Medical Diagnosis Prediction using Genetic Programming

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Abstract

Medical decision making is one of the most demanding tasks in modern medicine. Based on a huge amount of solved cases and rapidly growing number of new findings, medical decision making is supposed to become more and more reliable and effective. However, physicians and medical experts are facing a new arising problem – information overload, which they are not able to overcome. A solution might be found in decision support systems with intelligent information processing abilities that help to process a huge amount of data and suggest a possible decision for each new case. Regarding the simplicity of decision trees and effectiveness of evolutionary programming techniques we developed a decision support system based on automatic programming and used it to solve the mitral valve prolapse classification problem.

1: Introduction

Decision support systems that help physicians are becoming very important part of medical decision making, especially in medical diagnostic processes and particularly in those where decision must be made effectively and reliably [1,2]. They are based on different models and the best of them are providing an explanation together with an accurate, reliable and quick response. Since conceptual simple decision making models with the possibility of automatic learning should be considered for performing such tasks [3], according to recent reviews [1,4,5] decision trees are a very suitable candidate. Decision trees have been already successfully used for many medical decision making purposes. Although effective and reliable, the traditional decision tree construction approach still contains several deficiencies. Therefore we decided to develop a decision support model, that uses genetic programming techniques to overcome the deficiencies of the traditional decision trees induction method. Using our genetic programming kernel we constructed a tool that helps to predict a correct diagnosis of a new patient, based on the knowledge it retrieves from a set of already solved cases. Several solutions were evolved for the classification of mitral valve prolapse syndrome [6,7] and a comparison has been made with the traditional induction of decision trees.

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Diagnostic decisions during the diagnostic process in mitral valve prolapse (MVP) must be supported by suitable decision support model. In the majority of children with MVP, the diagnosis should be made before the complete diagnosis procedure has been accomplished. Our aim is to support the rationalization by reducing the number of necessary diagnostic steps to find a final diagnosis. This is done by deriving a genetic program that solves the given diagnosis prediction problem in accordance with the maximization of the information gain from each diagnostic step and the minimization of its complexity. Therefore, our final goal while developing the method was to achieve: maximal information (possible probability of correct diagnosis 1.00) with minimal risk for patient and doctor (the minimal needed number of steps) and cost benefit.

2: Mitral valve prolapse

Prolapse is defined as the displacement of a bodily part from its normal position. The term mitral valve prolapse (MVP) [6,7], therefore, implies that the mitral leaflets are displaced relative to some structure, generally taken to be the mitral annulus. The silent prolapse is the prolapse which can not be heard with the auscultation diagnosis and is especially hard to diagnose. The implications of the MVP are the following: disturbed normal laminar blood flow, turbulence of the blood flow, injury of the chordae tendinae, the possibility of thrombus' composition, bacterial endocarditis and finally hemodynamic changes defined as mitral insufficiency and mitral regurgitation.

Mitral valve prolapse is one of the most prevalent cardiac conditions, which may affect up to five to ten percent of normal population and one of the most controversial one. The commonest cause is probably myxomatous change in the connective tissue of the valvar liflets that makes them excessively pliable and allows them to prolapse into the left atrium during ventricular systole. The clinical manifestations of the Syndrome are multiple. The great majority of patients are asymptomatic. Other patients, however may present atypical chest-pain or supraventricular tachyarrhythmyas. Rarely, patients develop significant mitral regurgitation and, as with any valvar lesions, bacterial andocarditis is a risk.

Uncertainty persists about how it should be diagnosed and about its clinical importance. Historically, MVP was first recognized by auscultation of mid systolic "click" and late systolic murmur, and its presence is still usually suggested by auscultatory findings. However, the recognition of the variability of the auscultatory findings and of the high level of skill needed to perform such an examination has prompted a search for reliable laboratory methods of diagnosis. M-mod echocardiography and 2D echocardiography have played an important part in the diagnosis of mitral valve prolapse because of the comprehensive information they provide about the structure and function of the mitral valve.

Medical experts propose [6,7] that echocardiography enables properly trained experts armed with proper criteria to evaluate mitral valve prolapse (MVP) almost 100%. Unfortunately however, there are some problems concerned with the use of echocardiography. The first problem is that current MVP evaluation criteria are not strict enough [private communication and 1]. The second problem is the incidence of the MVP in the general population and the unavailability of the expensive ECHO - machines to general practitioners.

3: Decision trees

Inductive inference is the process of moving from concrete examples to general models, where the goal is to learn how to classify objects by analyzing a set of instances (already solved cases) whose classes are known. Instances are typically represented as attribute-value vectors. Learning input consists of a set of such vectors, each belonging to a known class, and the output consists of a mapping from attribute values to classes. This mapping should accurately classify both the given instances and other unseen instances.

A decision tree [5] is a formalism for expressing such mappings and consists of tests or attribute nodes linked to two or more subtrees and leafs or decision nodes labeled with a class which means the decision. A test node computes some outcome based on the attribute values of an instance, where each possible outcome is associated with one of the subtrees. An instance is classified by starting at the root node of the tree. If this node is a test, the outcome for the instance is determined and the process continues using the appropriate subtree. When a leaf is eventually encountered, its label gives the predicted class of the instance.

4: Genetic programming

Genetic programming is one of the most interesting approach in the field of evolutionary computation, that was developed relatively recently by Koza [8]. In comparison with more usual genetic algorithms Koza suggests that the desired program should evolve itself during the evolution process. In other words, instead of solving a problem, and instead of building an evolution program to solve the problem, we should rather search the space of possible computer programs for the best one (the most fit). Koza developed a new methodology, named genetic programming, which provides a way to run a search. A population of executable computer programs is created, individual programs compete against each other, weak programs die, and strong ones reproduce (crossover, mutation).

There are five major steps in using genetic programming for a particular problem. These are 1) selection of terminals, 2) selection of a function, 3) identification of the evaluation function, 4) selection of parameters of the system, and 5) selection of the termination condition. It is important to note that the structure which undergoes evolution is a hierarchically structured computer program. The search space is a hyperspace of valid programs, which can be viewed as a space of rooted trees. Each tree is composed of functions and terminals appropriate to the particular problem domain; the set of all functions and terminals are selected a priori in such a way that some of the composed trees yield a solution. The initial population of programs is composed of randomly constructed program trees, which then undergo the evolution process: evaluation, selection, reproduction, crossover, and mutation until the termination condition is fulfilled.

5: Automatic programming for the decision making

In defining a diagnostic procedure we have to consider a lot of examinations (103 in the case of MVP), each of them revealing new information about the patient's condition and threatening with possible risks for patients and doctor, not to forget economic aspects. When considering also a patient's specific medical history it becomes obvious that we are dealing with a huge, multi-parameterized, dynamic, noisy search space. In order to solve this problem we decided to use a decision support system approach that is very similar to decision trees, but uses different techniques for the induction of solution – a diagnostic procedure in our case. The most obvious difference of the two is the way in which they partition the description space, used for the classification of new patients. Fig. 1 presents an example of such partitioning for only two continuous numerical attributes (for the classification of MVP we used 103 attributes).

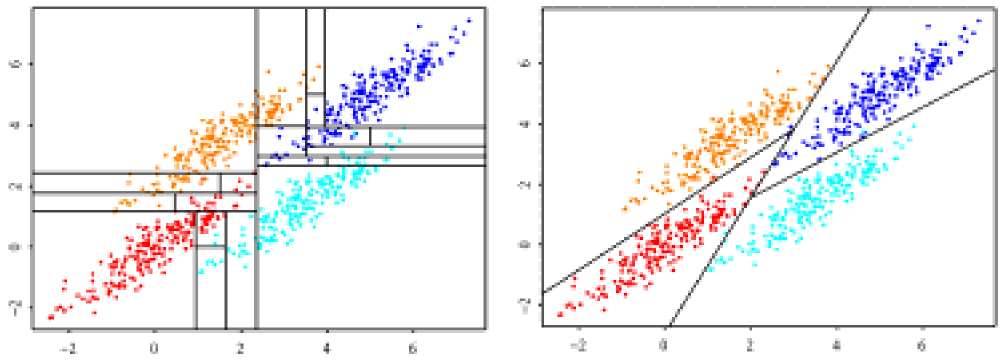

Figure 1. Partitioning of the description space: (i) axis-parallel in decision trees, and (ii) oblique decision boundaries in our approach. Colors correspond to different decisions.

For the construction of a decision program that would be able to classify the MVP for each patient we developed an automatic programming system that is able to develop programs in arbitrary programming language, based on context-free grammar. For this purpose we defined a simple programming language in which we would like to present a solution to MVP classification problem.

6: Decision trees vs. decision programs

To clarify the difference between traditional decision trees and evolved decision programs, we have to stress two major differences: the induction method and the representation. In the case of decision trees, the induction uses the heuristic function that selects attributes based on the information gain from each of the existing attributes. The result of this process is a decision tree (Fig. 2). In the case of automatic programming the final decision program is obtained through the evolutionary process as the most fit individual for solving the given problem (MVP classification in our case). The result of this evolutionary process is a decision program (Fig. 3).

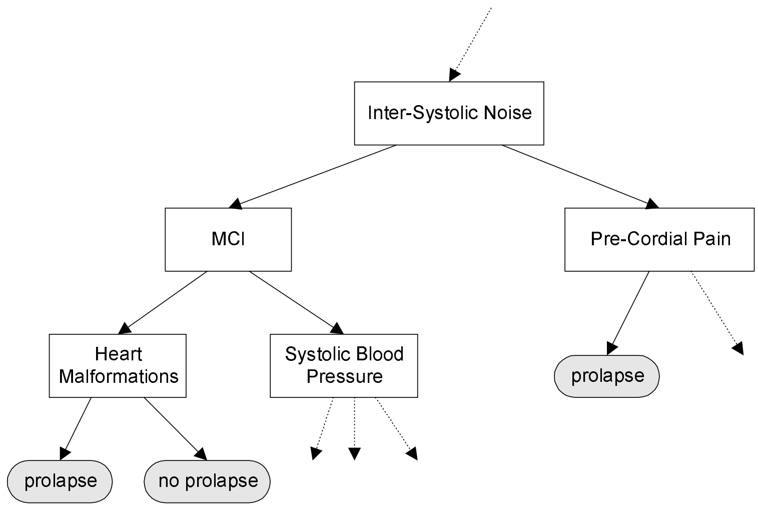

Figure 2. A part of a decision tree for the MVP classification.

```
if (InterSystolicNoise=true) then
  if (MCI=true) then
    if (InjuryMother=true) then return "silent prolapse"
    else return "no prolapse"
    endif
  else
    if (SystolicBloodPressure<=107) then
      if (AuscultationClick=true) then return "silent prolapse"
      else return "prolapse"
      endif
    else if (SystolicBloodPressure>107 and SystolicBloodPressure<=120) then
      if (Anestesy=true) then return "no prolapse"
      else return "silent prolapse"
      endif
    ...
```

Figure 3. A part of a decision program for the MVP classification.

7: Results

Using the Monte Carlo sampling method we have selected 900 children and adolescents representing the whole population under eighteen years of life. All of them were born in the Maribor region and all were white. Routinely they were called for an echocardiography with no prior findings. We examined 631 volunteers.

They all had an examination of their health state in the form of a carefully prepared protocol specially made for the Syndrome of MVP. The protocol consisted of general data, mothers' health, fathers' health, pregnancy, delivery, post-natal period, injuries of chest or any other kind, cronical diseases, sports, physical examination, subjective difficulties like headaches, chest-pain, palpitation, perspiring, dizziness etc., auscultation, phonocardiography, EKG and finally ECHO. In that manner, we gathered 103 parameters that can possibly indicate the presence of MVP.

All 631 patients were divided into a learning and a testing set, 500 patients were selected for the learning and the rest, 131, for the testing set. First we constructed several traditional decision trees (with different parameters settings). Then a few decision programs were evolved through our new evolutionary approach for the same learning and testing sets. A comparison of the best traditionally constructed decision tree (Table 1.a), with our new evolved decision program (Table 1.b) has been made.

Table 1. Classification of MVP problem with a) traditional decision tree, and b) automatically evolved decision program.

	Classified as **prolapse**	Classified as **sil. prolapse**	Classified as **no prolapse**
prolapse	3	0	4
silent prolapse	0	4	0
no prolapse	8	4	108

	Classified as **prolapse**	Classified as **sil. prolapse**	Classified as **no prolapse**
prolapse	4	0	3
silent prolapse	0	4	0
no prolapse	2	2	116

A comparison of the effectiveness of different diagnostic methods is usually described in the field of machine learning by accuracy and in the field of medicine by sensitivity and specificity (Table 2). The accuracy of a diagnostic method is calculated as the relation between the correctly classified and all testing objects. Sensitivity is based on ratio of correctly classified positive patients (patients having prolapse or silent prolapse in our case) compared to all positive patients, and specificity is based on ratio of correctly classified negative patients (without prolapse or silent prolaspe) compared to all negative patients. All values are given as percentages. From table 2 it is obvious that the evolutionary approach greatly improves all measures of effectiveness, especially accuracy and sensitivity.

Table 2. A comparison of the complexity between traditional decision tree and automatically evolved decision program.

	Traditional decision tree	Automatically evolved decision program
accuracy	78,79	94,66
sensitivity	63,64	72,73
specificity	90,00	96,67

8: Conclusion

The introduction of automatic programming techniques into medical decision making has shown some very good results, at least in the case of MVP classification problem. Regarding the possibilities of automatic programming, they could be also used for several other medical decision making purposes, especially in those situations, where the number of attributes that describe one case is large, when a lot of already solved cases are available and when the number of discrete attributes is much higher than the number of continuous ones.

References

[1] Kokol P, et al: Decision Trees and Automatic Learning and Their Use in Cardiology, Journal of Medical Systems 19(4), 1994.

[2] Kokol P, Podgorelec V, Malcic I: Diagnostic Process Optimisation with Evolutionary Programming, Proceedings of the 11th IEEE Symposium on Computer-based Medical Systems CBMS'98, pp. 62-67, Lubbock, Texas, USA, June 1998.

[3] Kokol P, Stiglic B, Zumer V: Metaparadigm: a soft and situation oriented MIS design approach, International Journal of Bio-Medical Computing, 39:243 - 256, 1995.

[4] Kokol P, et al: Spreadsheet Software and Decision making in Nursing, Nursing Informatics'91, (Honvenga E J S et al. eds.), Springer Verlag, 1991.

[5] Quinlan J R: C4.5: Programs for Machine Learning, Morgan Kaufmann, 1993.

[6] Anderson H R, et al: Clinicians Illustrated Dictionary of Cardiology. Science Press, London, 1991.

[7] Devereoux R: Diagnosis and Prognosis of Mitral Valve Prolaps, The New England Journal of Medicine 320(16)1077-1079, 1989.

[8] Koza J R: Genetic Programming: On the Programming of Computers by Natural Selection, MIT Press, 1992.