

PAINULIM: A Neuromuscular Diagnosis Expert System Based On Multiply Sectioned Bayesian Belief Networks

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Abstract

An expert system PAINULIM in neuromuscular diagnosis involving painful impaired upper limbs has been developed based on Bayesian belief networks. Although the startling advance has been made on probabilistic reasoning in Bayesian networks, when application domains are large as is the case for PAINULIM, the computation overhead (both time and space) is still forbidding. The problem gets more serious when application systems are to be constructed on microcomputers which are currently the major computational equipments in hospitals and clinics. Construction of medical expert systems on hospital equipments is often desired due to the tight schedule of medical professionals and lengthy process of knowledge acquisition and system refinement as in the case of PAINULIM. The problem can be traced to the current representation of Bayesian networks which does not consider domain structures and lumps all variables into a homogeneous network. In a large domain, new evidence and queries are often directed to a small subdomain in a period of time, which we term as *locality*. We developed the multiply sectioned Bayesian network technique to treat the above problem by representing and exploiting locality naturally existing in the PAINULIM application domain. We present major issues in knowledge acquisition and representation in PAINULIM.

1 Introduction

We present our research in development of PAINULIM expert system for neuromuscular diagnosis involving painful impaired upper limbs. As the limitation of rule-based systems for reasoning under uncertainty has

been identified [4, 5, 15], we have chosen to build PAINULIM based on Bayesian belief networks.

Bayesian nets combine the probability theory with graphic representation of domain models. In Bayesian nets, the probability theory provides a language which embeds many intuitive inference patterns of reasoning under uncertainty and guarantees the consistency of inference made upon the representation [15]. The graphical domain models convey directly to users the dependence and independence assumptions made of the domains, which facilitates knowledge acquisition and makes the representation transparent. They also allow quick identification of dependence relations such that efficient computation for inference are possible and the difficulty associated with general probabilistic reasoning [19] can be avoided when the networks are sparse.

PAINULIM has a large representation domain. This slows down the system response during system testing and demands more powerful computation equipments not available in the hospital lab. On the other hand, the tight schedule of medical staff demands knowledge acquisition and system testing within hospital environments and demands short response time in system testing. These conflicting demands have motivated us to develop the multiply sectioned Bayesian network (MSBN) technique to reduce the computational complexity in expert systems with the size of PAINULIM or larger.

In this paper, we discuss the issues on the knowledge representation and acquisition in PAINULIM. We emphasize the representation using the MSBN technique to implement large application systems in smaller computers. We present a case consultation using PAINULIM, and our initial system testing results.

2 PAINULIM Application Domain

PAINULIM is an expert system in neuromuscular diagnosis. It is intended to cover diagnosis of patients characterized by painful impaired upper limbs due to

diseases of spinal cord and/or peripheral nervous system. The 15 most common diseases considered by PAINULIM include: the Amyotrophic Lateral Sclerosis, the Parkinsons disease, the Anterior horn cell disease, the Root diseases, the Intrinsic cord disease, the Carpal tunnel syndrome, the Radial nerve lesion, the Thoracic outlet syndrome, etc.

Trying to serve all levels of users would greatly increase the size and complexity of a knowledge based system. This in turn demands more resource for the system development, and after the system is completed demands computation equipments possibly not attainable for all levels of users. PAINULIM is intended for users with the following knowledge and experience:

- minimum competence in clinical medicine especially in neuromuscular diseases;
- basic knowledge of nerve conduction study techniques; and
- minimum experience of EMG patterns in common neuromuscular diseases.

Users who can benefit from PAINULIM are

- students and residents in neurology, physical medicine and neuromuscular diseases;
- doctors who are practicing EMG and nerve conduction in their offices;
- experienced EMGers as a formal peer review (self evaluation); and
- hopefully different labs to adapt uniform procedures and criteria for diagnosis.

Clinical diagnosis is performed in steps as anatomical, pathological and etiological. PAINULIM currently works at anatomical level only. With its performance satisfactory at this level, we plan to extend it into the other levels.

3 Bayesian Belief Networks For Expert Systems

Most medical expert systems require reasoning under uncertainty. As the limitation of rule-based systems for reasoning under uncertainty has been identified [4, 5, 15], there has been active research in recent years on knowledge based system methodologies based on Bayesian belief networks (Bayes belief net, causal probabilistic network, causal network,

and influence diagram are other terms used in literature). Although it has been shown [3] that the probabilistic inference in a general Bayesian net is NP-complete, several algorithms have been developed for efficient inference computation in networks with special topologies or with general but sparse topologies [15, 16, 17, 8, 12, 11, 2]. We also see that several expert systems in medicine based on Bayesian networks have been emerged: QMR [18] in internal medicine, MUNIN [1] in EMG, PATHFINDER [6], INTELLIPATH [18] in pathology, and QUALICON [21] in nerve conduction studies.

Bayesian nets combine the probability theory with graphic representation of domain models. Nodes in graphs represent random variables each of which has a set of *mutually exclusive* and *exhaustive* outcomes. We use 'node' and 'variable' interchangeably under the context of Bayesian nets. The graphs in Bayesian nets are directed acyclic graphs. The arcs in the graphs signify the existence of direct causal influences between the linked variables. The basic dependence assumption embedded in Bayesian nets is: a variable is independent of its non-descendants given its parents. Each Bayesian net has an underlying joint probability distribution quantifying the strengths of the causal influences signified by the arcs. The joint distribution specifies the distribution of each variable E_i conditioned by the values of its parents π_i in the form of a conditional probability table $p(E_i|\pi_i)$.

Since Bayesian nets have demonstrated to be a natural, concise knowledge representation and a consistent inference formalism for expert systems reasoning under uncertainty, we have chosen to base PAINULIM's representation on Bayesian belief networks.

4 Locality In Large Application Domain

PAINULIM's Bayesian net representation has 78 variables representing disease hypotheses, clinical symptoms, EMG and nerve conduction study results with 180 arcs connecting them. Each variable has up to 3 possible outcomes. During the system development, the tight schedule of medical staff demands (1) knowledge acquisition and system testing within hospital environments where most computing equipments are personal computers; and (2) short response time in system testing. On the other hand, the space and time complexity of PAINULIM system tends to slow down the response and to demand more powerful computing equipments not available in the hospital lab. This motivates us to improve the current Bayesian network representation in order to reduce the computa-

tion complexity. We made the following observation of PAINULIM domain.

A neurologist, making clinical examination on a patient complaining painful impaired upper limbs, may temporarily consider only his findings' implication on a set of diseases candidates. He may not start to consider the diagnostic significance of each available laboratory test until he has finished the clinical examination. After each clinical finding, he dynamically change the most likely disease candidates and based on that he chooses the best question to ask the patient next or the best examination to perform on the patient next. After the clinical examination of the patient, findings highlight certain disease candidates and make others less likely, which may suggest that further nerve conduction studies are of no help at all, while EMG tests are diagnostically beneficial. Since EMG tests are usually not comfortable on the part of patients, the neurologist would not perform a test unless it is diagnostically necessary. Thus he would perform each test depending on results in previous ones.

From this scene, we see an important phenomenon - *locality*. That is, during the clinical examination, only clinical findings and disease candidates are of current interests to the neurologist. And during EMG tests, only EMG test results and their implications on a subset of the diseases are under the neurologist's attention. Furthermore, for certain percentage of patient population, either EMG tests or nerve conduction studies are not needed. If the neurologist is assisted by a Bayesian network, the evidence and queries would repeatedly towards a "small" part of the network during each diagnostic period (clinical examination or EMG tests for the above scene); and for some patients certain part of the network (nerve conduction for the above scene) may not be interested at all. If we can construct the Bayesian network in a way corresponding to this locality, we would be able to restrict our computation to only "interesting" part of the network and substantially reduce the complexity.

To summarize, by locality, we mean that during a particular consultation session in a large application domain (1) new evidence and queries are directed to small part of a large network repeatedly within a period of time; and (2) certain part of the network may not be of interest to users at all. Current Bayesian net representations do not consider structure in the domain and lump all variables into a *homogeneous* network. When locality exists the homogeneous network is inefficient since the overall network has to be updated each time. We discuss the multiply sectioned Bayesian network technique in the next section which

exploits the locality in PAINULIM.

5 Representation Of Locality In PAINULIM

We have developed general techniques which allows the representation of locality preserving subdomains in Bayesian networks [22]. The corresponding representation is termed *multiply sectioned Bayesian networks (MSBN)*. Using this technique, we partitioned PAINULIM domain into 3 natural locality preserving subdomains (clinical, EMG and nerve conduction) which are separately represented by 3 Bayesian subnets (CLINICAL, EMG, and NCV) in PAINULIM. With MSBN technique, all the system construction steps can be conducted with only 1 subnet at a time. Since the representation preserves the locality, the run time computation can also be restricted to only 1 subnet. Thus the time and space requirements are governed by the size of 1 subnet, not the size of the overall system. When a user's attention is shifted from the current active subnet to another, the technique allows the latter to be swapped into memory and all previously acquired evidence are absorbed. The answers to queries are always based on all the available knowledge and evidence embedded in the overall system. The computational savings thus obtained translate immediately to smaller hardware requirement and quicker response time. Therefore, with MSBN technique, we have been able to use hospital equipments (IBM AT compatible computers) to construct, refine and run PAINULIM interactively with neurologists right in the hospital lab. This greatly speeded up the development of PAINULIM.

In this section, we discuss how to represent locality in multiply sectioned Bayesian nets. We illustrate the technique using a simple network example, and describe how it relates to the representation in PAINULIM.

5.1 Representation of locality in MSBNs

We aim to partition a large domain such as the one for PAINULIM according to natural locality into subdomains such that each subdomain can be represented separately by a Bayesian subnet; and that these subnets (the collection of them is termed a MSBN) can cooperate with each other during inference by exchanging minimum amount of information between them. This imposes a technical constraints on the interface between subnets. MSBN technique requires the interface between 2 subnets to be a *d-sepset*. A set of nodes in a Bayesian net is a *d-sepset* if it separates 2 subnets and every node in the set has all its parent

nodes contained in one of the 2 subnets. A node in a d-sepset is called a *d-sepnode*. d-sepsets impose conditional independence on subnets which they interface. The union of d-sepsets of a subnets with its neighbor subnets render the variables in the subnet conditionally independent of the variables not contained in the subnet.

For example, in figure 1, the network Θ is sectioned into a MSBN consists of Θ^1 , Θ^2 and Θ^3 . $\{H_1, H_2, H_3\}$ is the d-sepset between Θ^1 and Θ^3 . H_2 has 2 parents A_1 and A_2 in Θ which are both contained in Θ^1 . In PAINULIM, the MSBN consists of 3 subnets (clinical, EMG, and nerve conduction) which are interfaced by disease variables having no parents.

The network Θ is a multiply connected network (more than 2 pathes can exist between 2 nodes). Many medical domains have to be represented in multiply connected networks. For such networks, when sparse, we can transform them into secondary structures as permanent representation in order to perform efficient inference computation. When doing so in MSBNs, it is important that resultant secondary structures still preserve the locality. A sectioning which allows the preservation of locality in secondary structure is termed as a *sound* sectioning. We call the resultant MSBN a sound MSBN. This imposes another technical constraint for sectioning. One of the rules is: if there is a subnet which contains nodes of all the d-sepsets in the network, then this sectioning is sound. The subnet is termed a *covering subnet*. Other conditions for sound sectioning are discussed in [22].

For example, in figure 1, the subnet Θ^1 is the covering subnet since it contains all the d-sepnodes between each pair of subnets. In PAINULIM, the CLINICAL subnet is the covering subnet which contains all the disease variables considered by the system. This is natural because clinical examination is the stage where doctors would consider all the disease hypotheses.

5.2 Transform MSBNs into locality preserving junction forests

After we have a sound MSBN, the transformation into a secondary structure can take place. MSBN technique allows the transformation to be conducted by local computation at the level of subnets. Thus computation during transformation is governed by the size of only 1 subnet. The first step of transformation is to *moralize* the subnets, which adds links between parents for every node and then drops the directions. The second step is to *triangulate* the graphs, which adds links to the graphs until every cycle of length 4 or more has a chord. During these 2 steps, communication between subnets is necessary to ensure that links be-

tween d-sepnodes are added identically in subnets containing them. With proper communication conducted, the triangulation in each subnet can be performed by maximum cardinality search [20].

For example, in figure 1, after the moralization, Θ^1 , Θ^2 and Θ^3 become Υ^1 , Υ^2 and Υ^3 respectively. And after triangulation, they become Λ^1 , Λ^2 and Λ^3 respectively. The purpose of the operations is to change the network topology such that (1) the hints for construction of an equivalent probability distribution in the secondary structure becomes graphically explicit; and (2) the coordination needed for information propagation through multiple pathes becomes graphically explicit.

The third step is to identify *cliques* in each resultant graph. A *clique* is a maximal set of nodes pairwise connected. The fourth step is to assign local probability distributions for cliques [22]. The fifth step is to organize the collection of cliques corresponding to each subnet into a *junction tree* (or join tree). A junction tree is a tree with its nodes labeled by cliques, and the intersection of any 2 cliques on the tree is contained in every clique in the unique path between them. This can be done by a maximum spanning tree algorithm [10, 13].

For example, in figure 1, Γ^1 , Γ^2 and Γ^3 are the junction trees constructed from Λ^1 , Λ^2 and Λ^3 respectively.

The sixth step is to create linkages between junction trees such that evidence can be propagated from one to another when the attention shift happens. The *linkages* between 2 junction trees are maximum intersections of cliques and the d-sepset between the 2 corresponding subnets. It is show in [22] that without the introduction of multiple linkages between junction trees, one would either lost locality in the secondary structure or would have to increase the size of the total state space exponentially.

For example, in figure 1, there are 2 linkages between Γ^1 and Γ^3 which are $\{H_2, H_3\}$ and $\{H_3, H_4\}$. All the linkages are illustrated by bands.

The junction trees corresponding to original Bayesian subnets and linkages between them are collectively termed a *junction forest* which constitutes the permanent representation of the application domain where evidential reasoning takes place. The original MSBN still serves as the user interface while the computation for inference is only performed in the junction forest.

5.3 Evidential reasoning in junction forests

After a junction forest is constructed, an initialization [22] is performed to propagate background knowledge

Figure 1: Top left: a Bayesian network Θ ; top right: a MSBN corresponding to Θ ; middle left: moralized graphs for the MSBN at the top right; middle right: triangulated graphs for the moral graphs at the middle left; bottom: a junction forest for the MSBN at the top right.

stored in different junction trees into the rest of junction forest. This operation is done once for all. After the initialization, the prior marginal probability (background belief) for each variable in the MSBN can be obtained by efficient computation at any junction tree which contains it.

Due to locality preserving property of junction forest, at any time during a consultation session, only 1 junction tree needs to be active in memory. When several pieces of evidence are available to the current active junction tree, they are entered to cliques which contain them such that corresponding variables are instantiated, and the local probability distributions are updated. Then the evidence are propagated to the rest of the junction tree by an operation UnifyBelief started at any clique in the junction tree. After that, updated marginal probabilities for all the variables in the junction tree can be obtained efficiently by local computation at each clique. The same happens for each new batch of evidence and queries. Thus computational savings are gained by not having to compute all the current inactive subnets.

For PAINULIM, if the current active junction tree is

the EMG tree, after each EMG test, the result can be entered and updated probabilities for all the relevant diseases and EMG tests unperformed can be obtained by computation at only the EMG junction tree.

Suppose a MSBN has a covering subnet which is the case in PAINULIM. When the user's attention shifts from the junction tree corresponding to covering subnet to another junction tree or the other way around, the target tree will be swapped into memory and an operation UpdateBelief is performed to absorb all previously acquired evidence. If the attention shift happens from a noncovering junction tree to another noncovering junction tree, the covering junction tree is swapped and UpdateBelief is performed first and then the target junction tree. Thus up to 2 UpdateBelief operations are required for a system with n subnets and a covering subnet. The more general case is discussed in [22]. Due to the locality, several batches of evidence and queries are usually computed before an attention shift happens; and some subnets will catch no attention during a query session. Therefore the run time computation complexity for a MSBN/junction forest is about $1/n$ of that required by a corresponding

homogeneous Bayesian network. By adopting MSBN technique and representing PAINULIM domain into 3 subnets, we have been able to reduce the computation complexity (both space and time) in PAINULIM by half taking into account the repetition of d-sepnodes and computation required for attention shift.

6 Other Issues in Knowledge Acquisition and Representation

6.1 Multiple Diseases

Many probability-based medical expert systems have assumed that diseases are mutually exclusive [6], for example, PATHFINDER [6] and MUNIN [1]. A few did not, for example, QMR [7]. When this assumption is valid, diseases can be lumped into 1 variable in the Bayesian network which simplify the network topology.

PAINULIM considers 15 most common diseases in patients complaining painful impaired upper limbs. Since a patient could suffer from multiple neuromuscular diseases, the assumption of mutually exclusive diseases is not valid in PAINULIM domain. We have therefore represented each disease by a separate node.

Although this representation is acceptable for most of the 15 diseases, there is an exception: the Amyotrophic lateral sclerosis (ALS), and the Anterior horn cell disease (AHCD). Both are disorders of the motor system. AHCD involves only the lower motor neuronal system (between the spinal cord and the muscle), but ALS additionally involves the upper motor neuron (between the brain and the spinal cord). However when one speaks of ALS it is not considered as an AHCD plus disease, but an entity by itself. Therefore, conceptually, a neurologist would never diagnose a patient to have both ALS and AHCD. We have represented this conceptual exclusion by an arc directed from ALS to AHCD with probability $p(AHCD = yes|ALS = yes) = 0$. A more concise representation is to combine the 2 into 1 variable which is Motor Neurone Disease (MND). The variable will have 3 exclusive and exhaustive outcomes: ALS, AHCD, NEITHER. We are now adopting the second representation in newer version of PAINULIM.

6.2 Acquisition of probability distribution

In PAINULIM, a clinical finding or a lab test result can have up to 7 parent disease nodes. In binary case, this will require $2^8 - 1 = 255$ numbers to fully specify the required conditional probability distribution at the finding node. It would be frustrating if all these numbers have to be elicited from a human neurologist.

We have found that the *leaky noisy OR gate* model [15, 9] is a powerful tool for managing distribution ac-

quisition. When a symptom can be caused by n explicitly represented diseases, the model assumes (1) each disease has a probability of being sufficient to produce the symptom in the absence of all other diseases; (2) the probability of each disease being sufficient is independent of the presence of other diseases; and (3) due to the incompleteness of representation there is a non-zero probability that the symptom will manifest in the absence of any of the diseases represented explicitly.

We found that the above assumptions are quite valid in PAINULIM domain. A symptom will occur in any given disease with a unique frequency. Should there exist more than one disease that could cause the same symptom, the frequency of occurrence of this particular symptom will be heightened. Using the leaky noise OR gate model, we have been able to assess the above mentioned distribution by eliciting only 8 numbers.

7 Shell Implementation

We implemented an expert system shell WEBWEAVR which incorporates the MSBN technique and leaky noisy OR gate model. This shell is in turn used to construct the PAINULIM expert system.

WEBWEAVR shell is written in *C* and is implemented in IBM PC to suit the computing environment in Neuromuscular Disease Unit, Vancouver General Hospital (VGH) where PAINULIM is constructed. It can be run in XT, AT or 386 although AT or above is recommended. The shell consists of a graphical editor, a structure transformer, and consultation inference engine. The graphical editor allows users to construct MSBNs in a visually intuitive manner. The structure transformer transforms constructed MSBNs into junction forests. The consultation inference engine does the evidence entering and evidential reasoning.

Figure 2 illustrate the WEBWEAVR shell with 6 screen dumps. In the upper left screen, a Bayesian subnet is drawn using a mouse. In the upper right screen, the name of a variable and its possible outcomes are entered. In the middle left screen, the conditional probability distribution for a child variable is entered. Each subnet can be constructed in this way separately. In the middle right screen, the composition of the MSBN for PAINULIM is specified. In the bottom left screen, a menu is displayed which allows a user to specify the d-sepset to be entered next. In the bottom right screen, the d-sepset between CLINICAL and EMG subnets is specified.

WEBWEAVR supports the construction of any MSBN which has a covering subnet.

Figure 2: Top left: drawing a Bayesian subnet with mouse operation; top right: naming a variable and specifying its outcomes; middle left: specifying the conditional probability distribution for a variable; middle right: specifying the subnets composing the MSBN of PAINULIM; bottom left: specifying the d-sepset to be entered next; bottom right: specifying a d-sepset.

8 A Query Session With PAINULIM

In this section, we snapshot several major steps of a query session with PAINULIM in the diagnosis of a particular patient to illustrate its capability.

Since clinical examination is always the first stage in the diagnosis of a patient, correspondingly the CLINICAL subnet is always the one to start with PAINULIM. Before any evidence is available, the prior probabilities for all the diseases and symptoms can be obtained which reflect the background knowledge about a patient population. The top screen in Figure 3 shows the CLINICAL subnet with prior probabilities displayed in histograms. The middle screen shows the same subnet with the same probabilities but a different layout is adopted with full names of variables displayed and arcs omitted. Users of PAINULIM can select one of the layouts depending on their perspective. The former layout provides richer information while the latter gives neat screen. We use the latter layout in the fol-

lowing illustration.

The patient presents with weakness of flexion (curling inwards) of the fingers and the thumb, as well as extension (straightening back) of the thumb. Other symptoms and signs are not known. After this 3 pieces of evidence are entered, the bottom screen in Figure 3 shows the updated (posterior) probabilities for diseases and symptoms above 30% of chance. The possible sites of involvement based on the available clinical evidence are: the Median Nerve (79%), the Root C6,7 (33%), the Radial Nerve (30%), and the Plexus Posterior Cord (30%).

Further evidence is to be obtained from EMG tests and we move to the EMG subnet. Before any EMG test result is entered, the up-to-date probabilities for variables in EMG subnet are displayed in the upper screen in Figure 4. The display threshold (set by the button RATE) is still 30%. We see the same 4 diseases are highlighted with the same posterior probabilities. The likely abnormal EMG findings are also highlighted

Figure 3: Top: CLINICAL subnet with prior probabilities; middle: same subnet with a neater layout; bottom: updated probabilities after clinical evidence is entered.

Figure 4: Top: EMG subnet with clinical evidence absorbed; bottom: updated probabilities after EMG findings are entered.

to help the user to plan EMG tests.

After several EMG tests are performed with abnormalities found in the following muscles: the Abductor pollicis brevis, the First dorsal interosseous, the Extensor digitorum communis, the Paraspinals C6,7 and the Paraspinals C8,T1; and with the status of other muscles in the limb not available, the revised disease candidates are: the Root C6,7 (90%), the Root C8,T1 (71%), the Median nerve (65%), and the Ulnar nerve (39%) (the lower screen in Figure 4).

Evidence from the above two subnets is *positive* evidence. Moving to the NCV subnet, we see in the upper screen of Figure 5 that the previous evidence has been absorbed and up-to-date probabilities of relevant diseases and nerve conduction findings are displayed. The first study is done on motor and sensory conduction in the Ulnar nerve with results being normal. This is considered as *negative* evidence. After the results are entered into the NCV subnet, the Ulnar

nerve lesion becomes unlikely and disappeared from highlighted diseases (the middle screen in Figure 5). The 3 nodes with centers whitened correspond to the new evidence.

With results of further nerve conduction studies in the Median and Radial nerves being also normal, posterior probabilities for the Median and Ulnar nerves drop to near 0. The final diagnosis is narrowed to Root C6,7 (98%) as well as Root C8,T1 (98%), or multiple root disease. An experienced physician would come up with the same diagnosis.

9 Remarks

Bayesian belief networks have demonstrated to be a natural, concise knowledge representation and a consistent inference formalism for expert systems reasoning under uncertainty. Although the startling advance has been made on probabilistic reasoning us-

Figure 5: Top: NCV subnet with clinical and EMG evidence absorbed; middle: updated probabilities after the results from nerve conduction studies in Ulnar nerve are entered; bottom: final diagnosis after nerve conduction studies are finished.

ing Bayesian networks in recent years, when application domain is large, the computational overhead (both time and space) is still forbidding. The problem gets more serious when the application systems are to be constructed, refined and used on microcomputers which are currently the major computational equipments in hospitals and clinics. Construction of medical expert systems on hospital equipments is often desired due to the tight schedule of medical professionals and lengthy process of knowledge acquisition and system refinement.

The problem is traced to the current homogeneous representation in Bayesian nets. We developed a solution (the MSBN technique) to the problem by representing and exploiting locality naturally existing in the PAINULIM application domain. Although our experience is from the domain of neuromuscular diagnosis, we believe that the locality is a general feature for many large application domains.

The MSBN technique is implemented in WEBWEAVR shell which supports the construction of large expert systems based on Bayesian networks. Using the shell we have developed the PAINULIM system in neuromuscular diagnosis of patients with painful impaired upper limbs. The computation complexity of PAINULIM is reduced by half with MSBN technique. About 30 clinical cases in Neuromuscular Disease Unit, Vancouver General Hospital have been used to test PAINULIM with agreement rate to neurologists very high. The system is under further refinement and evaluation currently.

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