Supervised Classification with Gaussian Networks. Filter and Wrapper Approaches

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Abstract. Bayesian network based classifiers are only able to handle discrete variables. They assume that variables are sampled from a multinomial distribution and most real-world domains involves continuous variables. A common practice to deal with continuous variables is to discretize them, with a subsequent loss of information. The continuous classifiers presented in this paper are supported by the Gaussian network paradigm, which assumes that variables follow a Gaussian distribution. A great advantage of Gaussian network is that they need $\mathcal{O}(n^2)$ parameters to model a complete graph. This work shows how classifiers, supported by the Bayesian network paradigm, can be adapted to deal with continuous variables without discretizing them. In addition, two novel classifier learning algorithms are introduced. The presented learning algorithms are ordered and grouped according to their structural complexity: from the simplest naive Bayes structures to k-dependence Bayesian classifiers and semi naive Bayes. Moreover, for each structure a filter and wrapper approaches are presented. All these classifiers are empirically evaluated using the Brier score and the predictive accuracy. The obtained results with both scores suggest that *semi naive Bayes* is the best classifier.

1 Introduction

Supervised classifi cation is a basic task in data analysis and pattern recognition. It requires the construction of a classifi er, that is, a function that assigns a class label to instances described by a set of variables. There are numerous classifi er paradigms and one of the most effective and well-known in domains with uncertainty are *Bayesian networks* [24], which are based on *probabilistic graphical models* [16] (*PGM*).

A Bayesian network is a directed acyclic graph of nodes representing variables and arcs representing conditional independence relations among the variables. A Bayesian network assumes that all random variables are multinomial. They handle discrete variables, and when a continuous variable is present, it must be discretized, with a subsequent loss of information.

The *Gaussian network* [8] is an alternative to work with continuous variables without the need of discretizing them. It is also based on *PGM*. A Gaussian network is similar to a Bayesian network, but it assumes that variables are sampled from a Gaussian density distribution, instead of a multinomial distribution. Although it is a strong assumption, Gaussian distribution usually provides a reasonable approximation to many real world distributions.

The paper is organized as follows. Section 2 presents five well known paradigms of discrete classifiers (naive Bayes, selective naive Bayes, tree augmented naive Bayes, k-dependence Bayesian classifier, and semi naive Bayes). For each paradigm, two classifier induction algorithms (wrapper and filter versions) to handle continuous variables are introduced. In the same section, two new algorithms are presented: *selective ranking naive Bayes*, and *wrapper k-dependence Bayesian classifier*. In addition, two new theorems about mutual information are proved. In Section 3, the experimental results in classification tasks are presented for Gaussian network-based classifiers using two different scores: the predictive accuracy and the Brier score. Finally, our conclusions and future works are presented.

2 Adapting Bayesian network classifiers to continuous domains

Bayesian and Gaussian networks are used to encode the joint distribution among the domain variables, based on the conditional independencies described by the graph structure. This fact, combined with the Bayes rule, can be used for classification. In order to induce a classifier from data, all classifiers have two types of variables: the class variable or class C, and the rest of variables or predictors, $\boldsymbol{X} = (X_1, \ldots, X_n)$. Although it is not mandatory, the class variable C is the root of the directed acyclic graph in the models presented in this paper. The process of classifying an instance $\boldsymbol{x} = (x_1, \ldots x_n)$ consists in selecting the class with the highest *a posteriori* $p(c \mid \boldsymbol{x})$ value:

$$p(c \mid \boldsymbol{x}) \propto f(c, \boldsymbol{x}) = p(c) \prod_{i=1}^{n} f(x_i \mid \boldsymbol{pa}_i) \tag{1}$$

where $\boldsymbol{pa}_i$ denotes a value of $\boldsymbol{Pa}_i$, the set of variables that are the parents of X_i in the graph. Moreover

$$f(x_i \mid \boldsymbol{pa}_i) \sim \mathcal{N}(\mu_i^c + \sum_{j=1}^{i-1} \rho_c^2(X_i, X_j)(x_j - \mu_j^c), (\sigma_i^c)^2) \tag{2}$$

[8], where μ_i^c and $(\sigma_i^c)^2)$ are the mean and variance of X_i conditioned to a class value $C = c$, and $\rho_c^2(X_i, X_j)$ is c conditioned correlation coefficient between X_i and X_j [18].

The process of induction of a Bayesian or Gaussian network can be divided in two parts: *structural learning* and *parametric learning*.

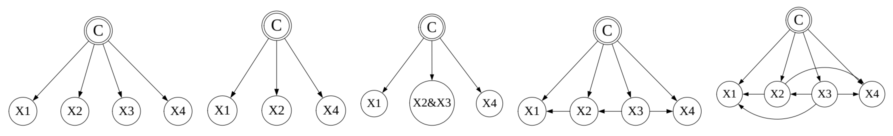
Structural learning usually involves a search process, led by a score value, in the space of possible graph structures. The search process tries to optimize the score, and it generally finishes when a local optimum is found. Depending on the nature of the search score, we consider that structural learning can be carried out in two different ways. A structural learning process is a *filter* approach when the score which guides the search process is based on intrinsic characteristics of the data. For example, a structural learning process is considered a *filter* approach if the score used is the mutual information between variables. On the other hand, we consider that a structural learning process is a *wrapper* approach when the score is a classification goodness measure of the structure given the data. In our case, the predictive accuracy score is used for this purpose.

These *filter* and *wrapper* concepts are adapted from the feature subset selection literature [11, 17] and are originally related to the nature of the scores used in the feature selection task.

Parametric learning consists in estimating parameters from the data. These parameters model the dependence relations between variables, represented by the classifier structure.

One of the main advantages of Gaussian networks with respect to Bayesian networks is that any graph structure can be modelled with a fixed number of parameters, which can be computed *a priori* in a single pass over the data. The needed parameters are an array of class conditional covariance matrixes, $\boldsymbol{\Sigma} = (\Sigma^1, \ldots \Sigma^r)$, and another array of class conditional mean vectors $\boldsymbol{\mu} = (\boldsymbol{\mu}^1, \ldots \boldsymbol{\mu}^r)$, where r is the number of class values. In contrast to the usually large number of parameters needed to learn a complete graph in Bayesian networks $r \prod_{i=1}^{n} r_i - 1$, where r_i is the number of values of variable X_i, the number of parameters needed to model a Gaussian network is $\mathcal{O}(n^2 r)$. This allows us to induce a classifier in a filter (using mutual information or entropy) or a wrapper way reading the train database only once. Another advantage is that this allows a more reliable and robust computation of the necessary statistics because the parameters are only class conditioned.

The following subsections presents different classifier paradigms in order of structure complexity: from the simplest *naive Bayes* to *k-dependence Bayesian classifier* and *semi naive Bayes*. The structure complexity is related to the type and the number of allowed dependencies between variables. Examples of each presented classifier structure are shown in Figure 1.



(a) Naive Bayes. (b) SelectiveNB. (c) SemiNB. (d) TAN. (e) KDB, K=2.

Fig. 1. Different structure complexity classifiers.

2.1 Naive Bayes

The *naive Bayes* classifier (*nB*) [5, 13, 19] is characterized by the conditional independence assumption between variables given the class. Moreover, all variables are included in the model so the classifier structure is given a priori. Thanks to the independence assumption, the factorization of the joint probability is greatly simplified. A *nB* structure example is shown in Figure 1(a), where each variable is a class-conditioned independent variable. After adapting Equation 1 to *nB* structure particularities, the following factorization is obtained:

$$p(c \mid \boldsymbol{x}) \propto p(c) \prod_{i=1}^{n} f(x_i \mid c) \tag{3}$$

with $f(x_i \mid c) \sim \mathcal{N}(\mu_i^c, \sigma_i^c)$. For example, the factorization of Figure 1(a) results in $p(c \mid \boldsymbol{x}) \propto p(c)f(x_1|c)f(x_2|c)f(x_3|c)f(x_4|c)$.

The accuracy obtained with this classifier, is surprisingly high, even in data bases, that do not obey the strong independence assumption [4] between variables.

2.2 Selective naive Bayes

The *selective naive Bayes* (*selectiveNB*)[14] is a modification of *nB*, which maintains its strong conditional independence assumption. *SelectiveNB* performs a variable selection process in a *wrapper* way, searching in the space of possible structures guided by the estimated accuracy. *SelectiveNB* achieves notable improvement accuracies with respect to *nB* especially in domains with redundant variables.

As the search space has 2^n structures, an exhaustive search of the space is impractical, so the induction algorithm performs a search in a greedy way. In other words, at each point in the search process, the algorithm considers the addition of each variable not included in the current naive Bayes model, selecting the best choice by the estimated accuracy. The search continues adding non-included variables until no option improves the accuracy of the last induced classifier.

A filter version of *selectiveNB* paradigm is based on the *mutual information* [3] between predictor variables and the class. For this purpose, a novel theorem about mutual information between Gaussian and multinomial variables is presented.

Theorem 1. *Let C be a multinomial random variable with r possible values been $p(C = c) = p(c)$. Let X be a random variable with a normal density function of parameters (μ_X, σ_X^2). We assume that the random variable X conditioned to $C = c$ follows a normal density with parameters $(\mu_X^c, (\sigma_X^c)^2)$. The mutual information between the variables X and C is given by:*

$$I(X,C) = \frac{1}{2}[\log(\sigma_X^2 - \sum_{c=1}^{r} p(c)\log((\sigma_X^c)^2))]$$

Proof. The definition of mutual information verifies that:

$$I(X,C) = \sum_{c=1}^{r} \int_x f(c,x) log \frac{f(c,x)}{p(c)f(x)} dx = \sum_{c=1}^{r} \int_x p(c) f(x \mid c) log \frac{f(x|c)}{f(x)} dx$$
$$= \sum_{c=1}^{r} p(c) \int_x f(x \mid c) \log f(x|c) dx - \sum_{c=1}^{r} \int_x p(c) f(x \mid c) \log f(x) dx$$

where the integral of the first term agrees with the entropy[1] of a normal distributed variable with parameters μ_X^c and $(\sigma_X^c)^2$.The second term can be expressed as follows:

$$\sum_{c=1}^{r} \int_x p(c) f(x \mid c) \log f(x) dx = \int_x \sum_{c=1}^{r} f(x,c) \log f(x) dx$$
$$= \int_x f(x) \log f(x) dx = -\frac{1}{2} \log(2\pi e \sigma_X^2)$$

[1] The entropy of a normal distributed variable with parameters μ_X and σ_X^2 is given by [3]: $-\frac{1}{2}\log(2\pi e \sigma_X^2)$

and then

$$\begin{aligned} I(X,C) &= \sum_{c=1}^{r} p(c)(-\frac{1}{2}log(2\pi e(\sigma_X^c)^2) + \frac{1}{2}\log(2\pi e\sigma_X^2) \\ &= -\frac{1}{2}\log(2\pi e) - \frac{1}{2}\sum_{c=1}^{r} p(c)\log((\sigma_X^c)^2) + \frac{1}{2}\log(2\pi e) + \frac{1}{2}\log(\sigma_X^2) \\ &= \frac{1}{2}[\log(\sigma_X^2) - \frac{1}{2}\sum_{c=1}^{r} p(c)\log((\sigma_X^c)^2)] \;\; \square \end{aligned}$$

In order to construct a pure *filter* algorithm, it must be known the distribution of $I(X_i, C)$ in order to fix a threshold value, τ, and select the variables that verify $I(X_i, C) \geq \tau$. At the moment, this distribution is unknown, so a future work line is to find this distribution to obtain the above-mentioned threshold. Based on the results of theorem 1, we propose an algorithm called *selective ranking naive Bayes* (*rankingNB*) shown in Figure 2. *RankingNB* is a *semi-filter* approach which guides the search process by the mutual information and the estimated accuracy. *RankingNB*, compared with the wrapper version, has less computational cost: only $\mathcal{O}(n)$ classifiers are constructed compared with $\mathcal{O}(n^2)$ of the wrapper approach.

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Step 0. Compute the mutual information $I(X_i, C)$ for $i = 1 \ldots n$, and use $I(X_i, C)$ to sort
        the variables from the greatest $X_1$ to the smallest $X_n$.
Step 1. Initialize predictor set $\aleph$ to empty. Classify all cases as the most frequent class.
Step 2. For $i = 1 \ldots n$ do:
        Add $X_i$ variable to $\aleph$. Construct the naive Bayes classifier with $\aleph$ and obtain its
        estimated accuracy.
Step 3. Return the classifier associated with the variable set $X_1 \ldots X_k$ which has achieved the
        best estimated accuracy in the search process.
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Fig. 2. Proposed *selective ranking naive Bayes* algorithm.

Due to the independence assumption, the factorization represented by the structure is as simple as the *nB* factorization shown in Equation 3. For example, the factorization of Figure 1(b) results in $p(c|\boldsymbol{x}) \propto p(c)f(x_1|c)f(x_2|c)f(x_4|c)$.

2.3 Semi naive Bayes

The *Semi naive Bayes* (*semiNB*) classifier [12, 23] breaks with the strong independence assumption of *NB*. With this purpose, a new kind of variable called *joint variable* $\boldsymbol{Y}_k$ is presented. This kind of variable is composed by the joint of some of the original variables, where each of the original variables can be in nor more than one *joint variable*. The fact that two variables, X_i and X_j, compose a *joint variable*, $\boldsymbol{Y}_k$, implies that these two variables are correlated, assuming that they are not conditionally independent. If a *joint variable* is composed of multinomial random variables, the states of the *joint variable* consist in the cartesian product of the states of the multinomial random variables [23]. The main problem of *joint variables* composed by multinomial variables X_i is the estimation of their class conditional probability tables because they have a number of exponential states in m_k, $\prod_{i=1}^{m_k} r_i^{(k)} - 1$, where $r_i^{(k)}$ is the number of states of the multinomial random variable $X_i^{(k)}$, and m_k is the number of original variables which constitute the *joint variable* $\boldsymbol{Y}_k$.

If a *joint variable* is composed of a set of Gaussian variables, it follows a *multidimensional normal distribution* [1] conditioned to the class variable. This is one of the contributions of this work. The joint node distribution function follows:

$$f(\boldsymbol{y}_k \mid c) = (2\pi)^{-\frac{1}{2}m_k} \mid \Sigma_k^c \mid^{-\frac{1}{2}} e^{-\frac{1}{2}(\boldsymbol{y}_k - \boldsymbol{\mu}_k^c)^t (\Sigma_k^c)^{-1} (\boldsymbol{y}_k - \boldsymbol{\mu}_k^c)} \qquad (4)$$

where Σ_k^c is the covariance matrix conditioned to a class value, and $\boldsymbol{\mu}_k^c$ is the mean vector conditioned to a class value of the joint variable $\boldsymbol{Y}_k$. In order to model this distribution function a number of parameters $m_k^2 * r$ is needed. This fact solves the problem of the probability table size needed to model the *joint variable* relation with the class variable when the component random variables are considered multinomial.

Depending on the direction of the greedy search process (forward and backward) Pazzani [23] presents two ways to detect dependencies among variables. Our adaptation of the called *Forward Sequential Selection and Joining (FSSJ)* to handle continuous variables is based on Equation 4 to model the class dependence relation of *joint variables*. The adaptation of the algorithm in a backward search direction can be easily done by the application of the same equation.

The *FSSJ* algorithm initializes the set of variables to be used by the Bayesian classifi ers to an empty set. It considers two operators to do the search in the space of possible structures:

1. Add a variable not used by the current classifi er as a new variable class conditionally independent of all other variables used in the classifi er.
2. Joint a variable not used by the current classifi er with a variable currently used by the classifi er.

At each step in the classifi er construction, every addition and every joining of an unused variable with a used variable is considered and evaluated by the estimated accuracy using a leave one out validation on the training data. If no change makes an accuracy improvement, the current classifi er is returned.

This is a pure wrapper algorithm that constructs $\mathcal{O}(2^n)$ classifi ers. A future work line consists in the implementation of a fi lter *semiNB* version based on *(*CFS) feature subset selection.

As *semiNB* considers independent *joint variables*, the factorization of a *semiNB* structure is very similar to the *NB* factorization. It is obtained from equation 3 using equation 4 instead of 2 to factorize terms like $p(X_i \mid C)$. For example, the factorization of the structure shown in fi gure 1(c), assuming that $\boldsymbol{Y}_1 = (X_1)$, $\boldsymbol{Y}_2 = (X_2, X_3)$ and $\boldsymbol{Y}_3 = (X_4)$, results in $p(c|\boldsymbol{x}) \propto p(c)f(x_1|c)f(x_2,x_3|c)f(x_4|c)$.

2.4 Tree augmented naive Bayes

The *tree augmented naive Bayes* (*TAN*) [7, 10] also breaks with the strong independence assumption made by *nB* classifi er, allowing probabilistic dependencies among predictors.

In this subsection, the adaptation to handle continuous value variables of two well-known algorithms to induce *TAN* structures among the variables is exposed, corresponding to fi lter [7] and wrapper [10] approaches.

As in the original algorithms, in the fi lter version (*fTAN*) the permitted graph structures are limited to tree structures between predictor variables and with arcs from the class variable to all predictors as shown in Figure 1(d). In the wrapper version (*wTAN*), we allow graphs with arcs from class variable only to selected predictors and with arcs between predictors taking into account that the maximum number of parents of a variable is one. It has a forest between predictors variables instead of the tree structure among predictors.

The well-known *fTAN* induction algorithm fi nds the tree structures that maximize the likelihood given the data. It can be considered an adaptation of the algorithm proposed by Chow and Liu [2], where they reduce the problem of constructing a maximum likelihood tree to construct a maximal weighted spanning tree in a graph. The algorithm proposed by Friedman et al. (1997)(*wTAN*) follows the general outline of Chow and Liu's procedure, but instead of using the mutual information between two variables, it uses class conditional mutual information between predictors to construct the maximal weighted tree. In order to adapt this algorithm to continuous variables we need to calculate the mutual information between every pair of predictor variables conditioned by the class variable. The following theorem shows how this computation can be done.

Theorem 2. *Let C be a multinomial random variable. If the joint density function of variables X_i and X_j conditioned to $C = c$ follows a bivariate normal distribution, then the mutual information between variables X_i and X_j conditioned to C verifies:*

$$I(X_i, X_j \mid C) = -1/2 \sum_{c=1}^{r} p(c) \log(1 - \rho_c^2(X_i, X_j))$$

Proof. The defi nition of mutual information between X_i and X_j conditioned to C verifi es that:

$$I(X_i, X_j \mid C) = \sum_{c=1}^{r} p(c) I(X_i, X_j \mid C = c) = -\frac{1}{2} \sum_{c=1}^{r} p(c) \log(1 - \rho_c^2(X_i, X_j)) \quad \square$$

The *fTAN* preserves the Chow-Liu algorithm computational cost, requiring a polynomial time in the number of variables [2], and so maintaining *nB*'s computational simplicity. This algorithm has two problems: fi rst, the maximization of the structure likelihood does not necessarily imply a minimization of the predictive error. Second, a tree between all predictors should be formed, so several irrelevant relations between variables are inevitably added. In order to solve this problem, Keogh and Pazzani present a wrapper version of the algorithm [10], that we call *wrapper tree augmented Bayesian network* (*wTAN*).

The *wTAN* [10] implies a different approach to constructing tree-augmented Bayesian networks. More than a direct attempt to approximate the underlying probability distribution, they solely concentrate on using the same representation to improve classifi cation accuracy. As the space of possible structures is exponential in number of variables, the authors use a hill climbing greedy search algorithm guided by the estimated accuracy.

For each arc added to the network $\mathcal{O}(n^2)$, classifi er structures are considered and evaluated, where n is the number of predicted variables. In each considered structure $\mathcal{O}(n)$, arcs may be added. So the complexity for *wTAN* is $\mathcal{O}(n^3)$.

The factorization of the implied *TAN* structure (in its fi lter and wrapper versions) is more complex than the case of *nB* and *selectiveNB* structures. This is due to the class conditional independence property of groups of variables. The factorization is obtained from equations 1 and 2 taking into account the particularity that $\boldsymbol{Pa}_i = \{X_j, C\}$ or $\boldsymbol{Pa}_i = \{C\}$. For example, the factorization of the Figure 1(d) is:
$p(c|\boldsymbol{x}) \propto p(c)f(x_1|x_2,c)f(x_2|x_3,c)f(x_3|c)f(x_4|x_3,c)$.

2.5 K-dependence Bayesian classifier

Sahami (1996) introduces an algorithm called *k-dependence Bayesian classifier* [25] *kDB*. This framework can be regarded as a spectrum of allowable dependence in a given probabilistic model with the *NB* algorithm at the most restrictive end and the learning of full *BN* at the most general extreme.

We regard the structure of the *kDB* as the structure of the *NB* which allows each predictor X_i to have a maximum of k predictor variables as parents, apart from C. In other words, $\mid \boldsymbol{Pa}_i \mid \leq k+1$ [25]. As in the case of *TAN* paradigm, there are two reasons to restrict the number of parents of a variable. First, the reduction of the search space. Second, the probability estimated for a multinomial variable becomes more unreliable as additional multinomial parents are added, because the size of the conditional probability tables increases exponentially with the number of parents [10] and fewer cases can be used to compute the needed statistics. As explained in the introduction of Section 2, the number of required parameters in our continuous adaptations is fi xed, so the second problem is avoided. In addition to estimating these parameters, instead of learning from database partition, the entire database is used. This allows to construct classifi ers with a high number of dependencies between variables.

As the implementation of the *kDB* algorithm proposed by Sahami [25] uses the class conditional mutual information between the variables $I(X_i, X_j \mid C)$ and the mutual information between class and the variables $I(X_i, C)$ to lead the structure search process, it is considered a fi lter paradigm. Hence, we call his approach *fkDB*. In the introduced continuous adaptation, the introduced mutual information defi nitions, shown in equations 1 and 2, are used again. The *fkDB* algorithm allows the construction of classifi ers at arbitrary values for the maximum number of dependencies between variables (values of k), maintaining much of the computational effi ciency of the *nB* model.

At this point we present the novel wrapper approach of *kDB* called *wkDB*. *wkDB* has the same motivation as *wTAN* with respect respect to *fTAN*. The *wkDB* algorithm follows the idea of Keogh and Pazzani's [10] *wTAN* with Friedman et al's [7] *fTAN* algorithm introducing the parameter K, for each $i, 1 < i < n$, $|\boldsymbol{Pa}_i| \leq K+1$, where K is the number of continuous variables. Our novel *wkDB* algorithm is shown in Figure 3.

The factorization of *kDB* and *TAN* structures are equivalent. For example, the factorization of Figure 1(e) is:
$p(c|\boldsymbol{x}) \propto p(c)f(x_1|x_2,x_3,c)f(x_2|x_3,c)f(x_3|c)f(x_4|x_2,x_3,c)$.

```
Step 1. Initialize predictor set to empty. Classify all the cases as the most frequent class.
Step 2. Repeat in each step. Select the best between:
        (a) Each variable not included in the model is considered a new predictor. This new
        predictor must be conditionally independent with respect to the others given, the class.
        (b) Include an arc $\alpha_{i,j}$ between predictors included in the model $X_i, X_j, i \neq j$ ,
        as long as the inclusion of $\alpha_{i,j}$ comes with the k-dependent Bayesian classifier
        structure.

        Evaluate each possible option through the correct classified percentage.
        Until No option improves the inducted classifier.
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Fig. 3. Proposed *wkDB* algorithm.

3 Experimental results

In this section, we present the estimated predictive accuracies and *Brier score* values [22, 26] obtained with the models of the adapted *GN* classifi er learning algorithms. The results have been obtained in eleven *UCI repository* data sets [20] which only contain continuous predictor variables. All the included databases, except waveform, do not obey the assumption that variables follow a Gaussian distribution, done by Gaussian network paradigm. In spite of that, the classifi ers presented in this work obtains results comparable to their discrete versions.

The results for each classifi er in each database have been obtained by a 10-fold cross-validation process with both scores. The performed study has been divided in three steps, with both scores:

1. Select the classifi er with the better score average, taking into account the estimated score for each database.
2. Based on the 10-fold cross-validation score estimation, for each classifi er in all databases, establish if the selected classifi er has obtained better estimated scores at $\alpha = 5\%$ signifi cance level in a paired Wilcoxon [6] test.
3. Based on the scores obtained with each fold of the 10-fold cross-validation process, for each classifi er in each database, establish if the selected classifi er has obtained better results than others in a non-paired Mann-Whitney[6] test. The study has been performed at $\alpha = 10\%$ and $\alpha = 5\%$ signifi cance levels, represented in Tables 1 and 2 by "∘" and "•" respectively. The tested databases are presented in tables in order of the number of parameters needed to model a complete Gaussian network (proportional to $n * r$).

3.1 Estimated predictive accuracy

The results obtained are summarized in Table 1. The classifi er with the best estimated score average is *semiNB*. A conclusion drawn from the second step of the study is that *semiNB* has obtained better estimated scores at $\alpha = 5\%$ signifi cance level in the selected databases. The third step of the study suggests that the accuracy differences obtained by the *semiNB*are more statistically signifi cant as the number of needed parameters to model a complete graph increases.

Data Base	nB	selectiveNB	rankingNB	semiNB	fTAN	wTAN	fkDB	wkDB
HABERMAN	0.74 ± 0.05	0.73± 0.10	0.73 ± 0.10	0.75 ± 0.08	0.75 ± 0.06	0.74 ± 0.07	● 0.75 ± 0.08	0.73 ± 0.06
BUPA	● 0.42 ± 0.10	0.59± 0.09	● 0.42 ± 0.06	0.58 ± 0.07	0.52 ± 0.08	0.59 ± 0.08	0.59 ± 0.07	0.58 ± 0.04
LIVER	● 0.42 ± 0.08	0.59 ± 0.06	● 0.42 ± 0.06	0.63 ± 0.04	● 0.52 ± 0.09	0.59 ± 0.08	0.59 ± 0.10	0.59 ± 0.07
IRIS	● 0.94 ± 0.04	○ 0.94± 0.05	○ 0.93 ± 0.06	0.98 ± 0.03	0.93 ± 0.08	● 0.93 ± 0.05	0.97 ± 0.03	0.93 ± 0.06
HAYES	● 0.60 ± 0.19	● 0.68± 0.09	● 0.60 ± 0.15	0.83 ± 0.05	○ 0.76 ± 0.09	● 0.68 ± 0.12	0.77 ± 0.09	● 0.68 ± 0.07
PIMA	● 0.65 ± 0.05	● 0.65± 0.05	● 0.65 ± 0.05	0.78 ± 0.03	0.75 ± 0.06	0.65 ± 0.04	● 0.74 ± 0.04	● 0.65 ± 0.05
WINE	● 0.69 ± 0.13	● 0.93± 0.06	● 0.90 ± 0.07	0.99 ± 0.02	0.98 ± 0.02	● 0.91 ± 0.07	1.00 ± 0.00	○ 0.95 ± 0.07
TEXT-BLOCK	● 0.55 ± 0.03	● 0.90± 0.00	● 0.90 ± 0.01	0.95 ± 0.08	● 0.94 ± 0.01	● 0.92 ± 0.01	● 0.91 ± 0.01	● 0.93 ± 0.01
WAVEFORM	● 0.77 ± 0.01	● 0.79± 0.02	● 0.77 ± 0.01	0.83 ± 0.01	○ 0.82 ± 0.02	● 0.82 ± 0.01	0.71 ± 0.01	● 0.82 ± 0.02
VEHICLE	● 0.34 ± 0.06	● 0.39± 0.04	● 0.34 ± 0.04	0.77 ± 0.05	● 0.56 ± 0.05	0.39 ± 0.03	● 0.53 ± 0.04	● 0.42 ± 0.05
Average	0.58	0.70	0,65	0.82	0.74	0.72	0.70	0.74

Table 1. Estimated accuracy results.

3.2 Estimated Brier score

The *Brier score* reflects the mean confidence of the learned classifier in the real class of the training data. The formulation of the Brier score is shown in Equation 5:

$$B = \sum_{l=1}^{N} \sum_{c=1}^{r} (p(C = c \mid \boldsymbol{X} = \boldsymbol{x}^{(l)}) - \delta_c^{(l)})^2 \tag{5}$$

where $p(c|\boldsymbol{x}^{(l)})$ function is factorized by the classifier, $\boldsymbol{x}^{(l)}$ represents the values for predictive variables of the case l, N is the number of cases, and $\delta_c^{(l)}$ is the Kronecker delta. The Kronecker delta is defined as follows:

$$\delta_c^{(l)} = \begin{cases} 1 & c = c^{(l)} \\ 0 & \text{otherwise} \end{cases}$$

where $c^{(l)}$ is the real class of the case l, and c is the predicted class value. A high *Brier score* indicates that the learned classifier assigns low confidence levels to the real class of the instances.

The problem is that f function must be a probability and $\sum_{c=1}^{r} f(C = c \mid \boldsymbol{X} = \boldsymbol{x}^{(l)}) = 1$. Discrete classifiers directly handle probabilities and so comply with this idea, but continuous classifiers must be normalized because they handle distribution functions (Equations 1 and 2) instead of probabilities. The normalization of the discrete classifier f process is given by

$$\rho(C = c^{(l)} \mid \boldsymbol{X} = \boldsymbol{x}^{(l)}) = \frac{f(C = c^{(l)} \mid \boldsymbol{X} = \boldsymbol{x}^{(l)})}{\sum_{c=1}^{r} f(C = c \mid \boldsymbol{X} = \boldsymbol{x}^{(l)})}$$

The obtained results for the *Brier score* are summarized in Table 2. The performed study throws similar results than the estimated accuracy study, highlighting the competitive results of *semiNB*.

4 Conclusions and future work

A battery of filter and wrapper classifiers, based on Gaussian networks, is proposed to deal with continuous variables without discretizing them. The classifiers have been compared in 7 databases with two different scores: estimated accuracy and Brier score.

Data Base	nB	selectiveNB	rankingNB	semiNB	fTAN	wTAN	fkDB	wkDB
HABERMAN	0.42 ± 0.01	0.39 ± 0.01	0.41 ± 0.01	0.40 ± 0.05	0.38 ± 0.01	0.39 ± 0.00	0.38 ± 0.06	0.39 ± 0.00
BUPA	● 0.76 ± 0.03	0.50 ± 0.00	● 0.53 ± 0.00	0.50 ± 0.05	0.54 ± 0.01	0.51 ± 0.00	0.51 ± 0.06	0.49 ± 0.00
LIVER	● 0.76 ± 0.02	0.50 ± 0.00	0.52 ± 0.00	0.50 ± 0.00	0.55 ± 0.01	0.50 ± 0.00	0.51 ± 0.10	0.50 ± 0.00
IRIS	○ 0.14 ± 0.01	○ 0.13 ± 0.01	○ 0.12 ± 0.00	0.06 ± 0.00	● 0.13 ± 0.01	0.15 ± 0.02	0.06 ± 0.06	○ 0.13 ± 0.01
HAYES	0.46 ± 0.04	● 0.53 ± 0.01	0.48 ± 0.03	0.42 ± 0.01	0.44 ± 0.00	0.50 ± 0.01	0.46 ± 0.04	0.50 ± 0.01
PIMA	● 0.61 ± 0.01	● 0.46 ± 0.00	● 0.55 ± 0.01	0.33 ± 0.00	0.37 ± 0.01	● 0.45 ± 0.00	● 0.39 ± 0.05	● 0.45 ± 0.00
WINE	● 0.66 ± 0.08	● 0.18 ± 0.01	● 0.20 ± 0.02	0.06 ± 0.03	0.05 ± 0.00	0.10 ± 0.01	● 0.02 ± 0.05	0.08 ± 0.01
TEXT-BLOCK	● 0.86 ± 0.01	● 0.18 ± 0.01	● 0.20 ± 0.00	0.09 ± 0.05	● 0.12 ± 0.00	● 0.15 ± 0.00	● 0.17 ± 0.06	● 0.13 ± 0.00
WAVEFORM	● 0.40 ± 0.00	● 0.32 ± 0.00	● 0.40 ± 0.00	0.25 ± 0.02	0.26 ± 0.00	○ 0.27 ± 0.00	● 0.44 ± 0.02	● 0.28 ± 0.00
VEHICLE	● 1.13 ± 0.01	● 0.82 ± 0.01	● 1.13 ± 0.00	0.39 ± 0.00	● 0.67 ± 0.01	● 0.75 ± 0.00	● 0.83 ± 0.07	● 0.73 ± 0.00
Average	0.69	0.45	0,50	0.28	0.38	0.40	0.40	0.36

Table 2. Estimated Brier results

In sum, *semiNB* obtains statistically significant improvements (using accuracy and Brier score) with respect to the rest of the algorithms in the presented databases.

Table 3 presents a work summary: the proposed novel contributions and the adaptations of previous works to the continuous domains presented in the article.

nB	selectiveNB	rankingNB	semiNB	fTAN	wTAN	fkDB	wkDB
adapted	adapted	novel	adapted	adapted	adapted	adapted	novel
		Theorem 1	Equation 4	Theorem 2			

Table 3. Contributions of the article in each included algorithm.

A future work line, related to the wrapper approach, consists in the adaptation of more classifiers supported by *BN*s for operating directly with continuous variables. The idea consists in the use of randomized heuristics (such as Genetic Algorithms or *Estimation Distribution Algorithms* [15]) as the search engine in the space of classifier structures. Following with the wrapper approaches, the Brier score shows the confidence of the classifier in the real class more in depth than accuracy. This fact suggests that it could be interesting to use the *Brier score*, instead of accuracy, to lead the structure search.

Another work line consists in obtaining a threshold for the mutual information introduced here (Equations 1 and 2). This will allow us to implement a pure filter algorithm based on the mentioned thresholds. Following with the filter approaches, a possible future work is the implementation of a *semi naive Bayes* classifier based on the *Correlation Based Feature Selection* [9] to select the groups of variables highly correlated with the class and not correlated among them.

Finally, another interesting study could consist in obtaining the results for Brier score and estimated accuracy using two new validation methods called *conservative Z* and *corrected resampled t-test* [21], instead of the used *K-Fold cross-validation*.

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