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First International Conference on Rough Sets and Knowledge Technology (RSKT 2006) [Proceedings], 2006

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Valdés, J., and Barton, A.
July 2006

* published at the First International Conference on Rough Sets and Knowledge Technology (RSKT 2006). Chonggin, P.R. China. July 24-26, 2006. NRC 48721.

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Relevant Attribute Discovery in High Dimensional Data: Application to Breast Cancer Gene Expressions.

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Abstract. In many domains, the data objects are described in terms of a large number of features. The pipelined data mining approach introduced in [12] using two clustering algorithms in combination with rough sets and extended with genetic programming, is investigated with the purpose of discovering important subsets of attributes in high dimensional data. Their classification ability is described in terms of both collections of rules and analytic functions obtained by genetic programming (gene expression programming). The Leader and several k-means algorithms are used as procedures for attribute set simplification of the information systems later presented to rough sets algorithms. Visual data mining techniques including virtual reality were used for inspecting results. The data mining process is setup using high throughput distributed computing techniques. This approach was applied to Breast Cancer gene expression data and it led to subsets of genes with high discrimination power with respect to the decision classes.

1 Introduction

As a consequence of the information explosion and the development of sensor, observation, computer and communication technologies, it is common in many domains to have data objects characterized by a large number of attributes. This situation leads to high dimensional databases in terms of the set of fields. For example, in biological gene expression experiments, the genetic content of samples of tissues are obtained with high throughput technologies (microchips) with thousands of genes being investigated. In addition, some kinds of bio-medical research involve samples described by large numbers of spectral properties (infrared, ultraviolet, etc). The common denominator in many domains is that the set of data objects has a very high dimensional nature.

A hybrid soft-computing approach for finding relevant attributes in high dimensional datasets based on a combination of clustering and rough sets techniques in a high throughput distributed computing environment was presented in [13]. It also uses virtual reality data representations to aid data analysis. The methodology was applied to Leukemia gene expression data with good results. In this paper, that methodology is extended by incorporating evolutionary computation techniques (genetic programming) at a post processing stage, in order to analytically characterize the relationships between the interesting attributes emerging from the pipeline analysis and the decision classes. This extended approach is applied to Breast Cancer gene expression data.

Each of the formed clusters of attributes is represented by exactly one of the original data attributes. By the nature of the leader algorithm, the representative is the leader (called an *l-leader*), whereas for a k-means algorithm, a cluster is represented by the most similar object with respect to the centroid of the corresponding cluster (the *k-leader*). As a next step, a new information system is built from the original by retaining the l-leaders (or the k-leaders). The filtered information system undergoes a segmentation with the purpose of learning classification rules, and testing their generalization ability in a cross-validation framework. N-folds are used as training sets; where the numeric attributes present are converted into nominal attributes via a discretization process, and from them, reducts are constructed. Finally, classification rules are built from the reducts, and applied to a discretized version of the test fold (according to the cuts obtained previously), from which the generalization ability of the generated rules is evaluated. Besides the numeric descriptors associated with the application of classification rules to data, the use of visual data mining techniques, like the virtual reality space representation [10] [11], enables structural understanding of the data described in terms of the selected subset of attributes and/or the rules learned from them. Each stage feeds its results to the next stage of processing, yielding a pipelined data analysis stream.

Distributed and Grid computing involves coordinating and sharing computing, application, data, storage, or network resources across dynamic and geographically dispersed organizations. The use of grid technologies is an obvious choice for many data mining tasks within the knowledge discovery process.

Condor (<http://www.cs.wisc.edu/condor/>) is a specialized workload management system for compute-intensive jobs in a distributed computing environment, developed at the University of Wisconsin-Madison (UW-Madison). It provides a job queuing mechanism, scheduling policy, priority scheme, resource monitoring, and resource management. All of the experiments in this paper were conducted on a Condor pool of the Institute for Information Technology, National Research Council Canada.

A visual data mining technique -virtual reality spaces- (VR-spaces) was used as an aid for data exploration and the interpretation of the datasets described in terms of the subsets of attributes resulting from the data processing pipelines. This technique extends the concept of 3D modelling to relational structures and was introduced in <http://www.hybridstrategies.com> [10], [11]. The construction of a VR-space requires the specification of several sets and a collection of mappings. Criteria for computing the VR space may be measures of structure preservation, maximization of class separability or combinations of several, possibly conflicting properties.

A detailed explanation about the implementation of the computational paradigm involved in the methodology in the context of a high throughput pipeline based on Condor is given in [12] [13].

2.2 Gene Expression Programming

Analytic functions are among the most important building blocks for modeling, and are a classical form of knowledge. Direct discovery of general analytic functions can be approached from a computational intelligence perspective via evolutionary computation.

There are other possibilities, such as logistic regression, but they do not have as general model representation flexibility. Genetic programming techniques aim at evolving computer programs, which ultimately are functions. Among these techniques, gene expression programming (GEP) is appealing [3]. It is an evolutionary algorithm as it uses populations of individuals, selects them according to fitness, and introduces genetic variation using one or more genetic operators. GEP individuals are nonlinear entities of different sizes and shapes (expression trees) encoded as strings of fixed length. For the interplay of the GEP chromosomes and the expression trees (ET), GEP uses a translation system to transfer the chromosomes into expression trees and vice versa [3]. The set of genetic operators applied to GEP chromosomes always produces valid ETs.

The chromosomes in GEP itself are composed of genes structurally organized in a head and a tail [4]. The head contains symbols that represent both functions (from a function set F) and terminals (from a terminal set T), whereas the tail contains only terminals. Two different alphabets occur at different regions within a gene. For each problem, the length of the head h is chosen, whereas the length of the tail t is a function of h and the number of arguments of the function with the largest arity.

As an example, consider a gene composed of the function set $F=\{Q, +, -, *, /\}$, where Q represents the square root function, and the terminal set $T=\{a, b\}$. Such a gene looks like (the tail is shown in **bold**): $*Q-b+++a/-b\mathbf{baabaaabaab}$, and encodes the ET which corresponds to the mathematical equation $f(a, b) = \sqrt{b} \cdot \left(\left(a + \frac{b}{a} \right) - ((a - b) + b) \right)$ simplified as $f(a, b) = \frac{b \cdot \sqrt{b}}{a}$

GEP chromosomes are usually composed of more than one gene of equal length. For each problem the number of genes as well as the length of the head has to be chosen. Each gene encodes a sub-ET and the sub-ETs interact with one another forming more complex multi-subunit ETs through a connection function. To evaluate GEP chromosomes, different fitness functions can be used.

3 Breast Cancer Experimental Settings and Results

The breast cancer data as used in [2] was downloaded from the Gene Expression Omnibus (GEO) (See http://www.ncbi.nlm.nih.gov/projects/geo/gds/gds_browse.cgi?gds=360) and consists of 24 core biopsies taken from patients found to be *resistant* (greater than 25% residual tumor volume, of which there are 14 biopsies) or *sensitive* (less than 25% residual tumor volume, of which there are 10 biopsies) to docetaxel treatment. The number of genes (probes) placed onto (and measured from) the microarray is 12,625. Therefore, the data contains two classes *resistant* and *sensitive*, with 12,625 attributes.

The experimental settings used in the investigation of the breast cancer data with the distributed pipeline [13] are reported in Table 1. A total of 168 k-leader experiments were completed, each requiring the generation of 86 files (for 10-fold cross-validation). For each experiment, the discretization, reduct computation and rule generation algorithms are those included in the Rosetta system[8].

From the series of k -leader Breast Cancer experiments performed, those experiments having a mean cross-validated accuracy ≥ 0.7 using the rules as applied to test

Table 1. The set of parameters and values used in the experiments with the Breast Cancer data set using the distributed pipeline environment.

Algorithm/Parameter	Values
K-means Variant	Forgy, Jancey, Convergent, MacQueen
Number of Clusters	2, 5, 10, 100, 300, 500
Cross-validation	10 folds
Discretization	BROrthogonalScaler, EntropyScaler, NaiveScaler, RSESOOrthogonalScaler, SemiNaiveScaler
Reduct Computation	JohnsonReducer, Holte1RReducer, RSESExhaustiveReducer, RSESJohnsonReducer
Rule Generation	RSESRuleGenerator

folds are reported in Table-2. Experiment 227 is the overall best result from those selected, with a mean (0.917), median (1.0), standard deviation (0.18), minimum (0.5) and maximum (1.0) 10-fold cross-validated classification accuracy. Table-2 shows that 14 of the 22 selected experimental results have a median classification accuracy of 1.0, while all selected experiments have a maximum classification accuracy of 1.0 over all of the 10 folds. In other words, the 22 selected experiments have classification accuracies skewed towards the maximum obtainable, with the majority of those attaining the maximum in at least one of the test folds. The k-means algorithms used, with the specific k , are also shown in Table-2. The majority of the results use the MacQueen algorithm (9); with Convergent (7), Forgy (3) and Jancey (3) having fewer experiments leading to results that meet the selection criteria. The Convergent algorithm leads to experiments that rank at the lowest and at the highest of the list, while the majority algorithm (MacQueen) leads to experiments that rank second lowest, and second highest. The Forgy and Jancy algorithms appear to come in pairs (e.g. experiments 129 and 130, experiments 177 and 154, and experiments 153 and 178).

Table-2 and Table-3 demonstrate at least two possible ways in which a small number of attributes may be produced from the pipeline. If the investigated k value is small then the rough-set portion of the pipeline will be constrained to output a set of genes of cardinality less than or equal to k . If the investigated k value is large, then the rough-set portion of the pipeline will be given many attributes from which to derive reducts. In the afore-mentioned tables, the selected experiments with large k (the latter case) used the Holte1RReducer algorithm. For example, experiment 359 has a large k value and used a Holte1RReducer and likewise for experiment 355.

Each experiment selects a subset of the original attributes through preprocessing, which are then passed to a cross-validation procedure. This results in the creation of training and test sets, from which a set of reducts and rules are generated.

From the set of selected experiments, the overall best (227) experiment's reducts for each of the 10 folds, are listed in Table-4. Nine of the ten folds produce the same reducts, with the largest reduct containing 3 attributes, and all other reducts containing 1 attribute. The tenth fold results in the production of 1 extra reduct as compared to the 9 other folds. Informally, the largest reduct has been split into 2 reducts in Fold 9.

Table 2. k-leader Breast Cancer experiments for which mean 10-fold cross-validated classification accuracy ≥ 0.7 . Experiment 227 is the overall best result.

No.	Experiment	Mean	Median	Standard Deviation	Min.	Max.	K-means	k
1	347	0.7	0.75	0.35	0.0	1.0	Convergent	10
2	344	0.7	0.75	0.35	0.0	1.0	MacQueen	5
3	127	0.717	0.583	0.25	0.5	1.0	Convergent	5
4	348	0.717	0.833	0.34	0.0	1.0	MacQueen	10
5	343	0.717	1.0	0.42	0.0	1.0	Convergent	5
6	359	0.717	1.0	0.42	0.0	1.0	Convergent	500
7	276	0.733	1.0	0.42	0.0	1.0	MacQueen	10
8	228	0.733	0.917	0.34	0.0	1.0	MacQueen	10
9	300	0.733	1.0	0.42	0.0	1.0	MacQueen	10
10	204	0.733	1.0	0.42	0.0	1.0	MacQueen	10
11	129	0.733	0.917	0.34	0.0	1.0	Forgy	10
12	130	0.733	0.917	0.34	0.0	1.0	Jancey	10
13	131	0.767	0.833	0.25	0.5	1.0	Convergent	10
14	296	0.767	1.0	0.34	0.0	1.0	MacQueen	5
15	272	0.767	1.0	0.34	0.0	1.0	MacQueen	5
16	177	0.783	1.0	0.34	0.0	1.0	Forgy	10
17	154	0.783	1.0	0.34	0.0	1.0	Jancey	10
18	153	0.783	1.0	0.34	0.0	1.0	Forgy	10
19	178	0.783	1.0	0.34	0.0	1.0	Jancey	10
20	355	0.85	1.0	0.34	0.0	1.0	Convergent	500
21	224	0.85	1.0	0.24	0.5	1.0	MacQueen	5
22	227	0.917	1.0	0.18	0.5	1.0	Convergent	10

These 2 reducts contain the same 3 attributes as the largest reduct in the other 9 folds, indicating that the attributes still contain discriminatory power on the whole data matrix.

It can be seen that the reducts listed in Table-4 for experiment 227, the highest ranked result, contain the following set of 10 attributes selected from the original 12,625 attributes. They are listed here, along with their simplified identifier in parenthesis: *36480_at* (v0), *38230_at* (v1), *1511_at* (v2), *38445_at* (v3), *31697_s_at* (v4), *36604_at* (v5), *38010_at* (v6), *39288_at* (v7), *1180_g_at* (v8), and *34211_at* (v9). The next best mean cross-validated experiment (224) yielded 5 attributes from the original 12,625, which are: *1961_f_at*, *34811_at*, *41293_at*, *38449_at*, and *41741_at*. A further investigation of the properties of these attributes should be performed. Therefore, experiment 227 was selected.

A VR-space of 10 attributes from the original 12,625 given to experiment 227 is shown in Fig-2. Convex hulls wrap each of the two classes. It is difficult to perceive on a static medium, but one object from the sensitive class is contained within that of the resistant class. In the dynamic virtual world, it is possible to, for example, rotate and more closely inspect the properties of each of the objects. This virtual reality representation indicates the feasibility of possibly obtaining a class discrimination function.

Table 3. k-leader Breast Cancer experiments for which mean 10-fold cross-validated classification accuracy ≥ 0.7 . Experiment 227 is the overall best result.

No.	Exp. Discretization	Reduct Algorithm
1	347 BROrthogonalScaler	Holte1RReducer
2	344 BROrthogonalScaler	Holte1RReducer
3	127 RSESOOrthogonalScaler	RSESExhaustiveReducer
4	348 BROrthogonalScaler	Holte1RReducer
5	343 BROrthogonalScaler	Holte1RReducer
6	359 BROrthogonalScaler	Holte1RReducer
7	276 SemiNaiveScaler	Holte1RReducer
8	228 BROrthogonalScaler	RSESExhaustiveReducer
9	300 NaiveScaler	Holte1RReducer
10	204 EntropyScaler	RSESExhaustiveReducer
11	129 RSESOOrthogonalScaler	RSESExhaustiveReducer
12	130 RSESOOrthogonalScaler	RSESExhaustiveReducer
13	131 RSESOOrthogonalScaler	RSESExhaustiveReducer
14	296 NaiveScaler	Holte1RReducer
15	272 SemiNaiveScaler	Holte1RReducer
16	177 NaiveScaler	RSESExhaustiveReducer
17	154 SemiNaiveScaler	RSESExhaustiveReducer
18	153 SemiNaiveScaler	RSESExhaustiveReducer
19	178 NaiveScaler	RSESExhaustiveReducer
20	355 BROrthogonalScaler	Holte1RReducer
21	224 BROrthogonalScaler	RSESExhaustiveReducer
22	227 BROrthogonalScaler	RSESExhaustiveReducer

The 10 attributes from experiment 227 were then provided to an expression finding system (GEP), from which a functional model (discrimination function) was found. The model contains 9 of the 10 attributes (v_8 is not used) and the explicit model is:

$$\begin{aligned}
 f(v_0, v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9) = & \quad (1) \\
 & v_6^3 * v_0 * v_9 + (-2) * v_6^2 * v_0 * v_9 * v_7 + v_6^2 * v_0 * v_9 * v_4 - v_6^2 * v_0 * v_9 * v_3 \\
 & - v_6^2 * v_0^2 * v_9 + 2 * v_6 * v_0^2 * v_9 * v_7 + v_6 * v_0^2 * v_9 * v_3 - v_6 * v_0^2 * v_9 * v_4 \\
 & + v_6 * v_0^2 * v_4 * v_1 + v_6 * v_0^2 * v_1 * v_5 - (v_6 * v_0^2 * v_7 * v_5 + v_6 * v_0^2 * v_7 * v_4) \\
 & - (v_6 * v_0^3 * v_5 + v_6 * v_0^3 * v_4) + v_0^2 * v_7 * v_4 * v_2 - v_0^2 * v_3 * v_4 * v_2 \\
 & + v_0 * v_3 * v_4 * v_1 * v_2 + v_0 - v_0 * v_7 * v_4 * v_1 * v_2 + v_9
 \end{aligned}$$

The model was found after 12,954 generations. Additive, multiplicative and subtractive binary operations along with quadratic and cubic unary operations are found. The two variables v_6 and v_0 appear in the model containing both cubic and quadratic forms. These two attributes, therefore, have a greater influence upon the overall functional value of the model.

The two attributes, v_6 and v_0 were extracted from the 10 attribute data matrix in order to construct a new 2 attribute data matrix. This 2 attribute data matrix was then

Table 4. The reducts computed within Experiment 227 for each of the 10-fold cross-validated results. Fold-9 results in the production of 1 extra reduct.

Fold-0,1,2,3,4,5,6,7,8 Reducts	Fold-9 Reducts
{36480_at, 31697_s_at, 36604_at}	{36480_at}
	{31697_s_at, 36604_at}
{38230_at}	{38230_at}
{1511_at}	{1511_at}
{38445_at}	{38445_at}
{38010_at}	{38010_at}
{39288_at}	{39288_at}
{1180_g_at}	{1180_g_at}
{34211_at}	{34211_at}

used in order to find a model that might have discriminatory power over the 2 classes. The highly non-linear model that GEP found is:

$$f(v_0, v_6) = \cos(\tan(v_0) * v_0) * v_0 * \tan(v_6) + v_0 * \tan(v_6) \quad (2)$$

$$+ v_0 * \log(v_6) * \sin(\tan(v_6) - v_6) - \tan(v_6) * v_6$$

The model uses both of the attributes, and contains more complex functions (e.g. sine). Superficially, no attribute seems to have higher influence than the other, so one particular attribute was chosen (v_6) and a new 1 attribute data matrix was constructed (also including the decision attribute). The GEP found the following highly non-linear model:

$$f(v_6) = \sin(v_6) + \cos(v_6 * (\cos(v_6^2) + \sin(\sin(v_6)))) \quad (3)$$

$$+ \sin(v_6 * (v_6 * \cos(v_6) + \cos(v_6)))$$

A property of each of the three models, is that they all produce high classification accuracies over the 2 classes. In particular, the latter single attribute model, when visualized in Fig-3 can be seen to produce almost perfect class separability. The X's represent objects from class *sensitive* and the O's represent objects from class *resistant*. In particular, one object from class *sensitive* is contained within the class *resistant*, which is in agreement with the virtual reality representation of the 10 attributes in Fig-2. The classification rule for Fig-3 is:

$$IF f(v_6) \geq 0.5 \longrightarrow class = sensitive \quad (4)$$

$$otherwise \longrightarrow class = resistant$$

4 Conclusions

Good results were obtained with the proposed high throughput pipeline for the discovery of relevant attributes in high dimensional data. The data mining procedure is based on a combination of clustering and rough sets techniques within a distributed

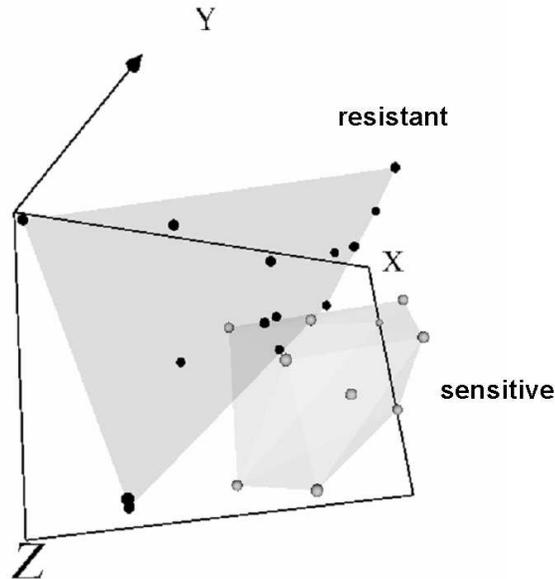


Fig. 2. The 2 classes are wrapped by convex hulls in this static virtual reality representation of 10 attributes from experiment 227. Sammon error: 0.07400. Number of iterations: 150.

computing framework and genetic programming. The attribute reduction procedure using rough set reduces within a cross-validated experimental scheme applied to Breast Cancer gene expression data demonstrates the possibilities of the proposed approach. More thorough studies are required to correctly evaluate the impact of the experimental settings on the data mining effectiveness. The gene expression programming technique produced sets of analytic functions with high discriminatory power. Visual exploration of the results was useful for understanding the properties of the pipeline outputs, and the relationships between the discovered attributes and the class structure.

5 Acknowledgements

This research was conducted within the scope of the BioMine project (National Research Council Canada (NRC), Institute for Information Technology (IIT)). The authors would like to thank Robert Orchard and Ratilal Haria from NRC-IIT.

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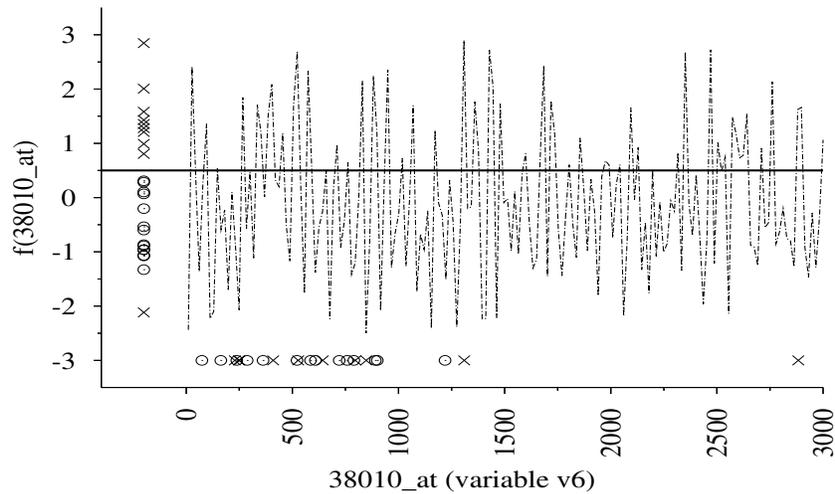


Fig. 3. Decision function found by GEP (Eq-3) for attribute *38010_at*. *x* = class sensitive, *o* = class resistant. No. of generations=4, 490. No. of misclassifications=1.

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