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A Fast Clustering-Based Feature Subset Selection Algorithm for High Dimensional Data

Qinbao Song, Jingjie Ni and Guangtao Wang

Abstract—Feature selection involves identifying a subset of the most useful features that produces compatible results as the original entire set of features. A feature selection algorithm may be evaluated from both the efficiency and effectiveness points of view. While the efficiency concerns the time required to find a subset of features, the effectiveness is related to the quality of the subset of features. Based on these criteria, a fast clustering-based feature selection algorithm, FAST, is proposed and experimentally evaluated in this paper. The FAST algorithm works in two steps. In the first step, features are divided into clusters by using graph-theoretic clustering methods. In the second step, the most representative feature that is strongly related to target classes is selected from each cluster to form a subset of features. Features in different clusters are relatively independent, the clustering-based strategy of FAST has a high probability of producing a subset of useful and independent features. To ensure the efficiency of FAST, we adopt the efficient minimum-spanning tree clustering method. The efficiency and effectiveness of the FAST algorithm are evaluated through an empirical study. Extensive experiments are carried out to compare FAST and several representative feature selection algorithms, namely, FCBF, ReliefF, CFS, Consist, and FOCUS-SF, with respect to four types of well-known classifiers, namely, the probability-based Naive Bayes, the tree-based C4.5, the instance-based IB1, and the rule-based RIPPER before and after feature selection. The results, on 35 publicly available real-world high dimensional image, microarray, and text data, demonstrate that FAST not only produces smaller subsets of features but also improves the performances of the four types of classifiers.

Index Terms—Feature subset selection, filter method, feature clustering, graph-based clustering

1 Introduction

With the aim of choosing a subset of good features with respect to the target concepts, feature subset selection is an effective way for reducing dimensionality, removing irrelevant data, increasing learning accuracy, and improving result comprehensibility [43], [46]. Many feature subset selection methods have been proposed and studied for machine learning applications. They can be divided into four broad categories: the Embedded, Wrapper, Filter, and Hybrid approaches.

The embedded methods incorporate feature selection as a part of the training process and are usually specific to given learning algorithms, and therefore may be more efficient than the other three categories[28]. Traditional machine learning algorithms like decision trees or artificial neural networks are examples of embedded approaches[44]. The wrapper methods use the predictive accuracy of a predetermined learning algorithm to determine the goodness of the selected subsets, the accuracy of the learning algorithms is usually high. However, the generality of the selected features is limited and the computational complexity is large. The filter methods are independent of learning algorithms, with good generality. Their computational complexity is low, but the accuracy of the learning algorithms is not guaranteed [13], [63], [39]. The hybrid methods are a combination of filter and wrapper methods [49], [15], [66], [63], [67] by using a filter method to reduce search space that will be considered by the subsequent wrapper. They mainly focus on combining filter and wrapper methods to achieve the best possible performance with a particular learning algorithm with similar time complexity of the filter methods. The wrapper methods are computationally expensive and tend to overfit on small training sets [13], [15]. The filter methods, in addition to their generality, are usually a good choice when the number of features is very large. Thus, we will focus on the filter method in this paper.

With respect to the filter feature selection methods, the application of cluster analysis has been demonstrated to be more effective than traditional feature selection algorithms. Pereira et al. [52], Baker et al. [4], and Dhillon et al. [18] employed the distributional clustering of words to reduce the dimensionality of text data.

In cluster analysis, graph-theoretic methods have been well studied and used in many applications. Their results have, sometimes, the best agreement with human performance [32]. The general graph-theoretic clustering is simple: Compute a neighborhood graph of instances, then delete any edge in the graph that is much longer/shorter (according to some criterion) than its neighbors. The result is a forest and each tree in the forest represents a cluster. In our study, we apply graph-theoretic clustering methods to features. In particular, we adopt the minimum spanning tree (MST) based clustering algorithms, because they do not assume that data points are grouped around centers or separated by a regular geometric curve and have been widely used in practice.

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Based on the MST method, we propose a Fast clustering-bAsed feature Selection algoriThm (FAST).The FAST algorithm works in two steps. In the first step, features are divided into clusters by using graph-theoretic clustering methods. In the second step, the most representative feature that is strongly related to target classes is selected from each cluster to form the final subset of features. Features in different clusters are relatively independent, the clustering-based strategy of FAST has a high probability of producing a subset of useful and independent features. The proposed feature subset selection algorithm FAST was tested upon 35 publicly available image, microarray, and text data sets. The experimental results show that, compared with other five different types of feature subset selection algorithms, the proposed algorithm not only reduces the number of features, but also improves the performances of the four well-known different types of classifiers.

The rest of the article is organized as follows: In Section 2, we describe the related works. In Section 3, we present the new feature subset selection algorithm FAST. In Section 4, we report extensive experimental results to support the proposed FAST algorithm. Finally, in Section 5, we summarize the present study and draw some conclusions.

2 Related work

Feature subset selection can be viewed as the process of identifying and removing as many irrelevant and redundant features as possible. This is because: (i) irrelevant features do not contribute to the predictive accuracy [33], and (ii) redundant features do not redound to getting a better predictor for that they provide mostly information which is already present in other feature(s).

Of the many feature subset selection algorithms, some can effectively eliminate irrelevant features but fail to handle redundant features [23], [31], [37], [34], [45], [59], yet some of others can eliminate the irrelevant while taking care of the redundant features [5], [29], [42], [68]. Our proposed FAST algorithm falls into the second group.

Traditionally, feature subset selection research has focused on searching for relevant features. A well known example is Relief [34], which weighs each feature according to its ability to discriminate instances under different targets based on distance-based criteria function. However, Relief is ineffective at removing redundant features as two predictive but highly correlated features are likely both to be highly weighted [36]. Relief-F [37] extends Relief, enabling this method to work with noisy and incomplete data sets and to deal with multi-class problems, but still cannot identify redundant features.

However, along with irrelevant features, redundant features also affect the speed and accuracy of learning algorithms, and thus should be eliminated as well [36], [35], [31]. CFS [29], FCBF [68] and CMIM [22] are examples that take into consideration the redundant features. CFS [29] is achieved by the hypothesis that a good feature subset is one that contains features highly correlated with the target, yet uncorrelated with each other. FCBF ([68], [71]) is a fast filter method which can identify relevant features as well as redundancy among relevant features without pairwise correlation analysis. CMIM [22] iteratively picks features which maximize their mutual information with the class to predict, conditionally to the response of any feature already picked. Different from these algorithms, our proposed FAST algorithm employs clustering based method to choose features.

Recently, hierarchical clustering has been adopted in word selection in the context of text classification (e.g., [52], [4], and [18]). Distributional clustering has been used to cluster words into groups based either on their participation in particular grammatical relations with other words by Pereira et al. [52] or on the distribution of class labels associated with each word by Baker and McCallum [4]. As distributional clustering of words are agglomerative in nature, and result in sub-optimal word clusters and high computational cost, Dhillon et al. [18] proposed a new information-theoretic divisive algorithm for word clustering and applied it to text classification. Butterworth et al. [8] proposed to cluster features using a special metric of Barthelemy-Montjardet distance, and then makes use of the dendrogram of the resulting cluster hierarchy to choose the most relevant attributes. Unfortunately, the cluster evaluation measure based on Barthelemy-Montjardet distance does not identify a feature subset that allows the classifiers to improve their original performance accuracy. Further more, even compared with other feature selection methods, the obtained accuracy is lower.

Hierarchical clustering also has been used to select features on spectral data. Van Dijk and Van Hullefor [64] proposed a hybrid filter/wrapper feature subset selection algorithm for regression. Krier et al. [38] presented a methodology combining hierarchical constrained clustering of spectral variables and selection of clusters by mutual information. Their feature clustering method is similar to that of Van Dijk and Van Hullefor [64] except that the former forces every cluster to contain consecutive features only. Both methods employed agglomerative hierarchical clustering to remove redundant features.

Quite different from these hierarchical clustering based algorithms, our proposed FAST algorithm uses minimum spanning tree based method to cluster features. Meanwhile, it does not assume that data points are grouped around centers or separated by a regular geometric curve. Moreover, our proposed FAST does not limit to some specific types of data.

3 Feature subset selection algorithm

3.1 Framework and definitions

Irrelevant features, along with redundant features, severely affect the accuracy of the learning machines [31], [35]. Thus, feature subset selection should be able

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to identify and remove as much of the irrelevant and redundant information as possible. Moreover, "*good feature subsets contain features highly correlated with (predictive of) the class, yet uncorrelated with (not predictive of) each other.*" [30]

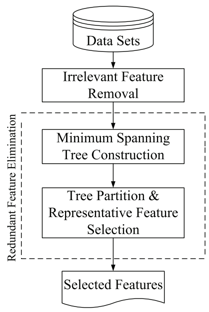

Fig. 1: Framework of the proposed feature subset selection algorithm

Keeping these in mind, we develop a novel algorithm which can efficiently and effectively deal with both irrelevant and redundant features, and obtain a good feature subset. We achieve this through a new feature selection framework (shown in Fig.1) which composed of the two connected components of *irrelevant feature removal* and *redundant feature elimination*. The former obtains features relevant to the target concept by eliminating irrelevant ones, and the latter removes redundant features from relevant ones via choosing representatives from different feature clusters, and thus produces the final subset.

The *irrelevant feature removal* is straightforward once the right relevance measure is defined or selected, while the *redundant feature elimination* is a bit of sophisticated. In our proposed FAST algorithm, it involves (i) the construction of the minimum spanning tree (MST) from a weighted complete graph; (ii) the partitioning of the MST into a forest with each tree representing a cluster; and (iii) the selection of representative features from the clusters.

In order to more precisely introduce the algorithm, and because our proposed feature subset selection framework involves irrelevant feature removal and redundant feature elimination, we firstly present the traditional definitions of relevant and redundant features, then provide our definitions based on variable correlation as follows.

John et al. [33] presented a definition of relevant features. Suppose F to be the full set of features, $F_i \in F$ be a feature, $S_i = F - \{F_i\}$ and $S_i^{'} \subseteq S_i$. Let $s_i^{'}$ be a value-assignment of all features in $S_i^{'}$, f_i a value-assignment of feature F_i, and c a value-assignment of the target concept C. The definition can be formalized as follows.

***Definition** 1: (Relevant feature)* F_i is relevant to the target concept C if and only if there exists some $s_i^{'}$, f_i and c, such that, for probability $p(S_i^{'} = s_i^{'}, F_i = f_i) > 0$,

$$p(C = c \mid S_i^{'} = s_i^{'}, F_i = f_i) \neq p(C = c \mid S_i^{'} = s_i^{'}).$$

Otherwise, feature F_i is an *irrelevant feature*.

Definition 1 indicates that there are two kinds of relevant features due to different $S_i^{'}$: (i) when $S_i^{'} = S_i$, from the definition we can know that F_i is directly relevant to the target concept; (ii) when $S_i^{'} \subsetneq S_i$, from the definition we may obtain that $p(C|S_i, F_i) = p(C|S_i)$. It seems that F_i is irrelevant to the target concept. However, the definition shows that feature F_i is relevant when using $S_i^{'} \cup \{F_i\}$ to describe the target concept. The reason behind is that either F_i is interactive with $S_i^{'}$ or F_i is redundant with $S_i - S_i^{'}$. In this case, we say F_i is indirectly relevant to the target concept.

Most of the information contained in redundant features is already present in other features. As a result, redundant features do not contribute to getting better interpreting ability to the target concept. It is formally defined by Yu and Liu [70] based on Markov blanket [36]. The definitions of Markov blanket and redundant feature are introduced as follows, respectively.

***Definition** 2: (Markov blanket)* Given a feature $F_i \in F$, let $M_i \subset F$ ($F_i \notin M_i$), M_i is said to be a Markov blanket for F_i if and only if

$$p(F - M_i - \{F_i\}, C \mid F_i, M_i) = p(F - M_i - \{F_i\}, C \mid M_i).$$

***Definition** 3: (Redundant feature)* Let S be a set of features, a feature in S is redundant if and only if it has a Markov Blanket within S.

Relevant features have strong correlation with target concept so are always necessary for a best subset, while redundant features are not because their values are completely correlated with each other. Thus, notions of feature redundancy and feature relevance are normally in terms of feature correlation and feature-target concept correlation.

Mutual information measures how much the distribution of the feature values and target classes differ from statistical independence. This is a nonlinear estimation of correlation between feature values or feature values and target classes. The *symmetric uncertainty* (SU) [53] is derived from the mutual information by normalizing it to the entropies of feature values or feature values and target classes, and has been used to evaluate the goodness of features for classification by a number of researchers (e.g., Hall [29], Hall and Smith [30], Yu and Liu [68], [71], Zhao and Liu [72], [73]). Therefore, we choose symmetric uncertainty as the measure of correlation between either two features or a feature and the target concept.

The *symmetric uncertainty* is defined as follows

$$SU(X, Y) = \frac{2 \times Gain(X|Y)}{H(X) + H(Y)}. \tag{1}$$

Where,

1) $H(X)$ is the entropy of a discrete random variable X. Suppose $p(x)$ is the prior probabilities for all values of X, $H(X)$ is defined by
$$H(X) = -\sum_{x \in X} p(x) \log_2 p(x). \tag{2}$$
2) *Gain*$(X|Y)$ is the amount by which the entropy of Y decreases. It reflects the additional information about Y provided by X and is called the information gain [55] which is given by
$$\begin{aligned} Gain(X|Y) &= H(X) - H(X|Y) \\ &= H(Y) - H(Y|X). \end{aligned} \tag{3}$$

Where $H(X|Y)$ is the conditional entropy which quantifies the remaining entropy (i.e. uncertainty) of a random variable X given that the value of another random variable Y is known. Suppose $p(x)$ is the prior probabilities for all values of X and $p(x|y)$ is the posterior probabilities of X given the values of Y, $H(X|Y)$ is defined by

$$H(X|Y) = -\sum_{y \in Y} p(y) \sum_{x \in X} p(x|y) \log_2 p(x|y). \quad (4)$$

Information gain is a symmetrical measure. That is the amount of information gained about X after observing Y is equal to the amount of information gained about Y after observing X. This ensures that the order of two variables (e.g.,(X, Y) or (Y, X)) will not affect the value of the measure.

Symmetric uncertainty treats a pair of variables symmetrically, it compensates for information gain's bias toward variables with more values and normalizes its value to the range [0,1]. A value 1 of $SU(X, Y)$ indicates that knowledge of the value of either one completely predicts the value of the other and the value 0 reveals that X and Y are independent. Although the entropy-based measure handles nominal or discrete variables, they can deal with continuous features as well, if the values are discretized properly in advance [20].

Given $SU(X, Y)$ the symmetric uncertainty of variables X and Y, the relevance *T-Relevance* between a feature and the target concept C, the correlation *F-Correlation* between a pair of features, the feature redundancy *F-Redundancy* and the representative feature *R-Feature* of a feature cluster can be defined as follows.

***Definition** 4: (T-Relevance)* The relevance between the feature $F_i \in F$ and the target concept C is referred to as the *T-Relevance* of F_i and C, and denoted by $SU(F_i, C)$.

If $SU(F_i, C)$ is greater than a predetermined threshold θ, we say that F_i is a strong *T-Relevance* feature.

***Definition** 5: (F-Correlation)* The correlation between any pair of features F_i and F_j ($F_i, F_j \in F \wedge i \neq j$) is called the *F-Correlation* of F_i and F_j, and denoted by $SU(F_i, F_j)$.

***Definition** 6: (F-Redundancy)* Let $S = \{F_1, F_2, ..., F_i, ..., F_{k<|F|}\}$ be a cluster of features. if $\exists F_j \in S$, $SU(F_j, C) \geq SU(F_i, C) \wedge SU(F_i, F_j) > SU(F_i, C)$ is always corrected for each $F_i \in S$ ($i \neq j$), then F_i are redundant features with respect to the given F_j (i.e. each F_i is a *F-Redundancy*).

***Definition** 7: (R-Feature)* A feature $F_i \in S = \{F_1, F_2, ..., F_k\}$ ($k < |F|$) is a representative feature of the cluster S (i.e. F_i is a *R-Feature*) if and only if,

$$F_i = \mathrm{argmax}_{F_j \in S}\, SU(F_j, C).$$

This means the feature, which has the strongest *T-Relevance*, can act as a *R-Feature* for all the features in the cluster.

According to the above definitions, feature subset selection can be the process that identifies and retains the strong *T-Relevance* features and selects *R-Feature*s from feature clusters. The behind heuristics are that

1) irrelevant features have no/weak correlation with target concept;
2) redundant features are assembled in a cluster and a representative feature can be taken out of the cluster.

3.2 Algorithm and analysis

The proposed FAST algorithm logically consists of tree steps: (i) removing irrelevant features, (ii) constructing a MST from relative ones, and (iii) partitioning the MST and selecting representative features.

For a data set D with m features $F = \{F_1, F_2, ..., F_m\}$ and class C, we compute the *T-Relevance* $SU(F_i, C)$ value for each feature F_i ($1 \leq i \leq m$) in the first step. The features whose $SU(F_i, C)$ values are greater than a predefined threshold θ comprise the target-relevant feature subset $F' = \{F'_1, F'_2, ..., F'_k\}$ ($k \leq m$).

In the second step, we first calculate the *F-Correlation* $SU(F'_i, F'_j)$ value for each pair of features F'_i and F'_j ($F'_i, F'_j \in F' \wedge i \neq j$). Then, viewing features F'_i and F'_j as vertices and $SU(F'_i, F'_j)$ ($i \neq j$) as the weight of the edge between vertices F'_i and F'_j, a weighted complete graph $G = (V, E)$ is constructed where $V = \{F'_i \mid F'_i \in F' \wedge i \in [1, k]\}$ and $E = \{(F'_i, F'_j) \mid (F'_i, F'_j \in F' \wedge i, j \in [1, k] \wedge i \neq j\}$. As symmetric uncertainty is symmetric further the *F-Correlation* $SU(F'_i, F'_j)$ is symmetric as well, thus G is an undirected graph.

The complete graph G reflects the correlations among all the target-relevant features. Unfortunately, graph G has k vertices and $k(k-1)/2$ edges. For high dimensional data, it is heavily dense and the edges with different weights are strongly interweaved. Moreover, the decomposition of complete graph is NP-hard [26]. Thus for graph G, we build a MST, which connects all vertices such that the sum of the weights of the edges is the minimum, using the well-known Prim algorithm [54]. The weight of edge (F'_i, F'_j) is *F-Correlation* $SU(F'_i, F'_j)$.

After building the MST, in the third step, we first remove the edges $E = \{(F'_i, F'_j) \mid (F'_i, F'_j \in F' \wedge i, j \in [1, k] \wedge i \neq j\}$, whose weights are smaller than both of the *T-Relevance* $SU(F'_i, C)$ and $SU(F'_j, C)$, from the MST. Each deletion results in two disconnected trees T_1 and T_2.

Assuming the set of vertices in any one of the final trees to be $V(T)$, we have the property that for each pair of vertices ($F'_i, F'_j \in V(T)$), $SU(F'_i, F'_j) \geq SU(F'_i, C) \vee SU(F'_i, F'_j) \geq SU(F'_j, C)$ always holds. From Definition 6 we know that this property guarantees the features in $V(T)$ are redundant.

This can be illustrated by an example. Suppose the MST shown in Fig.2 is generated from a complete graph G. In order to cluster the features, we first traverse all the six edges, and then decide to remove the edge (F_0, F_4) because its weight $SU(F_0, F_4) = 0.3$ is smaller than both $SU(F_0, C) = 0.5$ and $SU(F_4, C) = 0.7$. This makes the MST is clustered into two clusters denoted as $V(T_1)$ and $V(T_2)$. Each cluster is a MST as well. Take $V(T_1)$ as an example. From Fig.2 we know that $SU(F_0, F_1) >$

$SU(F_1, C)$, $SU(F_1, F_2) > SU(F_1, C) \wedge SU(F_1, F_2) > SU(F_2, C)$, $SU(F_1, F_3) > SU(F_1, C) \wedge SU(F_1, F_3) > SU(F_3, C)$. We also observed that there is no edge exists between F_0 and F_2, F_0 and F_3, and F_2 and F_3. Considering that T_1 is a MST, so the $SU(F_0, F_2)$ is greater than $SU(F_0, F_1)$ and $SU(F_1, F_2)$, $SU(F_0, F_3)$ is greater than $SU(F_0, F_1)$ and $SU(F_1, F_3)$, and $SU(F_2, F_3)$ is greater than $SU(F_1, F_2)$ and $SU(F_2, F_3)$. Thus, $SU(F_0, F_2) > SU(F_0, C) \wedge SU(F_0, F_2) > SU(F_2, C)$, $SU(F_0, F_3) > SU(F_0, C) \wedge SU(F_0, F_3) > SU(F_3, C)$, and $SU(F_2, F_3) > SU(F_2, C) \wedge SU(F_2, F_3) > SU(F_3, C)$ also hold. As the mutual information between any pair $(F_i, F_j)(i, j = 0, 1, 2, 3 \wedge i \neq j)$ of F_0, F_1, F_2, and F_3 is greater than the mutual information between class C and F_i or F_j, features F_0, F_1, F_2, and F_3 are redundant.

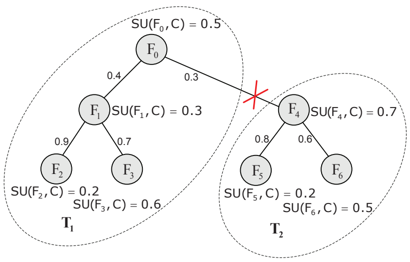

Fig. 2: Example of the clustering step

After removing all the unnecessary edges, a forest *Forest* is obtained. Each tree $T_j \in$ *Forest* represents a cluster that is denoted as $V(T_j)$, which is the vertex set of T_j as well. As illustrated above, the features in each cluster are redundant, so for each cluster $V(T_j)$ we choose a representative feature F_R^j whose *T-Relevance* $SU(F_R^j, C)$ is the greatest. All F_R^j $(j = 1...|Forest|)$ comprise the final feature subset $\cup F_R^j$.

The details of the FAST algorithm is shown in Algorithm 1.

Algorithm 1: FAST

inputs: $D(F_1, F_2, ..., F_m, C)$ - the given data set
θ - the *T-Relevance* threshold.
output: S - selected feature subset .
//==== *Part 1 : Irrelevant Feature Removal* ====
for *i = 1 to m* **do**
  T-Relevance = SU (F_i, C)
  if *T-Relevance* $> \theta$ **then**
    $S = S \cup \{F_i\}$;

//==== *Part 2 : Minimum Spanning Tree Construction* ====
G = NULL; *//G is a complete graph*
for *each pair of features* $\{F_i', F_j'\} \subset S$ **do**
  F-Correlation = SU (F_i', F_j')
  Add F_i' *and/or* F_j' *to* G *with F-Correlation as the weight of the corresponding edge;*
minSpanTree = Prim (G); *//Using Prim Algorithm to generate the minimum spanning tree*
//==== *Part 3 : Tree Partition and Representative Feature Selection* ====
Forest = *minSpanTree*
for *each edge* $E_{ij} \in$ *Forest* **do**
  if $\mathrm{SU}(F_i', F_j') < \mathrm{SU}(F_i', C) \wedge \mathrm{SU}(F_i', F_j') < \mathrm{SU}(F_j', C)$ **then**
    Forest = *Forest* $-$ E_{ij}

$S = \phi$
for *each tree* $T_i \in$ *Forest* **do**
  $F_R^j = \mathrm{argmax}_{F_k' \in T_i} \mathrm{SU}(F_k', C)$
  $S = S \cup \{F_R^j\}$;
return S

Time complexity analysis. The major amount of work for Algorithm 1 involves the computation of SU values for *T-Relevance* and *F-Correlation*, which has linear complexity in terms of the number of instances in a given data set. The first part of the algorithm has a linear time complexity $O(m)$ in terms of the number of features m. Assuming $k(1 \leq k \leq m)$ features are selected as relevant ones in the first part, when $k = 1$, only one feature is selected. Thus, there is no need to continue the rest parts of the algorithm, and the complexity is $O(m)$. When $1 < k \leq m$, the second part of the algorithm firstly constructs a complete graph from relevant features and the complexity is $O(k^2)$, and then generates a MST from the graph using Prim algorithm whose time complexity is $O(k^2)$. The third part partitions the MST and chooses the representative features with the complexity of $O(k)$. Thus when $1 < k \leq m$, the complexity of the algorithm is $O(m+k^2)$. This means when $k \leq \sqrt{m}$, FAST has linear complexity $O(m)$, while obtains the worst complexity $O(m^2)$ when $k = m$. However, k is heuristically set to be $\lfloor \sqrt{m} * \lg m \rfloor$ in the implementation of FAST. So the complexity is $O(m * \lg^2 m)$, which is typically less than $O(m^2)$ since $lg^2 m < m$. This can be explained as follows. Let $f(m) = m - \lg^2 m$, so the derivative $f'(m) = 1 - 2\lg e/m$, which is greater than zero when $m > 1$. So $f(m)$ is a increasing function and it is greater than $f(1)$ which is equal to 1, i.e., $m > \lg^2 m$, when $m > 1$. This means the bigger the m is, the farther the time complexity of FAST deviates from $O(m^2)$. Thus, on high dimensional data, the time complexity of FAST is far more less than $O(m^2)$. This makes FAST has a better runtime performance with high dimensional data as shown in Subsection 4.4.2.

4 EMPIRICAL STUDY

4.1 Data source

For the purposes of evaluating the performance and effectiveness of our proposed FAST algorithm, verifying whether or not the method is potentially useful in practice, and allowing other researchers to confirm our results, 35 publicly available data sets[1] were used.

The numbers of features of the 35 data sets vary from 37 to 49152 with a mean of 7874. The dimensionality of the 54.3% data sets exceed 5000, of which 28.6% data sets have more than 10000 features.

The 35 data sets cover a range of application domains such as text, image and bio microarray data classification. Table 1[2] shows the corresponding statistical information.

Note that for the data sets with continuous-valued features, the well-known off-the-shelf MDL method [74] was used to discretize the continuous values.

4.2 Experiment setup

To evaluate the performance of our proposed FAST algorithm and compare it with other feature selection

1. The data sets can be downloaded at: http://archive.ics.uci.edu/ml/, http://tunedit.org/repo/Data/Text-wc, http://featureselection.asu.edu/datasets.php, http://www.lsi.us.es/aguilar/datasets.html

2. F, I, and T denote the number of features, the number of instances, and the number of classes, respectively.

algorithms in a fair and reasonable way, we set up our experimental study as follows.

1) The proposed algorithm is compared with five different types of representative feature selection algorithms. They are (i) FCBF [68], [71], (ii) ReliefF [57], (iii) CFS [29], (iv) Consist [14], and (v) FOCUS-SF [2], respectively.
   FCBF and ReliefF evaluate features individually. For FCBF, in the experiments, we set the relevance threshold to be the SU value of the $\lfloor m/\log m \rfloor_{th}$ ranked feature for each data set (m is the number of features in a given data set) as suggested by Yu and Liu [68], [71]. ReliefF searches for nearest neighbors of instances of different classes and weights features according to how well they differentiate instances of different classes.
   The other three feature selection algorithms are based on subset evaluation. CFS exploits best-first search based on the evaluation of a subset that contains features highly correlated with the target concept, yet uncorrelated with each other. The Consist method searches for the minimal subset that separates classes as consistently as the full set can under best-first search strategy. FOCUS-SF is a variation of FOCUS [2]. FOCUS has the same evaluation strategy as Consist, but it examines all subsets of features. Considering the time efficiency, FOUCS-SF replaces exhaustive search in FOCUS with sequential forward selection.
   For our proposed FAST algorithm, we heuristically set θ to be the SU value of the $\lfloor \sqrt{m}*\lg m \rfloor_{th}$ ranked feature for each data set.

TABLE 1: Summary of the 35 benchmark data sets

Data ID	Data Name	F	I	T	Domain
1	chess	37	3196	2	Text
2	mfeat-fourier	77	2000	10	Image,Face
3	coil2000	86	9822	2	Text
4	elephant	232	1391	2	Microarray,Bio
5	arrhythmia	280	452	16	Microarray,Bio
6	fqs-nowe	320	265	2	Image,Face
7	colon	2001	62	2	Microarray,Bio
8	fbis.wc	2001	2463	17	Text
9	AR10P	2401	130	10	Image,Face
10	PIE10P	2421	210	10	Image,Face
11	oh0.wc	3183	1003	10	Text
12	oh10.wc	3239	1050	10	Text
13	B-cell1	4027	45	2	Microarray,Bio
14	B-cell2	4027	96	11	Microarray,Bio
15	B-cell3	4027	96	9	Microarray,Bio
16	base-hock	4863	1993	2	Text
17	TOX-171	5749	171	4	Microarray,Bio
18	tr12.wc	5805	313	8	Text
19	tr23.wc	5833	204	6	Text
20	tr11.wc	6430	414	9	Text
21	embryonal-tumours	7130	60	2	Microarray,Bio
22	leukemia1	7130	34	2	Microarray,Bio
23	leukemia2	7130	38	2	Microarray,Bio
24	tr21.wc	7903	336	6	Text
25	wap.wc	8461	1560	20	Text
26	PIX10P	10001	100	10	Image,Face
27	ORL10P	10305	100	10	Image,Face
28	CLL-SUB-111	11341	111	3	Microarray,Bio
29	ohscal.wc	11466	11162	10	Text
30	la2s.wc	12433	3075	6	Text
31	la1s.wc	13196	3204	6	Text
32	GCM	16064	144	14	Microarray,Bio
33	SMK-CAN-187	19994	187	2	Microarray,Bio
34	new3s.wc	26833	9558	44	Text
35	GLA-BRA-180	49152	180	4	Microarray,Bio

2) Four different types of classification algorithms are employed to classify data sets before and after feature selection. They are (i) the probability-based Naive Bayes (NB), (ii) the tree-based C4.5, (iii) the instance-based lazy learning algorithm IB1, and (iv) the rule-based RIPPER, respectively.
   Naive Bayes utilizes a probabilistic method for classification by multiplying the individual probabilities of every feature-value pair. This algorithm assumes independence among the features and even then provides excellent classification results.
   Decision tree learning algorithm C4.5 is an extension of ID3 that accounts for unavailable values, continuous attribute value ranges, pruning of decision trees, rule derivation, and so on. The tree comprises of nodes (features) that are selected by information entropy.
   Instance-based learner IB1 is a single-nearest-neighbor algorithm, and it classifies entities taking the class of the closest associated vectors in the training set via distance metrics. It is the simplest among the algorithms used in our study.
   Inductive rule learner RIPPER (Repeated Incremental Pruning to Produce Error Reduction) [12] is a propositional rule learner that defines a rule based detection model and seeks to improve it iteratively by using different heuristic techniques. The constructed rule set is then used to classify new instances.
3) When evaluating the performance of the feature subset selection algorithms, four metrics, (i) the proportion of selected features (ii) the time to obtain the feature subset, (iii) the classification accuracy, and (iv) the Win/Draw/Loss record [65], are used.
   The proportion of selected features is the ratio of the number of features selected by a feature selection algorithm to the original number of features of a data set.
   The Win/Draw/Loss record presents three values on a given measure, i.e. the numbers of data sets for which our proposed algorithm FAST obtains better, equal, and worse performance than other five feature selection algorithms, respectively. The measure can be the proportion of selected features, the runtime to obtain a feature subset, and the classification accuracy, respectively.

4.3 Experimental procedure

In order to make the best use of the data and obtain stable results, a (M = 5)×(N = 10)-cross-validation strategy is used. That is, for each data set, each feature subset selection algorithm and each classification algorithm, the 10-fold cross-validation is repeated M = 5 times, with each time the order of the instances of the data set being randomized. This is because many of the algorithms exhibit order effects, in that certain orderings dramatically improve or degrade performance [21]. Randomizing the order of the inputs can help diminish the order effects.

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In the experiment, for each feature subset selection algorithm, we obtain M×N feature subsets *Subset* and the corresponding runtime *Time* with each data set. Average |*Subset*| and *Time*, we obtain the number of selected features further the proportion of selected features and the corresponding runtime for each feature selection algorithm on each data set. For each classification algorithm, we obtain M×N classification *Accuracy* for each feature selection algorithm and each data set. Average these *Accuracy*, we obtain mean accuracy of each classification algorithm under each feature selection algorithm and each data set. The procedure *Experimental Process* shows the details.

Procedure *Experimental Process*

```
M = 5, N = 10
DATA = {D_1, D_2, ..., D_35}
Learners = {NB, C4.5, IB1, RIPPER}
FeatureSelectors = {FAST, FCBF, ReliefF, CFS, Consist, FOCUS-SF}
for each data ∈ DATA do
    for each times ∈ [1, M] do
        randomize instance-order for data
        generate N bins from the randomized data
        for each fold ∈ [1, N] do
            TestData = bin[fold]
            TrainingData = data - TestData
            for each selector ∈ FeatureSelectors do
                (Subset, Time) = selector(TrainingData)
                TrainingData' = select Subset from TrainingData
                TestData' = select Subset from TestData
                for each learner ∈ Learners do
                    classifier = learner(TrainingData')
                    Accuracy = apply classifier to TestData'
```

4.4 Results and analysis

In this section we present the experimental results in terms of the proportion of selected features, the time to obtain the feature subset, the classification accuracy, and the Win/Draw/Loss record.

For the purpose of exploring the statistical significance of the results, we performed a nonparametric Friedman test [24] followed by Nemenyi post-hoc test [47], as advised by Demsar[17] and Garcia and Herrerato [25] to statistically compare algorithms on multiple data sets. Thus the Friedman and the Nemenyi test results are reported as well.

4.4.1 Proportion of selected features

Table 2 records the proportion of selected features of the six feature selection algorithms for each data set. From it we observe that

1) Generally all the six algorithms achieve significant reduction of dimensionality by selecting only a small portion of the original features. FAST on average obtains the best proportion of selected features of 1.82%. The Win/Draw/Loss records show FAST wins other algorithms as well.
2) For image data, the proportion of selected features of each algorithm has an increment compared with the corresponding average proportion of selected features on the given data sets except Consist has an improvement. This reveals that the five algorithms are not very suitable to choose features for image data compared with for microarray and text data. FAST ranks 3 with the proportion of selected features of 3.59% that has a tiny margin of 0.11% to the first and second best proportion of selected features 3.48% of Consist and FOCUS-SF, and a margin of 76.59% to the worst proportion of selected features 79.85% of ReliefF.
3) For microarray data, the proportion of selected features has been improved by each of the six algorithms compared with that on the given data sets. This indicates that the six algorithms work well with microarray data. FAST ranks 1 again with the proportion of selected features of 0.71%. Of the six algorithms, only CFS cannot choose features for two data sets whose dimensionalities are 19994 and 49152, respectively.
4) For text data, FAST ranks 1 again with a margin of 0.48% to the second best algorithm FOCUS-SF.

TABLE 2: Proportion of selected features of the six feature selection algorithms

Data set	Proportion of selected features (%) of FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF
chess	16.22	21.62	10.81	62.16	81.08	18.92
mfeat-fourier	19.48	49.35	24.68	98.70	15.58	15.58
coil2000	3.49	8.14	11.63	50.00	37.21	1.16
elephant	0.86	3.88	5.60	6.03	0.86	0.86
arrhythmia	2.50	4.64	9.29	50.00	8.93	8.93
fqs-nowe	0.31	2.19	5.63	26.56	4.69	4.69
colon	0.30	0.75	1.35	39.13	0.30	0.30
fbis.wc	0.80	1.45	2.30	0.95	1.75	1.75
AR10P	0.21	1.04	2.12	62.89	0.29	0.29
PIE10P	1.07	1.98	2.52	91.00	0.25	0.25
oh0.wc	0.38	0.88	1.10	0.38	1.82	1.82
oh10.wc	0.34	0.80	0.56	0.40	1.61	1.61
B-cell1	0.52	1.61	1.07	30.49	0.10	0.10
B-cell2	1.66	6.13	3.85	96.87	0.15	0.15
B-cell3	2.06	7.95	4.20	98.24	0.12	0.12
base-hock	0.58	1.27	0.82	0.12	1.19	1.19
TOX-171	0.28	1.41	2.09	64.60	0.19	0.19
tr12.wc	0.16	0.28	0.26	0.59	0.28	0.28
tr23.wc	0.15	0.27	0.19	1.46	0.21	0.21
tr11.wc	0.16	0.25	0.40	0.37	0.31	0.31
embryonal-tumours	0.14	0.03	0.03	13.96	0.03	0.03
leukemia1	0.07	0.03	0.03	41.35	0.03	0.03
leukemia2	0.01	0.41	0.52	60.63	0.08	0.08
tr21.wc	0.10	0.22	0.37	2.04	0.20	0.20
wap.wc	0.20	0.53	0.65	1.10	0.41	0.41
PIX10P	0.15	3.04	2.35	100.00	0.03	0.03
ORL10P	0.30	2.61	2.76	99.97	0.04	0.04
CLL-SUB-111	0.04	0.78	1.23	54.35	0.08	0.08
ohscal.wc	0.34	0.44	0.18	0.03	NA	NA
la2s.wc	0.15	0.33	0.54	0.09	0.37	NA
la1s.wc	0.17	0.35	0.51	0.06	0.34	NA
GCM	0.13	0.42	0.68	79.41	0.06	0.06
SMK-CAN-187	0.13	0.25	NA	14.23	0.06	0.06
new3s.wc	0.10	0.15	NA	0.03	NA	NA
GLA-BRA-180	0.03	0.35	NA	53.06	0.02	0.02
Average(Image)	3.59	10.04	6.68	79.85	3.48	3.48
Average(Microarry)	0.71	2.34	2.50	52.92	0.91	0.91
Average(Text)	2.05	3.25	2.64	10.87	11.46	2.53
Average	1.82	4.27	3.42	42.54	5.44	2.06
Win/Draw/Loss	-	33/0/2	31/0/4	29/1/5	20/2/13	19/2/14

The Friedman test [24] can be used to compare k algorithms over N data sets by ranking each algorithm on each data set separately. The algorithm obtained the best performance gets the rank of 1, the second best ranks 2, and so on. In case of ties, average ranks are assigned. Then the average ranks of all algorithms on all data sets are calculated and compared. If the null hypothesis, which is all algorithms are performing equivalently, is rejected under the Friedman test statistic, post-hoc tests such as the Nemenyi test [47] can be used to determine which algorithms perform statistically different.

The Nemenyi test compares classifiers in a pairwise manner. According to this test, the performances of two classifiers are significantly different if the distance of

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the average ranks exceeds the critical distance $CD_\alpha = q_\alpha\sqrt{\frac{k(k+1)}{6N}}$, where the q_α is based on the Studentized range statistic [48] divided by $\sqrt{2}$.

In order to further explore whether the reduction rates are significantly different we performed a Friedman test followed by a Nemenyi post-hoc test.

The null hypothesis of the Friedman test is that all the feature selection algorithms are equivalent in terms of proportion of selected features. The test result is $p = 0$. This means that at $\alpha = 0.1$, there is evidence to reject the null hypothesis and all the six feature selection algorithms are different in terms of proportion of selected features.

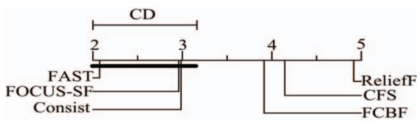

Fig. 3: Proportion of selected features comparison of all feature selection algorithms against each other with the Nemenyi test.

In order to further explore feature selection algorithms whose reduction rates have statistically significant differences, we performed a Nemenyi test. Fig. 3 shows the results with $\alpha = 0.1$ on the 35 data sets. The results indicate that the proportion of selected features of FAST is statistically smaller than those of RelieF, CFS and FCBF, and there is no consistent evidence to indicate statistical differences between FAST , Consist, and FOCUS-SF, respectively.

4.4.2 Runtime

TABLE 3: Runtime (in ms) of the six feature selection algorithms

Data set	FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF
chess	105	60	352	12660	1999	653
mfeat-fourier	1472	716	938	13918	3227	660
coil2000	866	875	1483	304162	53850	1281
elephant	783	312	905	20991	2439	1098
arrhythmia	110	115	821	3684	3492	2940
fqs-nowe	977	97	736	1072	1360	1032
colon	166	148	12249	744	1624	960
fbis.wc	14761	16207	66058	79527	579376	479651
AR10P	706	458	57319	3874	3568	2083
PIE10P	678	1223	77579	7636	4149	2910
oh0.wc	5283	5990	59624	4898	488261	420116
oh10.wc	5549	6033	28438	5652	428459	402853
B-cell1	160	248	103871	1162	2476	1310
B-cell2	626	1618	930465	4334	5102	2556
B-cell3	635	2168	1097122	7001	4666	2348
base-hock	8059	21793	146454	728900	999232	1017412
TOX-171	1750	1558	1341345	9757	17185	8446
tr12.wc	3089	3585	51360	2558	53304	34270
tr23.wc	4266	2506	32647	1585	29165	16649
tr11.wc	5086	5575	136063	4418	111073	79000
embryonal-tumours	754	314	10154	1681	5045	1273
leukemia1	449	278	10900	790	5708	1263
leukemia2	1141	456	216888	894	10407	3471
tr21.wc	4662	5543	218436	4572	89761	55644
wap.wc	25146	28724	768642	33873	1362376	1093222
PIX10P	2957	9056	25372209	11231	9875	4292
ORL10P	2330	12991	30383928	11547	13905	5780
CLL-SUB-111	1687	1870	6327479	12720	17554	12307
ohscal.wc	353283	391761	981868	655400	NA	NA
la2s.wc	70776	99019	2299244	118624	7400287	NA
la1s.wc	79623	107110	2668871	128452	7830978	NA
GCM	9351	4939	3780146	32950	39383	26644
SMK-CAN-187	4307	5114	NA	34881	67364	38606
new3s.wc	790690	960738	NA	2228746	NA	NA
GLA-BRA-180	29854	17348	NA	97641	220734	152536
Average(Image)	1520	4090	9315452	8213	6014	2793
Average(Microarry)	1468	1169	1152695	8059	9590	5385
Average(Text)	6989	8808	137232	107528	381532	327341
Average	3573	4671	2456366	45820	149932	126970
Win/Draw/Loss	-	22/0/13	33/0/2	29/0/6	35/0/0	34/0/1

Table 3 records the runtime of the six feature selection algorithms. From it we observe that

1) Generally the individual evaluation based feature selection algorithms of FAST, FCBF and ReliefF are much faster than the subset evaluation based algorithms of CFS, Consist and FOCUS-SF. FAST is consistently faster than all other algorithms. The runtime of FAST is only 0.1% of that of CFS, 2.4% of that of Consist, 2.8% of that of FOCUS-SF, 7.8% of that of ReliefF, and 76.5% of that of FCBF, respectively. The Win/Draw/Loss records show that FAST outperforms other algorithms as well.
2) For image data, FAST obtains the rank of 1. Its runtime is only 0.02% of that of CFS, 18.50% of that of ReliefF, 25.27% of that of Consist, 37.16% of that of FCBF, and 54.42% of that of FOCUS-SF, respectively. This reveals that FAST is more efficient than others when choosing features for image data.
3) For microarray data, FAST ranks 2. Its runtime is only 0.12% of that of CFS, 15.30% of that of Consist, 18.21% of that of ReliefF, 27.25% of that of FOCUS-SF, and 125.59% of that of FCBF, respectively.
4) For text data, FAST ranks 1. Its runtime is 1.83% of that of Consist, 2.13% of that of FOCUS-SF, 5.09% of that of CFS, 6.50% of that of ReliefF, and 79.34% of that of FCBF, respectively. This indicates that FAST is more efficient than others when choosing features for text data as well.

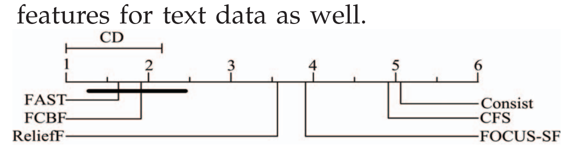

Fig. 4: Runtime comparison of all feature selection algorithms against each other with the Nemenyi test.

In order to further explore whether the runtime of the six feature selection algorithms are significantly different we performed a Friedman test. The null hypothesis of the Friedman test is that all the feature selection algorithms are equivalent in terms of runtime. The test result is $p = 0$. This means that at $\alpha = 0.1$, there is evidence to reject the null hypothesis and all the six feature selection algorithms are different in terms of runtime. Thus a post-hoc Nemenyi test was conducted. Fig. 4 shows the results with $\alpha = 0.1$ on the 35 data sets. The results indicate that the runtime of FAST is statistically better than those of ReliefF, FOCUS-SF, CFS, and Consist, and there is no consistent evidence to indicate statistical runtime differences between FAST and FCBF.

4.4.3 Classification accuracy

Tables 4, 5, 6 and 7 show the 10-fold cross-validation accuracies of the four different types of classifiers on the 35 data sets before and after each feature selection algorithm is performed, respectively.

Table 4 shows the classification accuracy of Naive Bayes. From it we observe that

1) Compared with original data, the classification accuracy of Naive Bayes has been improved by FAST, CFS, and FCBF by 12.86%, 6.62%, and 4.32%,

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respectively. Unfortunately, ReliefF, Consist, and FOCUS-SF have decreased the classification accuracy by 0.32%, 1.35%, and 0.86%, respectively. FAST ranks 1 with a margin of 6.24% to the second best accuracy 80.60% of CFS. At the same time, the Win/Draw/Loss records show that FAST outperforms all other five algorithms.

2) For image data, the classification accuracy of Naive Bayes has been improved by FCBF, CFS, FAST, and ReliefF by 6.13%, 5.39%, 4.29%, and 3.78%, respectively. However, Consist and FOCUS-SF have decreased the classification accuracy by 4.69% and 4.69%, respectively. This time FAST ranks 3 with a margin of 1.83% to the best accuracy 87.32% of FCBF.
3) For microarray data, the classification accuracy of Naive Bayes has been improved by all the six algorithms FAST, CFS, FCBF, ReliefF, Consist, and FOCUS-SF by 16.24%, 12.09%, 9.16%, 4.08%, 4.45%, and 4.45%, respectively. FAST ranks 1 with a margin of 4.16% to the second best accuracy 87.22% of CFS. This indicates that FAST is more effective than others when using Naive Bayes to classify microarray data.
4) For text data, FAST and CFS have improved the classification accuracy of Naive Bayes by 13.83% and 1.33%, respectively. Other four algorithms ReliefF, Consist, FOCUS-SF, and FCBF have decreased the accuracy by 7.36%, 5.87%, 4.57%, and 1.96%, respectively. FAST ranks 1 with a margin of 12.50% to the second best accuracy 70.12% of CFS.

TABLE 4: Accuracy of Naive Bayes with the six feature selection algorithms

	Classification accuracy of Naive Bayes with						
Data set	FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF	Full set
chess	92.92	92.12	90.43	88.56	89.50	94.34	87.68
mfeat-fourier	80.05	78.57	79.31	76.32	76.72	76.72	76.07
coil2000	94.04	93.53	92.59	76.96	84.64	94.03	78.04
elephant	99.47	67.96	85.98	87.54	99.94	99.94	82.34
arrhythmia	73.01	65.98	69.64	64.53	69.24	69.24	63.06
fqs-nowe	69.81	71.57	70.45	66.44	71.35	71.35	65.61
colon	95.08	84.81	84.81	68.33	85.48	85.48	56.33
fbis.wc	70.04	49.79	61.26	38.75	39.20	39.20	61.89
AR10P	69.23	81.08	82.77	80.77	62.46	62.46	72.62
PIE10P	96.83	95.71	94.57	93.97	73.90	73.90	90.67
oh0.wc	72.31	67.75	75.97	49.38	73.44	73.44	80.10
oh10.wc	69.65	70.02	69.54	58.79	69.73	69.73	72.40
B-cell1	100.00	100.00	100.00	100.00	91.50	91.50	91.30
B-cell2	96.63	83.53	83.47	77.63	62.71	62.71	74.58
B-cell3	98.22	82.47	85.47	79.26	82.24	82.24	75.40
base-hock	93.18	90.09	90.98	51.05	81.92	81.92	90.12
TOX-171	85.56	90.53	93.09	79.93	74.27	74.27	76.27
tr12.wc	84.88	57.77	60.01	66.33	49.50	49.50	56.08
tr23.wc	93.77	53.86	55.25	51.11	54.80	54.80	55.96
tr11.wc	82.47	50.72	53.49	63.92	46.58	46.58	54.39
embryonal-tumours	92.22	97.00	97.00	96.39	97.00	97.00	94.33
leukemia1	100.00	100.00	100.00	75.00	100.00	100.00	92.17
leukemia2	100.00	77.33	78.00	95.00	55.33	55.33	62.00
tr21.wc	89.97	48.26	53.61	70.43	44.04	44.04	47.01
wap.wc	65.64	61.23	68.19	60.43	58.82	58.82	73.05
PIX10P	98.00	98.20	96.80	98.00	90.00	90.00	96.00
ORL10P	99.00	98.80	95.60	94.33	84.60	84.60	86.20
CLL-SUB-111	85.45	84.97	87.86	69.32	74.71	74.71	67.00
ohscal.wc	68.06	58.48	59.24	23.81	NA	NA	NA
la2s.wc	69.68	60.48	71.89	40.99	61.94	NA	75.27
la1s.wc	71.96	60.46	70.42	33.51	58.74	NA	75.16
GCM	70.90	77.00	81.33	57.65	62.62	62.62	66.83
SMK-CAN-187	85.96	75.63	NA	68.14	73.78	73.78	60.36
new3s.wc	56.69	33.73	NA	16.13	NA	NA	NA
GLA-BRA-180	76.48	77.89	NA	69.07	63.44	63.44	67.00
Average(Image)	85.49	87.32	86.58	84.97	76.51	76.51	81.20
Average(Microarry)	91.38	84.30	87.22	79.22	79.59	79.59	75.13
Average(Text)	82.62	66.83	70.12	61.43	62.92	64.22	68.79
Average	86.84	78.30	80.60	73.66	72.63	73.12	73.98
Win/Draw/Loss	-	25/2/8	24/2/9	31/2/2	29/1/5	28/1/6	28/0/7

TABLE 5: Accuracy of C4.5 with the six feature selection algorithms

	Classification accuracy of C4.5 with						
Data set	FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF	Full set
chess	94.02	94.02	90.43	97.83	99.44	94.34	99.44
mfeat-fourier	71.25	75.74	77.80	76.40	71.06	71.06	75.93
coil2000	94.03	94.03	94.03	94.03	93.97	94.03	93.93
elephant	99.90	99.94	99.94	99.90	99.94	99.94	95.27
arrhythmia	71.53	70.05	69.21	66.15	66.59	66.59	65.23
fqs-nowe	69.81	73.35	69.13	66.46	68.42	68.42	66.96
colon	90.40	90.76	89.14	82.38	86.90	86.90	82.33
fbis.wc	69.41	69.35	77.52	57.03	68.70	68.70	NA
AR10P	77.69	75.54	79.54	71.54	64.92	64.92	70.92
PIE10P	84.13	82.95	86.10	80.32	81.33	81.33	79.14
oh0.wc	71.88	75.45	84.20	57.43	83.47	83.47	81.37
oh10.wc	69.33	73.75	74.65	67.65	75.60	75.60	72.38
B-cell1	87.33	81.80	82.90	78.17	88.60	88.60	74.90
B-cell2	71.00	63.24	64.07	65.85	60.80	60.80	64.31
B-cell3	78.07	81.07	77.02	83.04	72.84	72.84	77.96
base-hock	92.02	89.81	89.57	49.92	90.57	90.57	91.54
TOX-171	76.85	64.92	68.69	60.24	68.66	68.66	58.44
tr12.wc	81.68	85.43	31.96	74.02	43.76	84.47	81.19
tr23.wc	89.87	94.80	46.38	86.78	67.07	96.57	92.93
tr11.wc	80.22	82.04	36.95	69.25	46.81	84.11	79.09
embryonal-tumours	87.78	97.00	97.00	88.89	97.00	97.00	87.50
leukemia1	100.00	97.00	97.00	61.11	97.00	97.00	89.17
leukemia2	100.00	75.00	78.00	88.89	81.33	81.33	60.33
tr21.wc	90.47	88.32	69.23	80.26	68.76	88.21	80.72
wap.wc	62.26	67.60	32.87	64.32	21.86	63.27	NA
PIX10P	97.00	95.40	98.80	93.33	92.20	92.20	93.00
ORL10P	90.33	82.60	90.20	74.67	84.00	84.00	72.40
CLL-SUB-111	83.64	73.85	74.36	64.80	78.76	78.76	60.89
ohscal.wc	67.73	66.69	68.42	27.30	NA	NA	NA
la2s.wc	72.40	72.53	79.08	51.52	75.53	NA	NA
la1s.wc	72.45	72.57	77.63	47.05	75.33	NA	NA
GCM	58.73	59.16	60.92	52.73	45.79	45.79	51.81
SMK-CAN-187	85.19	71.42	NA	66.14	77.83	77.83	62.17
new3s.wc	55.64	60.51	NA	17.83	NA	NA	NA
GLA-BRA-180	71.30	68.22	NA	65.00	64.56	64.56	63.22
Average(Image)	81.70	80.93	83.60	77.12	76.99	76.99	76.39
Average(Microarry)	83.77	79.48	79.85	74.35	78.68	78.68	72.35
Average(Text)	81.38	83.15	66.16	72.59	69.09	83.94	85.84
Average	82.44	81.17	75.43	74.25	74.69	80.33	77.74
Win/Draw/Loss	-	17/2/16	21/1/13	28/2/5	27/0/8	19/1/10	30/0/5

Table 5 shows the classification accuracy of C4.5. From it we observe that

1) Compared with original data, the classification accuracy of C4.5 has been improved by FAST, FCBF, and FOCUS-SF by 4.69%, 3.43%, and 2.58%, respectively. Unfortunately, ReliefF, Consist, and CFS have decreased the classification accuracy by 3.49%, 3.05%, and 2.31%, respectively. FAST obtains the rank of 1 with a margin of 1.26% to the second best accuracy 81.17% of FCBF.
2) For image data, the classification accuracy of C4.5 has been improved by all the six feature selection algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 5.31%, 4.54%, 7.20%, 0.73%, 0.60%, and 0.60%, respectively. This time FAST ranks 2 with a margin of 1.89% to the best accuracy 83.6% of CFS and a margin of 4.71% to the worst accuracy 76.99% of Consist and FOCUS-SF.
3) For microarray data, the classification accuracy of C4.5 has been improved by all the six algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 11.42%, 7.14%, 7.51%, 2.00%, 6.34%, and 6.34%, respectively. FAST ranks 1 with a margin of 3.92% to the second best accuracy 79.85% of CFS.
4) For text data, the classification accuracy of C4.5 has been decreased by algorithms FAST, FCBF, CFS, ReliefF, Consist and FOCUS-SF by 4.46%, 2.70%, 19.68%, 13.25%, 16.75%, and 1.90% respectively. FAST ranks 3 with a margin of 2.56% to the best accuracy 83.94% of FOCUS-SF and a margin of 15.22% to the worst accuracy 66.16% of CFS.

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TABLE 6: Accuracy of IB1 with the six feature selection algorithms

Data set	Classification accuracy of IB1 with						
	FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF	Full set
chess	90.18	91.47	84.78	96.86	95.09	90.79	90.60
mfeat-fourier	77.87	81.69	83.72	80.00	77.71	77.71	80.13
coil2000	88.42	89.27	89.42	89.16	89.96	67.62	89.87
elephant	98.97	99.99	99.99	100.00	99.97	99.97	99.31
arrhythmia	64.48	60.10	63.67	54.35	55.22	55.22	53.27
fqs-nowe	56.59	66.20	70.48	70.74	63.02	63.02	65.32
colon	91.90	78.76	84.38	82.54	85.95	85.95	76.14
fbis.wc	60.09	61.91	72.94	43.69	60.83	60.83	NA
AR10P	73.33	79.08	86.77	71.79	80.46	80.46	49.54
PIE10P	99.21	99.90	99.05	99.37	92.19	92.19	99.62
oh0.wc	67.33	63.19	75.53	48.12	68.34	68.34	20.64
oh10.wc	64.06	63.56	66.46	56.67	63.41	63.41	8.40
B-cell1	100.00	94.90	95.40	92.17	93.30	93.30	73.00
B-cell2	97.00	87.02	86.42	71.78	58.00	58.00	70.20
B-cell3	98.96	95.02	95.02	83.48	80.20	80.20	83.98
base-hock	89.06	92.24	92.60	50.86	92.95	92.95	78.81
TOX-171	75.60	95.92	97.90	96.32	65.14	65.14	86.44
tr12.wc	82.11	83.43	84.92	61.02	84.91	84.91	40.13
tr23.wc	90.18	86.55	88.90	67.62	86.80	86.80	56.11
tr11.wc	78.43	79.65	81.89	59.81	81.26	81.26	49.58
embryonal-tumours	90.56	97.00	97.00	90.56	97.00	97.00	89.50
leukemia1	100.00	97.00	97.00	67.22	97.00	97.00	76.50
leukemia2	100.00	84.33	75.00	79.72	71.00	71.00	59.67
tr21.wc	87.98	85.34	91.23	76.41	87.23	87.23	67.85
wap.wc	56.47	57.31	68.49	61.03	58.74	58.74	NA
PIX10P	99.00	99.00	99.00	99.00	95.00	95.00	99.00
ORL10P	100.00	97.60	95.20	94.67	95.00	95.00	94.40
CLL-SUB-111	79.09	74.94	81.62	68.66	65.83	65.83	NA
ohscal.wc	52.94	49.52	57.98	19.67	NA	NA	NA
la2s.wc	68.33	68.16	79.88	39.95	73.43	NA	NA
la1s.wc	67.44	67.01	76.41	33.98	71.42	NA	NA
GCM	68.49	66.71	69.50	58.59	52.54	52.54	58.87
SMK-CAN-187	76.28	66.08	NA	70.40	70.58	70.58	63.57
new3s.wc	49.46	52.38	NA	8.82	NA	NA	NA
GLA-BRA-180	72.96	73.89	NA	68.33	73.00	73.00	61.78
Average(Image)	84.33	87.25	89.04	85.93	83.90	83.90	81.34
Average(Microarry)	88.75	85.97	86.91	78.78	76.76	76.76	75.17
Average(Text)	77.66	77.63	81.56	64.66	79.05	76.63	55.78
Average	83.63	83.07	85.32	74.90	79.11	78.19	69.88
Win/Draw/Loss	-	18/1/16	14/1/20	25/2/8	20/0/15	23/0/12	27/1/7

Table 6 shows the classification accuracy of IB1. From it we observe that

1) Compared with original data, the classification accuracy of IB1 has been improved by all the six feature selection algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 13.75%, 13.19%, 15.44%, 5.02%, 9.23%, and 8.31%, respectively. FAST ranks 2 with a margin of 1.69% to the best accuracy 85.32% of CFS. The Win/Draw/Loss records show that FAST outperforms all other algorithms except for CFS, winning and losing on 14 and 20 out of the 35 data sets, respectively.
   Although FAST does not perform better than CFS, we observe that CFS is not available on the three biggest data sets of the 35 data sets. Moreover, CFS is very slow compared with other algorithms as reported in Section 4.4.2.
2) For image data, the classification accuracy of IB1 has been improved by all the six feature selection algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 3.00%, 5.91%, 7.70%, 4.59%, 2.56%, and 2.56%, respectively. FAST ranks 4 with a margin of 4.70% to the best accuracy 89.04% of CFS.
3) For microarray data, the classification accuracy of IB1 has been improved by all the six algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 13.58%, 10.80%, 11.74%, 3.61%, 1.59%, and 1.59%, respectively. FAST ranks 1 with a margin of 1.85% to the second best accuracy 86.91% of CFS and a margin of 11.99% to the worst accuracy 76.76% of Consist and FOCUS-SF.
4) For text data, the classification accuracy of IB1 has been improved by the five feature selection algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 21.89%, 21.85%, 25.78%, 8.88%, 23.27%, and 20.85%, respectively. FAST ranks 3 with a margin of 3.90% to the best accuracy 81.56% of CFS.

TABLE 7: Accuracy of RIPPER with the six feature selection algorithms

Data set	Classification accuracy of RIPPER with						
	FAST	FCBF	CFS	ReliefF	Consist	FOCUS-SF	Full set
chess	94.09	94.09	90.43	97.81	99.17	94.34	99.16
mfeat-fourier	70.40	73.46	75.35	72.58	69.13	69.13	73.36
coil2000	94.02	94.03	94.03	94.03	93.93	94.03	93.89
elephant	72.57	66.84	78.85	77.31	98.62	98.62	79.38
arrhythmia	68.36	72.21	70.97	71.01	71.27	71.27	71.36
fqs-nowe	69.81	73.66	69.15	69.05	68.52	68.52	63.62
colon	93.41	80.14	79.76	77.14	84.05	84.05	74.19
fbis.wc	65.58	68.18	75.49	53.29	65.10	65.10	NA
AR10P	73.08	64.62	65.08	59.23	57.23	57.23	56.62
PIE10P	88.57	80.57	80.00	79.37	76.67	76.67	79.33
oh0.wc	65.90	69.93	78.98	41.27	79.12	79.12	NA
oh10.wc	67.90	69.41	70.08	62.22	71.47	71.47	NA
B-cell1	86.50	79.50	85.50	80.67	89.60	89.60	74.10
B-cell2	80.67	61.31	55.13	58.56	53.53	53.53	53.42
B-cell3	82.52	76.24	59.42	72.07	72.31	72.31	60.67
base-hock	91.04	89.29	90.72	51.13	92.34	92.34	88.26
TOX-171	78.22	67.61	70.59	63.39	60.12	60.12	62.58
tr12.wc	82.53	81.13	79.67	71.56	83.07	83.07	77.94
tr23.wc	91.15	95.96	93.22	84.80	95.11	95.11	89.91
tr11.wc	80.13	79.52	80.72	66.67	81.46	81.46	NA
embryonal-tumours	80.56	97.00	97.00	85.28	97.00	97.00	82.83
leukemia1	100.00	97.00	97.00	64.44	97.00	97.00	86.67
leukemia2	100.00	70.67	71.00	92.50	76.33	76.33	63.67
tr21.wc	91.07	89.75	90.53	84.63	87.59	87.59	NA
wap.wc	50.90	63.54	67.06	58.48	60.00	60.00	NA
PIX10P	96.67	93.00	85.80	86.67	92.00	92.00	82.60
ORL10P	85.33	73.80	62.40	66.00	75.60	75.60	54.20
CLL-SUB-111	83.99	74.91	70.61	68.76	81.83	81.83	66.77
ohscal.wc	62.34	62.98	62.06	24.98	NA	NA	NA
la2s.wc	69.37	70.06	79.73	40.93	76.52	NA	NA
la1s.wc	67.56	68.03	78.50	41.11	74.26	NA	NA
GCM	53.13	49.86	50.32	47.41	46.26	46.26	44.09
SMK-CAN-187	77.53	68.88	NA	61.81	72.47	72.47	59.55
new3s.wc	44.46	52.69	NA	9.69	NA	NA	NA
GLA-BRA-180	70.19	68.11	NA	59.44	65.22	65.22	60.56
Average(Image)	80.64	76.52	72.96	72.15	73.19	73.19	68.29
Average(Microarry)	81.66	74.44	73.85	71.55	77.33	77.33	68.31
Average(Text)	79.48	81.35	82.81	69.63	82.58	82.15	89.83
Average	80.62	77.49	77.06	70.94	78.46	78.30	72.98
Win/Draw/Loss	-	20/1/14	22/0/13	28/0/7	21/0/14	22/0/13	30/0/5

Table 7 shows the classification accuracy of RIPPER. From it we observe that

1) Compared with original data, the classification accuracy of RIPPER has been improved by the five feature selection algorithms FAST, FCBF, CFS, Consist, and FOCUS-SF by 7.64%, 4.51%, 4.08%, 5.48%, and 5.32%, respectively; and has been decreased by ReliefF by 2.04%. FAST ranks 1 with a margin of 2.16% to the second best accuracy 78.46% of Consist. The Win/Draw/Loss records show that FAST outperforms all other algorithms.
2) For image data, the classification accuracy of RIPPER has been improved by all the six feature selection algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 12.35%, 8.23 %, 4.67%, 3.86%, 4.90%, and 4.90%, respectively. FAST ranks 1 with a margin of 4.13% to the second best accuracy 76.52% of FCBF.
3) For microarray data, the classification accuracy of RIPPER has been improved by all the six algorithms FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 13.35%, 6.13%, 5.54%, 3.23%, 9.02%, and 9.02%, respectively. FAST ranks 1 with a mar-

TABLE 8: Rank of the six feature selection algorithms under different types of data

	Image Data						Microarray Data						Text Data						All Data					
	FAST	FCBF	CFS	ReliefF	Consist	FOCUS -SF	FAST	FCBF	CFS	ReliefF	Consist	FOCUS -SF	FAST	FCBF	CFS	ReliefF	Consist	FOCUS -SF	FAST	FCBF	CFS	ReliefF	Consist	FOCUS -SF
NB	3	1	2	4	5	5	1	3	2	6	4	4	1	3	2	6	5	4	1	3	2	4	6	5
C4.5	2	3	1	4	5	5	1	3	2	6	4	4	3	2	6	4	5	1	1	2	4	6	5	3
IB1	4	2	1	3	5	5	1	3	2	4	5	5	3	4	1	6	2	4	2	3	1	6	4	5
RIPPER	1	2	1	6	3	3	1	4	5	6	2	2	5	3	1	6	2	4	1	4	5	6	2	3
Sum	10	8	5	17	18	18	4	13	11	22	15	15	12	12	10	22	14	13	5	12	12	22	17	16
Rank	3	2	1	4	5	5	1	3	2	6	4	4	2	2	1	6	5	4	1	2	2	6	5	4

gin of 4.33% to the second best accuracy 77.33% of Consist and FOCUS-SF.

4) For text data, the classification accuracy of RIPPER has been decreased by FAST, FCBF, CFS, ReliefF, Consist, and FOCUS-SF by 10.35%, 8.48%, 7.02%, 20.21%, 7.25%, and 7.68%, respectively. FAST ranks 5 with a margin of 3.33% to the best accuracy 82.81% of CFS.

In order to further explore whether the classification accuracies of each classifier with the six feature selection algorithms are significantly different, we performed four Friedman tests individually. The null hypotheses are that the accuracies are equivalent for each of the four classifiers with the six feature selection algorithms. The test results are $p = 0$. This means that at $\alpha = 0.1$, there are evidences to reject the null hypotheses and the accuracies are different further differences exist in the six feature selection algorithms. Thus four post-hoc Nemenyi tests were conducted. Figs. 5, 6, 7, and 8 show the results with $\alpha = 0.1$ on the 35 data sets.

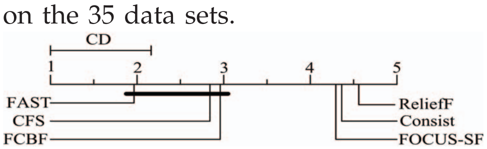

Fig. 5: Accuracy comparison of Naive Bayes with the six feature selection algorithms against each other with the Nemenyi test.

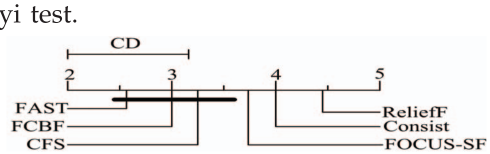

Fig. 6: Accuracy comparison of C4.5 with the six feature selection algorithms against each other with the Nemenyi test.

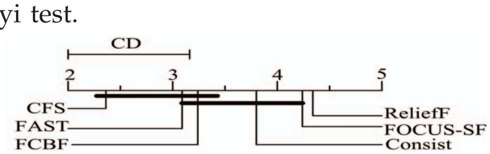

Fig. 7: Accuracy comparison of IB1 with the six feature selection algorithms against each other with the Nemenyi test.

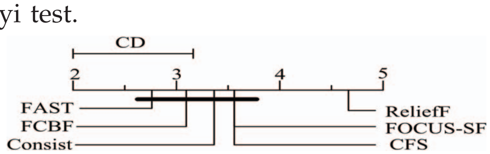

Fig. 8: Accuracy comparison of RIPPER with the six feature selection algorithms against each other with the Nemenyi test.

From Fig. 5 we observe that the accuracy of Naive Bayes with FAST is statistically better than those with ReliefF, Consist, and FOCUS-SF. But there is no consistent evidence to indicate statistical accuracy differences between Naive Bayes with FAST and with CFS, which also holds for Naive Bayes with FAST and with FCBF.

From Fig. 6 we observe that the accuracy of C4.5 with FAST is statistically better than those with ReliefF, Consist, and FOCUS-SF. But there is no consistent evidence to indicate statistical accuracy differences between C4.5 with FAST and with FCBF, which also holds for C4.5 with FAST and with CFS.

From Fig. 7 we observe that the accuracy of IB1 with FAST is statistically better than those with ReliefF. But there is no consistent evidence to indicate statistical accuracy differences between IB1 with FAST and with FCBF, Consist, and FOCUS-SF, respectively, which also holds for IB1 with FAST and with CFS.

From Fig. 8 we observe that the accuracy of RIPPER with FAST is statistically better than those with ReliefF. But there is no consistent evidence to indicate statistical accuracy differences between RIPPER with FAST and with FCBF, CFS, Consist, and FOCUS-SF, respectively.

For the purpose of exploring the relationship between feature selection algorithms and data types, i.e. which algorithms are more suitable for which types of data, we rank the six feature selection algorithms according to the classification accuracy of a given classifier on a specific type of data after the feature selection algorithms are performed. Then we summarize the ranks of the feature selection algorithms under the four different classifiers, and give the final ranks of the feature selection algorithms on different types of data. Table 8 shows the results.

From Table 8 we observe that (i) for image data, CFS obtains the rank of 1, and FAST ranks 3; (ii) for microarray data, FAST ranks 1 and should be the undisputed first choice, and CFS is a good alternative; (iii) for text data, CFS obtains the rank of 1, and FAST and FCBF are alternatives; and (iv) for all data, FAST ranks 1 and should be the undisputed first choice, and FCBF, CFS are good alternatives.

From the analysis above we can know that FAST performs very well on the microarray data. The reason lies in both the characteristics of the data set itself and the property of the proposed algorithm.

Microarray data has the nature of the large number of features (genes) but small sample size, which can cause "curse of dimensionality" and over-fitting of the training data [19]. In the presence of hundreds or thousands of

This article has been accepted for publication in a future issue of this journal, but has not been fully edited. Content may change prior to final publication.

features, researchers notice that it is common that a large number of features are not informative because they are either irrelevant or redundant with respect to the class concept [66]. Therefore, selecting a small number of discriminative genes from thousands of genes is essential for successful sample classification [27], [66].

Our proposed FAST effectively filters out a mass of irrelevant features in the first step. This reduces the possibility of improperly bringing the irrelevant features into the subsequent analysis. Then, in the second step, FAST removes a large number of redundant features by choosing a single representative feature from each cluster of redundant features. As a result, only a very small number of discriminative features are selected. This coincides with the desire happens of the microarray data analysis.

4.4.4 Sensitivity analysis

Like many other feature selection algorithms, our proposed FAST also requires a parameter θ that is the threshold of feature relevance. Different θ values might end with different classification results.

In order to explore which parameter value results in the best classification accuracy for a specific classification problem with a given classifier, a 10 fold cross-validation strategy was employed to reveal how the classification accuracy is changing with value of the parameter θ.

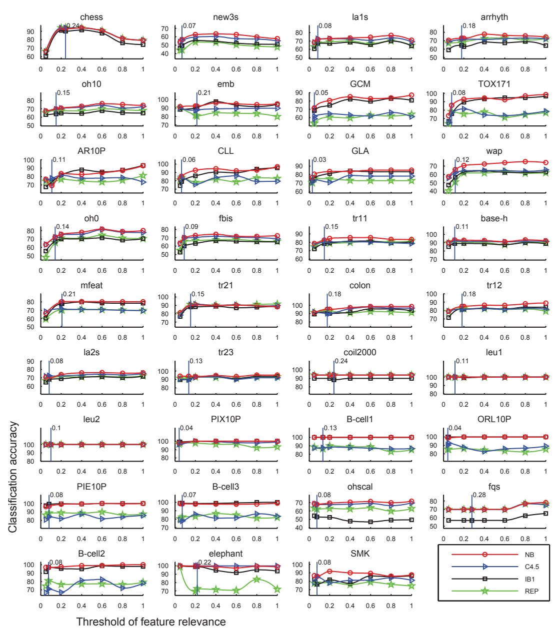

Fig. 9: Accuracies of the four classification algorithms with different θ values.

Fig. 9 shows the results where the 35 subfigures represent the 35 data sets, respectively. In each subfigure, the four curves denotes the classification accuracies of the four classifiers with the different θ values. The cross points of the vertical line with the horizontal axis represent the default values of the parameter θ recommended by FAST, and the cross points of the vertical line with the four curves are the classification accuracies of the corresponding classifiers with the θ values. From it we observe that:

1) Generally, for each of the four classification algorithms, (i) different θ values result in different classification accuracies; (ii) there is a θ value where the corresponding classification accuracy is the best; and (iii) the θ values, in which the best classification accuracies are obtained, are different for both the different data sets and the different classification algorithms. Therefore, an appropriate θ value is desired for a specific classification problem and a given classification algorithm.
2) In most cases, the default θ values recommended by FAST are not the optimal. Especially, in a few cases (e. g., data sets GCM, CLL-SUB-11, and TOX-171), the corresponding classification accuracies are very small. This means the results presented in Section 4.4.3 are not the best, and the performance could be better.
3) For each of the four classification algorithms, although the θ values where the best classification accuracies are obtained are different for different data sets, The value of 0.2 is commonly accepted because the corresponding classification accuracies are among the best or nearly the best ones.

When determining the value of θ, besides classification accuracy, the proportion of the selected features should be taken into account as well. This is because improper proportion of the selected features results in a large number of features are retained, and further affects the classification efficiency.

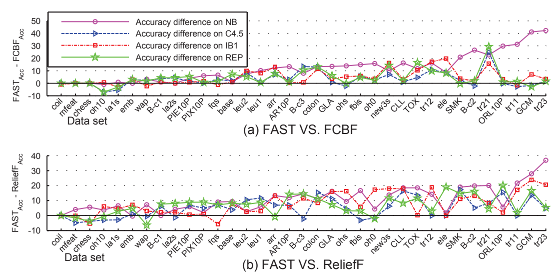

Fig. 10: Accuracy differences between FAST and the comparing algorithms

Just like the default θ values used for FAST in the experiments are often not the optimal in terms of classification accuracy, the default threshold values used for FCBF and ReliefF (CFS, Consist, and FOCUS-SF do not require any input parameter) could be so. In order to explore whether or not FAST still outperforms when optimal threshold values are used for the comparing algorithms, 10-fold cross-validation methods were firstly used to determine the optimal threshold values and then were employed to conduct classification for each of the four classification methods with the different feature subset selection algorithms upon the 35 data sets. The results reveal that FAST still outperforms both FCBF and ReliefF for all the four classification methods, Fig. 10 shows the full details. At the same time, Wilcoxon signed ranks tests [75] with α = 0.05 were performed to confirm the results as advised by Demsar [76]. All the p values are smaller than 0.05, this indicates that the FAST is significantly better than both FCBF and ReliefF (please refer to Table 9 for details).

TABLE 9: p values of the Wilcoxon tests

Alternative hypothesis	NB	C4.5	IB1	REPPER
FAST > FCBF	8.94E-07	0.0013	5.08E-05	8.78E-05
FAST > ReliefF	4.37E-07	3.41E-04	4.88E-06	7.20E-06

Note that the optimal θ value can be obtained via the cross-validation method. Unfortunately, it is very time consuming.

5 Conclusion

In this paper, we have presented a novel clustering-based feature subset selection algorithm for high dimensional data. The algorithm involves (i) removing irrelevant features, (ii) constructing a minimum spanning tree from relative ones, and (iii) partitioning the MST and selecting representative features. In the proposed algorithm, a cluster consists of features. Each cluster is treated as a single feature and thus dimensionality is drastically reduced.

We have compared the performance of the proposed algorithm with those of the five well-known feature selection algorithms FCBF, ReliefF, CFS, Consist, and FOCUS-SF on the 35 publicly available image, microarray, and text data from the four different aspects of the proportion of selected features, runtime, classification accuracy of a given classifier, and the Win/Draw/Loss record. Generally, the proposed algorithm obtained the best proportion of selected features, the best runtime, and the best classification accuracy for Naive Bayes, C4.5, and RIPPER, and the second best classification accuracy for IB1. The Win/Draw/Loss records confirmed the conclusions.

We also found that FAST obtains the rank of 1 for microarray data, the rank of 2 for text data, and the rank of 3 for image data in terms of classification accuracy of the four different types of classifiers, and CFS is a good alternative. At the same time, FCBF is a good alternative for image and text data. Moreover, Consist and FOCUS-SF are alternatives for text data.

For the future work, we plan to explore different types of correlation measures, and study some formal properties of feature space.

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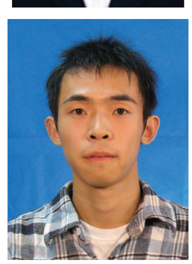

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