# Learning on Vertically Partitioned Data based on Chi-square Feature Selection and Naive Bayes Classification

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Abstract: In the last few years, distributed learning has been the focus of much attention due to the explosion of big databases, in some cases distributed across different nodes. However, the great majority of current selection and classification algorithms are designed for centralized learning, i.e. they use the whole dataset at once. In this paper, a new approach for learning on vertically partitioned data is presented, which covers both feature selection and classification. The approach splits the data by features, and then uses the $\chi^2$ filter and the naive Bayes classifier to learn at each node. Finally, a merging procedure is performed, which updates the learned model in an incremental fashion. The experimental results on five representative datasets show that the execution time is shortened considerably whereas the classification performance is maintained as the number of nodes increases.

## 1 INTRODUCTION

In the last decades, the dimensionality of the datasets involved in data mining has increased dramatically until the size of zetabytes. In fact, if one analyzes the dimensionality of the datasets posted in the UC Irvine Machine Learning Repository (Frank and Asuncion, 2010) from 1987 to 2010, this circumstance can be confirmed (Zhao and Liu, 2011). Dimensionality can be defined as the product of the number of samples and features. In the 1980s, the maximal dimensionality of the data was about 100; then in the 1990s, this number increased to more than 1500; and finally in the 2000s, it further increased to about 3 million. Theoretically, having such a high amount of data available could lead to better results, but this is not always the case due to the so-called curse of dimensionality (Bellman, 1966). This phenomenon happens when the dimensionality increases and the time required for training the machine learning algorithm on the data increases exponentially. To overcome these problems, feature selection is a well-known dimensionality reduction technique.

Feature selection consists of detecting the relevant features and discarding the irrelevant and the redundant ones (Guyon et al., 2006). A correct selection of the features can lead to an improvement of the inductive learner, either in terms of learning speed, generalization capacity or simplicity of the induced model. Feature selection, since it is an important activity in data preprocessing, has been an active research area in the last decade, finding success in many different real world applications (Bolón-Canedo et al., 2011; Forman, 2003; Saari et al., 2011; Saeys et al., 2007).

Most of the feature selection methods belong to one of the three following types: filters, wrappers and embedded methods. While wrapper models involve optimizing a predictor as part of the selection process, filter models rely on the general characteristics of the training data to select features with independence of any predictor. The embedded methods generally use machine learning models for classification, and then an optimal subset of features is built by the classifier algorithm. Nevertheless, the most common approach in feature selection is the filter model and will be the approach selected for this research, As stated in (Saeys et al., 2007), even when the subset of features is not optimal, filters are preferable due to their computational and statistical scalability.

Most existing feature selection techniques are designed to run in a centralized computing environment. Traditionally, it is assumed that all data can be held in the memory or, at least, all data are stored in one central storage space. However, in the contemporary world, huge databases are developed and maintained in meteorological, financial, medical, in-

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dustrial or science domains (Czarnowski, 2011), and traditional centralized techniques are not fit to effectively deal with such massive datasets. Not only is the large size of the datasets the problem facing feature selection, but also that the datasets may be geographically, physically or logically distributed. In both these situations, distributed feature selection techniques are often required. In this manner, allocating the learning process among several nodes is a natural way of scaling up learning algorithms at the same time that it allows to deal with datasets that are naturally distributed. There are two common types of data distribution: (a) horizontal distribution, where data are distributed in subsets of instances; and (b) vertical distribution, where data are distributed in subsets of features. The great majority of approaches distribute the data horizontally (Chan et al., 1993; Ananthanarayana et al., 2000; Tsoumakas and Vlahavas, 2002) when datasets are too large for batch learning in terms of samples. While not common, there are some other developments that distribute the data by features (Skillicorn and McConnell, 2008; McConnell and Skillicorn, 2004), which is appropriate when the number of features is large. Besides of the type of partition, another important issue when dealing with distributed learning is privacy preserving. The goal of privacy preserving is to learn valuable knowledge from different sources without leakage of any sensitive data, in other words, share non-sensitive data to infer sensitive data (Wang et al., 2009).

The idea of this research is to deal with distributed learning problems through distributing vertically the data and performing a feature selection process which can be carried out at separate nodes. Since the computational complexity of most of feature selection methods is affected by the number of features, the complexity in each node will be reduced with respect to the centralized approach. Then, the selection procedure required for the data reduction will be integrated with the classifier learning. For the feature selection step, we choose the $\chi^2$ metric (Liu and Setiono, 1995), because of its simplicity and effectiveness. However, this filter requires data to be discrete, so a discretization stage has to be added to preprocess the data. Finally, a classifier is necessary, and the well-known naive Bayes (Rish, 2001) was chosen. This decision has been made because after performing the three stages in each node (discretization, selection and classification), the learned models are combined in a incremental manner, and naive Bayes has some characteristics that makes it inherently incremental. With the proposed methodology, it is expected that the global learning process will be sped up and so become more computationally efficient.

The rest of the paper is organized as follows: section 2 presents the state of the art in the field of distributed learning, section 3 describes the method proposed in this research, section 4 introduces the experimental settings and results and, finally, section 5 reveals the conclusions and future lines of research.

## 2 BACKGROUND AND RELATED WORK

Most of the research in the literature concerning distributed learning proposes privacy-preserving methods for horizontally partitioned data. A meta-learning approach has been developed that uses classifiers trained at different sites to develop a global classifier (Prodromidis et al., 2000). In (Wolpert, 1992; Chawla et al., 2002; Tsoumakas and Vlahavas, 2002; Kantarcioglu and Clifton, 2004; Tsoumakas and Vlahavas, 2009), the authors proposed several privacy-preserving classification methods for horizontally partitioned data. However, previous research in distributed classification for vertically partitioned data is rather sparse. In (Vaidya and Clifton, 2005), it is introduced a generalized privacy preserving variant of the ID3 algorithm for vertically partitioned data distributed over two or more parties. In (Vaidya and Clifton, 2004), the authors addressed classification over vertically partitioned data where either all the parties hold the class attribute, or only a subset of the parties have the class attribute. The basic idea behind their protocol is that each party ends up with shares of the conditionally independent probabilities that constitute the parameters of a Naïve Bayes classifier. In (Gangrade and Patel, 2013), all party calculates probabilities (model parameters of a Naïve Bayes classifier) of all class value for each attribute value for every attribute individually, causing no privacy breaches. They use secure multiplication protocol for multiplying the probabilities of particular values of all attributes for all class value and compare total probability of all class value and find out the maximum total probability. Other research has addressed classification using Bayesian networks in vertically partitioned data (Chen et al., 2001), and situations where the distribution is itself interesting with respect to what is learned (Wirth et al., 2001).

On the other hand, regarding distributed feature selection, a distributed privacy-preserving method to perform feature subset selection that handles both horizontal as well as vertical data partitioning is proposed in (Banerjee and Chakravarty, 2011). In that paper a secure distributed protocol was proposed. It allows feature selection for multiple parties without revealing their own data evolving from a method called virtual dimension reduction. This method is used in the field of hyperspectral image processing for selection of subset of hyperspectral bands for further analysis. In (Ye et al., 2010), the authors addressed attribute reduction over vertically partitioned data, where two parties, each having a private dataset want to collaboratively conduct global attribute reduction. By using a semi-trusted third party and commutative encryption, they presented some secure multi-party computation (SMC) protocols (Yao, 1982) into privacy preserving attribute reduction algorithms. But the method is only proven secure under the semi-honest model, and security under this adversary model is insufficient. SMC protocols under the malicious adversary model generally have impractically high complexities for privacy-preserving data mining.

As can be seen, distributed classification algorithms are becoming more popular in machine learning. Moreover, some first steps are taken towards developing distributed feature selection methods. However, to the best knowledge of the authors, none of the previous research addresses both distributed feature selection and classification simultaneously on vertically partitioned data.

## 3 THE PROPOSED METHOD

As stated before, distributed feature selection on vertically partitioned data has not been deeply explored yet. Distributed methods usually consist of three stages:

1. Partition of the dataset (if the dataset is not distributed from origin).
2. Application of learning methods in each node. In the case of the method proposed herein, it consists of three steps:
   (a) Discretization.
   (b) Feature selection.
   (c) Classification.
3. Combination of the results.

The interest of this work relies on the independence of the methodology, that can be performed on all the nodes at the same time. Besides, the novelty in the combination stage is that it is done in an incremental manner. As explained before, the learning methodology to be applied to each node consists of three steps: discretization, feature selection and classification (see Figure 1).

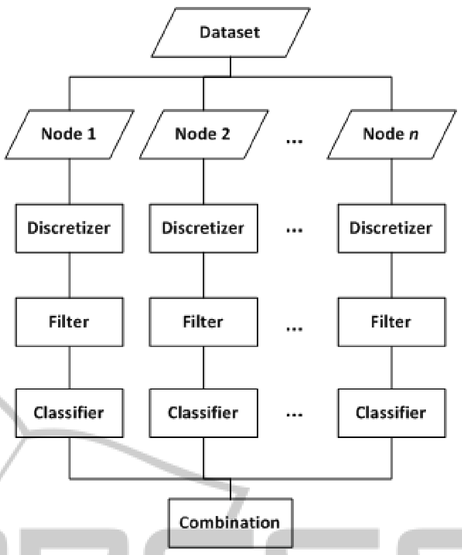


Figure 1: Flow chart of proposed methodology.

### 3.1 Partition of the Dataset

In some cases, data can be originally distributed by features. In this manner, different features belonging to the same sample are recorded in different locations. Each node gathers the values for one or more features for a given instance and then, each node has a different "view" of the data. For instance, a sensor network usually records a single feature in each sensor. Another example may be a patient that performs several medical tests in different hospitals. In such these situations, a distributed learning approach can be much more efficient computationally than moving all distributed datasets into a centralized site for learning the global model. Moreover, even when data are stored in a single site, distributed learning can be also useful to speed up the process.

As most of the datasets publicly available are stored in a centralized manner, the first step consists of partitioning the dataset, i.e. dividing the original dataset into several disjoint subsets of approximately the same size that cover the full dataset. As mentioned in the introduction, in this research the partition will be done vertically, as can be seen in Figure 2. Notice that this step could be eliminated in a real distributed situation.

### 3.2 Learning Methods

In this research, the learning stage consists of three steps: discretizer, filter and classifier, which will be following described.

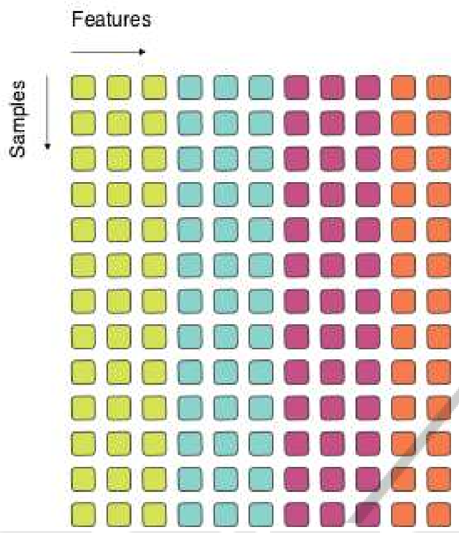


Figure 2: Vertical partition of the data.

### 3.2.1 Discretizer

Many filter algorithms are shown to work effectively on discrete data (Liu and Setiono, 1997), so discretization is a recommended as a previous step. The well-known $k$-means discretization algorithm (Tou and González, 1977; Ventura and Martinez, 1995) was chosen because of its simplicity and effectiveness. $K$-means moves the representative weights of each cluster along an unrestrained input space, where each feature is discretized independently, making it suitable for our purposes. This clustering algorithm operates on a set of data points and assumes that the number of clusters to be determined ($k$) is given. The partition is done based on certain objective function. The most frequently used criterion function in $k$-means is minimizing the squared error $\varepsilon$ between the centroids $\mu_i$ of clusters $c_i, i = 1, \ldots, k$ and the samples in those clusters

$$\varepsilon = \sum_{x \in c_i} |x - \mu_i|^2$$

Let $C$ be the set of clusters and $|C|$ its cardinality. For each new sample $x$, the discretizer works as follows,

- *If* $|C| < k$ and $x \notin C$ *then* $C = \{x\} \cup C$, i.e. if the maximum number of cluster was not reached already and the new sample is not in $C$, then create a new cluster with its centroid in $x$.
- *else*
  1. Find the closest cluster to $x$.
  2. Update its centroid $\mu$ as the average of all values in that cluster.

The method assigns at most $k$ clusters. Notice that the number of clusters is the minimum between the parameter $k$ and the number of different values in the feature.

### 3.2.2 Filter

The $\chi^2$ method (Liu and Setiono, 1995) evaluates features individually by measuring their chi-squared statistic with respect to the class labels. The $\chi^2$ value of an attribute is defined as:

$$\chi^2 = \sum_{i=1}^{t} \sum_{j=1}^{l} \frac{(A_{ij} - E_{ij})^2}{E_{ij}} \quad (1)$$

where

$$E_{ij} = R_i * L_j / S \quad (2)$$

$t$ being the number of intervals (number of different values in a feature), $l$ the number of class labels, $A_{ij}$ the number of samples in the $i$-th interval, $j$-th class, $R_i$ the number of samples in the $i$-th interval, $L_j$ the number of samples in the $j$-th class, $S$ the total number of samples, and $E_{ij}$ the expected frequency of $A_{ij}$. Note that the size of the matrices is related to the number of intervals. In this manner, a very large $k$ in the discretizer will lead to a very large size of the matrices $A$ and $E$. A very large matrix is computationally expensive to update and this should be taken into account for real-time applications.

After calculating the $\chi^2$ value of all considered features in each node, these values can be sorted with the largest one at the first position, as the larger the $\chi^2$ value, the more important the feature is. This will provide an ordered ranking of features, and a threshold needs to be established. In this research, the choice is to estimate the threshold from the effect on the training set, specifically using 10% of the training dataset available at each node so as to speed up the process. The selection of this threshold must take into account two different criteria: the training error, $e$, and the percentage of features retained, $m$. Both values must be minimized to the extent possible. The fitness function is showed in equation (3), in which the function $f(v)$ is calculated using those features for which the $\chi^2$ value is above $v$.

$$f(v) = \alpha e(v) + (1 - \alpha) m(v) \quad (3)$$

$\alpha$ being a value in the interval [0,1] that measures the relative relevance of both values. Following the recommendations in (de Haro García, 2011), a value of $\alpha = 0.75$ was chosen, since in general the error minimization is more important than storage reduction. For the possible values of the threshold $v$, three options were considered for the experimental part:

- $v = mean(\chi^2)$
- $v = mean(\chi^2) + std(\chi^2)$
- $v = mean(\chi^2) + 2std(\chi^2)$

#### 3.2.3 Classifier

Among the broad range of classifiers available in the literature, the naive Bayes method (Rish, 2001) was chosen for the classification step. This classifier is simple, efficient and robust to noise and irrelevant attributes. Besides, it requires a small amount of input data to estimate the necessary parameters for classification.

Given a set of $l$ mutually exclusive and exhaustive classes $c_1, c_2, \ldots, c_l$, which have prior probabilities $P(c_1), P(c_2), \ldots, P(c_l)$, respectively, and $n$ attributes $a_1, a_2, \ldots, a_n$ which for a given instance have values $v_1, v_2, \ldots, v_n$ respectively, the posterior probability of class $c_i$ occurring for the specified instance can be shown to be proportional to

$$P(c_i) \times P(a_1 = v_1 \text{ and } a_2 = v_2 \ldots \text{ and } a_n = v_n | c_i) \tag{4}$$

Making the assumption that the attributes are independent, the value of this expression can be calculated using the product

$$P(c_i) \times P(a_1 = v_1 | c_i) \times P(a_2 = v_2 | c_i) \times \cdots \times P(a_n = v_n | c_i) \tag{5}$$

This product is calculated for each value of $i$ from 1 to $l$ and the class which has the largest value is chosen. Notice that this method is suitable for a dynamic space of input features.

### 3.3 Combination of the Results

After performing the previous stages, the methodology will return as many trained classifiers as nodes we have. These classifiers are trained using only the features selected in each node. The final step consists of combining all the trained classifiers in an incremental manner, in order to have a unique classifier trained on the subset of features resulted of the union of the features selected in every node. This combination is possible because the naive Bayes classifier is inherently incremental. In this algorithm each feature makes an independent contribution towards the prediction of a class as stated in the previous section.

Notice that the main contribution of this paper relies in this merging step. The formulation of the naive Bayes classifier allows to build an exact solution, i.e. the same as would be obtained in batch learning. For this reason, the solution achieved is more reliable than other schemes, such as voting. Moreover, this methodology is flexible, since it can work independently of the number of nodes, the number of features selected and so on.

## 4 EXPERIMENTAL STUDY

### 4.1 Materials

Table 1 summarizes the number of input features, samples, and output classes of the data sets. A more detailed description of the data sets can be found in (Frank and Asuncion, 2010).

Table 1: Brief description of the binary data sets.

| Name | Features | Training samples | Test samples |
|---|---|---|---|
| Madelon | 500 | 1,600 | 800 |
| MNIST | 717 | 40,000 | 20,000 |
| Mushrooms | 112 | 5,416 | 2,708 |
| Ozone | 72 | 1,691 | 845 |
| Spambase | 52 | 3,068 | 1,533 |

### 4.2 Performance Metrics

In addition to the traditional approach of evaluating the performance of an algorithm in terms of test accuracy, a distributed algorithm can be also evaluated in terms of speed-up (Bramer, 2013). Speed-up experiments evaluate the performance of the system with respect to the number of nodes for a given dataset. We measure the training time as the number of nodes is increased. This shows how much a distributed algorithm is faster than the serial (one processor) version, as the dataset is distributed to more and more nodes. We can define two performance metrics associated with speep-up:

- The *speedup factor* $S_n$ is defined by $S_n = \frac{R_1}{R_n}$, where $R_1$ and $R_n$ are the training times of the algorithm on a single and $n$ nodes, respectively. This factor measures how much the training time is faster using $n$ nodes instead of just one. The ideal case is that $S_n = n$, but the usual situation is that $S_n < n$ because of communication or other overheads. Occasionally, it can be a value greater than $n$, in the case of what is known as *superlinear* speedup.
- The *efficiency* $E_n$ of using $n$ nodes instead of one is defined by $E_n = \frac{S_n}{n}$, i.e. the speedup factor divided by the number of nodes.

## 4.3 Experimental Procedure

The evaluation of the methods has been done using holdout validation. Training data have been scattered across either 2, 4, or 8 nodes; 1 node was also considered to perform a comparative study with the standard centralized approach. Experiments were run 10 times with random partitions of the datasets in order to ensure reliable results. We use the methodology proposed by Demsar (Demšar, 2006) to perform a statistical comparison of the algorithms over the multiple data sets. First a Friedman test (Friedman, 1940) is done and then, if significant differences are found, the Bonferroni-Dunn test (Dunn, 1961) is considered.

## 4.4 Results

Table 2 shows the training time of the algorithm for the different datasets and number of nodes. As can be seen, the training time is dramatically reduced as the number of nodes is increased. Statistical tests demonstrate that doubling the number of nodes obtains significantly better results in terms of time.

Table 2: Training time (s).

| | Number of nodes | | | |
|---|---|---|---|---|
| | 1 | 2 | 4 | 8 |
| Madelon | 127.74 | 63.96 | 31.89 | 16.18 |
| MNIST | 4643.43 | 2336.79 | 1165.28 | 585.93 |
| Mushrooms | 94.28 | 46.96 | 23.58 | 11.82 |
| Ozone | 19.95 | 9.96 | 4.99 | 2.50 |
| Spambase | 28.20 | 14.14 | 7.10 | 3.57 |

Table 3 shows the test accuracy on the different datasets for the different number of nodes. In general terms, the accuracy is maintained as the number of nodes in increased. Statistical tests prove this fact. However, this is not the case of MNIST dataset. The accuracy of the algorithm on this dataset when using 8 nodes is significantly worse in comparison with its performance when using 1 (batch), 2, or 4 nodes. This dataset has a large number of classes, so the less features in each node, the more difficult to find a correlation between them and the classes. For this kind of multiclass datasets, it seems that it is necessary a more exhaustive experimentation to find the optimal number of nodes.

Finally, Figure 3 shows three graphs representing the different measures related with the time performance of the algorithm. Figure 3(a) plots the training time versus the number of nodes. Figure 3(b) shows a graph of speedup factor against the number of nodes. This form of display is often preferred to the more obvious plot of training time versus the number of nodes, as it makes straightforward to see the impact on the training time of increasing the number of nodes. As can be deduced from Figure 3(c), the efficiency of the proposed method is close to 1, i.e. increasing the number of nodes by *n* divides the training time by the same *n*. Notice the implications of these results when dealing with high dimensional datasets. The training time may be notably reduced without compromising the classification accuracy. In this manner, the proposed methodology allows to deal with problems which were intractable with classical approaches.

Table 3: Test accuracy (%).

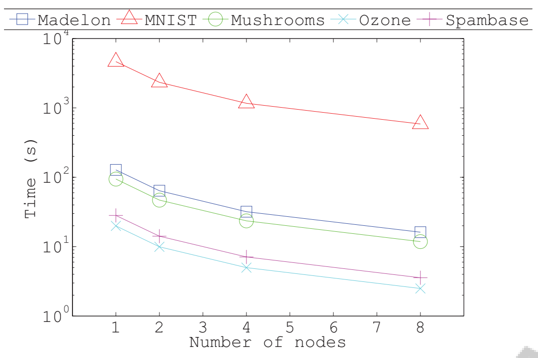
| | Number of nodes | | | |
|---|---|---|---|---|
| | 1 | 2 | 4 | 8 |
| Madelon | 71.38 | 71.27 | 71.05 | 70.82 |
| MNIST | 76.26 | 76.31 | 76.36 | 67.06 |
| Mushrooms | 93.25 | 92.04 | 91.81 | 91.78 |
| Ozone | 86.15 | 85.93 | 85.76 | 85.73 |
| Spambase | 88.78 | 88.72 | 88.76 | 88.81 |

## 5 CONCLUSIONS

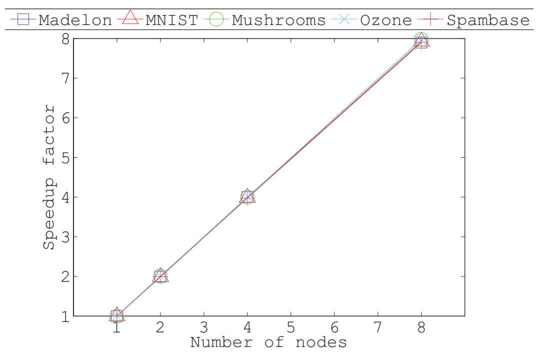
In this work, a new method for scaling up feature selection was proposed. The idea was to vertically distribute the data and then performing a feature selection process which could be carried out at separate nodes. Thus, the proposed methodology consists of three different steps: discretization of the data, feature selection, and classification. All the stages are executed in parallel and finally, the learned models obtained from each node are combined in an incremental manner. For this reason, the classical naive Bayes classifier was modified so as to be able to make it work incrementally.

The proposed methodology has been tested on five datasets considered representative of problems from medium to large size, and different numbers of nodes to distribute the data were considered. As expected, the larger the number of nodes, the shorter the time required for the computation. However, in most of the datasets, increasing the number of the nodes did not lead to a significative degradation in classification accuracy.

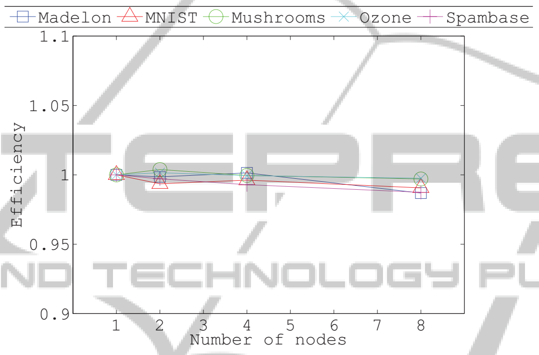
As future work, we plan to continue this research using other feature selection algorithms and classifiers, and trying another distributed approach where all nodes share their results after each step (discretization, feature selection and classification). In this sense, the difficult of this future line of research lies on the fact that for this approach, all the methods have to be adapted to work in an incremental fashion.



(a) Nodes vs time



(b) Speed up



(c) Efficiency

Figure 3: Plots regarding time performance of the algorithm.

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