Exploring Medical Data using Visual Spaces with Genetic Programming and Implicit Functional Mappings

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ABSTRACT

Two medical data sets (Breast cancer and Colon cancer) are investigated within a visual data mining paradigm through the unsupervised construction of virtual reality spaces using genetic programming and classical optimization (for comparison purposes). The desired visual spaces are such that a modified genetic programming approach was proposed in order to generate programs representing vector functions. The extension leads to populations that are composed of forests, instead of single expression trees. No particular kind of genetic programming algorithm is required due to the generic nature of the approach taken in the paper. The results (visual spaces) show that the relationships between the data objects and their classes can be appreciated in all of the obtained spaces regardless of the mapping error. In addition, the spaces obtained with genetic programming resulted in lower mapping errors than a classical optimizer and produced relatively simple equations. Further, the set of obtained equations can be statistically analyzed in terms of the original attributes in order to further the understanding of the derivation of the new nonlinear features that are constructed. Thus, explicit mappings provided by genetic programming can be used for feature selection and generation in data mining where scalar and/or vector functions are involved.

Categories and Subject Descriptors

I.5 [**Computing Methodologies**]: Pattern Recognition; E.0 [**Data**]: General; I.1 [**Computing Methodologies**]: Symbolic and Algebraic Manipulation; J.3 [**Computer Applications**]: Life and Medical Sciences

General Terms

Algorithms

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Keywords

vector functions, virtual reality, genetic programming, breast cancer, colon cancer

1. INTRODUCTION

Proper exploration and understanding of medical data requires significant domain knowledge. To begin such an investigation, many approaches may be considered possible avenues for research. This paper takes a visual approach due to the increasing complexity of data analysis procedures that inhibit the user from extracting useful information out of results generated by the various techniques.

This paper explores an extension of genetic programming to vector valued functions; that is, from single expressions to forests of expression trees. The extension is not constrained to a particular form of genetic programming but is a generic approach that is used for constructing explicit analytic mappings for visualization and exploration purposes. This occurs within a visual data mining paradigm using virtual reality that enables the decision maker to not only visualize, but also navigate and interact with the presented information. A comparison of the evolutionary technique to classical optimization is also presented and applied to medical data for both Breast and Colon cancer.

2. SPACE VISUALIZATION

There are many possible paradigms for creating visual spaces within data mining. In particular Virtual Reality (VR) is a suitable paradigm for several reasons. It is *flexible*: allows the choice of different ways to represent the objects according to the differences in human perception. VR allows *immersion*: the user can navigate inside the data and interact with the objects in the world. It creates a *living* experience: the user is not a passive observer, but an actor in the world. VR is *broad and deep*: the user may see the VR world as a whole, or concentrate on details. Also very important is that its use does not require any special background knowledge. A virtual reality technique for visual data mining on heterogeneous, imprecise and incomplete information systems was introduced in [14, 15].

One of the steps in the construction of a VR space for data representation is the transformation of the original set of attributes describing the objects under study, often defining a heterogeneous high dimensional space, into another space of small dimension (typically 2-3) with an intuitive metric (e.g. Euclidean). The operation usually involves a non-linear transformation; implying some information loss. There are basically two kinds of spaces sought: *i)* spaces preserving the structure of the objects as determined by the original set of attributes, and *ii*) spaces preserving the distribution of an existing class defined over the set of objects.

2.1 Space Taxonomy

From the point of view of the property(s) which the objects in the space must satisfy, several paradigms can be considered for building a transformed space for constructing visual representations [16]:

- *Unsupervised*: The location of the objects in the space should preserve some structural property of the data, dependent only on the set of descriptor attributes.
- *Supervised*: The goal is to produce a space where the objects are maximally discriminated w.r.t. a class distribution. The space is distorted in order to maximize class discrimination.
- *Mixed*: A space compromising the two goals is sought. Very often these two goals are conflicting.

For the purposes of this study, unsupervised spaces are constructed because data structure is one of the most important elements to consider when the location and adjacency relationships between the objects should give an indication of the *similarity relationships* [3, 2] between the objects as given by the set of original attributes [15]. Let $\mathcal{H}^n$ be the space defined by the original n-attributes (not necessarily numeric) and $\mathbb{R}^m$ a m-dimensional space given by a Cartesian product of the reals s.t. $m < n$. A mapping $\varphi : \mathcal{H}^n \to \mathbb{R}^m$ creates images of the objects in $\mathcal{H}^n$ in $\mathbb{R}^m$. The mappings of interest are those which maximize some metric or non-metric structure preservation criteria as has been done for decades in multidimensional scaling [10, 2], or to minimize some error measure of information loss [13]. If δ_{ij} is a dissimilarity measure between any two objects i, j ($i, j \in \mathcal{H}^n$), and $\zeta_{i^v j^v}$ is another dissimilarity measure defined on objects $i^v, j^v \in \mathbb{R}^m$ ($i^v = \varphi(i), j^v = \varphi(j)$), examples of error measures frequently used are:

$$\text{S stress} = \sqrt{\frac{\sum_{i<j} (\delta_{ij}^2 - \zeta_{ij}^2)^2}{\sum_{i<j} \delta_{ij}^4}}, \quad (1)$$

$$\text{Sammon error} = \frac{1}{\sum_{i<j} \delta_{ij}} \frac{\sum_{i<j} (\delta_{ij} - \zeta_{ij})^2}{\delta_{ij}} \quad (2)$$

$$\text{Quadratic Loss} = \sum_{i<j} (\delta_{ij} - \zeta_{ij})^2 \quad (3)$$

2.2 Mapping Taxonomy

From the point of view of their mathematical nature, the mappings can be:

- *Implicit*: the images of the transformed objects are computed directly and the algorithm does not provide a function representation.
- *Explicit*: the function performing the mapping is found by the procedure and the images of the objects are obtained by applying the function. Two sub-types are:
  - *analytical functions.*
  - *general function approximators*: neural networks, fuzzy systems, or others.

2.3 Mapping Computation

Explicit mappings can be constructed in the form of analytical functions (e.g. via genetic programming), or using general function approximators like neural networks or fuzzy systems. An explicit mapping (e.g. φ) is useful for both practical and theoretical reasons. On one hand, in dynamic data sets (e.g. systems being monitored or incremental data bases) an explicit transform φ will increase the update rate of the VR information system. On another hand, it can give semantics to the attributes of the VR space, thus acting as a general dimensionality reducer.

Classical algorithms have been used for directly optimizing these measures, like Steepest descent, conjugate gradient Fletcher-Reeves, Powell, Levenberg-Marquardt, and others. The number of different similarity, dissimilarity and distance functions definable for the different kinds of source sets is immense. Moreover, similarities and distances can be transformed into dissimilarities according to a wide variety of schemes, thus providing a rich framework.

For this study, the Fletcher-Reeves method, which is a well known technique used in deterministic optimization [12] was used. It assumes that the function f is roughly approximated as a quadratic form in the neighborhood of an N dimensional point $\mathbf{P}$ and it uses the information given by the partial derivatives of the original function f. This is the conjugate gradient family of minimization methods and requires an initial approximation to the solution (typically random), which is then refined in a sequence of iterative steps. The convergence of these methods is relatively fast, but they suffer from the entrapment effect, by means of which the obtained solutions are locally optimal.

3. MAPPING COMPUTATION USING GENETIC PROGRAMMING

Genetic programming techniques aim at evolving computer programs, which ultimately are functions. Genetic Programming is an extension of the Genetic Algorithm introduced in [6] and further elaborated in [7], [8] and [9]. The algorithm starts with a set of randomly created computer programs. This initial population goes through a domain-independent breeding process over a series of generations. It employs the Darwinian principle of survival of the fittest with operations similar to those occurring naturally, like sexual recombination of entities (crossover), occasional mutation, duplication and gene deletion. A computer program is understood as an entity that receives inputs, performs computations which transform these inputs and produces some output in a finite amount of time. The operations include arithmetic computation (possibly involving many other functions), conditionals, iterations, recursions, code reuse and other kinds of information processing organized into a hierarchy. It is considered that a system for automatically creating computer programs should create entities covering the above mentioned features as much as possible. Genetic programming combines the expressive high level symbolic representations of computer programs with the near-optimal search efficiency of the genetic algorithm. For a given problem, this process often results in a computer program which solves it exactly, or if not, at least provides a fairly good approximation. Those programs which represent functions are of particular interest and can be modeled as $y = F(x_1, \cdots, x_n)$, where $(x_1, \cdots, x_n)$ is the set of independent or predictor variables, and y the dependent or predicted variable, so that $x_1, \cdots, x_n, y \in \mathbb{R}$, where $\mathbb{R}$ are the reals. The function F is built by assembling functional subtrees using a set of predefined primitive functions (the function set), defined beforehand. In general terms, the model describing the program is given by $y = F(\vec{x})$, where $y \in \mathbb{R}$ and $\vec{x} \in \mathbb{R}^n$. Most implementations of genetic programming for modeling fall within this paradigm.

However, there are problems involving vector functions which require an extension of this paradigm. In these cases the model associated to the evolved programs must be $\vec{y} = F(\vec{x})$. Note that these are *not* multi-objective problems, but problems where the fitness function depends on vector variables. The mapping problem between vectors of two spaces of different dimension (n and m) is one of that kind. In this case a transformation like $\varphi : \mathbb{R}^n \to \mathbb{R}^m$ mapping vectors $\vec{x} \in \mathbb{R}^n$ to *vectors* $\vec{y} \in \mathbb{R}^m$ would allow a reformulation of Eq. 2 (and the others) as in Eq. 4:

$$\text{Sammon error} = \frac{1}{\sum_{i<j} \delta_{ij}} \frac{\sum_{i<j} (\delta_{ij} - d(\vec{y}_i, \vec{y}_j))^2}{\delta_{ij}}, \qquad (4)$$

where $\vec{y}_i = \varphi(\vec{x}_i)$, $\vec{y}_j = \varphi(\vec{x}_j)$. The implication from the point of view of genetic programming is that instead of evolving expression trees, where there is a one-to-one correspondence between an expression tree and a fitness function evaluation (the classical case), the evolution has to consider populations of *forests* such that the evaluation of the fitness function depends on the set of trees within a forest. In these cases, the cardinality of any forest within the population is equal to the dimension of the target space m.

3.1 Gene Expression Programming

Gene Expression Programming (GEP) [4] is used to build mathematical models. The algorithm starts with a generated population of individuals (i.e. the initial population) that each embody a mathematical model. The individuals in the population are evaluated to determine their fitness (how well they represent the data) and those with the most suitable fitness are chosen to move along to the next generation, with various types of "genetic" operators applied to them. Over a number of generations the population evolves towards better models. In the GEP algorithm, the individuals are encoded as simple strings of fixed length, referred to as chromosomes. Each chromosome can be composed of one or more genes which hold individual mathematical expressions that are linked together to form a larger expression.

To facilitate experimentation with the GEP algorithm, an extension to an existing Java-based Evolution Computing Research System called ECJ [1] from George Mason University has been made. ECJ has an infrastructure to support various types of evolutionary computing, including Genetic Programming (GP). The extension, ECJ-GEP, implements almost all of the features of GEP allowing one to tackle four basic types of problem: function finding, classification, time series, and logical. It supports a large set of fitness functions and allows expressions to be created using many types of arithmetic functions in such a way that additions are straightforward. The problem parameters that determine which functions to use in expressions, how to perform the evolutionary operations, the size of the population, the number of generations to run, etc. are defined within parameter files. The system has been designed so that for most problems no code should need to be written. However, for those other problems, code may be incorporated in order to address the special need (e.g. to generate data, do something special with the fitness calculation, etc). There is a graphical interface that allows for the sequential execution of problems. Batch files may be constructed (outside of ECJ-GEP) for execution upon distributed systems (e.g. Condor: `http://www.cs.wisc.edu/condor/`) to allow for large scale experimentation.

For the particular research described in this paper, a new idea led to an extension of the GEP algorithm, whereby an individual in the population may have multiple chromosomes. The chromosomes are independent but evolve together from generation to generation. This supports the population of *forests* needed for such problems.

3.2 Distributed Computing Environment

Among distributed computing systems for delivering high throughput computing, the Condor system stands out. Condor is a specialized workload management system for compute-intensive jobs in a distributed computing environment, developed by the Condor Research Project at the University of Wisconsin-Madison (UW-Madison). Like other full-featured batch systems, Condor provides a job queueing mechanism, scheduling policy, priority scheme, resource monitoring, and resource management. Users submit their serial or parallel jobs to Condor, Condor places them into a queue, chooses when and where to run the jobs based upon a policy, carefully monitors their progress, and ultimately informs the user upon completion.

4. EXPERIMENTAL SETTINGS

Two data sets (Breast Cancer and Colon Cancer) were used along with both a classical and a genetic programming technique for the construction of visual spaces. The experimental settings associated with each such experimental condition are detailed subsequently.

The University of California, Irvine (UCI) maintains an international machine learning (ML) database repository (`http://www.ics.uci.edu/~mlearn/`), containing an archive of over 100 databases used specifically for evaluating machine learning algorithms. As such, a breast cancer database created by Dr. William H. Wolberg of the University of Wisconsin Hospitals, Madison, Wisconsin, was obtained from the UCI ML Repository [11]. The database contains 699 objects, 9 integer-valued attributes and is composed of 2 classes (241 malignant and 458 benign). In addition, 16 objects contain missing values, which, for the purposes of our study, were removed from consideration (leaving 683 objects).

A previous study [17] analyzed a human colon cancer cell line (called EcR-RKO/KLF4) that was treated for up to 24 hours with ponasterone A to induce expression of a full-length, transgenic Krüppel-like factor 4 (KLF4). KLF4 is an epithelially-enriched, zinc finger transcription factor. The study's results provide insight into the biochemical function of KLF4. Fig. 1 shows a typical cell cycle [18], with it being known that KLF4 exhibits checkpoint function during the G_1/S and G_2/M transitions. This cell cycle [18] is the se-

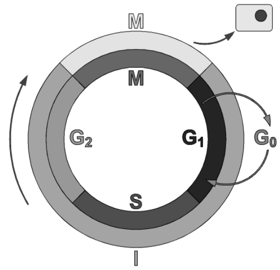

Figure 1: Schematic of a cell cycle. Outer Ring: I=Interphase, M=Metaphase; Inner Rring: M=Mitosis. Mitosis duration in relation to the other phases has been exaggerated.

ries of events in a eukaryotic cell between one cell division and the next. Thus, it is the process by which a single-cell fertilized egg develops into a mature organism and the process by which hair, skin, blood cells, and some internal organs are renewed. It consists of four distinct phases: G1 phase, S phase, G2 phase (collectively known as interphase) and M phase. M phase is itself composed of two tightly coupled processes: mitosis, in which the cell's chromosomes are divided between the two daughter cells, and cytokinesis, in which the cell's cytoplasm physically divides. Cells that have temporarily or reversibly stopped dividing are said to have entered a state of quiescence called G0 phase, while cells that have permanently stopped dividing due to age or accumulated DNA damage are said to be senescent. The molecular events that control the cell cycle are ordered and directional; that is, each process occurs in a sequential fashion and it is impossible to "reverse" the cycle. Data was obtained from `http://www.ncbi.nlm.nih.gov/geo/gds/gds_browse.cgi?gds=1942` and consists of $44,566$ objects, 8 time points (0h, 1h, 2h, 4h, 6h, 8h, 12h, 24h) (only the last 7 used) and 2 classes ($22,283$ control and $22,283$ induced). After application of the classical leader algorithm [5] the class distribution was (224 control and 335 induced for a total of 559 objects).

4.1 Implicit Classical Algorithm Settings

The Fletcher-Reeves-Polak-Ribiere (FRPR) method (a slight modification of this method, believed to improve the original), is the one used here as a standard for comparison. When Eq. 4 is solved for the $\vec{y}_k \in \mathbb{R}^m, k \in [1, N]$, where N is the number of objects, with this method (or a similar one), the obtained mapping is implicit. In order to reduce the chance of entrapment in local minima, 100 runs of the algorithm were made, that were started with the corresponding number of random initial approximations (in this case random 3D matrices). This procedure was applied to each investigated data set. The solutions were used for constructing the corresponding virtual reality spaces with which those obtained with vectorial genetic programming are compared.

4.2 Explicit GEP Algorithm Settings

The major experimental settings that were used for the ECJ-GEP experiments are listed in Table 2. It can be seen that the mathematical expressions composed for each of the chromosomes in an idividual will be made from 5 gene expressions, each linked by the addition operator. The gene

Table 1: Example of a mathematical expression and its respective encoding.

Mathematical expression:	b*(c-d)
Karva Encoding of Expression:	*b-cd/bdaac

expressions can be formed using constants, the independent variables associated with each problem, and any of the functions listed. The weightings for the functions allow us to give a preference to some operators over others. In this case we decided to favour addition, subtraction and multiplication. The number of *characters* (constants, functions, variables) in each gene is determined by the gene's head size and the maximum arity of any function being used and consequently is calculated according to Eq.5:

$$headSize + headSize * (maximumArity - 1) + 1 \qquad (5)$$

In this study a head size of 5 and a maximum arity of 2 were used leading to genes that have 11 characters that encode expressions in a special notation called Karva [4]. Each gene also stores 4 constants randomly chosen between 1 and 10 that can be used in the formation of Karva expressions. A Karva expression with 11 characters and the expression it encodes is shown in Table 1; depending on the expression being encoded, not all characters are part of the expression.

The great advantage of the encoding scheme is that it is compact and any combination of the allowed characters will always represent a valid mathematical expression.

The parameters related to evolution determine how the genes (Karva expressions) are transformed from generation to generation. It is beyond the scope of this paper to discuss this in detail but as an example, the mutation rate determines the number of characters that will be mutated (replaced by another character) in the population. If we have 100 individuals in the population and each individual has 1 chromosome with a single gene of size 11 characters, then we would randomly select 100*11*0.044 or 48 characters to mutate. Note that it may be that the character is in a region of the gene that is not part of the expression encoded by the gene and the effect will be no change to the expression. The parameters rnc-mutation rate, dc-mutation rate and dc-inversion rate control how the 4 constants associated with each gene evolve from generation to generation while the others are related to evolution of the genes.

For each of the three experiments a set of 75 runs was performed with random seeds and varying values for the number of generations and population size.

5. RESULTS

The mapping errors (Eq. 4) for the best models found for all data sets are shown in Table. 3. For the Breast cancer data, the FRPR method outperformed GP-GEP by a factor of 2.6, but for Colon cancer data, GP-GEP outperformed FRPR by a factor of 10.

5.1 Breast Cancer Results

It is impossible to represent a VR space on hard media. Snapshots of the visual spaces computed over the Breast Cancer data set using GP-GEP (Fig. 4(b), Fig. 5(a)) and FRPR (Fig. 5(b)) show the similarity structure and the original classes (benign and malignant tumors). In addition, the

Table 2: Experimental Settings used for the investigation of the Breast and Colon Cancer data.

GEP Parameter	Experimental Values
No. Generations	100, 500 and 1000
Population Size	100, 200 and 500
No. Chromosomes / Individual	3
No. Genes / Chromosome	5
Gene Head Size	5
Linking function	Addition
No. Constants / Gene	4
Bounded Range of Constants	$[1, 10]$
Inversion Rate	0.1
Mutation Rate	0.044
is-transposition Rate	0.1
ris-transposition Rate	0.1
One-point Recomb. Rate	0.3
Two-point Recomb. Rate	0.3
Gene Recombination Rate	0.1
Gene Transposition Rate	0.1
rnc-mutation Rate	0.01
dc-mutation Rate	0.044
dc-inversion Rate	0.1
Breast Cancer Data	
5 Functions(weight)	add(2), sub(2), mult(2), div(1), pow(1)
Breast and Colon Cancer Data	
8 Functions(weight)	add(2), sub(2), mult(2), div(1), pow(1), exp(1), sin(1), cos(1)

Table 3: Sammon errors for the different datasets and methods.

Dataset	Method	Sammon Error
Breast Cancer	GP-GEP (5 functions)	0.026616
	GP-GEP (8 functions)	0.027823
	FRPR	0.009945
Colon Cancer	GP-GEP (8 functions)	0.002874
	FRPR	0.024015

classes are wrapped with transparent membranes as an aid and Fig. 4(a) may be compared to Fig. 4(b) to appreciate the enhancement. Both algorithms, GP-GEP and FRPR, succeeded in showing the benign class (light objects) more densely packed and homogeneous than the malignant class. In addition, it can be observed that both classes have an important intersection making it difficult to expect perfect classification of this data with machine learning techniques. The same class structure is exhibited by the FRPR space (Fig. 5(b)) despite its lower mapping error.

The analytical expression for the vector function φ (Eq. 6) shows that slight nonlinear combinations of the original variables may achieve a good level of dimensionality reduction. However, increasing the function set with more nonlinear functions, led to more complex equations (Eq. 7) without improving the error. Not all of the variables appear in the best model equations, suggesting that this technique may help in identifying irrelevant variables.

The best Breast cancer data experiment (No. 4) using 5

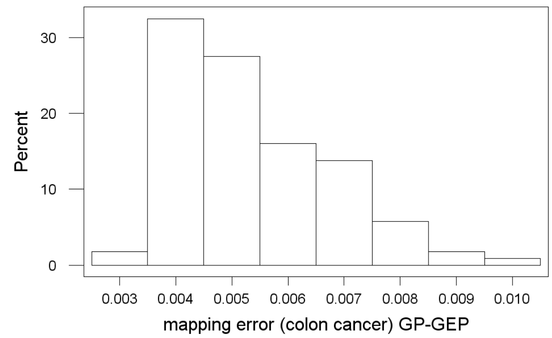

Figure 2: Error Histogram - Colon Cancer 8 functions - GP-GEP

functions yielded the vector function mapping (φ) of Eq.6:

$$\begin{aligned}\varphi_X &= v2 + v6 + v3 + ((v3/v2) - v3) \\ &\quad + ((v6 - (v9 + v6))/v5) \\ \varphi_Y &= (v7/((v1 + v4) + k_{y1})) + ((v7 * v3)/(v3 + v3)) \\ &\quad + (v4 - v7) + (v7/((v2 + v3) * pow(v6, v4))) + v7 \\ \varphi_Z &= v5 + (v6/(k_{z1}/v9)) + ((v6 + v6)/(v5 + v9)) \\ &\quad + (v8 - v5) + (v1 - v6)\end{aligned} \tag{6}$$

where
$k_{y1} = 3.7319260767682723$, and $k_{z1} = 9.948321752508829$.

The best Breast cancer data experiment (No. 28) using 8 functions yielded the vector function mapping (φ) of Eq.7:

$$\begin{aligned}\varphi_X &= v3 + sin(exp(v6)) + (((v5/v5) + v9)/v8) \\ &\quad + cos((sin(v7)/pow(v8, k_{x1}))) + v6 \\ \varphi_Y &= k_{y1} + cos(cos((k_{y2} * cos(v5)))) + v7 + k_{y3} \\ &\quad + \quad (v4 + (v5/v6)) \\ \varphi_Z &= sin(v4) + v1 + k_{z1} + v8 + sin((sin(v2)/v9))\end{aligned} \tag{7}$$

where
k_{x1} =8.532346535090838, k_{y1} $=exp(1.4970654475170435)$, k_{y2} =9.392340674168233, k_{y3} $=cos(7.062490411699605)$, k_{z1} =4.786257036832491.

5.2 Colon Cancer Results

In this case, the best GP-GEP error solution is one order of magnitude better than the one obtained with the FRPR method. In addition, the distribution of GP-GEP errors (when 5 functions were used) is positively skewed (Fig. 2) indicating the tendency of the algorithm to produce low error solutions. But the distribution for FRPR (Fig. 3) is negatively skewed, which is a non-desirable behavior.

The VR spaces for GP-GEP are shown in Fig. 6(a) and Fig. 6(b) while those for FRPR are shown in Fig. 7(a) and Fig. 7(b). The difference in behavior between the control and the induced classes is clear. The latter is linear (in the non-linear space), whereas the control is not. In addition, the control class is much larger and scattered. The larger error of the FRPR space is visually associated with the scattering of the data at one extreme (Fig. 7(a), Fig. 7(b)) and with a general bending of the space (particularly affecting the induced class). The mapping function for the GP-GEP algorithm (Eq. 8) exhibits a more evident nonlinear character that disregards some of the original attributes.

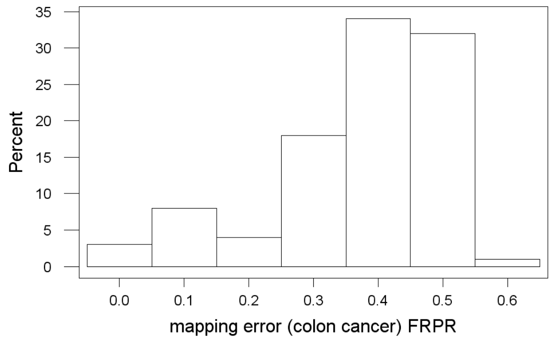

Figure 3: Error Histogram - Colon Cancer 8 functions - FRPR

The best Colon cancer data experiment (No. 94) using 8 functions yielded the vector function mapping (φ) of Eq.8:

$$\begin{aligned}\varphi_X &= (v6 - ((v2 - v5)/k_{x1})) + v4 + exp(cos(v1)) \\ &\quad + cos(v3) \\ \varphi_Y &= ((v5 + v3)/(k_{y1} - v7)) + v1 + cos(v1) + (v2/k_{y2}) \\ &\quad + (v2/v1) \\ \varphi_Z &= cos(v5) + k_{z1} + sin((cos(v7) * (v7 * k_{z2}))) \\ &\quad + ((v3 - v6)/k_{z3}) + v3\end{aligned} \tag{8}$$

where
k_{x1} =3.651359087092545, k_{y1} =3.2137460764913106, k_{y2} =1.9151269649790634 , k_{z1} =1.2251144232153708, k_{z2} =6.183231644681386, k_{z3} =6.860155877701824.

6. CONCLUSIONS

This paper presented a method for computing virtual reality spaces for visual data mining based on genetic programming, oriented to the generation of programs representing vector functions. Populations composed of forests, instead of single expression trees, are evolved in an generic approach; that is, not associated with a particular kind of genetic programming algorithm. Virtual reality spaces for representing two medical data sets are constructed and compared with similar ones computed using classical optimization methods. The mapping errors obtained with the genetic programming generated vector functions were similar or much better than their counterparts obtained with classical techniques. The spaces correspond to unsupervised mappings. Nevertheless, the relationships between the data objects and their classes (shown within the paper for comparison) can be appreciated in all of the spaces computed regardless of the mapping error. An additional advantage of the GP approach is the possibility of explicitly examining the role of the data attributes by examining the corresponding vector equations responsible for the mappings. This can be seen as a GP contribution to feature selection and generation in data mining. These results are preliminary but also promising.

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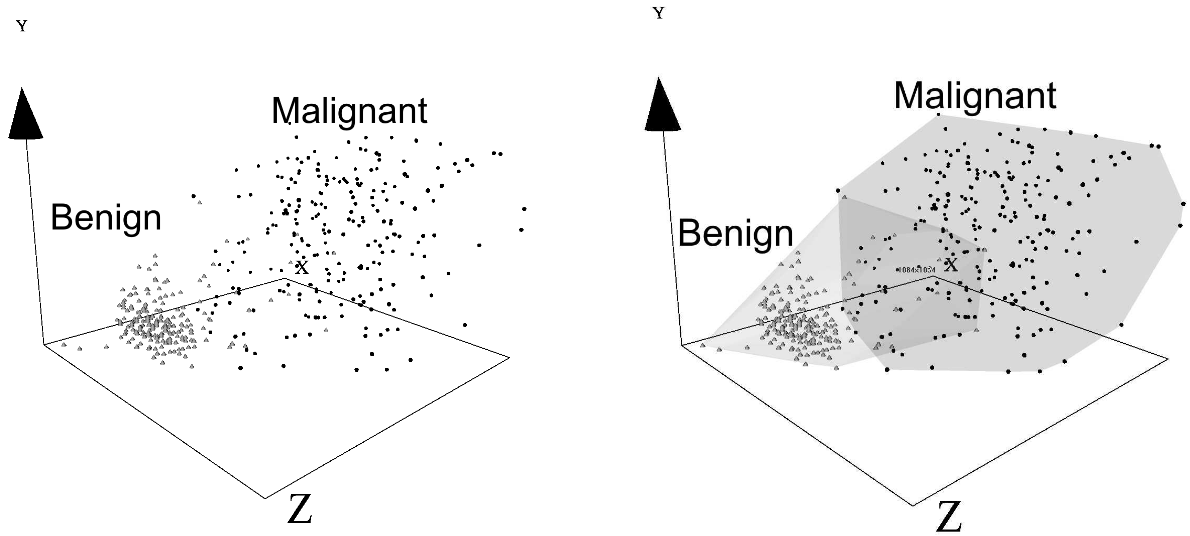
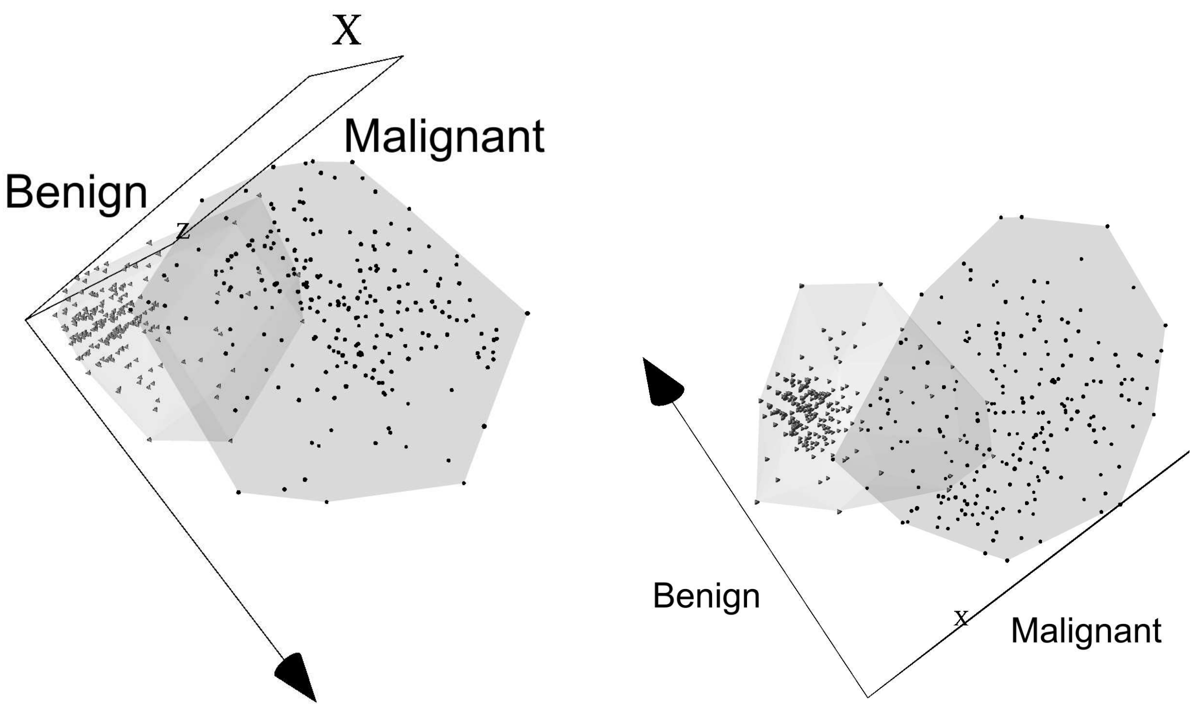


(a) Object (gene) locations after mapping using Eq.6.

(b) Convex Hulls wrap the two classes.

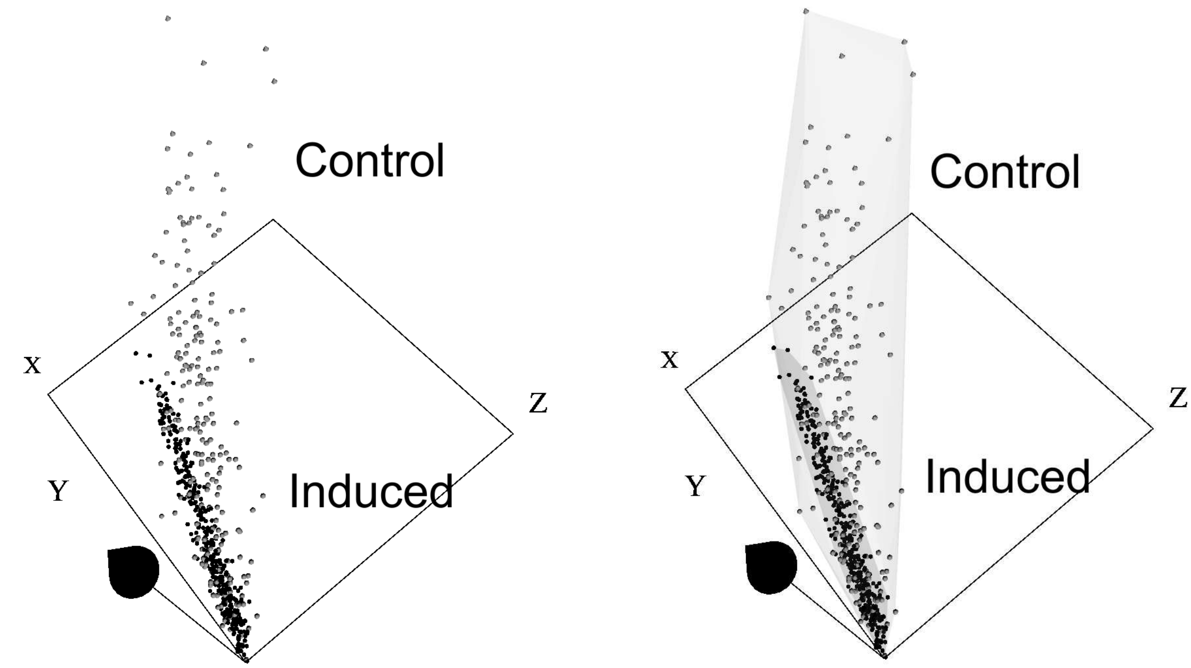
Figure 4: Breast Cancer Data (GP-GEP with 5 functions). Light objects: benign. Dark objects: malignant.



(a) Object (gene) locations after mapping using Eq.7. Convex Hulls wrap the two classes.

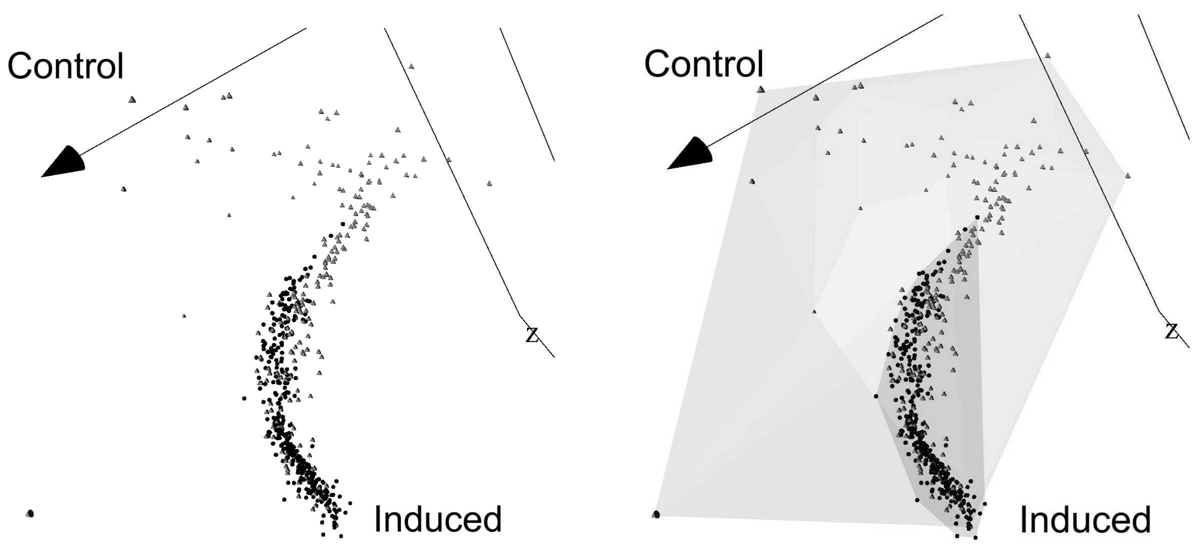
(b) Object (gene) locations after implicit mapping. Convex Hulls wrap the two classes.

Figure 5: Breast Cancer Data Left: GP-GEP with 8 functions. Right: FRPR. Light objects: benign. Dark objects: malignant.



(a) Object (gene) locations after mapping using Eq.8. (b) Convex Hulls wrap the two classes.

Figure 6: Colon Cancer Data (GP-GEP with 8 functions). Light objects: control. Dark objects: induced.



(a) Object (gene) locations after implicit mapping. (b) Convex Hulls wrap the two classes.

Figure 7: Colon Cancer Data (FRPR). Light objects: control. Dark objects: induced.