New Filter method for categorical variables' selection

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Abstract

It is worth noting that the variable-selection process has become an increasingly exciting challenge, given the dramatic increase in the size of databases and the number of variables to be explored and modelized. Therefore, several strategies and methods have been developed with the aim of selecting the minimum number of variables while preserving as much information for the interest variable of the system to be modelized (variable to predict). In this work, we will present a novel Filter method useful for selecting variables, distinct for its joint application of both simple as well as multivariate analyses to select variables. In the first place, we will deal with the major prevailing strategies and methods already underway. Secondly, we will expose our new method and establish a comparison of its achieved results with those of the existing methods. The experiments have been implemented on two different databases, namely, a cardiac diagnosis disease labeled "Spect Heart", and a car diagnosis, called "Car Diagnosis 2". As for the ultimate section, it will bear the conclusion as well some highlights for future research perspectives and potential horizons.

Keywords: *Variables selection; Filter method; Wrapper strategy; Clustering.*

1. Introduction

In the early 1990s, most publications pertaining to variables selection covered areas often described by only a few dozens of variables. Most recently, however, owing to the increase in the capacity for collecting, storing and handling data, the situation has greatly changed. It is not uncommon, however, to meet in some areas, particularly in bioinformatics or text mining, hundreds or even thousands of variables. Consequently, new variable-selection techniques have emerged in a bid to address this change of scale, and above all, to consider the abundance of redundant as well as irrelevant variables in the data processing [5].

This problem appears to be even more serious with respect to several learning applications, especially in the case of a supervised process. Most often, we have a fixed-size learning set available at our disposal whether regarding variables or regarding individuals. Based on this set, we have to construct a classification model for individuals. This model is then used to predict the class of new individuals. Intuitively, one might well consider that an algorithm's discriminating power increases with the number of variables. The situation is not that simple, since an increase in the number of variables might engender a dramatic increase in the algorithm's execution time. In addition to this computational complexity, there is a problem of the difficulties inherent in the content of processed information to be posed: certain variables are redundant while some others are irrelevant for the prediction of classes. In this respect, three major categories or families of approaches have been highlighted in the literature. First, the Filter approaches [1, 2, 3, 4, 5, 10] involve introducing the selection procedures prior to, and independently of, the learning algorithm to be implemented thereafter. Second, the Embedded approaches [6, 9], according to which the selection process is part of learning. This approach is perfectly illustrated by the decision-tree inducing algorithms, whereby consistency is the major advantage. Yet, consistency does not necessarily mean performance, since one of the selection's primary objective is to produce a classifier having the most effective generalization capabilities. As for the idea of the Wrapper approach [8, 7, 10], it consists in explicitly applying a performance criterion for the purpose of retrieving the subset of relevant predictors.

It is as well-known fact that a single variable's impact on an information system's interest variable or class may be limited as compared to a subset's impact, in which the variables jointly react in a complementary manner (Provided that these variables are not redundant) [11]. This can be made clear, for instance, in the case study of the variables responsible for a complex genetic disease in which variables' subsets complementarily react to develop the disease. We can also refer to the example of marketing variables, where separated subsets of variables influence consumer behavior, although a single variable's role might seem insignificant. The major Filter methods sort out and sift the variables by individual importance and select the most important ones. This might lead to the possibility of eliminating a variable whose individual impact is

relatively weak on the variable to predict, while on combining it with a variables' group, it turns out to be very important and selectable. This problem is partially resolved by means of the Wrapper strategy, as it undertakes to select the subset that optimizes best a classifier's performance criterion, although the calculation is the result of the addition or removal of a single variable rather than a subset of variables. It is also a well-known fact that the Wrapper strategy is greedy in algorithmic complexity, as it is classified as an NP-Hard rated problem [12]. Therefore, several heuristics have been adopted to help optimize this problem, the most simple and best known among which are: the Backward method (starting from the whole set of variables, then eliminating variable by variable) as well as the Forward method (addition variable by variable). It is worth noting, however, that in our present work, we undertake to jointly apply the single variable analysis along with the multivariate analysis to select variables associated with a variable to predict (or class). Our conceived method is going to be tested on two databases (well-known among data mining practitioners) and compared to the two major approaches: Filter and Wrapper. To note, the Embedded methods have been excluded from the comparison owing to the fact that they, predominantly, constitute specific learning methods and their application cannot be generalized.

The remaining parts of this article are organized as follows: in the next section, we will present some methods pertaining to the Filter and Wrapper strategy. Then, a new approach will be exposed which can be classified as a Filter method, based primarily on the selection of variables following ranking scores. Our method's results will be compared to those of the different methods presented in "section 2." with regard to a "car diagnosis" and a "cardiac disease diagnosis" databases. Finally, we will close this research work with a conclusion and some prospects for future research.

2. State of art

2.1 The Wrapper strategy

The idea of the Wrapper approach [8] is to explicitly use the performance criterion for finding and the subset of relevant predictors. Most often, this lies in the error rate. Actually, however, any criterion might fit well and can be agreed upon. This may, for instance, be the cost if we introduce a cost matrix of maladjusted classifications; it can also be the under-curve area when evaluating the classifier using a ROC curve; etc. In such cases, the learning method should act as a black box, to which we exhibit different groups of predictor variables, and ultimately select the most appropriate one that best optimizes the criterion. The solutions' search strategy plays a crucially-important role in the Wrapper strategy. It can be very simple, with greedy approaches, adding (Forward) or removing (Backward) a variable to the current solution. It can also be very elaborate and intricate, with approaches based on meta heuristics (genetic algorithms, ants' colonies, etc.). In this area, we consider that the best is the enemy of good. Actually, an excessive exploration of the solutions' space leads us to over-learning. In most cases, the greedy simplistic approaches turn out to be the most suitable and appropriate. Indeed, they permit to naturally smooth the path of the solutions' space.

2.2 The Filter approach

The Filter approach consists in undertaking some independent selection procedures of learning algorithms to be implemented thereafter. The major advantage of such methods is their high speed and flexibility. The "Ranking" methods are certainly the most representative of this family. The process consists in calculating an indicator, individually, featuring the connection between the class and each predictor. Variables' are, then, arranged according to the criterion's decreasing value. We choose the primary *X* variables' using a statistical hypotheses test to select the variables having a significant relationship with the variable to predict. In the upcoming part, we will present some Filter methods, most frequently mentioned or cited in the literature [10, 1, 2, 3, 4, 5], and that will be compared experimentally with our new method in "section 4.".

The Correlation Feature Selection (CFS) method: The CFS method [1] is based on an overall measure of measure of "merit" of a subset *M* of *m* variables, considering both their relevance and redundancy. It is written as:

$$merit = \frac{m * \overline{\rho_{y,x}}}{\sqrt{m + m * (m-1) * \overline{\rho_{x,x}}}}$$

The CFS method [1] is based on an overall Where $\overline{\rho_{y,x}}$ is the mean of correlations between predictor variables and the target variable; $\overline{\rho_{x,x}}$, the mean of cross-correlations among predictor variables.

Thus, the selection problem becomes an optimization problem. We need to maximize the amount of "merit" starting from all the candidate variables' set. In this respect, we can apply either some simple greedy strategies (such methods as step by step, Forward or Backward) or sophisticated ones (e.g. genetic algorithms, simulated annealing, etc.). In practice, a simple technique, smoothing the solutions' space exploration, is largely sufficient. It avoids the over-learning pitfall.

The algorithm (greedy selection "Forward") is linear in respect of the observations' number. All correlations can be pre-calculated through a single pass on the data. Yet, it is quadratic in respect of the number of descriptors.

Therefore, it is more advantageous especially for the huge databases with a large number of observations but, relatively, few descriptors.
Inversely, however, when the descriptors are very numerous, calculation and memory storage of all cross-correlations become a problem. It becomes more practical and advantageous to calculate (and recalculate) correlations on the fly. Experiments have shown that the number of ultimately-selected variables is often very low.

The Mutual Information Feature Selection (MIFS) method: The MIFS method [2] rests on a step-by-step "Forward" algorithm. The evaluation criterion of adding a supplementary variable X to the set M (of cardinal m) of the already-selected variables can be written as:

$$I(Y, X / M) = I(Y,X) - \beta \times \sum_{Z \in M} \frac{I(X,Z)}{m}$$

At each step, we choose the quantity-maximizing variable $I(Y, X / M)$, which is a partial mutual information. A variable is considered to be interesting if its connection to the target Y exceeds its average connection with the already-selected predictors, taking into account relevance and redundancy. The search ends when the best variable X^* is such that $I(Y, X^* /M) \leq 0$. The selection algorithm is also quadratic with respect to the number of variables in the database.

The Fast Correlation-Based Filter (FCBF) method: The FCBF [4, 5] method is based on the criterion "symmetrical uncertainty - ρ". However, it differs for the implemented search strategy, based on the notion of "predominance". Actually, the correlation between a variable X^* and the target Y is said to be predominant if and only if:

$$\rho_{y,x^*} \geq \delta \; et \; \forall \; X (X \neq X^*), \rho_{x,x^*} < \rho_{y,x^*}$$

Concretely, a variable is considered interesting if:

- its correlation with the target variable is sufficiently high, δ is the parameter that serves to modulate this;
- there does not exist in the database any variable which is more strongly correlated to it.

In terms of computing time, the approach is particularly interesting, especially when we have to process databases involving thousands of candidate predictors. Regarding the capacity to detect "good" variables, the experiments have shown that this method highly outperforms the other approaches mentioned in this section.

The MODTREE method: Similarly, the MODTREE [3] method is based on the notions of relevance and redundancy, through it does not use the same correlation measure, as it rests on the principle of pair-wise comparison. The calculation is linear in number of observations n, even if the criterion is based on the principle of pair-wise comparisons. This makes it operational for processing databases involving a large number of lines. The partial correlation is applied to achieve the step-by-step "Forward" selection. It measures the correlation degree between two variables X and Y by subtracting the effect of a third variable Z.
Similar to the CFS and the MIFS, the algorithm is quadratic in terms of the number of predictor candidates. It is especially worth noting that it obliges us to calculate the cross-partial correlations' table (initially, a simply raw cross-correlations' table), which has to be updated whenever a new variable is added to the set M. The memory footprint and computation time constraints become stronger when we have to process databases encompassing a large number of descriptors. Compared to the CFS and FCBF methods, the experiments have shown that MODTREE is also useful and able to detect the most interesting predictors [3].

3. New Filter method of categorical variables

With our new Filter method, we propose, on a first stage, to process the selection via a simple variable analysis with an initial selection. On a second stage, we undertake to use a multivariate analysis for a second and final selection.

3.1 Stages pursued by our new approach

• The first stage is consecrated to eliminating redundant variables as well as the variables providing no information (variables with a single categorical value with respect to a database entire examples).
• The second step is devoted, in the first place, to the simple-variable statistical analysis, then, in a second place, to eliminating variables with very low statistical significance.
• The third step consists in the variables' clustering (a non-supervised classification).
• The fourth step consists in merging the individual scores of each cluster's variables into a single representative score and ranking all the clusters according to their new scores.
• The fifth step is the selection of the r first clusters (see Fig. 1).

3.2 Applied Methodologies and algorithms

Elimination of redundant variables: Throughout this stage, a special course will be undertaken for the purpose of eliminating redundant variables (for two or more identical variables, only a single one will be selected) as well as the variables having a single categorical value according to all the data samples (as they provide no information).

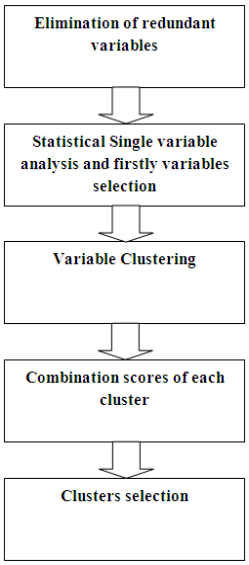

Fig. 1 Stages of our approach

Single variable analysis: The chi-square test is a widely applied test to measure the association between categorical variables. For binary variables (two categories), such as the disease status and a risk factor in epidemiological studies, the chi-square is easily calculated [13].

The idea of the Pearson χ^2 is to compare the observed effectives o_k with a referential basic state: the theoretical effectives e_k that would be obtained should the variables *X* and *Y* be independent. Thus, the procedure heavily relies on a hypothesis-testing mechanism. The null hypothesis signifies independence. In this case, the table's content is entirely defined by its margins, actually, under H_0: $P(Y = y_l \cap X = x_c) = P(Y = y_l) \times P(X = x_c)$

χ^2 statistic quantifies the gap (distance) between the observed effectives and the theoretical ones.

$\chi^2 = \sum_{k=1}^{k} \frac{(o_k - e_k)^2}{e_k}$ where ek correspond to effectives under H_0 : $e_k = \frac{n_{l.} * n_{.c}}{n}$.

The chi-square test will be applied to calculate a p-value corresponding to each variable according to its dependence on the variable to predict. Thus, variables whose p-value exceeds *10% (0.1)* will be removed thereupon.

The variables' clustering: The automatic type of clustering is the most frequently used and widespread technique among the data-analysis and data mining descriptive techniques. It is often applied when we get a huge amount of data, within which we intend to distinguish some homogeneous subsets suitable for processing and for differential analyses [14].

Actually, there exist two major well-known algorithm classifying families in the literature, namely, the partition methods as well as the ascending hierarchical-clustering ones. The advantage of the ascending-hierarchical methods, as compared to the partitioning one, lies in the fact that they enable to choose, appropriately, the optimum number of clusters. Nevertheless, the partitioning criterion is not global; it exclusively depends on the already-obtained clusters, since two variables placed in different clusters could by no means be compared any more. Contrary to the hierarchical methods, the partitioning algorithms might perpetually improve the clusters' quality [14], in addition to the fact that their algorithmic complexities are linear (for the most popular algorithms). Regarding our present work, however, we have chosen to use the K-means algorithm, as it is the most popular and applied in the literature, added to fact that its algorithmic complexity is linear ($O(n)$) [15]. We also propose to use a hierarchical clustering algorithm along with the bootstrap technique to obtain the optimal number of clusters that will be introduced as entries in the K-means algorithm. To note, the databases that will be applied to test our approach, in the experimentation section, consist of categorical variables. As regard the performance of clustering, we will use the toolbox ClustOfVar with the software R [16]. In particular, we will use the variant K-means for categorical variables [17] and the linkage-likelihood approach [18] (hierarchical clustering algorithm for categorical variables). To assess the stability of all possible partitions, *2* to *p-1* (where p is the total number of variables) clusters from the hierarchical clustering, we will use a feature called "Stability" (also developed in the ClustOfVar toolbox) based on the "bootstrap" technique, whose corresponding steps are:

- An ascendant hierarchical clustering is applied to the *B* bootstrap replications' sample of *n* initial observations.
- For each replication, scores of *2* to *p-1* clusters obtained are compared with the hierarchy's initial partitions through the calculation of adjusted Rand criterion [19].
- Averages (the *B* replications) of these calculated adjusted Rand are plotted against the number of clusters.

This graph is then a useful tool to help select the number of clusters. Thus, the user can choose the number K of clusters to the heights of the first increase in the stability as exemplified by Fig. 2 below:

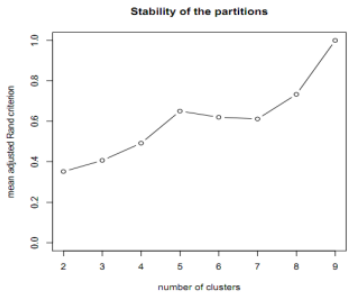

Fig. 2 Example of the partitions' graphic stability.

According to "Fig. 2", once stability is increased up to the level of five clusters, the user can then select the partition in five clusters.

Calculations of each cluster's score and ranking: The question raised in this step is how to derive a score for each class based on the scores of variables within clusters. Most of the methods used to combine scores in computer science literature, and specifically in knowledge discovery through database, are those that consist in merging scores of independent variables such as: Average and Maximum scores [20, 21], Sum, Minimum and product scores [22].
However, the statistical literature provides numerous score-combining methods by taking into account the correlations between variables. One of these is the Truncated Product Method (TPM) (case of dependant variable) [23] that combines p-values of correlated tests. This method has already been compared with other conventional methods and has proven its strength [24]. So, we propose to use it in this step.
After applying the TPM algorithms, scores are transformed as the logarithmic transformation $-Log_{10}(p\text{-}value)$ in such a way that a high score value implies a high degree of significance (association).

Selection of first *r* clusters: The purpose of this step is to select clusters of variables that are the most associated to the phenomenon (predicted variable). There are numerous methods for selecting most influential variables depicted in the statistical and computer-science literature. However, to our knowledge, there are only a few methods that deal with selecting clusters of variables. In this respect, we reckon to propose a new method inspired from [25]. It consists in calculating the empirical value of each cluster score with the contribution of the scores obtained by repeating steps *1*, *2* and *4* *B* times on simulated data (the initial clustering is to be kept). Selection is stopped once a cluster's empirical value increases for the first time reports by the other(s) first cluster's empirical value. On simulating data, each variable's states will be simulated with the same initial composition categorical values.
We set:
H_i^{obs} score of cluster ranked *i*.
H_i^{sim} : the score of a cluster ranked *i* obtained after applying steps *1*, *2*, and *4* to simulated data.
B: the number of simulations.
PT_i: Empirical value of each cluster ranked *i* calculated as $PT_i = \frac{Card(H_i^{sim} \leq H_i^{obs})}{B}$.
The number of would be selected clusters is the first *r* clusters before the first increase in PT_i.

4. Experiments

The clustering was performed via the R language, more specifically, the package ClustOfVar. The remainder of our method has been developed in *C* language. Noteworthy, the FCBF, CFS, MIFS and MODTREE methods have been executed with the Tnagra *1.4* software, available and free downloadable on the site: http://eric.univ-lyon2.fr/~ricco/tanagra/. As for the Wrapper strategy methods, they have been executed with the Spina Research software, available and free downloadable on the site: http://eric.univ-lyon2.fr/~ricco/sipina.html .

4.1 Databases

Firstly, we undertake to test our approach on a heart-diagnosis database (Spect Heart). It is made up of *23* variables (see Table 1.), among which is a status variable called "overall_Diagnosis", the global interest variable of the information system. This Spect Heart domain is available on the site http://archive.ics.uci.edu/ml/datasets/SPECT+Heart.
Among the *267* data instances, *32* have been left aside for the references' testing phase. In addition, we have applied our approach to a car diagnosis database (Car Diagnosis 2). It involves *18* variables (see "Table 2."), among which is a status variable called "Car starts", the information system's global interest variable. The parameters' generating file of this database is available on the site http://www.norsys.com/downloads/netlib/. Relying on these parameters, we have been able to generate *10000* examples, among which *32* have been left aside for the references' testing phase.

Table 1. "Spect Heart" variables.

Variables' names	Possible states
F1 to F22	(0, 1)
Overall_Diagnosis	(0, 1)

Table 2. "Car diagnosis 2" variables.

Variables' names	possible states
AL : Alternator	(Okay, Faulty)
CS : Charging System	(Okay, Faulty)
BA : Battery age	(new, old, very_old)
BV: Battery voltage	(strong, weak, dead)
MF: Main fuse	(okay, blown)
DS: Distributor	(Okay, Faulty)
PV: Voltage at plug	(strong, weak, none)
SM: Starter Motor	(Okay, Faulty)
SS: Starter system	(Okay, Faulty)
HL: Head lights	(bright, dim, off)
SP: Spark plugs	(okay, too_wide, fouled)
SQ: Spark Quality	(good, bad, very_bad)
CC: Car cranks	(True, False)
TM: Spark timing	(good, bad, very_bad)
FS: Fuel system	(Okay, Faulty)
AF: Air filter	(clean, dirty)
AS: Air system	(Okay, Faulty)
ST: Car starts	(True, False)

4.2 Results

The Spect Heart database: After an automated exploration of this database, there will be neither redundant variables nor any variables with a single categorical value. The chi-square test results are presented in "Table 3" below. The F7 variable, whose chi-square test value equals *0.17*, is automatically removed at this stage. Regarding the clustering, the optimal number of clusters chosen is equal to *4* (see Fig. 3). The results of applying the K-means algorithm are presented in "Table 4".

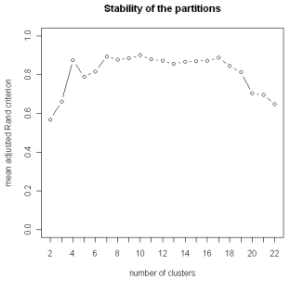

Fig. 3 Partitions' Stability of "Spect Heart" database.

Table 3. Variables chi-square tests results of « Spect Heart » database.

Variables names	Chi-square results
F1	0.10
F2	0.03
F3	0.02
F4	0.01
F5	0.32
F6	0.17
F7	0.5×10^{-2}
F8	0.4×10^{-3}
F9	0.04
F10	0.08
F11	0.5×10^{-2}
F12	0.9×10^{-2}
F13	0.2×10^{-4}
F14	0.02
F15	0.08
F16	0.4×10^{-3}
F17	0.2×10^{-2}
F18	0.01
F19	0.15
F20	0.03
F21	0.3×10^{-2}
F22	0.4×10^{-2}

Table 4. Clustering results of the "Spect Heart" database.

Cluster 1	Cluster 2	Cluster 3	Cluster 4
F1, F5, F10, F19	F2, F6, F7, F11, F12, F17	F3, F8, F13, F18, F21, F22	F4, F9, F14, F15, F16, F20

After merging each cluster's scores with the TPM algorithm, and following the logarithmic transfomation of these scores and the sorting of clusters, we obtain the results presented in "Table 5". As for the selection of clusters to be retained, we have obtained the empirical results PT_i, presented in "Table 5". As PT_i increases at the level of cluster *1*, it is, then, a breakpoint. As for clusters *2* (irrespective of the variable F7), *3* and *4*, they have been retained. The final number of selected variables has been equal to *17* (F2, F6, F11, F12, F17, F3, F8, F13, F18, F21, F22, F4, F9, F14, F15, F16, F20).

The variable-selection results of the methods: FCBF, CFS, MIFS, MODTREE, Forward Wrapper, Backward Wrapper as well as those of our designed approach are shown in "Table 6". Eventually, the achieved results' evaluation and comparison will be presented in "subsection *4.3*" of this work.

Table 5. Clusters' ranking by scores.

Cluster number	Variables names	Score	PT_i
3	F3 F8 F13 F18 F21 F22	2.1549	0.0000
4	F4 F9 F14 F15 F16 F20	0.6675	0.0000
2	F2 F6 F11 F12 F17	0.6326	0.0000
1	F1 F5 F10 F19	0.0814	0.0200

Table 6. Variables selected according to different methods.

FCBF	CFS	MODTREE	MIFS	Wrapper Forward	Wrapper Backward	Our Method
F10	F8	F13	F8	F13 F1	F2 F3 F5	F2 F6
F13	F11		F13	F2 F3	F7 F8 F9	F11
F16	F13		F16	F4 F11	F10 F11	F12
F17	F16		F17		F12 F13	F17 F3
	F17		F18		F14 F15	F8 F13
	F22		F20		F16 F17	F18
			F22		F18 F19	F21
					F21 F22	F22 F4
						F9 F14
						F15
						F16
						F20

The Car Diagnosis 2 database: Following this database's automated exploration, no redundant variable has been detected. However, the variable "AL", whose value has been equal to a single categorical value with respect to the entirety of the studied examples, has been rejected. As regard the variables CS, BA, HP, HL, DC and AF, whose chi-square test values has been higher than *0.1*, they are automatically removed at this stage. Regarding the clustering, the optimal number of selected clusters has been equal to *3* (see Fig. 4); the results of applying the K-means algorithm are presented in "Table 8".

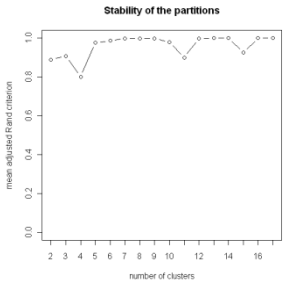

Fig. 4 The partitions' stability of "Car Diagnosis 2" database.

Table 7. Results of the chi-square test application on « Car Diagnosis 2 » database.

Variables names	Chi-square results
CS	0.35
BA	0.25
BV	0.7×10^{-2}
MF	0.1×10^{-10}
PV	0.19
SM	0.1×10^{-10}
SS	0.18×10^{-3}
HL	0.18
SP	0.2×10^{-2}
SQ	0.02
CC	0.17
DS	0.1×10^{-10}
TM	0.12×10^{-6}
FS	0.6×10^{-10}
AF	0.10
AS	0.2×10^{-14}

Table 8. Clustering results of the "Car diagnosis 2" database.

Cluster 1	Cluster 2	Cluster 3
CS : Charging System BA : Battery age BV: Battery voltage MF: Main fuse PV: Voltage at plug SM: Starter Motor SS: Starter system HL: Head lights SP: Spark plugs SQ: Spark Quality CC: Car cranks	DS: Distributor TM: Spark timing	FS: Fuel system AF: Air filter AS: Air system

After merging each cluster's scores with the TPM algorithm, and following the logarithmic transformation of these scores as well as the sorting of clusters, we obtain the results shown in "Table 9".

Concerning the selection of clusters to be retained, we have obtained the empirical results PT_i depicted in "Table 9". Actually, as PT_i has always been equal to *0*, no cluster will have to be eliminated. Hence, Clusters *1, 2* and *3* have been retained. The ultimate number of selected variables is equal to *10* (BV, MF, SM, SS, SP, SQ, DS, TM, FS, AS).

The variable-selection results of the methods: FCBF, CFS, MIFS, MODTREE, Forward Wrapper, Backward Wrapper as well as those of our designed approach are shown in "Table 10.". These results' evaluation and comparison will be presented in "subsection *4.3*.".

Table 9. Clusters' ranking by scores.

Cluster number	Variables names	Score	PT_i
3	FS AS	3.7300	0.0000
1	BV MF SM SS SP SQ	2.9067	0.0000
2	DS TM	1.7443	0.0000

Table 10. Variables selected according to the different applied methods.

FCBF	CFS	MODTREE	MIFS	Forward Wrapper	Backward Wrapper	Our Method
SS TM FS AS	AS	AS	FS AF AS	AS FS CS AL MF BV BA SQ	AL CS MF DS SM SS SP SQ TM FS AS	BV MF SM SS SP SQ DS TM FS AS

4.3 Inference and comparison of results

For the sake of evaluating the different methods' results, we will learn the Bayesian networks' structures and parameters of the variables selected via the methods: FCBF, CFS, MIFS, MODTREE, Forward Wrapper, Backward Wrapper as well as ours (variables selected with the variable to be predicted or class). For this purpose, we will use the Maximum Weight Spanning Tree (MWST) [27] algorithm to attain the variables' starting orders, with the introduction of the variable to be predicted as an initial variable repeatedly at each time [28]. Then, we will use the K2 algorithm [26] so as to learn the different structures. After the parameters' learning, we will use *32* database samples (evidently not used during the learning process) to infer each structure and calculate the states' probabilities of the variable to predict, with respect to both databases under study. Then, we will compare them with those obtained by inferring the resulting learning structure of all variables (without selection) with the variable to be predicted. The purpose of this evaluation is to recognize the methods that mostly preserve the information for the variables to predict while eliminating the maximum of variables. The results are presented graphically, comparing the probabilities of the variable to be predicted with those obtained by inferring all the variables' structure (we will test exclusively the probability for the predictable variable to be at the state *1*, as the variables to predict of both studied databases are binary). Eventually, the "Spect Heart" database attained results are presented in Appendix A, while those pertaining to the "Car Diagnosis 2" one are presented in Appendix B.

5. Discussion

On examining the achieved results, the Filter methods (FCBF, MIFS, MODTREE and CFS) turn out to be very selective, eliminating a great deal of variables. Actually, this is very beneficial in terms of computational complexity when exploiting the results; yet, there is still a considerable loss of information especially with respect to the CFS and MODTREE methods. Regarding the Wrapper strategy, results differ significantly between the Forward and Backward types of exploration. With the Backward one, fewer variables have been removed; still, the

inference results remain identical to those of the entire variables' structure inference. The inference results via the Forward Wrapper have been very close to the inference results of all the variables' structure, but not identical. Our conceived approach along with the Backward Wrapper strategy appear to be the only methods to safeguard and maintain the complete information after eliminating variables (inference results identical to those of all the variables' learning regarding both databases examined). Nevertheless, our approach turns out to be more effective since it has helped eliminate a higher number of variables (elimination of *5* variables with respect to the "Spect Heart" database, versus *4* variables eliminated with the Backward Wrapper strategy and the elimination of *7* variables via our method, regarding the "Car Diagnosis2" database, against *6* variables, too through the Backward Wrapper strategy). We can, therefore, conclude that our method appears to be more efficient than the Wrapper (Forward and Backward explorations) as well as the other Filter methods tested in this work. Regarding the algorithmic computational complexity, it appears clear that our envisaged framework along with the Wrapper strategy methods can be classified as NP-Hard problems. Noteworthy, in this respect, that our envisaged objective to be targeted in future works will lie in devising certain tools, or solutions, whereby to reduce the computational complexity even further, above all with respect to the clusters' selection section.

It is also worth noting that the positively good results achieved via our novel method may be due to its thorough focus on the impact of several subsets of variables on the variable to be predicted, in addition to the study of variables' separate association with that variable. To our knowledge, our Filter method appears to be the exclusive framework to jointly apply both the simple variable and multivariate analyses for variables' selection purposes. Hence, the originality of such a novel framework, whose contribution has led to a noticeable improvement in the study area.

6. Conclusion

Throughout the present study, we have earnestly tried to define a new Filter method useful for selecting categorical variables. In a first place, we have presented the key strategies and existing methods, while highlighting their advantages and drawbacks. In a second place, we have presented a novel Filter method that has been tested and compared with the main existing methods through a two-database experiment. On an ultimate stage, the different models' results have been evaluated, which has led to prove that our designed approach turns out to be the most efficient and accurate. Actually, it is the scheme that has enabled to fully preserve the whole information while eliminating the greatest number of variables. In future research, we shall try to find new techniques for the selection of clusters to reduce our method's computational complexity even more, and attempt to devise new evaluation methods using new learning strategies.

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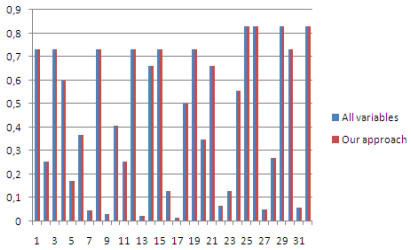
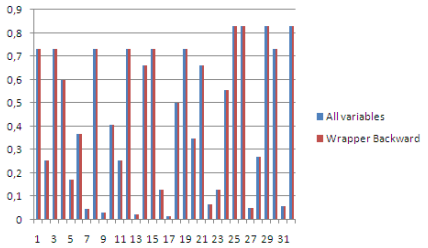
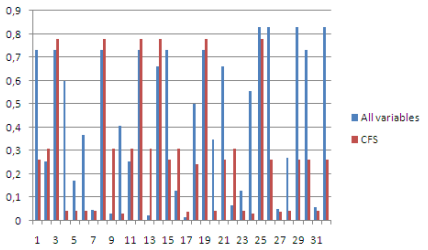
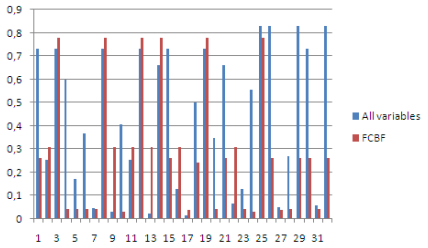
Appendix A

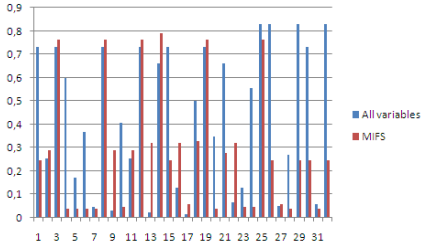
Inference results' comparisons under all variables' learning and selected variables' learning through each method studied for the "Spect Heart" database.

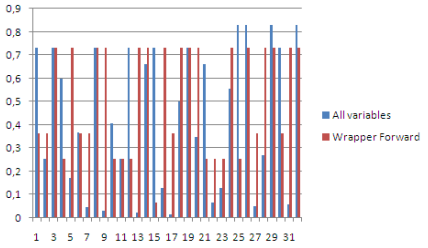


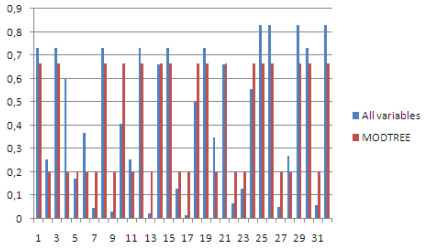






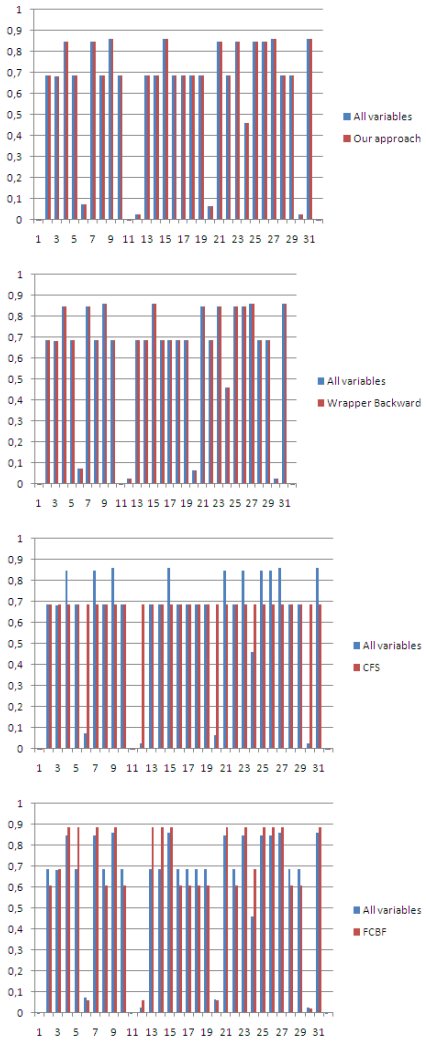


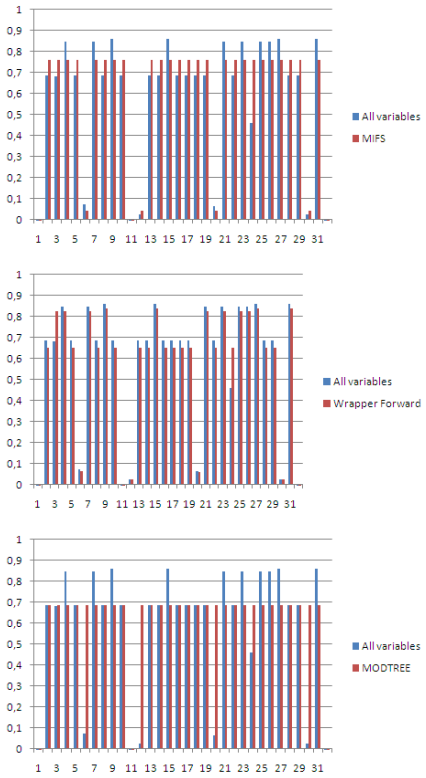




Appendix B

Inference results' comparisons under all variables' learning and selected variables' learning through each method studied for the "Car Diagnosis 2" database.





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