

An Analysis on the Performance of a K-Nearest-Neighbor Classification Based Outlier Detection System using Feature Selection and Dimensionality Reduction Techniques

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ABSTRACT - The general idea of classification-based outlier detection method is to train a classification model that can distinguish normal data from outliers. In the previous work, we have implemented and evaluated three classification based outlier detection algorithms and found that the k-neighborhood algorithm was capable of identifying and classifying the outliers better than the other two compared algorithm in terms of accuracy, f-score, Sensitivity/Recall, error rate. Further, the cpu time of the k-neighborhood algorithm also minimum. In this work, the performance of outlier detection is evaluated using dimensionality reduction algorithms. The results clearly shows that the impact of dimensionality reduction algorithm on the cancer dataset is significantly improved the overall classification performance to a considerable level.

1. INTRODUCTION

In Data Mining, Outliers are meaningful input signals, which represent the characteristic of the object. This work aims to study the performance of classification algorithms of data mining for outlier detection using dimensionality reductions. Before the elimination of points, one should study why these points appeared and whether it is likely to continue to appear.

1.1. Outlier Detection in High-Dimensional Data

In high dimensional data set, some attributes may be irrelevant. But by using feature selection approaches such as filter and wrapper, has to find the subset of the original attributes.

1.2. Problem Specification

The identification of outlier can be viewed as classification problem which can lead to the discovery of unexpected knowledge in the medical field. The general idea is to train a classification model that can distinguish normal data from outliers [7].

In medical cancer dataset, the available number of malignant/outlier samples are less than that of the normal/benign and it causes an inaccurate classifier model [25, 26]. Many solutions like eliminate variables using factor analysis and principle component methods were suggested to improve the efficiency of the algorithm.

This method proposes to use dimensionality reduction and feature selection algorithms to overcome the training performance and testing accuracy issues in the classification based outlier detection approaches.

2. MODELING CLASSIFICATION BASED OUTLIER DETECTION SYSTEM

The popular methods of outlier detection are supervised, semi supervised, unsupervised proximity-based. With the limitation of the Grubb's test and the Rosener test, there is a need for

more sophisticated and speedy method such as classification based outlier detection, which heavily depends of the quality and availability of training data set.

2.1. The Used Classification Algorithm

K-Nearest Neighbors Classifier

K-Nearest Neighbors is a method to assign the input instance to the class with the majority of K-Nearest Neighbors by considering the Euclidean distances between two instances

2.2. Feature Selection Technique

1. Chi Square, 2.Information Gain and 3.Gini Index are used.

2.3. Dimensionality Reduction Algorithm

The famous Algorithms for dimensionality reduction such as Principal Component Analysis, Kernel PCA and LPP (Locality preserving Projection) can be used.

3. THE EVALUATION

The performance of the classification algorithms under evaluation were tested with "Wisconsin Breast Cancer Database"

3.1. Breast cancer dataset

Breast cancer dataset (Wisconsin Breast Cancer Database) obtained from the UCI online machine-learning repository at <http://www.ics.uci.edu/~mllearn/MLRepository.html>

The Wisconsin breast cancer database (WBCD): The WBCD dataset is summarized in Table 1 and consists of 699 instances taken from fine needle aspirates (FNA) of human breast tissue. Each instance consists of nine measurements (without considering the sample's code number), namely clump thickness, uniformity of cell size, uniformity of cell shape, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal nucleoli, and mitoses. The measurements are assigned an integer value between 1 and 10, with 1 being the closest to benign and 10 the most anaplastic. Associated with each sample is its class label, which is either benign or malignant. This dataset contains 16 instances with missing attributes' values. Since many classification algorithms have discarded these data samples, for the ease of comparison, the same way is followed and the remaining 683 samples are taken for use. Therefore, the class is distributed with 444 (65.0%) benign samples and 239 (35.0%) malignant samples (Tan et al 2003).

3.2. Metrics Used For Evaluation

Random index and Run time are two measures for evaluating the algorithm under consideration. The total run time is the sum of the times taken for learning and testing and this model concentrate on the time taken for training which is higher than the time taken for testing.

3.2.1. Total Run Time

We calculated the total run time as the sum of time required for training and the time required for testing. Here we compare the CPU times only. Since the time taken for training is the very much higher and the time required for testing the network with same number of records is very in significant, in the following table we just only mention the time taken for training.

Table 1: Summary of the WBCD dataset

Attribute	Possible values
Clump thickness	Integer 1–10
Uniformity of cell size	Integer 1–10
Uniformity of cell shape	Integer 1–10
Marginal adhesion	Integer 1–10
Single epithelial cell size	Integer 1–10
Bare nuclei	Integer 1–10
Bland chromatin	Integer 1–10
Normal nucleoli	Integer 1–10
Mitoses	Integer 1–10
Class	Benign (65.5%), Malignant (34.5%)

3.3. The Metrics and Validation Method Used for Performance Evaluation

3.3.1. Confusion Matrix

A Confusion matrix shows the type of classification error a classifier produced. The advantage of using this matrix is that it not only tells us how many got misclassified but also what misclassifications occurred.

Predicted Class		Actual Class
Positives	Negatives	
a	b	Positives
c	d	Negatives

Figure 1: A confusion matrix.

The breakdown of a confusion matrix is as follows:

- a is the number of positive examples correctly classified (True Positives –TP)
- b is the number of positive examples misclassified as negative(False Negatives -FN)
- c is the number of negative examples misclassified as positive(False Positives –FP)
- d is the number of negative examples correctly classified(True Negatives –TN).

The performance of the algorithm is measured with metrics Sensitivity, Specificity, Accuracy, Precision, F-score, Error rate and CPU time.

$$\text{Sensitivity} = \text{TP} / (\text{TP} + \text{FN})$$

$$\text{Specificity} = \text{TN} / (\text{TN} + \text{FP})$$

Error Rate = $(T - C) / T$, The test data has total of T objects and C of the T objects are correctly classified.

3.3.2. Validation Methods

This work uses the K-fold cross validation method, in which the data set is divided into K-disjoint subsets of approximately equal size. One of the subsets is then used as the test set and the remaining k-1 sets are used for building the classifier. The test set is then used to estimate the accuracy. This is done repeatedly k times so that each subset is used as a test subset once. One of the K-subset is used as a test set and remain K-1 subsets are put together to form a training set. Thus every data point gets a chance to be in a test set exactly once.

In the first iteration , to obtain the first model, subset x_1, x_2, \dots, x_k , collectively serve as a training set , which is tested on x_1 : the second iteration is trained in subsets x_1, x_3, \dots, x_k and tested on x_2 : and so on.

About the Implementation

The proposed outlier detection software is developed with Matlab version 7.4.0 (R2007a) and uses some of the features of Weaka with Matlab interface code. The Mex and Java interface of matlab is used to implement this outlier detection software. Here, the standard weaka implementation of the classification algorithms is used and only passed the default parameters while invoking the classifier algorithms.

4. RESULTS AND DISCUSSION

In the second plot clearly shows that the benign records are grouped together and form a distinct cluster. The red points that are deviating from the black cluster are the outliers which signifies the malignant nature of that case.

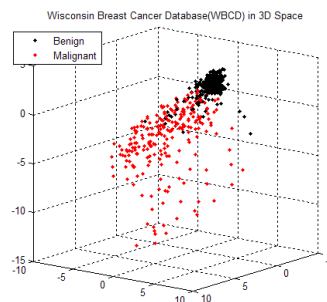


Figure 2: The Plot of WBDC Data Clearly Showing the Benign Cluster and Malignant Outliers

The following table lists the performance of the algorithm with respect to different metrics. In fact, each value is an average of 10 trials. In each trial we did a 10- fold validation. So, each table cell value is the average of 100 separate runs with different training and testing data sets.

With the concept of the number dimension as five, first five features, the above table shows an improvement in the performance of outlier detection with different number of dimensionality reduction algorithms.

4.1. The Effect of Feature Selection Algorithms

This table reveals that there is no improvement in accuracy or reduction in error rate. So it is clear that there is no performance improvement in result by considering less number of features than original one.

Table 2: The Performance of Outlier Detection with different Feature Dimensionality Reduction Algorithms and Classification Algorithms

Algorithm	Precision %	F-Score %	Sensitivity %	Specificity %	Accuracy %	Error Rate %
k-Neighbourhood	96.07	96.66	97.31	92.23	95.57	4.43
Chi-square + k-Neighbourhood	96.44	95.75	95.20	93.34	94.56	5.44
Information Gain + k-Neighbourhood	96.49	96.16	95.94	93.27	95.00	5.00
Gini Index + k-Neighbourhood	96.02	96.55	97.16	92.28	95.47	4.53
PCA + k-Neighbourhood	96.65	96.83	97.07	93.69	95.85	4.15
kPCA + k-Neighbourhood	95.25	94.38	93.66	91.08	92.75	7.25
LPP + k-Neighbourhood	96.89	97.20	97.57	94.23	96.37	3.63

The following table shows the comparison of previous results with this work.

Table 3: The Comparison with Recent Works

Sl No	Classifiers	Classification accuracy
1	CART with feature selection (Chi-square)[11]	94.56%
2	C4.5 [12]	94.74%
3	Hybrid Approach[14]	95.96%
4	Neuron-Fuzzy[16]	95.06%
5	Supervised Fuzzy Clustering [17]	95.57%
6	Proposed PCA* + k-Neighborhood	95.85

* The First Five Principal Components were used for classification

4.2. The Effect of Dimensionality Reduction Algorithms

In this case, accuracy measures the capability of the algorithms to correctly identify the normal as well as outliers in the data. It means, Proposed PCA+ k-neighborhood and proposed LPP+ k-neighborhood classifiers are capable of marking normal as well as the outliers correctly.

This table shows the performance of the algorithm in terms of f-score. In this case, f-score measures the capability of the algorithms to correctly identify the normal as well as outliers in the data. As shown in the table, with respect to f-score, proposed PCA+ k-neighborhood and proposed LPP+ k-neighborhood classifiers performed well.

In this case, error rate measures how much the algorithm wrongly identifies both the normal as well as outliers in the data. The lower value of error rate of proposed PCA+ k-neighborhood and proposed LPP+ k-neighborhood classifiers reveals that classifiers are making less error while identifying the malignant as well as outlier data.

5. CONCLUSION

This work is implemented with the classification based outlier detection software under Matlab and evaluated its performance using different metrics and thus arrived at significant and comparable results. The table and graphs in the previous section shows the overall results. In this work, the performance of outlier detection algorithm K-Neighborhood with dimensionality reduction algorithms is evaluated and the result clearly shows that the impact of dimensionality reduction algorithm on the cancer dataset improves the overall classification performance. Also it is clear that there is no significant effect on the result by using the feature selection algorithms. Future works may address these issues and improve the performance of the outlier detection in cancer data with other algorithms.

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