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Using Combined Descriptive and Predictive Methods of Data Mining for Coronary Artery Disease Prediction: a Case Study Approach

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Abstract

Heart disease is one of the major causes of morbidity in the world. Currently, large proportions of the healthcare data are not processed properly, and thus fail to be effectively used for decision-making purposes. The risk of heart disease may be predicted via investigation of heart disease risk factors coupled with data mining knowledge. This paper presents a model developed using the combined descriptive and predictive techniques of data mining that aims to aid specialists in the healthcare system to effectively predict patients with Coronary Artery Disease (CAD). In order to achieve this objective, some clustering and classification techniques are used. First, the number of clusters are determined using clustering indices. Next, some types of decision tree methods and artificial neural network are applied to each cluster in order to predict the CAD patients. The results obtained show that the C&RT decision tree method performs best on all the data used in this work with 0.074 error. The data used in this work is real, and was collected from a heart clinic database.

Keywords: Data Mining, Coronary Heart Disease, Clustering, Classification, Decision Tree.

1. Introduction

Coronary artery disease (CAD) is the most common type of heart disease in the United States. For some people, the first sign of CAD is a heart attack. CAD is caused by plaque build-up in the walls of the arteries that supply blood to the heart (called coronary arteries) and other parts of the body. Plaque is made up of deposits of cholesterol and other substances in the artery. Plaque build-up causes the inside of the arteries to narrow over time, which could partially or totally block the blood flow. This process is called atherosclerosis. Excessive plaque build-up and narrowed artery walls can make it harder for blood to flow through the body. When the heart muscle does not get enough blood, it may cause chest pain or discomfort, called angina. Angina is the most common symptom of CAD.

Over time, CAD can weaken the heart muscle. This may lead to heart failure, a serious condition where the heart fails to pump blood the way it should. An irregular heartbeat or arrhythmia can also develop. Coronary Heart Disease (CHD) is a result of CAD. The prediction of CHD risk is a vital and complicated task of medicine, which is closely linked with lifestyle behaviors [1]. Narrowing of the coronary arteries results from the reduction of blood and oxygen supply to the heart and leads to CHD. Myocardial infarctions, generally known as heart attack and angina pectoris or chest pain, are encompassed in CHD. A sudden blockage in the coronary artery generally due to a blood clot results in heart attack. Chest pains arise when the blood received by the heart muscles is inadequate [2].

Knowledge discovery is the process of the effort to understand, analyze, and eventually make use of the huge volume of data available. According to Fayyad et al., Knowledge Discovery in Databases (KDDs) is the non-trivial process of identifying valid, novel, potentially useful, and ultimately understandable patterns of data. Data mining is the process of applying machine learning and other techniques to classical databases in order to extract implicit, previously unknown, and potentially useful patterns from a database. Data mining can be viewed as an essential step in knowledge discovery. It combines statistical analysis and machine learning to extract hidden patterns and relationships from large datasets [3]. Data mining is an essential step in knowledge

Data mining is an essential step in knowledge discovery. It is the exploration of large datasets to discover hidden and previously unknown patterns, relationships, and knowledge that are otherwise difficult to detect with the traditional statistical methods.

Data mining in healthcare is an emerging field of high importance that has a potential for providing a deeper understanding of the medical data [4]. The CAD risk factors could be identified by physicians to prevent the occurrence of CAD in a near future. Invasive coronary angiography, a current diagnostic method, is costly and associated with morbidity and mortality in CAD patients [5].

In what follows, efforts for identification of patients with CHD in historical datasets using different algorithms and techniques are discussed. Mobley et al. have studied the Artificial Neural Network (ANN) methods and designed an ANN model for the prediction of CHD in 2000, 2002, and 2005 [6-8]. Two years later, Lee et al. used various experiments on the linear and non-linear features of Heart Rate Variability (HRV) indices to evaluate several classifiers, e.g. Bayesian classifiers, CMAR, C4.5, and Support Vector Machine (SVM). In their experiments, SVM outperformed its counterparts [9].

In 2008, Tsipouras et al. provided CAD diagnosis based on easily acquired features. This tool is capable of providing interpretations on decisions made using the decision tree and fuzzy modeling algorithms [10]. In the same year, Kurt et al. compared the performance of various machine learning approaches, namely logistic regression, classification and regression tree, multi-layer perceptron, radial basis function, and selforganizing feature maps in order to predict the presence of CAD using demographic and medical data [11]. Sitar-taut et al. used the Weka tool to investigate naïve Bayes and J4.8 decision trees for the detection of CHD. The results obtained demonstrated no significant difference between naïve Bayes and decision trees in the correct prediction of CHD in 2009 [12]. A year later, Karaolis et al. used the C4.5 decision tree towards targeted algorithm the three aforementioned events. The most important risk factors as extracted from the classification rules analysis were: 1) age, smoking history, and history of hypertension for myocardial infarction (MI); 2) family history, history of hypertension, and history of diabetes for percutaneous coronary

intervention (PCI); and 3) age, history of hypertension, and smoking history for Coronary Artery Bypass Graft (CABG). Data-mining analysis was performed using the C4.5 decision tree algorithm [13].

In 2012, A. Sheik Abdullah et al. developed a mining model capable of predicting the occurrence of various events corresponding to the record of each patient. This model was developed based on the random forest classification algorithm, whose accurate performance requires the patient history to comprise at least one of the followings: Angina, Acute Myocardial (AMI), PCI, and CABG. The Infarction developed model will have functionalities such as prediction of the occurrence of various events related to each patient record, prevention of risk factors and its associated cost metrics, and improvement in the overall prediction accuracy [14]. Muthukaruppan & E presented a particle swarm optimization (PSO)based fuzzy expert system for the diagnosis of CAD in 2012 [15].

In 2013, Nitin Kumari et al. presented a survey on the diagnosis of CHD using ANN, fuzzy logic, and neuro-fuzzy integrated approaches. Here, these approaches were compared in an attempt to identify the most appropriate approach. For instance, ANN and fuzzy logic both exhibit numerous advantages but also some disadvantages. Neuro-fuzzy approaches consist of the combination of ANN and fuzzy logic. They combine the advantages of both ANN and fuzzy Advantages of ANNs include massive logic. parallelism, robustness, and learning in data-rich environments. The authors also presented a survey on the diagnosis of coronary heart disease using three soft computing techniques [16].

Later, in 2015, a model for CHD prediction was designed by Kim et al. according to the rule-based guidelines. In their study, a fuzzy logic and decision tree (classification and regression tree [CART])-driven CHD prediction model was developed for the Korean population [17]. Akila et al. presented a two-stage hybrid method for CHD identification and prediction in 2015. In the first stage, risk identification was carried out via classification of physical and biochemical factors using the C4.5 algorithm in DT, and in the second stage, the level prediction was performed via analysis of CHD risk instances identified from DT using MLP with habitation and medical history attributes [1]. In 2015, Jonnagaddala et al. also presented methods to extract Framingham risk factors of unstructured electronic health records using clinical text mining and calculated 10-year CAD risk scores in a cohort of diabetic patients [18]. In 2016, Wiharto et al. provided an intelligence system for the diagnosis of CHD

stage by taking into account the problem of data imbalance using K-star algorithms [19]. These are briefly shown in Table 1.

| Table 1. A sample of data minin | g techniques used on different coro | nary heart disease datasets. |
|---------------------------------|-------------------------------------|------------------------------|
|---------------------------------|-------------------------------------|------------------------------|

| Author | Year | Title | Techniques |
|---|------|---|---|
| B. A. Mobley, Schechter, | 2000 | | Decision trees, |
| Moore, McKee, & Eichner | 2000 | Predictions of coronary artery stenosis by artificial neural network | Fuzzy model |
| Lee, Noh, & Ryu | 2007 | Mining biosignal data: coronary artery disease diagnosis using linear and non-linear features of HRV | Bayesian classifiers, CMAR, C4.5, and SVM |
| Kurt, Ture, & Kurum | 2008 | Comparing performances of logistic regression, classification and regression tree, and neural networks for predicting coronary artery disease | logistic regression, classification and regression tree, multi-layer perceptron, radial basis |
| Tsipouras et al. | 2008 | Automated Diagnosis of Coronary Artery Disease based on Data Mining and Fuzzy Modeling | Decision tree, fuzzy model |
| Sitar-tăut, Zdrenghea, Pop, & Sitar-tăut | 2009 | Using machine learning algorithms in cardiovascular disease risk evaluation | naïve bayes, J4.8 decision trees |
| Karaolis, Moutiris, Hadjipanayi, & Pattichis | 2010 | Assessment of risk factors of coronary heart events based on data mining with decision trees | C4.5 Decision tree |
| Abdullah & Rajalaxmi | 2012 | A data mining model for predicting Coronary Heart Disease using Random Forest Classifier | Random Forest |
| Muthukaruppan & Er | 2012 | A hybrid particle swarm optimization based fuzzy expert system for diagnosis of coronary artery disease | fuzzy expert system |
| Kumari & Sunita | 2013 | Comparison of ANNs, Fuzzy Logic, and Neuro-Fuzzy Integrated Approach for Diagnosis of Coronary Heart Disease: A Survey | ANN, fuzzy logic, and neuro- fuzzy integrated approach |
| Kim, Lee, & Lee | 2015 | Data-Mining-Based Coronary Heart Disease Risk Prediction Model using Fuzzy Logic and Decision Tree | Fuzzy logic, CART |
| Akila & Chandramathi | 2015 | A Hybrid Method for Coronary Heart Disease Risk Prediction using Decision Tree and Multi-Layer Perceptron | C4.5 Decision tree and MLP |
| Jonnagaddala, Liaw, Ray, Kumar, Chang, & Dai | 2015 | Coronary artery disease risk assessment from unstructured electronic health records using text mining | Text mining |
| Wiharto, Kusnanto, & Herianto | 2016 | Intelligence System for Diagnosis Level of Coronary Heart Disease with K-Star Algorithm, Healthcare informatics research | K-Star algorithms |

Investigation of the previous works done on the prediction of CAD patients shows that only a single predictive or descriptive method have been used in these studies. In this work, a total of 282 records with 58 attributes were obtained from an actual clinical dataset as the case study. Therefore, we first divided the data into three clusters using clustering indices, and then used different decision tree algorithms for the three clusters. The results obtained showed that C&RT performed best on all data in terms of the CAD patient prediction.

In cluster 1&2, C&RT is the best decision tree algorithm, whereas in cluster 3, CHAID has a minimum error for predicting CAD patients. Here, we used combined descriptive and predictive methods for prediction of CAD patients, which showed a better performance than the other purely descriptive or merely predictive methods in working with real data and its analysis. Totally, it can be said that the novelty of this paper is seen in the definition of the problem, the combined prediction method as a new solving method, and its actual application based on the case study.

The remainder of this paper is organized as what follows. In Section 2, data preparation and study methods are briefly explained. The data used in this work is driven from a clinical dataset. In Section 3, results of the clustering and classification methods are presented. In Section 4, discussion is clearly noted. Finally, in Section 4, the work is concluded.

2. Materials and methods

2.1. Data description

For the automatic diagnosis of normal and CAD conditions, the HRV signal extracted from electrocardiogram (ECG) can be used but here, no patient had a history or electrocardiographic evidence of prior myocardial infarction or known valvular or cardiomyopathy diseases.

Therefore, we had to find another method to predict CAD patients. Marateb et al. [5] used the following 21 attributes in their work: age, gender, resting blood pressure (trestbps), CHOL, fasting blood sugar (FBS), resting electrocardiographic results (restecg), active smoker type, number of cigarettes per day, number of years as a smoker, family history of CAD (famhist), and chest pain type (cp). In addition, patients underwent 3 noninvasive tests as defined in the research protocol. The results of these tests (exercise electrocardiogram, thallium scintigraphy, and cardiac fluoroscopy) were not interpreted until after the invasive gold standard test (coronary angiograms) had been read. The CAD status was

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considered when narrowing of at least one of the coronary arteries was more than 50%, as indicated by angiography.

In this work, a total of 282 records with 58 attributes were obtained from an actual clinical dataset as the case study. Based on the literature, a set of cut points were extracted in this work for the properties of attributes for every individual, as shown in Table 2, in order to create ordinal-scale variables.

| Attribute | Measurement scale | Definition | Value |
|-----------|----------------------|--|--|
| Age | Interval | Age in years | |
| Gender | Nominal | Sex | 1 = male; $0 = $ female |
| Trestbps | Interval | Resting blood pressure (mmHg) | |
| CHOL | Interval | Serum CHOL (mg/dL) | |
| FBS | Nominal | FBS >120 (mg/dL) | Value (1): true; If greater than 120 mg/dl the attribute; Value (0): False; Other wise |
| Restecg | Nominal | Resting electrocardiographic results | Value 0: normal; Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV); Value 2: showing probable or definite left ventricular hypertrophy |
| Thalrest | Nominal | Resting heart rate (bpm) | |
| Smoke | Nominal | Active smoker type | |
| Cigs | Interval | Number of cigarettes per day | |
| Years | Interval | Number of years as a smoker | |
| Famhist | Nominal | Family history of CAD | |
| Ср | Nominal | Chest pain type | |
| Tpeakbps | Interval | Peak exercise systolic blood pressure (mmHg) | |
| Tpeakbpd | Interval | Peak exercise diastolic blood pressure (mmHg) | |
| Thalach | Interval | Maximum exercise heart rate achieved (bpm) | |
| Exang | Nominal | Exercise-induced angina | Value 1= Yes Value 0= No |
| Oldpeak | Interval | ST depression induced by exercise relative to rest | |
| Slope | Nominal | Slope of the peak exercise ST segment | Value 1: up sloping Value 2: flat Value 3: down sloping |
| Ca | Interval | Number of major vessels (0–3) colored by fluoroscopy | |
| Thal | Nominal | Thallium-201 stress scintigraphy | Value 3: normal Value 6: fixed defect Value 7: reversible defect |
| Num | Nominal | Diagnosis of heart disease (angiographic disease status) | Value 0: Normal: < 50% diameter narrowing Value 1: CAD > 50% diameter narrowing |

Table 2. Attributes of raw CAD dataset.

2.2. Proposed method

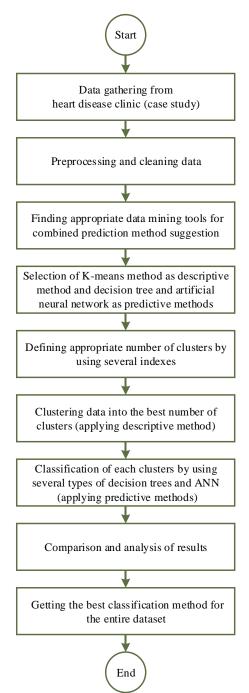
As mentioned earlier, the authors seeked to provide a combination model of descriptive and predictive methods of data mining tools for predicting coronary artery disease. Thus they first received the real data, along with their characteristics from the heart clinic. Then the received data was pre-processed in order to eliminate their annoying contamination. The preprocessing of the received actual data included the removal of records whose fields were missing values or appeared to be outliers. In the following, with a review of the literature on the topic, we found the descriptive and predictive methods of data mining that were possible to combine, and in previous literature, not considered significantly to diagnose CAD.

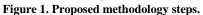
In order to better understand the subject, it should be mentioned that some data mining tools such as clustering methods, association rules, data summarization, and statistics are in the category of data mining descriptive methods because they can describe the current data interpretation but data mining tools such as regression, and classification are in the category of predictive methods because they are capable of being used for prediction and not limited to the current status of data.

Finally, after studying the literature, the k-means method was chosen as the clustering method (descriptive), and various types of classification methods (predictive) including CHAID, Quest, C5.0, C&RT decision tree, and ANN method for combination with the previous method.

In the clustering method, the number of clusters must be pre-defined. Therefore, various indices were used to determine the suitable number of clusters. Indices indicate that the optimal cluster number is 3. After the clean data was split into three clusters, we applied each of the five classification methods to each cluster for getting the optimal predictive approach in the next step and analyzed the results. Clean data refers to the data that has been pre-processed and does not have fluctuations such as noise, turbulence, outlier, and missing values.

The results obtained showed that according to the results, the C&RT decision tree method performed better than the other classification methods in predicting CAD patients in the entire database including CHAID, Quest, C5.0 decision tree, and ANN method. Figure 1 also shows the steps of the proposed methodology. In the following, it is briefly explained in relation to the data mining tools used.





2.2.1. Clustering

Cluster analysis is an unsupervised machine learning method. It offers the means for partitioning a dataset into subsets with similar patterns. Clustering methods partition objects into groups so that objects in one group are similar to each other, and as dissimilar as possible to objects in other groups. The similarity or dissimilarity between two data objects is typically measured as the distance between the multi-dimensional feature vectors that represent the objects. The feature vectors are also called data points. A large distance between the data points encodes a greater dissimilarity. Here, a number of available clustering methods are described [20]. Clustering is the process of partitioning a dataset with 'n' data points into 'k' groups or clusters. As a result, each cluster should have at least one data point, and each data point must belong to only one cluster. In this clustering approach, the number of clusters should be defined prior to partitioning. The partition clustering method is divided into two categories; K-means and K-mediods are based upon the choice of cluster centroid and similarity measures [21].

K-Means clustering is one of the most widely used clustering approaches that partition 'n' data points into 'k' clusters based on a similarity measure so that the data points in the same cluster exhibit a high similarity as compared to the data points of the other clusters [20].

An appropriate value of k must be somehow chosen if it cannot be inferred from a prior knowledge of the dataset properties. Several methods are available for selection of an appropriate k value, many of which rely on cluster evaluation metrics. In reference [22], during the presentation of an algorithm, the different values of the number of clusters are evaluated and the best number is determined. Thus in this work, a clustering algorithm was run with different values of k, and the value of k that provided the best results was chosen like [22], and the average silhouette method [23], gap statistic method [24], dunn Index [25], within sum of square [26], and elbow algorithms [27] were used for detecting the number of clusters. The results obtained for each method are shown in Section 3.

2.2.2. Classification

Classification and prediction are two forms of data analysis. Classification is the analysis of a training dataset in order to identify the typical characteristics of data in the same class based on the characteristics of the data, and the subsequent use of these characteristics to classify the new data. The key in classification is to export functions or models for classification. On the other hand, the term prediction is used when data objects are continuous rather than discrete [28]. In this work, decision trees and neural networks were used.

Classification methods are one of the predictive models in data mining. The inputs of predictive models are data of patients referring to the clinic in the form of the attributes of the raw CAD dataset in each cluster, and output of the predictive models is a decision tree or ANN that shows probability of CAD in the form of "Yes" and "No" labels. This process was applied to each cluster separately.

- Decision Tree

Decision tree is a data classification process that consists of a series of rules [29]. Determined by a series of "if then" logic (branching) relationships, this method infers a set of classified rules from a set with no order and no rule examples, and expresses the probabilities of all possible outcomes with a tree chart in the form of a decision tree so as to yield an accurate prediction or a correct classification [30]. The decision tree method is finding more and more application in the clinical studies, especially clinical diagnosis. Decision tree has many different algorithms, and this study uses the CHAID, C&RT, Quest, and C5.0 algorithms.

- Neural Network

ANN, often referred to as "neural network", is a mathematical or computational model developed based on the biological neural networks. In other words, it is the simulation of biological neural systems that are made up of inter-connections between the artificial neural information units. In most cases, neural networks are based upon adaptive systems in the learning stage where external or internal information flows through the network, thus changing its structure [31].

The structure of artificial neural network in the proposed methodology is as what follows.

- ANN type = one-layer perceptron
- Number of inputs = 20 (attributes of the raw CAD dataset)
- Number of hidden layers = 1
- Number of nodes in the hidden layer = 3
- Number of outputs = 1 (probability of CAD in the form of "Yes" and "No" labels)

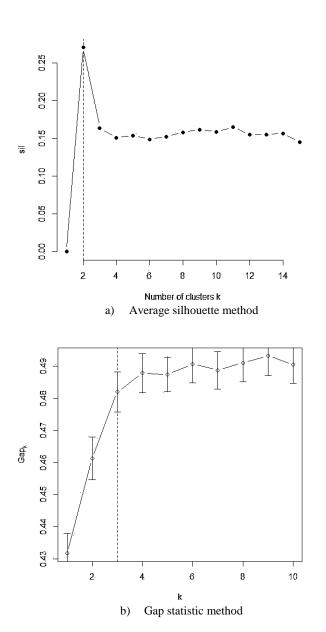
3. Results

When we use clustering methods, we need to define the number of clusters by using the indices for getting the appropriate number. Various types of indices help us to define the optimal cluster number regarding some indicators like minimizing the distance between data in clusters and maximizing the distances between clusters. After using some indices, we found that the appropriate number of clusters in our data was k =3. The results obtained are shown in table 3 and figure 2. Figure 2 shows the charts of the average silhouette method, gap statistic method, dunn index, within sum of square, and elbow algorithms that are used for detecting the number

of clusters. The horizontal axis in these charts shows the number of clusters and the vertical axis shows the value of the related axis. Table 3 summarizes the result of an appropriate number of cluster in the mentioned indices.

| Table 3. Outcome of different methods for defining |
|--|
| number of alustors |

| lusters. |
|--------------------|
| Number of clusters |
| 2 |
| 2 |
| 3 |
| 4 |
| 3 |
| |



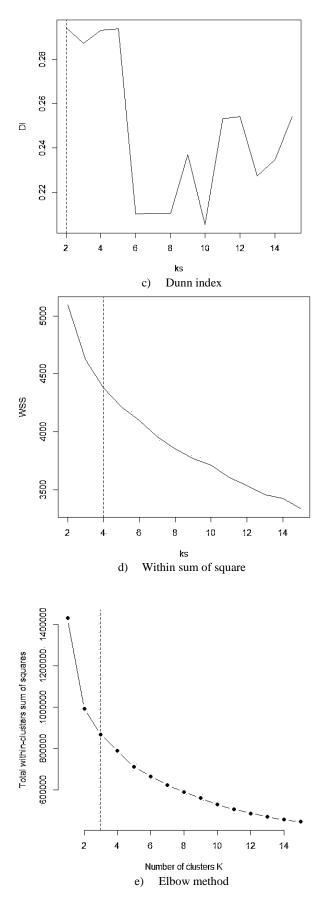


Figure 2. Using different methods to determine an appropriate number of clusters.

As mentioned earlier, to define an appropriate number of clusters, some indices were used. Recall that the basic idea behind partitioning methods such as k-means clustering is to define clusters such that the total intra-cluster variation [or total within-cluster sum of square (WSS)] is The total WSS measures the minimized. compactness of the clustering, and we want it to be as small as possible. The elbow method looks at the total WSS as a function of the number of clusters. One should choose a number of clusters so that adding another cluster does not improve much better the total WSS. Therefore, the location of a bend (knee) in the plot is generally considered as an indicator of the appropriate number of clusters. Also the dunn index is a wellestablished cluster index that identifies "compact, separate" clusters. If a dataset is well-separated by a clustering scheme, the distance among the clusters is usually large, and the diameters of the clusters are expected to be small. Therefore, a large value for dunn index corresponds to a good clustering scheme.

On one hand, a high average silhouette width indicates a good clustering. The optimal number of clusters k is the one that maximizes the average silhouette over a range of possible values for k. On the other hand, the gap statistic compares the total within intra-cluster variation for different values of k with their expected values under null reference distribution of the data. The estimate of the optimal clusters will be the value that maximizes the gap statistic (i.e. that yields the largest gap statistic). For getting the best number of clusters, we must choose the number of clusters as the smallest value of k such that the gap statistic is within one standard deviation of the gap at k + 1, where the number of clusters are from $k = 1, ..., k_{max}$. The enthusiasts can refer to reference [32] for a further study.

Using k = 3 as the number of clusters, the data was divided into groups of 90, 88, and 104 data points. Data points mean the number of data records. In fact, after applying the clustering method, the number of records in clusters 1, 2, & 3 was 90, 88, and 104, respectively. The results of applying the clustering method indicate that each cluster includes how people are:

- cluster 1: This cluster includes people who have smoked a lot over many years every day. So many of their major vessels were clogged up. These people had a lower age than the other people who referred to the clinic. Also totally, they had less chest pain, blood pressure, and depression. - cluster 2: This cluster includes people who have smoked amusingly every day for few years. So few of their major vessels were clogged up. These people were older than cluster 1, and had more chest pain, blood pressure, and depression but compared to cluster 3 that had a lower age, and less chest pain, blood pressure, and depression.

- cluster 3: Persons in cluster number 3 are high-age people who smoked less for years compared to cluster 1. Therefore, fewer of their major vessels were clogged up. However, they smoked more than cluster 2. Therefore, many of their major vessels were clogged up. These people had more chest pain, blood pressure, and depression than the other people who referred to the clinic.

I. Table 4 shows the average of each factor in these three clusters, which emphasizes the above-mentioned explanations, and

TABLE 5 shows the distance between centers of clusters. For example, distance between center of cluster 1 and center of cluster 2 was 1.214. These calculated values somehow represent dissimilarity between two classes. With these interpretations, the similarity between clusters 1 and 2 was greater than the similarity between clusters 2 and 3 and the similarity between clusters 1 and 3 was more than the similarity between clusters 2 and 3.

Table 4. Average of each factor in each cluster.

| Factors | Cluster 1 | Cluster 2 | Cluster 3 |
|----------|--------------|-------------|--------------|
| age | 52.033 | 54.727 | 56.202 |
| gender | 0.711 | 0.386 | 0.894 |
| ср | 2.778 | 2.875 | 3.740 |
| trestbps | 128.422 | 131.784 | 134.096 |
| chol | 239.356 | 252.659 | 254.500 |
| smoke | 1.000 | 0.011 | 0.683 |
| cigs | 28.144 | 0.034 | 20.683 |
| cigsyear | 25.411 | 0.068 | 18.606 |
| fbs | 0.167 | 0.125 | 0.154 |
| famhist | 0.556 | 0.614 | 0.683 |
| restecg | 0.644 | 1.080 | 1.279 |
| thalach | 160.322 | 154.080 | 136.981 |
| thalrest | 75.533 | 76.420 | 73.654 |
| tpeakbps | 171.156 | 169.375 | 164.260 |
| tpeakbpd | 75.033 | 81.284 | 79.808 |
| exang | 0.100 | 0.159 | 0.663 |
| oldpeak | 0.571 | 0.759 | 1.648 |
| slope | 1.322 | 1.523 | 1.865 |
| ca | 0.411 | 0.284 | 1.212 |
| thal | 3.856 | 3.466 | 6.404 |
| num | No → 88.89 % | No → 84.09% | Yes → 97.12% |

| Table 5. Approximately distance between clusters. | |
|---|--|
|---|--|

| Clusters | 1 | 2 | 3 |
|----------|-------|-------|---|
| 1 | | | |
| 2 | 1.214 | | |
| 3 | 1.436 | 1.608 | |

4. Discussion

In order to derive a classifier or predictor, we can use training dataset, and then to estimate the accuracy of the resulting learned model, we can use that classifier.

Sometimes due to over-fitting of the learning algorithm to the data, this accuracy is estimated over-optimistically but in fact, it is misleading. Instead, accuracy is better measured on a test set consisting of class-labeled tuples that were not used in the process of training the model. The accuracy of a classifier on a given test set is the percentage of test set tuples that are correctly classified by the classifier. Accuracy refers to the overall recognition rate of the classifier, i.e. it reflects how well the classifier recognizes tuples of the various classes.

Sometimes we would like to be able to assess how well the classifier can recognize "CAD" tuples (the positive tuples) and how well it can recognize "normal" tuples (the negative tuples). The sensitivity and specificity measures can be used for this purpose, respectively. Sensitivity is also referred to as the true positive rate, while specificity is the true negative rate. In addition, we may use precision to assess the percentage of tuples labeled as "CAD" that actually are "CAD" tuples. These measures are defined in [21].

The confusion matrix for positive and negative tuples is shown in Table 6. Also, accuracy, sensitivity, precision, and specificity are given in Equations 1-4.

$$Sensitivity = \frac{TP}{TP + FN}$$
(1)

Specificity =
$$\frac{TN}{TN+FP}$$
 (2)

$$Precision = \frac{TP}{TP+FP}$$
(3)

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$
(4)

 Table 6. A confusion matrix for positive and negative tuples.

| | Predicted Class = Yes | Predicted Class = No | |
|--------------------|--------------------------|-------------------------|--|
| Actual Class = Yes | True Positives (TP) | False Negative (FN) | |
| Actual Class = No | False Positives (FP) | True Negative (TN) | |

II. The results of comparing the performance of different algorithms on all data is shown in Table 7. According to the results obtained, the C&RT method has the minimum prediction error. Then

Table 8 shows the results of using different decision tree methods in three clusters.

III. According to the results, C&RT and CHAID perform best in predicting the CAD patients in clusters 1 & 2 and cluster 3, respectively.

Figure 3 shows the comparison error in all different methods for the three clusters. In this figure, the horizontal axis shows the methods used for analyzing three clusters and the vertical axis shows the error of each method in three clusters separately.

In general, clustering has helped us to put people who have the same features together, with the aim that the predictive method applied separately for each cluster would be a less predictive error.

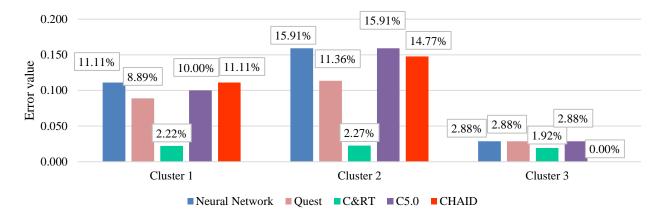
In other words, if we only used the predictive method and removed the clustering phase, the proposed methodology had more error in the diagnosis of CAD patients.

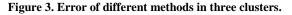
| | ТР | FN | FP | TN | Sensitivity | Specificity | Precision | Accuracy | Error |
|----------------|-----|----|----|-----|-------------|-------------|-----------|----------|-------|
| Neural network | 101 | 24 | 3 | 154 | 0.808 | 0.981 | 0.971 | 0.904 | 0.096 |
| Quest | 101 | 24 | 3 | 154 | 0.808 | 0.981 | 0.971 | 0.904 | 0.096 |
| C&RT | 113 | 12 | 9 | 148 | 0.904 | 0.943 | 0.926 | 0.926 | 0.074 |
| C5.0 | 104 | 21 | 3 | 154 | 0.832 | 0.981 | 0.972 | 0.915 | 0.085 |
| CHAID | 106 | 19 | 5 | 152 | 0.848 | 0.968 | 0.955 | 0.915 | 0.085 |

able 7. Comparison of different algorithm results for all data.

| | | ТР | FN | FP | TN | Sensitivity | Specificity | Precision | Accuracy | Error |
|----------|----------------|-----|----|----|----|-------------|-------------|-----------|----------|-------|
| Cluster1 | Neural network | 0 | 10 | 0 | 80 | 0 | 1 | 1 | 0.889 | 0.111 |
| | Quest | 2 | 8 | 0 | 80 | 0.200 | 1 | 1 | 0.911 | 0.089 |
| | C&RT | 9 | 1 | 1 | 79 | 0.900 | 0.988 | 0.900 | 0.978 | 0.022 |
| | C5.0 | 3 | 7 | 2 | 78 | 0.300 | 0.975 | 0.600 | 0.900 | 0.100 |
| | CHAID | 0 | 10 | 0 | 80 | 0 | 1 | 1 | 0.889 | 0.111 |
| Cluster2 | Neural network | 0 | 14 | 0 | 74 | 0 | 1 | 1 | 0.841 | 0.159 |
| | Quest | 4 | 10 | 0 | 74 | 0.286 | 1 | 1 | 0.886 | 0.114 |
| | C&RT | 12 | 2 | 0 | 74 | 0.857 | 1 | 1 | 0.977 | 0.023 |
| | C5.0 | 0 | 14 | 0 | 74 | 0 | 1 | 1 | 0.841 | 0.159 |
| | CHAID | 9 | 5 | 8 | 66 | 0.643 | 0.892 | 0.529 | 0.852 | 0.148 |
| Cluster3 | Neural network | 101 | 0 | 3 | 0 | 1 | 0 | 0.971 | 0.971 | 0.029 |
| | Quest | 101 | 0 | 3 | 0 | 1 | 0 | 0.971 | 0.971 | 0.029 |
| | C&RT | 100 | 1 | 1 | 2 | 0.990 | 0.667 | 0.990 | 0.981 | 0.019 |
| | C5.0 | 101 | 0 | 3 | 0 | 1 | 0 | 0.971 | 0.971 | 0.029 |
| | CHAID | 104 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 |

Table 8. Comparison of different algorithm results for different clusters.





5. Conclusion

In this work, a total of 282 patient records with 58 attributes were acquired from a clinical dataset and combined descriptive, and the predictive methods were applied for prediction of CAD in these patients. For this, the k-means method was chosen as the clustering method (descriptive) and various types of classification methods (predictive) including CHAID, Quest, C5.0, C&RT decision tree, and ANN method for combination with the previous method. Here, the appropriate number of clusters was first determined as 3 using several clustering indices. Then the decision tree methods were applied to each cluster to define the best prediction algorithm for each cluster. Briefly, we can say cluster 1 includes people who have smoked a lot over many years every day. Cluster 2 includes

people who have smoked amusingly every day for few years, and persons in cluster number 3 were high-age people who smoked less for years compared to cluster 1 but they smoked more than cluster 2.

Finally, C&RT appeared as the best method for the entire dataset with 0.074 error. However, the results obtained for each of the three clusters were different. The best method for prediction in clusters 1 and 2 was C&RT with 0.022 and 0.023 error, respectively, and CHAID appeared as the most appropriate method for cluster 3 with zero error.

Also as clinical implications of the suggested procedure, we can point out that a software can be designed easily in every heart clinic for entering new patient's data. For this, using the result of actual data analysis and applying the proposed combined method are sufficient to diagnose the CAD patients. If a patient is exposed to CAD, the new designed software-based system will alert and aware physicians.

As future suggestions, we can consider a combination of other descriptive and predictive methods for prediction of CAD patients. Also the use of real data from other clinics with complementary features can also provide better and more realistic analytical results.

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تشربه ہوش مصنوعی و دادہ کاوی



استفاده از ترکیب روشهای توصیفی و پیشبینانه دادهکاوی برای پیشبینی بیماریهای عروق کرونری: رویکرد مطالعه موردی

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چکیدہ:

بیماری قلبی یکی از علل عمده مرگ و میر در جهان است. در حال حاضر، بخش وسیعی از دادههای مراقبتهای بهداشتی به درستی مورد پردازش قرار نمی گیرد و متعاقباً نمی توان از آنها به طور موثر جهت تصمیم گیری استفاده نمود. در حالیکه، خطر ابتلا بـه بیماریهای قلبی را مـی تـوان از طریـق بررسی عوامل خطر آن با استفاده از دانش داده کاوی پیش بینی کرد. مدل پیشنهادی در این مقاله، با استفاده از ترکیب روشهای توصیفی و پیش بینانـه داده کاوی ارائه شده است و هدف آن کمک به متخصصان سیستم مراقبتهای بهداشتی می باشد تا بتوانند به طور موثری بیماران مبتلا به بیماری عـروق کرونر (CAD) را پیش بینی نمایند. به منظور دستیابی به این هدف، برخی از روشهای خوشهبندی و دستهبندی به کار برده شده است. در ابتـدا، تعـداد خوشهها با استفاده از شاخصهای خوشهبندی تعیین میشود. سپس به منظور پیش بینی بیماران C C می می از می ماران مبتلا به بیماری مروق تصمیم و شبکه عصبی مصنوعی (ANN) مورد استفاده قرار می گیرند. در نهایت، نتایج بدست آمده نشان می دهد که روش درخت تصمیم RT یک در تمام دادههای مورد استفاده در این کار تحقیقاتی با خطای ۲۰٬۷۲۴ بهترین است. تمام دادههای مورد استفاده در این کار واقعـی هستند و از پایگاه داده کرونر راینی می در استفاده در این کار تحقیقاتی با خطای ۲۰٬۷۲۴ بهترین است. تمام دادههای مورد استفاده در این کار واقعـی هستند و از پایگاه داده

كلمات كليدى: دادەكاوى، بيمارىھاى قلبى عروقى، خوشەبندى، طبقەبندى، درخت تصميم.