_j, G_i \cup G_k, 0.5)] \quad (1)$$

where A is an element of boolean algebra (Ω) derived from the universe of discourse $\Delta = \{G_1, \dots, G_k, \dots, G_n\}$, for example $A = \{G_1 \cup G_i\}$. $m_i(A)$ is the mass (basic probability assignment) derived from the evidence E_i , for example $E_i = Edema$. X and Y are elements of which meet the condition $X \cap Y = A$.

In an interactive manner, the system presents the possible evidence, asking the user if it is available for the case being studied. When the required evidence matches with the data provided by the user, the inference can be realized - the system displays the hypotheses (groups) and unions of hypotheses supported by this one and the corresponding beliefs. The user has the opportunity to enter a new value for the belief, or let the value provided by the system unchanged. In order to update the beliefs values according to the new available evidence, the program gives the control

to the Dempster-Shafer module.

3.2 Bayesian network Module

At the lower level, as generality decreases and the knowledge model is refined to include more variables and the complex interconnections among them, a more accurate evaluation method becomes necessary, thus emphasizing the increased precision decreased intelligence (IPDI) principle.

Bayesian networks consist of two components: the first is a quantitative component which provides a probabilistic model for representing uncertainty in the form of a joint probability distribution over the set of the variables of the domain. In solving the diagnostic problem, the task of the bayesian network is to compute the posterior probability distribution for a set of query variables (diagnostic hypotheses) given a set of evidence variables (symptoms). The second is the qualitative component, which encodes causal relations among the variables in the form of conditional dependence/independence assertions which can be read directly in the directed acyclic graph structure of the network. The independence assertions greatly reduce the computing complexity of network evaluation by allowing the global joint probability to be constructed of local distributions as $P(X) = \prod_{i=1}^n P(x_i|pa(x_i))$, where x_i is a variable (vertex of the graph) and $pa(x_i)$ represents the variables associated to the parent nodes of x_i .

Several algorithms have been developed for the evaluation of Bayesian networks, both exact and approximate. For the purpose of our system we have considered the Lauritzen-Spiegelhalter (L-S) algorithm implemented by B. Perry and J. Stilson in their Toolkit for Experimentation in Bayesian Networks (Perry and Stilson [2002]), which works efficiently for networks that are sparse and irregular, such is the case in our model, where the number of variables is fairly small and most of the variables are binary. The L-S algorithm is an exact probability inference algorithm in an arbitrary Bayes Network.

4. CASE STUDY

As an example of a medical application of the structure developed, we have considered a list of 26 diagnostic hypotheses characterized by a total of 207 symptoms at the finest granulation level (Munteanu [2006]). By applying the clustering algorithms described in section 2 on the 26 hypotheses considered and a restricted set of 110 symptoms, we obtained similar results as depicted in Fig. 4, and 5.

The arborescent structure in Fig. 4 corresponding to hierarchical clustering, is much more intuitive and permits an a posteriori decision on the number of groups according to the desired level of abstraction. In the FCM grouping algorithm the number of groups is given as an a-priori parameter for the algorithm, thus requiring some previous insight of the knowledge structure. However, the FCM algorithm allows for a representation of the inherent interrelations

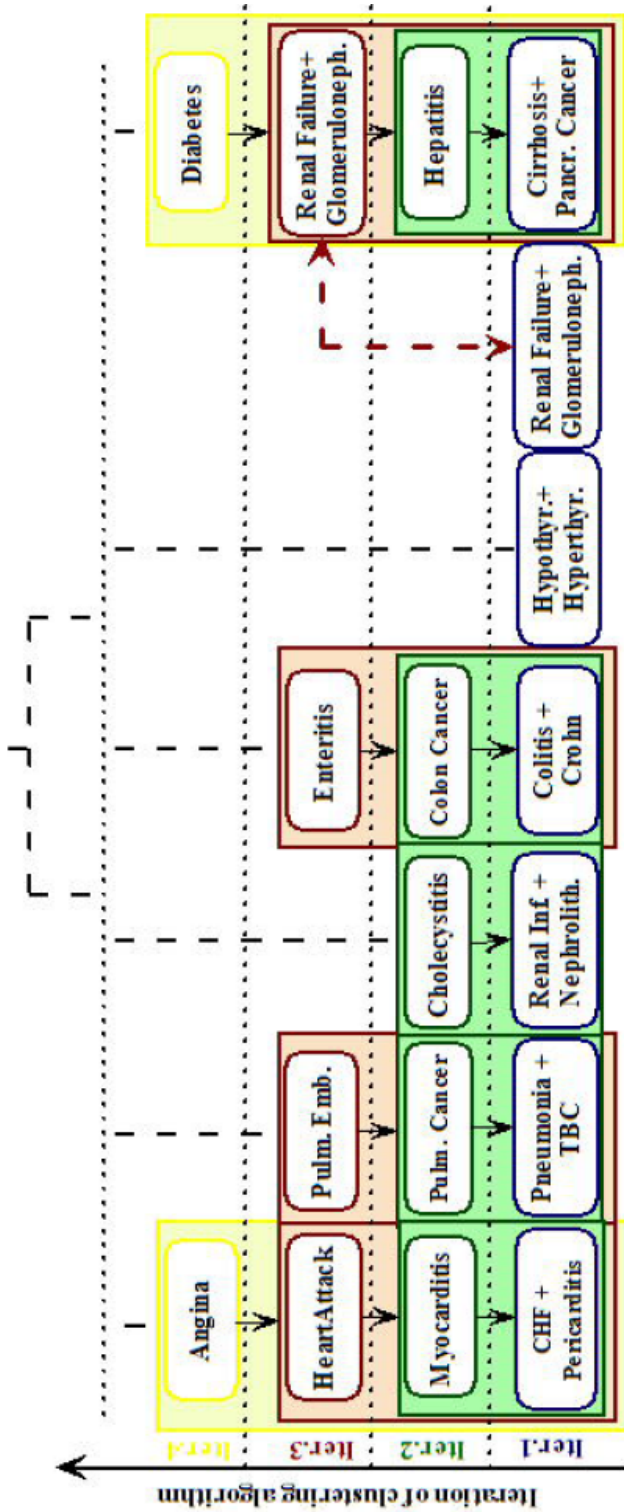


Fig. 4. Results for hierarchical clustering algorithm (partial representation)

among groups (side-effects, disease iter-influences) as can be seen in Fig. 5. Each group is represented at the lower level by a bayesian network model. An example is given in Fig.7.

Group formation described in the above paragraphs occurs in a preliminary phase of system set-up and will not

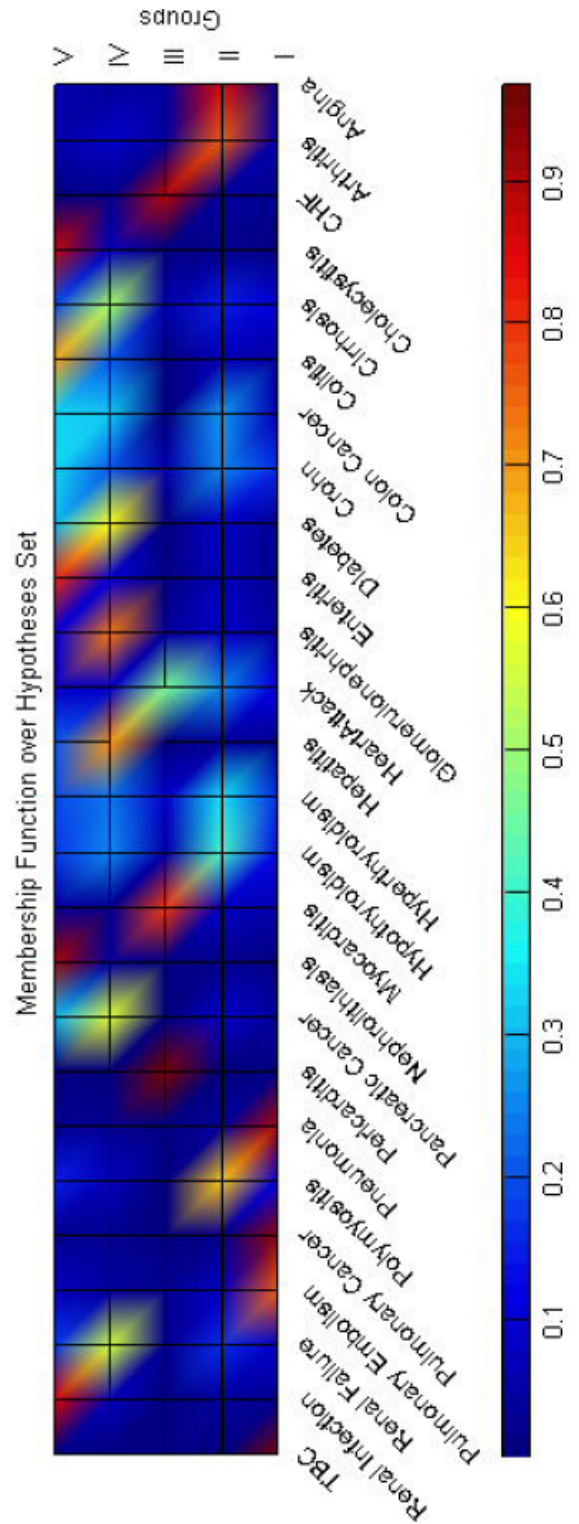


Fig. 5. Results of Fuzzy C-Means clustering algorithm

be reiterated in current usage. The end-user interaction sequence supported by the system comprises two stages which correspond to the decision making process implemented in our approach and described above.

A restricted set of symptoms which can be obtained in the first stage of the diagnosis process by physical examination or past medical history is used in the Dempster-Shafer

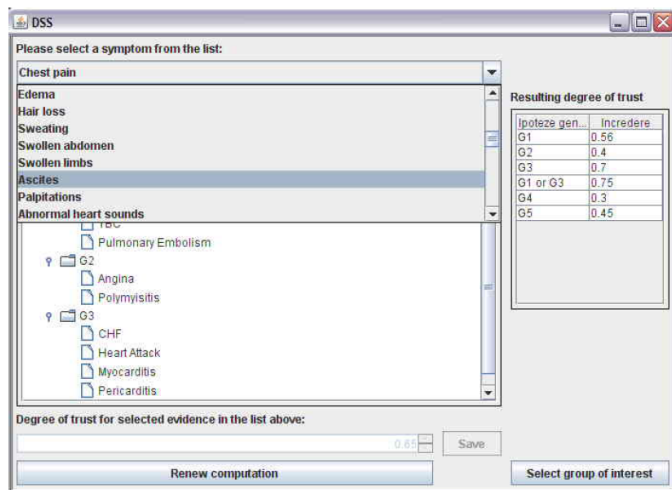


Fig. 6. Step one - Dempster-Shafer inference

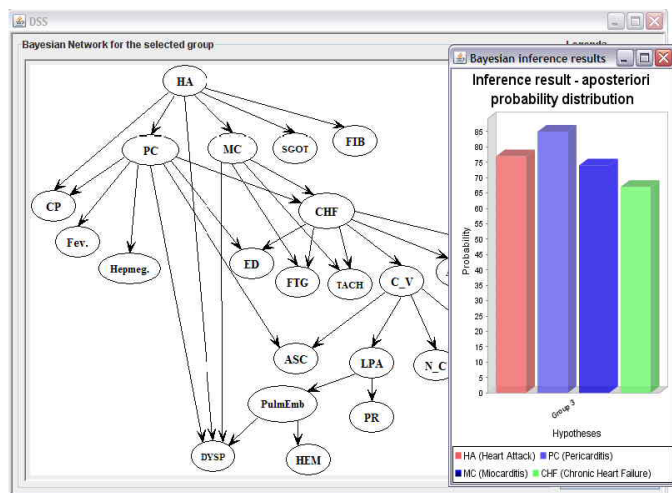


Fig. 7. Step two - Bayesian inference and results module for discriminating between groups.

The decision module displays the list evidence corresponding to the group of causes and asks the user to validate them. As an evidence is observed (chosen by the user from the list), the probabilistic masses are updated, Fig. 6, right side of the window. When the evidence list is finished, the decision module presents a list of hypotheses having the highest beliefs that resulted from the inference. The user is asked to choose the most probable candidate for inference at the lower level. In the second stage, the decision module presents the user with two options (Fig.7):

- to review the Bayesian network of the selected group, where he is given the opportunity to modify the probability distributions of the nodes and to select evidence nodes;
- to review the results of the evaluation of the network in a graphical manner, deciding either to continue or choose the final diagnosis.

5. CONCLUSIONS

In this paper a hierarchical structure implemented as a hybrid medical diagnosis system is presented. The com-

bination of heuristic (Dempster-Shafer) and probabilistic (Bayesian networks) models, emulates uncertain reasoning on two levels. We attempted to obtain a more intuitive analysis of the medical decision making process by decomposing the original diagnosis problem into sub-problems of more manageable complexity, using granular computing concepts such as Grouping, Focusing and Searching. A partitioning of the problem domain has been presented by cluster formation (Grouping), followed by a selection of the relevant sub-problem domain (Searching implemented by the DS inference on level 1), and finally, retrieving the finer representation of the constricted domain (Focusing) and searching for the solution by Bayesian inference on level 2.

Preliminary tests of the system were favorable, but mainly consisted of a comparison of results obtained by the proposed system and the system designed in Munteanu [2006], which was medically approved. This solution was chosen because the two systems were designed starting from the same pool of hypotheses and symptoms, so that a comparison basis existed. Further testing and validation in clinical settings is necessary. Also, some common performance measures should be defined and evaluated in order to attempt comparison to other systems.

Currently the restricted set of symptoms used in group formation is chosen on the basis of occurrence frequency. As future improvements of the system, the dimensionality reduction of the symptoms space will be further studied from the perspective of the theorems in information theory. We plan to introduce a more accurate method of pruning the symptoms set down to a sub-set of most relevant symptoms, by defining a measure to quantify the informational value of each symptom, such as a score based on the entropy and the specificity of the symptom in support of each particular hypothesis. Also, in defining the Bayesian models, the reduced symptoms space will be defined by selecting those candidates (symptoms) with the lowest cross-correlation, thus most representative for preserving maximum information from the higher dimensional space.

Once thoroughly tested and validated, the system could be extended to employ adaptive Bayesian models that learn from experience, such that the prior probabilities in the models adjust statistically from the posteriors of previous calculations. Additionally, online clustering procedures and Bayesian model learning from symptom data could be implemented to insure a greater autonomy for the system. However, this aspect requires extensive study, since complexity and run-time overload issues should also be considered.

Since the system presents a user-friendly interface, providing a graphical representations of the results and other explanatory facilities, it is more likely to obtain a wide acceptance and wide spread use by clinicians, as well as less experienced doctors.

A case study gives the possibility to verify this DSS proposal for medical diagnosis and to prove the viability of its hierarchical hybrid structure.

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