SEMI-SUPERVISED EVALUATION OF CONSTRAINT SCORES FOR FEATURE SELECTION

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Abstract: Recent feature constraint scores, that analyse must-link and cannot-link constraints between learning samples, reach good performances for semi-supervised feature selection. The performance evaluation is generally based on classification accuracy and is performed in a supervised learning context. In this paper, we propose a semi-supervised performance evaluation procedure, so that both feature selection and classification take into account the constraints given by the user. Extensive experiments on benchmark datasets are carried out in the last section. They demonstrate the effectiveness of feature selection based on constraint analysis.

1 INTRODUCTION

In machine learning and pattern recognition applications, the processing of high dimensional data requires large computation time and capacity storage. Though, it leads to poor performances when the dimensionality to sample size ratio is high. To improve performances of data classification, the sample dimensionality is reduced thanks to a feature selection scheme. It consists in selecting the most relevant features in order to build a low dimensional feature space. One generally assumes that a classifier scheme operating in this low dimensional feature space outperforms the same classifier operating in the initial feature space

The feature subspace can be selected thanks to a non-exhaustive sequential feature selection procedure which iteratively adds selected features (Kudo and Sklansky, 2000). However, such a strategy is time consuming since it evaluates properties of different multi-dimensional sub-spaces. That leads authors to sort the score of each feature, so that the feature subspace is composed of the most relevant ones (Liu and Motoda, 1998).

During the training step, the score of each feature is evaluated thanks to the subset of training samples. They can be either unlabelled or labelled, leading to the development of unsupervised and supervised feature selection techniques. Unsupervised feature score measures the feature ability of keeping the intrinsic data structure. In the supervised learning context, the feature score is based on the correlation between the feature and the class labels of the training samples.

However, in the supervised learning context, the sample labelling process achieved by the user is fastidious and expensive. That is the reason why for many real applications, the training data subset is composed of a few labelled samples and huge unlabelled ones. To deal with this 'lack labelled-sample problem', recent semi-supervised feature scores have been developed (Zhao and Liu, 2007),(Zhao et al., 2008).

Beside class labels of samples, there is another kind of user supervision information called the pairwise constraints. The user simply specifies whether a pair of training samples must be regrouped together (must-link constraints) or cannot be regrouped together (cannot-link constraints). Recent feature scores called constraint scores, that analyse must-link and cannot link constraints, have shown excellent performance of semi-supervised learning with a lot of datasets (Zhao et al., 2008),(Zhang et al., 2008).

To measure the performances reached by feature selection schemes based on constraint scores, authors use benchmark datasets composed of labeled samples. Each dataset is divided into the training and the test subsets according to the holdout strategy. A small number of must-link and cannot-link constraints are deduced from the labeled samples of the training subset. Finally, the training subset is only composed of

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constrained and unconstrained samples without any knowledge about their label. First, the features are selected by sorting their constraint scores obtained with the training samples. Then, the performance of the feature selection algorithm based on each constraint score is measured by the classification accuracy of test samples reached by a classifier operating in the feature space defined by the selected features. The nearest neighbor classifier is the most used for this purpose. As it requires a lot of prototypes of the classes, it uses training samples with their labels as prototypes whereas these labels have not been exploited by the constraint scores. Indeed, a constraint score only analyses unconstrained data samples and/or a few pairwise constraints. So, the test samples are classified in a supervised learning context (the prototypes are the training samples with their labels) whereas the features are selected in a semi-supervised learning context (only constraints on a few training samples are considered).

In this paper, we propose a semi-supervised evaluation procedure of performance reached with the constraint scores, so that both feature selection and test sample classification take into account the constraints given by the user.

The paper is organized as follows. Constraint scores used by semi-supervised feature selection schemes, are introduced in section 2. In section 3, we describe our semi-supervised procedure of constraint score evaluation. Finally, experiments presented in section 4, compare the performances of the different constraint scores thanks to the semi-supervised evaluation.

2 CONSTRAINT SCORES

Given the training subset composed of n samples defined in a d-dimensional feature space, let us denote $\mathcal{X} = (x_{ir})\ i = 1,\ldots,n;\ r = 1,\ldots,d$; the associated data matrix where x_{ir} is the r^{th} feature value of the i^{th} data. Each of the n rows of the matrix $\mathcal{X}$ represents a data sample $x_i = (x_{i1},\ldots,x_{id}) \in \mathbb{R}^d$, while each of the d columns of $\mathcal{X}$ defines the feature values $f_r = (x_{1r},\ldots,x_{nr})^T \in \mathbb{R}^n$.

2.1 Constraints

In the semi-supervised learning context, the prior knowledge about the data is usually represented by sample labels. Furthermore, another kind of knowledge is represented by pairwise constraints. Pairwise constraints simply mention for some pairs of data samples that they are similar, i.e. must be grouped together (must-link constraints), or that they are dissimilar, i.e. cannot be grouped together (cannot-link constraints). These pairwise constraints arise naturally in many applications since they are easier to be obtained by the user than the class labels. They simply formalize that two data samples belong or not to the same class without detailed information about the different classes.

The user has to build the subset $\mathcal{M}$ of must-link constraints and the subset $\mathcal{C}$ of cannot-link constraints defined as:

$\mathcal{M} = \{(x_i,x_j),\ \textit{such as } x_i \textit{ and } x_j \textit{ must be linked}\}$,

$\mathcal{C} = \{(x_i,x_j),\ \textit{such as } x_i \textit{ and } x_j \textit{ cannot be linked}\}$.

The cardinals of these subsets are usually much lower than the number $n(n-1)/2$ of all possible pairwise constraints defined by the data.

In the context of the spectral theory, two specific graphs are built from these two subsets:

- The must-link graph $G^{\mathcal{M}}$ where a connection is established between two nodes i and j if there is a must-link constraint between their corresponding samples (nodes) x_i and x_j.
- The cannot-link graph $G^{\mathcal{C}}$ where two nodes i and j are connected if there is a cannot-link constraint between their corresponding samples (nodes) x_i and x_j.

The connection weights between two nodes of the graphs $G^{\mathcal{M}}$ and $G^{\mathcal{C}}$ are respectively stored by the similarity matrices $S^{\mathcal{M}}$ $(n \times n)$ and $S^{\mathcal{C}}$ $(n \times n)$, and are built as:

$$s_{ij}^{\mathcal{M}} = \begin{cases} 1 & \text{if } (x_i,x_j) \in \mathcal{M} \text{ or } (x_j,x_i) \in \mathcal{M} \\ 0 & \text{otherwise,} \end{cases} \quad (1)$$

$$s_{ij}^{\mathcal{C}} = \begin{cases} 1 & \text{if } (x_i,x_j) \in \mathcal{C} \text{ or } (x_j,x_i) \in \mathcal{C} \\ 0 & \text{otherwise.} \end{cases} \quad (2)$$

2.2 Scores

This prior knowledge represented by the constraints has been integrated in many recent feature scores (Zhang et al., 2008) (Zhao et al., 2008) (Kalakech et al., 2011).

Zhang et al. propose two constraint scores C_r^1 and C_r^2 which use only the subset of must-link and cannot-link constraints (Zhang et al., 2008):

$$C_r^1 = \frac{\sum_i \sum_j (x_{ir} - x_{jr})^2 s_{ij}^{\mathcal{M}}}{\sum_i \sum_j (x_{ir} - x_{jr})^2 s_{ij}^{\mathcal{C}}} = \frac{f_r^T L^{\mathcal{M}} f_r}{f_r^T L^{\mathcal{C}} fr}, \quad (3)$$

$$C_r^2 = \sum_i \sum_j (x_{ir} - x_{jr})^2 s_{ij}^{\mathcal{M}} - \lambda \sum_i \sum_j (x_{ir} - x_{jr})^2 s_{ij}^{\mathcal{C}} = f_r^T L^{\mathcal{M}} f_r - \lambda f_r^T L^{\mathcal{C}} f_r, \quad (4)$$

where $L^{\mathcal{M}} = D^{\mathcal{M}} - S^{\mathcal{M}}$ and $L^{\mathcal{C}} = D^{\mathcal{C}} - S^{\mathcal{C}}$, are the constraint Laplacian matrices, $D^{\mathcal{M}}$ and $D^{\mathcal{C}}$ are the degree matrices defined by $D^{\mathcal{M}}_{ii} = d^{\mathcal{M}}_i$ ($d^{\mathcal{M}}_i = \sum_{j=1}^{n} s^{\mathcal{M}}_{ij}$) and $D^{\mathcal{C}}_{ii} = d^{\mathcal{C}}_i$ ($d^{\mathcal{C}}_i = \sum_{j=1}^{n} s^{\mathcal{C}}_{ij}$) and λ is a regularization coefficient used to balance the contribution of must-link and cannot-link constraints. Must-link constraints are favored by setting $0 < \lambda < 1$ and the lower these two scores are, the more efficient the feature is.

Zhao et al. define another score which uses both unconstrained data and pairwise constraints in order to retrieve both locality properties and discriminating structures of the data samples (Zhao et al., 2008). They build a new graph $G^{\mathcal{W}}$ that connects samples having high probability of sharing the same label:

- $G^{\mathcal{W}}$ is the within-class graph: two nodes i and j are connected if (x_i, x_j) or (x_j, x_i) belongs to $\mathcal{M}$, or if one of the two samples is unconstrained but they are sufficiently close to each other (by using the k-nearest neighbor graph denoted kNN)

The edges in the graph $G^{\mathcal{W}}$ are weighted by using the similarity matrix $S^{\mathcal{W}}$ $(n \times n)$ expressed as:

$$s^{\mathcal{W}}_{ij} = \begin{cases} \gamma \text{ if } (x_i, x_j) \in \mathcal{M} \text{ or } (x_j, x_i) \in \mathcal{M} \\ 1 \text{ if } x_i \text{ or } x_j \text{ is unlabeled} \\ \text{but } x_i \in kNN(x_j) \text{ or } x_j \in kNN(x_i) \\ 0 \text{ otherwise} \end{cases} \quad (5)$$

where γ is a suitable constant parameter which has been empirically set to 100 in (Zhao et al., 2008).

Zhao et al. also introduce a Laplacian score, called the locality sensitive discriminant analysis score and defined as:

$$C^3_r = \frac{\sum_i \sum_j (x_{ir} - x_{jr})^2 s^{\mathcal{W}}_{ij}}{\sum_i \sum_j (x_{ir} - x_{jr})^2 s^{\mathcal{C}}_{ij}} = \frac{f_r^T L^{\mathcal{W}} f_r}{f_r^T L^{\mathcal{C}} f_r}. \quad (6)$$

where $L^{\mathcal{W}} = D^{\mathcal{W}} - S^{\mathcal{W}}$, $D^{\mathcal{W}}$ being the degree matrix defined by $D^{\mathcal{W}}_{ii} = d^{\mathcal{W}}_i$ ($d^{\mathcal{W}}_i = \sum_{j=1}^{n} s^{\mathcal{W}}_{ij}$). The lower the score C^3 is, the more relevant the feature is.

The scores C^1 and C^2 do not take into account the unconstrained samples since they are only based on the must-link and cannot link constraints. C^3 considers mainly the must-link constraints, so it seems to be very close to C^2 and both neglect the unconstrained samples.

Though, taking into account the unconstrained samples should catch the data structure and make less sensitive a feature score against the given constraint subsets. That is why we have proposed a semi-supervised constraint score C^4 defined as (Kalakech et al., 2011):

$$C^4_r = \frac{\tilde{f}_r^T L \tilde{f}_r}{\tilde{f}_r^T D \tilde{f}_r} . \frac{f_r^T L^{\mathcal{M}} f_r}{f_r^T L^{\mathcal{C}} f_r}, \quad (7)$$

where D and L are respectively the degree and the Laplacian matrices ($L = D - S$) deduced from the similarity matrix S. S $(n \times n)$ is the similarity matrix between all the samples, expressed as:

$$s_{ij} = \exp\left(- \frac{\left\| x_i - x_j \right\|^2}{2t^2} \right). \quad (8)$$

t is a Gaussian parameter ajusted by the user.

The score C^4_r is the simple product between the unsupervised Laplacian score processed with samples (He et al., 2005) and the constraint score C^1_r (see Equation (3)) (Zhang et al., 2008). As for the other scores, the features are ranked in ascending order according to score C^4 in order to select the most relevant ones. We have experimentally demonstrated that this score is less sensitive to the constraint changes than the classical scores while selecting features with comparable classification performances (Kalakech et al., 2011) (Kalakech et al., 2010).

3 EVALUATION SCHEME

In this section, we present the classical supervised evaluation scheme used to evaluate the performances of the features selected by the constraint scores, and propose our new semi-supervised evaluation scheme.

3.1 Supervised Evaluation

In order to compare different feature scores, the dataset is divided into training and test subsets. The feature selection procedure is performed with the training subset. Then, the performance of each constraint score is measured by the accuracy rates of test sample obtained by a classifier such as kNN classifier operating in the feature space defined by the selected features.

The training samples with their true labels are used by the nearest neighbor classifier to classify the test data, whereas these true labels have not been used by the constraint scores. Indeed, these scores use only the unconstrained data and/or a few pairwise constraints given by the user. So, the test samples are classified in the supervised learning context (the prototypes are the training samples with their true labels) whereas the features are selected in the semi-supervised learning context (only constraints on a few training samples are analyzed).

Though, the selection and the evaluation should operate in the same learning context. That is why, unlike to classical supervised evaluation, we propose to perform the score evaluation in a semi-supervised context.

Algorithm 1: Constrained K-means.

1: Choose randomly K samples as the initial class centers.
2: Assign each sample to the closet class while verifying that constraint subsets $\mathcal{M}$ and $\mathcal{C}$ are not violated.
3: Update the center of each class.
4: Iterate 2 and 3 until converge.

3.2 Semi-supervised Evaluation

To compare the performances reached by different feature selection schemes operating in the semi-supervised learning context, the test samples are also classified in the semi-supervised context. For this purpose, feature selection and test sample classification take into account only the constraints given by the user as prior knowledge. To classify the test samples, the nearest neighbor classifier needs to define the labels of the training samples.

In the semi-supervised context, we have no prior knowledge about labels of these training samples. So, to build the prototypes of classes, we propose to estimate the labels of the training samples. As the prior knowledge is described by a few constraints between training samples, we propose to cluster the training samples thanks to the constrained K-means scheme developed by Wagstaff et al. (Wagstaff et al., 2001) (see Algorithm 1). The desired number of classes is set by the user and this scheme operates in the selected features space.

Once the labels of the training samples have been estimated, the nearest neighbor classifier use them as prototypes of classes to classify the test samples.

Since the true classes of the training samples can be different from those determined by the constrained K-means, we cannot directly use these labels to measure the classification accuracy of the test samples. For this purpose, we propose to match the true and estimated labels of the training samples thanks to Carpaneto and Toth algorithm (Carpaneto and Toth, 1980).

4 EXPERIMENTS

In this section, we compare the different constraint scores performances thanks to the semi-supervised evaluation. Experiments are achieved with six well known and largely used benchmark databases, and more precisely the 'Wine', 'Image segmentation' and 'Vehicle' databases from the UCI repository ((Blake et al., 1998)), the face database 'ORL' ((Samaria and Hartert, 1994)) and the two gene expression databases, i.e., 'Colon Cancer'((Alon et al., 1999)) and 'Leukemia'((Golub et al., 1999)). These databases have been retained since the features are numeric and since the label information of each sample is clearly defined.

4.1 Datasets

In our experiments, we first normalize the features between 0 and 1, so that the scale of the different features is the same. For each dataset, we follow a Hold-out partition and choose the half of samples from each class as the training data and the remaining data for testing.

Here is a brief description of the six considered databases:

- **'Wine' Database**
  This database contains 178 samples characterized by 13 features (d=13) composed of 3 classes having 59, 71 and 48 instances, respectively. We randomly select 30, 36 and 24 samples from each class to build the training subset. The remaining samples are considered as the test subset.
- **'Image Segmentation' Database**
  This database contains 210 samples characterized by 19 features (d=19) regrouped into 7 classes, each class having 30 instances. We randomly select 15 samples from each class to build the training subset and the remaining samples constitute the test subset.
- **'Vehicle' Database**
  This database contains 846 samples characterized by 18 features (d=18) regrouped into 4 classes, having 212, 217, 218 and 199 instances, respectively. We randomly select 106, 109, 109 and 100 samples from each class to build the training subset.

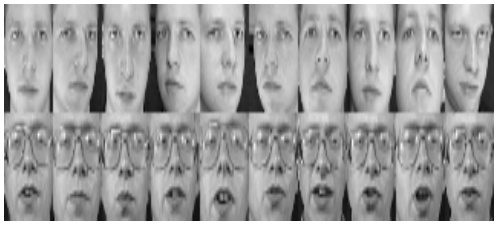


Figure 1: Sample face images from the ORL database (2 subjects).

The 'ORL' database (Olivetti Research Laboratory) contains a set of face images representing 40 distinct subjects. There are 10 different images per subject, so that the database contains 400

images. For each subject, the images have been acquired according to different conditions: lighting, facial expressions (open / closed eyes, smiling / not smiling) and facial details (glasses / no glasses) (see Figure 1).
In our experiments, original images are normalized (in scale and orientation) so that the two eyes are aligned at the same horizontal position. Then, the facial areas are cropped in order to build images of size 32×32 pixels, whose gray level is quantified with 256 levels. Thus, each image can be represented by a 1024-dimensional sample data.
We randomly select 5 images from each class (subject) to build the training subset. The remaining samples are organized as the test subset.

- **'Colon Cancer'** database
  This database contains 62 tissues (40 tumors and 22 normals) characterized by the expression of 2000 genes. We randomly select 20 and 11 samples from each class to build the training subset. The remaining data are organized as the test subset.
- **'Leukemia'** database
  This database contains information on gene-expression in samples from human acute myeloid (AML) and acute lymphoblastic leukemias (ALL). From the originally measured 6817 genes, the genes that are not measured in at least one sample, are removed. So a total of 5147 genes are examined in the experiments.
  Because Leukemia has a predefined partition of the data into training (27 ALL and 11 AML) and test (20 ALL and 14 AML) subsets ((Golub et al., 1999)), all the experiments on this dataset are performed on these predefined training and test subsets.

4.2 Experimental Procedure

In our experiments, the feature selection is performed on the training samples and features are ranked according to the different scores. At each feature selection run q, q=1,..., p, we simulate the generation of pairwise constraints as follow: we randomly select pairs of samples from the training subset and create must-link or cannot-link constraints depending on whether the underlying classes of the two samples are the same or different. We iterate this scheme until we obtain l must-link constraints and l cannot-link constraints, l being set by the user.

The classification accuracies of the test samples are used to evaluate the performance of each score. The rates of good classification are averaged over $p =$ 100 runs with different generations of constraints. 10 constraints (l=5) have been considered for the 'Wine', 'Image segmentation', 'Vehicle' and 'ORL' databases and 60 constraints (l=30) have been considered for the 'Colon Cancer' and 'Leukemia' ones.

4.3 Accuracy vs. Number of Features

We compare the accuracy rates of the different scores C^1, C^2, C^3 and C^4 thanks to our semi-supervised evaluation procedure. The labels of the training data are estimated by the constrained K-means algorithm operating in the selected feature space. These estimated labels are then used by the nearest neighbor classifier in order to measure the accuracy of the different scores.

Figure 2 shows the accuracy rates vs the desired number of selected features on the databases of 'Wine','Image segmentation', 'Vehicle', 'ORL', 'Colon cancer' and 'Leukemia.

From this figure, we can see that the accuracy rates of C^1, C^2, C^3 and C^4 are very close, because the different curves overlap. Since these results are averaged over 100 runs, it is hard to compare them.

That leads us to compare these scores by examining their accuracies at each of the 100 runs. For a fixed number of selected features, in each of the 100 runs, we propose to rank the 4 scores in descending order of their accuracy.

Let us denote $rank_q^*$ the rank of the criterion C^* at the run q. This rank takes the values 1, 2, 3 or 4. At each run q, the score having the highest accuracy is ranked as 1 and the score with the lowest accuracy value, is ranked as 4. Scores with the same accuracy have the same rank.

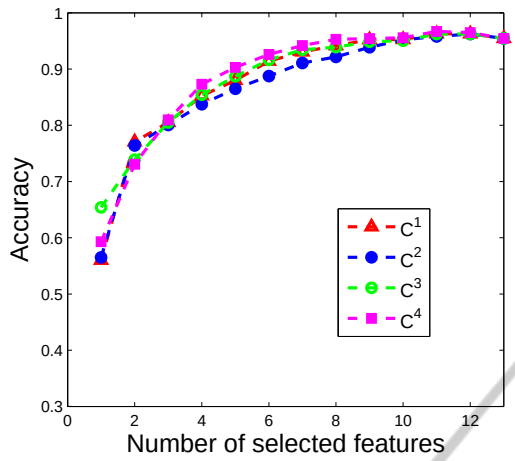
We calculate the rank sum T^* for each semi-supervised constraint score as follow:

$$T^* = \sum_{q=1}^{100} rank_q^*, \tag{9}$$

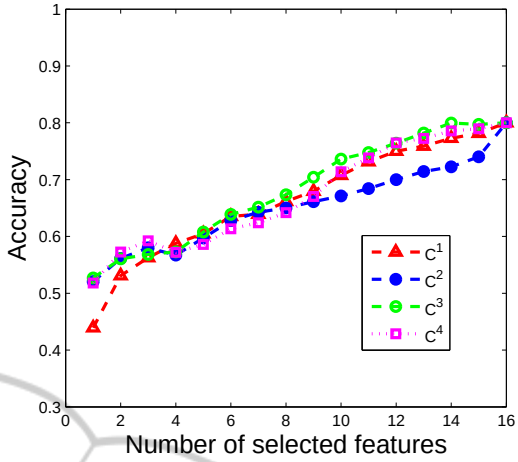
where * is 1, 2, 3 or 4 corresponding to the score C^1, C^2, C^3 or C^4 respectively. The method with the lowest rank sum is considered as being the score which provides the best results.

Table 1 shows the rank sum T^* for the different databases 'Wine', 'Image segmentation', 'Vehicle', 'ORL', 'Colon Cancer' et 'Leukemia'. The rank sum of each score is computed by considering respectively the first 6, 5, 8, 300, 1000 and 2576 features on the 'Wine', 'Image segmentation', 'Vehicle' and 'ORL' databases.

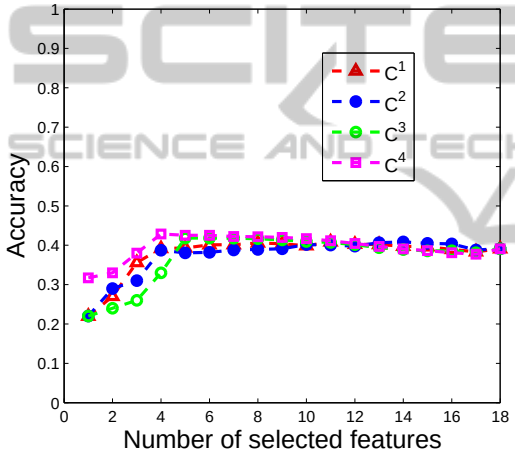
Our score C^4 has the lowest value 3 times (indicated as bold) over the 6 rows of table 1. The other three scores share each one a row.



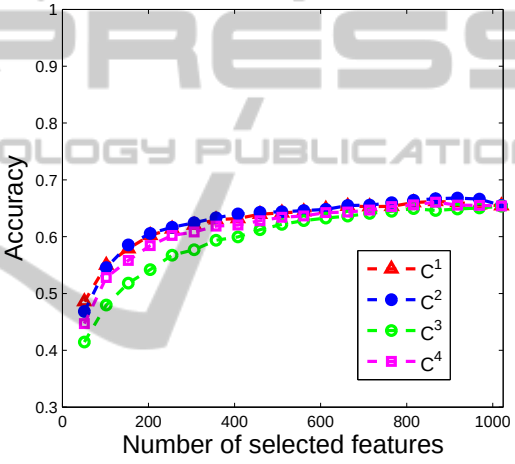
(a) 'Wine'.



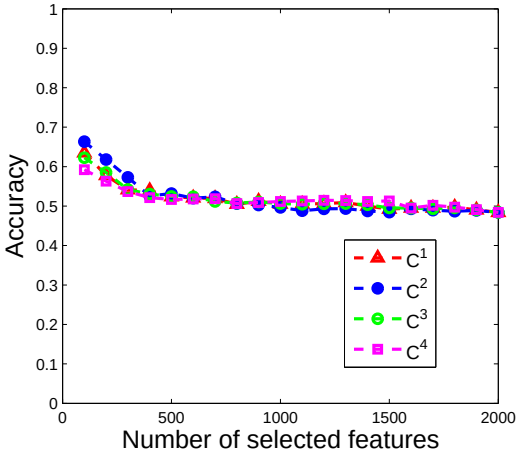
(b) 'Image segmentation'.



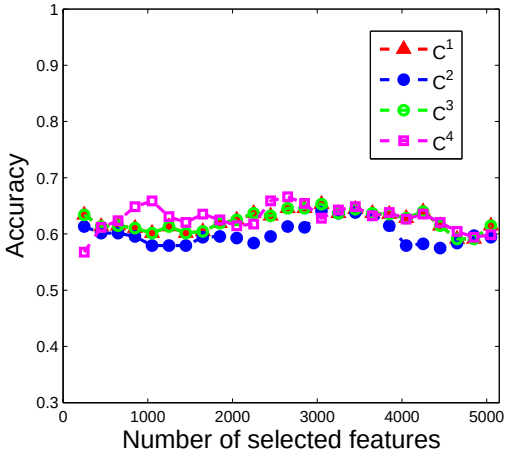
(c) 'Vehicle'.



(d) 'ORL'.



(e) 'Colon Cancer'.



(f) 'Leukemia'.

Figure 2: Accuracy rates vs. the desired number of selected features on the 6 databases. 10 constraints composed of 5 must-link et 5 cannot-link was used for the 'Wine', 'Image segmentation', 'Vehicle' and 'ORL' databases and 60 constraints composed of 30 must-link and 30 cannot-link was used for the 'Colon Cancer' and 'Leukemia' databases. The evaluation is performed in a semi-supervised learning context: the one nearest neighbor classifier uses the estimated labels of the training samples as prototypes of classes.

Table 1: The rank sum of the constraint scores on different databases.

Database $\backslash T$	T^1	T^2	T^3	T^4
'Wine'	191	277	206	**157**
'Image segmentation'	165	219	**161**	196
'Vehicle'	261	239	238	**209**
'ORL'	230	**200**	264	228
'Colon Cancer'	150	216	162	**150**
'Leukemia'	**140**	240	140	176

These results show that the features selected by C^4 provide accuracy rates that are higher than those obtained by features selected by the classical scores. This same conclusion was found in our earlier work that follows the classical supervised evaluation of the constraint scores (Kalakech et al., 2011) (Kalakech et al., 2010).

4.4 Accuracy vs. Number of Constraints

We compare the accuracy rates of the different scores with a fixed number of features vs. number of pairwise constraints.

Figure 3 displays the plot of accuracy with a fixed number of selected features (half of the number of original features (Sun and Zhang, 2010) vs. different number of pairwise constraints on the two gene expression databases. The accuracy of the test samples is measured thanks to the supervised evaluation scheme.

From this figure, we can see that, for almost all the number of constraints, our score C^4 provides higher accuracy than C^1, C^2 and C^3. We can also notice that the accuracy does not tend to increase with respect to the number of constraints. This is due to the constraints choice. Since these constraints are randomly generated, some of them could be less informative than the others.

Table 2: The rank sum of the constraint scores for different number $2l$ of constraints on the 'Colon Cancer' database.

$2l\backslash T$	T^1	T^2	T^3	T^4
4 constraints	**140**	157	153	224
10 constraints	242	**147**	201	153
40 constraints	153	268	169	**124**
60 constraints	257	171	194	**151**

Furthermore, Tables 2 and 3 show the rank sum T^* for different number $2l$ of constraints (4, 10, 40 and 60) on the 'Colon Cancer' and the 'Leukemia' databases, respectively. The rank sum of each of the semi-supervised criteria is calculated with the half of the original features of each of the gene expression databases.

Table 3: The rank sum of the constraint scores for different number $2l$ of constraints on the 'Leukemia' database.

$2l\backslash T$	T^1	T^2	T^3	T^4
4 constraints	194	215	210	**190**
10 constraints	234	176	159	**150**
40 constraints	148	198	196	**123**
60 constraints	167	170	184	**115**

We can see that, for the 'Colon Cancer' database, our score provides the lowest rank sum T (indicated in bold) for 2 times over the 4 rows of Table 2 (when the number of constraints is higher than 10). For the 'Leukemia database', our score provides the lowest rank sum T (indicated in bold) for the different numbers of constraints (4, 10, 40 and 60). These results show that the features selected thanks to our score C^4 provide accuracy rates which are higher than those obtained by the features selected by constraint scores C^1, C^2 and C^3. The same conclusions were found using the classical supervised evaluation (Kalakech et al., 2011).

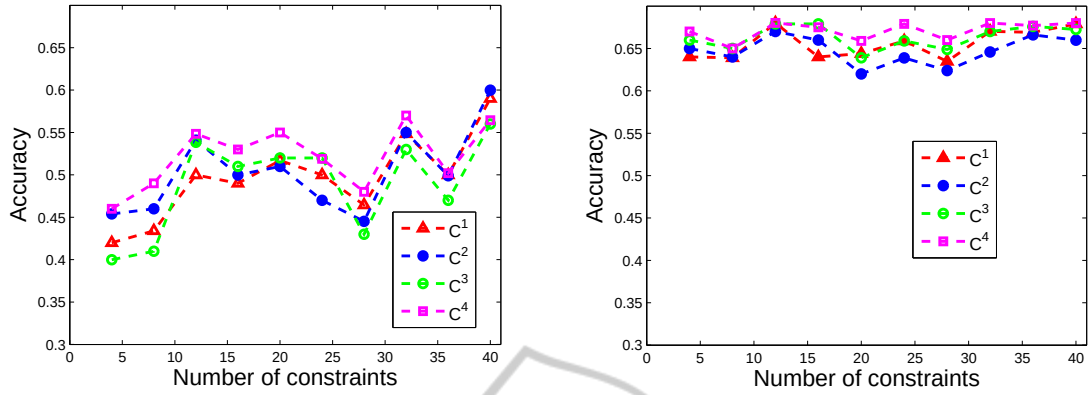
5 CONCLUSIONS

The accuracy rates of test samples reached by a classifier that analyses the features selected by the constraint scores, are generally compared in the supervised learning context. The nearest neighbor classifier uses the training sample labels as prototypes of classes. However, the feature selection has been performed in a semi-supervised context, since it uses the available constraint sets and/or the unconstrained samples.

So, we have proposed in this paper, to keep the same learning context for the feature selection as for the evaluation. The prior knowledge represented by must-link and cannot-link constraints is used for the selection and for the classification. The training sample labels are estimated by using the constrained K-means algorithm that tries to respect the constraints as much as possible. These estimated labels are then used as prototypes by the nearest neighbor classifier to classify the test samples. We called this approach semi-supervised evaluation to distinguish it from the classical supervised one.

The comparison between the different constraint scores thanks to this semi-supervised evaluation shows that the accuracy rates provided by our score are higher than those of the classical scores.

We notice that the constrained K-means used during the semi-supervised evaluation is a simple clustering algorithm. It does not guarantee the respect of all



(a) 'Colon Cancer'. (b) 'Leukemia'.

Figure 3: Accuracy rates vs. number of constraints for C^1, C^2, C^3 and C^4 on the gene expression databases thanks to the semi-supervised evaluation scheme. The desired number of selected features is half of the number of the original features.

the constraints specially when several constraints are defined with the same sample. So, it will be interesting to use another constrained classification algorithm that is more efficient than this one, as these presented by Kulis et al. (Kulis et al., 2009) and Davidson et al. (Davidson et al., 2006).

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