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Multivariate Regression Analysis for Coronary Heart Disease Using SPM Tool

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ABSTRACT

Regression is a data mining (machine learning) technique used to fit an equation to a dataset. In statistical modeling, regression analysis is a statistical process for estimating the relationships among variables. It includes many techniques for modeling and analyzing several variables, when the focus is on the relationship between a dependent variable and one or more independent variables (or 'predictors'). More specifically, regression analysis helps one understand how the typical value of the dependent variable (or 'criterion variable') changes when any one of the independent variables is varied, while the other independent variables are held fixed. Most commonly, regression analysis estimates the conditional expectation of the dependent variable given the independent variables – that is, the average value of the dependent variable when the independent variables are fixed. Then can implement multivariate attributes in coronary heart disease datasets. In regression, analyze the multivariate attribute model which is a generalization of the probit model used to estimate several correlated binary outcomes jointly. In this project, perform comparative study to various regression algorithms such as CART, Ensemble and bagger, Random forest and MARS. Classification and regression trees (CART), Ensemble and bagger, Random forest for tree prediction models can be implemented in prediction model for heart disease datasets. And also propose the MARS procedure which builds flexible regression models by fitting separate splines for multiple predicted variables. Finally compare the results in terms of RMSE, MSE, MAD and gain values metrics in data mining.

Keywords : Regression Analysis, Multivariate Attribute, Dependent Variable, Classification And Regression Tree, Ensemble And Bagger, Random Forest

I. INTRODUCTION

Coronary heart disease (CHD) is a serious threat to human health, especially for the elderly. Integrative medicine (IM) specialists have accumulated a large number of data in the clinical practice of CHD, which contain important information about diseases, syndromes, syndrome diagnosis and thinking skills, prescription medication, treatment, prognosis and evolution syndrome, and other aspects of development trends. How to do our clinical researches relying on these objective, dynamically updated massive clinical data of IM for CHD, is the primary challenge for us. At present, on current clinical research methods, due to the strict limitations in the included crowd and medication conditions for randomized controlled trials (RCTs), the studies have high internal validity but poor in external making difficulty for the findings in promoting practical application. On basis of practical international RCTs, real-world study (RWS) concepts and methods gradually rise, which is to reflect the real world as a whole through the “real world sample.” It is to choose interventions according to the actual condition and willingness of the patient and evaluate the effects of interventions with more comprehensive coverage of the crowd using statistical methods such as propensity score to control confounding bias. Thus, RWS has strong external validity than the traditional RCTs and can evaluate the effect of interventions in a real clinical setting. Therefore, the results are much closer to clinical practice. Integrative interventions emphasize individualized treatment, focusing on holistic, complex, and multiple effects in the evaluation of clinical efficacy. RWS undoubtedly opens up a new path for researches of integrative medical in CHD. However, clinical data of IM in CHD are large in amount and complex in data types. All are multivalued and multi-types data, the attribute and label of each record have one or more options, and the clinical research data also have more confounding factors, making exploring the appropriate methodology become a hot topic.

Regression is an interdisciplinary research field, which combines the latest research achievements such as statistics, data warehousing, information retrieval, machine learning, artificial intelligence, high performance computing, and data visualization. Data mining techniques are to analyze and dig out data useful information and knowledge from the mass data to guide people's practices, which is changing the use patterns of data with a new concept. To analyze clinical syndrome diagnosis and prescription experience of CHD in the real world with data mining methods, it cannot only find clinical rules and improve clinical diagnostic accuracy of CHD for IM physicians, but also get a deep understanding of IM academic thinking and grasp disease treatment rule. Therefore, using data mining methods for IM study in CHD will greatly improve the level of clinical diagnosis and treatment of IM study in CHD and has broad application prospects. The main features of regression include correlation analysis, classification and prediction, cluster analysis, and evolution analysis. Various types of regression in shown in figure 1.

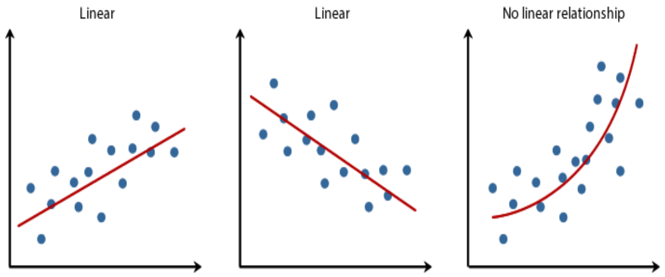


Figure 1. Types of regression

Following the paper describes methods and materials in Section 2, and followed by we present the results and discussion in Section 3. In Section 4 provides conclusion to this work.

II. METHODS AND MATERIALS

Objective of Regression analysis is to explain variability in dependent variable by means of one or more of independent or control variables. The determination of explicit form of regression equation is the ultimate objective of regression analysis. It is finally a good and valid relationship between study variable and explanatory variables. Such regression equation can be used for several purposes. For example, to determine the role of any explanatory variable in the joint relationship in any policy formulation, to forecast the values of response variable for given set of values of explanatory variables. The regression equation helps understands the interrelationships of variables among them. There are various types of regression are implemented in existing framework.

2.1 classification and regression tree

Classification and regression tree (CART), a statistical procedure introduced by Breiman et al. (1984), is primarily used as a classification tool, where the objective is to classify an object into two or more populations. As the name suggests, CART is a single procedure that can be used to analyze either categorical or continuous data using the same technology. The methodology outlined in Breiman et al. (1984) can be summarized into three stages. The first stage involves growing the tree using a recursive partitioning technique to select variables and split points using a splitting criterion. In addition to selecting the primary variables, surrogate variables, which are closely related to the original splits and may be used in classifying observations having missing values for the primary variables, can also be identified and selected. After a large tree is identified, the second stage of the CART methodology uses a pruning procedure that incorporates a minimal cost complexity measure. The result of the pruning procedure is a nested subset of trees starting from the largest tree grown and continuing the process until only one node of the tree remains. Cross-validation or a testing sample will be used to provide estimates of future classification errors for each sub tree. Cross-validation is used when only small numbers of data points are available in building the CART models. The last stage of the methodology is to select the optimal tree, which corresponds to a tree yielding the lowest cross-validated or testing set error rate. Trees in this stage have been identified as unstable. To avoid this instability, trees with smaller sizes, but comparable in accuracy (i.e. within one standard error), will be chosen as an alternative. This process is referred to as the one standard error rule and can be tuned to obtain trees of varying sizes and complexity. A measure of variable importance can be achieved by observing the drop in the error rate when another variable is used instead of the primary split. Basically the more frequent a variable appears as a primary or surrogate split, the higher the importance score assigned.

At the first step, all possible dichotomizations of all continuous variables (above vs. below a given threshold) and of all categorical variables are considered. Using each possible dichotomization, all possible ways of partitioning the sample into two distinct subsets is considered. That binary partition that results in the greatest reduction in impurity is selected. This process is then repeated iteratively until a predefined stopping rule is satisfied. For classification, a subject's class can be determined using the status that was observed for the majority of subjects within that subset to which the given subject belongs (i.e. classification by majority vote). For prediction, the predicted probability of the event for a given subject can be estimated using the proportion of subjects who have the condition of interest amongst all the subjects in the subset to which the given subject belongs. CART analysis uses binary recursive partitioning to split the original node into two nodes. Rood node was first split by trait anxiety, which indicating trait anxiety is the most significant independent variable and the second child node was split down by exercise habit. This process repeats until an optimal tree, for which each terminal node indicates a specific pattern of subgroups, is established. All of the information in the database was able to be analyzed in a decision tree model, rather than through linear regression, which usually selects certain independent variables based on the literature or clinical experience. The CART tree structure is shown in figure 2

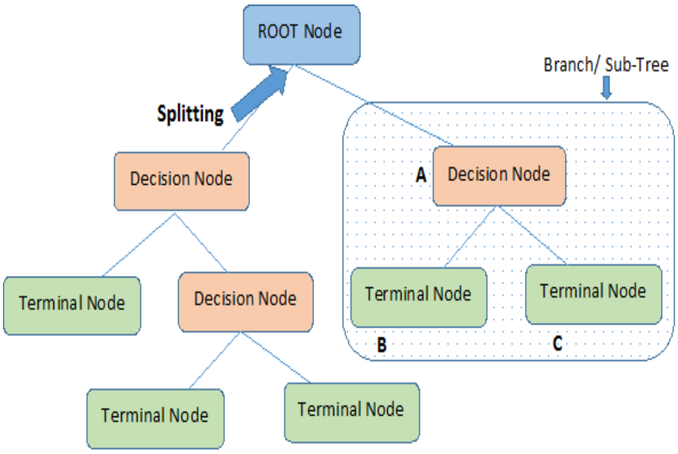


Figure 2. CART tree structure

2.2 ensemble bagging and boosting

Ensemble Data Mining Methods also known as Committee Methods or Model Combiners are machine learning methods that leverage the power of multiple models to achieve better prediction accuracy than any of the individual models could on their own.

Ensemble Classifier Methods:

- Bagging
- Boosting
- Random Subspace

Recently bagging, boosting and the random subspace method have become popular combining techniques for improving weak classifiers.

Bagging: Bootstrap aggregation, or bagging, is a technique proposed by that can be used with many classification methods and regression methods to reduce the variance associated with prediction, and thereby improve the prediction process. It is a relatively simple idea many bootstrap samples are drawn from the available data some prediction method is applied to each bootstrap sample, and then the results are combined, by averaging for regression and simple voting for classification, to obtain the overall prediction, with the variance being reduced due to the averaging.

Boosting: The Boost family of algorithms also known as boosting is another category of powerful ensemble methods. It explicitly alters the distribution of training data fed to every individual classifier specifically weight so each training sample. Initially the weights are uniform for all the training samples. During the boosting procedure adjusted after the training of each classifier is completed. For misclassified samples the weights are increased while for correctly classified samples are decreased. The final ensemble is constructed by combining individual classifiers according to their own accuracies.

Random Subspace: This method takes the advantage of high dimensionality and is an effective counter measure for the traditional problem of the curse of dimensionality. Its merit can be attributed to the high ensemble diversity which compensates for the possible deficiency of accuracies in individual classifiers. In random subspace feature subspaces are picked at random from the original feature space and individual classifiers are created only based on those attributes in the chosen feature subspaces using the original training set. The outputs from different individual classifiers are combined by the uniform majority voting to give the final prediction. The ensemble classifier is shown in figure 3

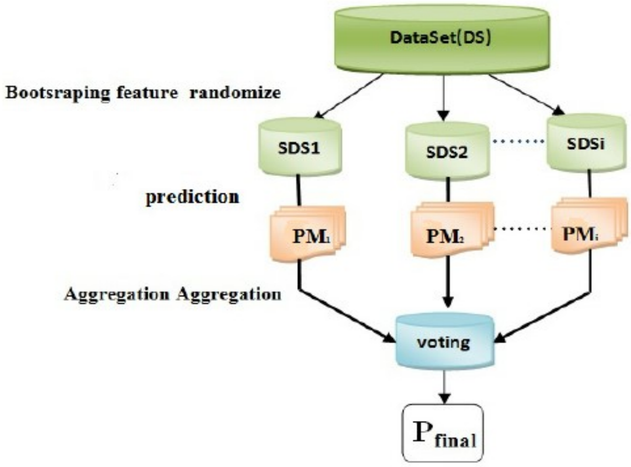


Figure 3. Ensemble Bagging and Boosting

2.3 random forest

Random Forest is essentially an ensemble of un-pruned classification trees. It gives excellent performance on a number of practical problems, largely because it is not sensitive to noise in the data set, and it is not subject to over-fitting. It works fast, and generally exhibits a substantial performance improvement over many other tree-based algorithms. Random forests are built by combining the predictions of several trees, each of which is trained in isolation. Unlike in boosting where the base models are trained and combined using a sophisticated weighting scheme, typically the trees are trained independently and the predictions of the trees are combined through averaging. There are three main choices to be made when constructing a random tree. These are

- The method for splitting the leafs.
- The type of predictor to use in each leaf.
- The method for injecting randomness into the trees.

In Brieman's early work each individual tree is given an equal vote and later version of Random Forest allows weighted and unweighted voting. The technique on which Random Forest ensemble is formed can be considered over following parameters:

i) Base Classifier: It describes the base classifier used in the Random Forest ensemble. Base classifier can be decision tree, Random tree, or extremely randomized tree.

ii) Split Measure: If base classifier of Random Forest is decision tree, then which split measure is found at each node of the tree to perform the splitting. To perform splitting Gini index, Info gain etc are used.

iii) Number of Passes: For building Random Forest classifier, if single pass is sufficient or multiple passes through data are needed

iv) Combine Strategy: In Random Forest ensemble, all the base classifiers generated are used for classification. At the time of classification, how the results of individual base classifiers are combined is decided by the combine strategy.

v) Number of attributes used for base classifier generation: This parameter gives the number of how many attributes are to be used which is randomly selected from the original set of attributes at each node of the base decision tree. Filter and Wrapper these are main techniques used for feature selection and extraction.

Each tree of Random Forest is grown, are described as follows: Suppose training data size containing N number of records, then N records are sampled at random but with replacement, from the original data, this is known as bootstrap sample along with M number of attributes. This sample will be used for the training set for growing the tree. If there are N input variables, a number n << N is selected such that at each node, n variables are selected at random out of N and the best split on these m attributes is used to split the node. The value of m is held constant during forest growing. The decision tree is grown to the largest extent possible. A tree forms "inbag" dataset by sampling with replacement member from the training set. It is checked whether sample data is correctly classified or not using out of bag error with the help of out of bag data which is normally one third of the "inbag" data. Prediction is made by aggregating (majority vote for classification or averaging for regression) the predictions of the ensemble

The overall process of Random forest algorithm is shown in figure 4

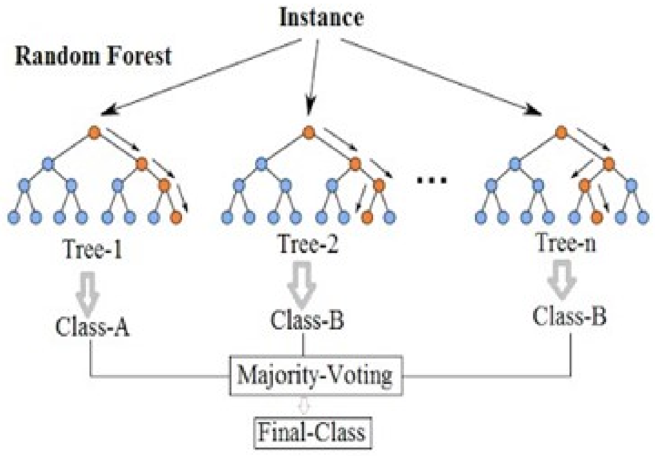


Figure 4. Random Forest Algorithm

2.4 multivariate adaptive regression splines (mars) tool

Nowadays healthcare industry generates massive amount of data about patients. Data analysis is essential for medical decision making and supervision. Analyzing and processing the enormous amounts of data generated by healthcare industry are too complex by conventional method. In data mining, classification is a technique used to predict the target classes accurately for each case. Prediction is a technique used to predict the future from the historical facts. In the healthcare sector, disease caused by a particular symptom cannot be well depicted using a single-label dataset, whereas multi-label dataset can be used to resolve this problem. Multi-label classification is the classification crisis where multiple labels should be assigned to each instance. Feature selection is an important step in regression and also for dimensionality reduction. As medical information is with multiple attributes, medical data mining differs from other one. Diagnosis of most of the diseases is expensive as many tests are required to predict the disease. By using data mining techniques we can reduce the cost of diagnosis by avoiding many tests by selection of those attributes which are really important for prediction of disease. Dimensionality reduction plays an important role in the field of medicine as it contains multiple attributes. Multi-label classification was mainly provoked by the task of text categorization, music, and medical analysis. Multi-label classification uses two methods for classification. First, problem transformation method which converts the multi-label problem into a set of binary classification problem then the problem can be handled by the single-label classifier. Second, algorithm adaptation method, adapts the algorithm directly to perform the multi-label classification. In multi-label, the main issue is to select the features for multiple classes. Features available in the multi-label dataset are entirely dependent on all the class labels. The feature selection is the process of selecting the relevant features which are the subset of the features. The features present in the dataset can be used to classify the data with accurate prediction. For this, multivariate adaptive regression splines (MARS) tool is used to handle the complex data and for the selection of optimistic feature subset for the multi-label data. MARS essentially builds flexible models by fitting piecewise linear regressions; that is, the nonlinearity of a model is approximated through the use of separate regression slopes in distinct intervals of the independent variable space. Therefore, the slope of the regression line is allowed to change from one interval to the other as the two “knot” points are crossed. The variables to use and the end points of the intervals for each variable are found via a fast but intensive search procedure. In addition to searching variables one by one, MARS also searches for interactions between variables, allowing any degree of interaction to be considered. Feature selection in the multi-label dataset is a challenging task due to complex interaction among features and class labels. Therefore, the multivariate adaptive regression spline (MARS) is used to classify and to select the important features. MARS handles large dataset and makes prediction quickly. The optimal MARS model is selected in a two-stage process. Firstly, MARS constructs a very large number of basis functions (BF), which are selected to over-fit the data initially, where variables are allowed to enter as continuous, categorical, or ordinal, the formal mechanism by which variable intervals are defined, and they can interact with each other or be restricted to enter in only as additive components. In the second stage, basis functions are deleted in the order of least contribution using the generalized cross-validation (GCV) criterion. A measure of variable importance can be assessed by observing the decrease in the calculated GCV when a variable is removed from the model. Missing values can also be handled in MARS by using dummy variables indicating the presence of the missing values. By allowing for any arbitrary shape for the function and interactions, and by using the above-mentioned two-stage model building procedure, MARS is capable of reliably tracking the very complex data structures that often hide in high-dimensional data.

Let y be the target output and X=($x_1, \ldots, x_p$) be a matrix of P input variables. Then it is assumed that the data are generated from an unknown 'true' model. In case of a continuous response this would be

$y = f(x_1, \ldots., x_p) + e$ = f(X)+e in which e is the distribution of the error. MARS approximates the function f by applying basis functions (BFs). BFs are splines (smooth polynomials), including piece-wise linear and piece-wise cubic functions. For simplicity, only the piece-wise linear function is expressed. Piece-wise linear functions are of the form max(0, x−t) with a knot occurring at value t. The equation max(.) means that only the positive part of (.) is used otherwise it is given a zero value. Formally

$$\max(0, x - t) = \begin{cases} x - t, \text{if } x \geq t \\ 0, \text{otherwise} \end{cases}$$

The MARS model, f(**X**), is constructed as a linear combination of BFs and their interactions, and is expressed as

$$f(x) = \beta_0 + \sum_{m=1}^{M} \beta_m \lambda_m(X)$$

where each λm is a basis function. It can be a spline function, or the product of two or more spline functions already contained in the model (higher orders can be used when the data warrants it; for simplicity, at most second order is assumed in this paper). The coefficients β are constants, estimated using the least-squares method. The aim of the backward deletion procedure is to find a close to optimal model by removing extraneous variables. The backward pass prunes the model by removing terms one by one, deleting the least effective term at each step until it finds the best sub-model. Model subsets are compared using the less computationally expensive method of Generalized Cross-Validation (GCV).

III. RESULTS AND DISCUSSION

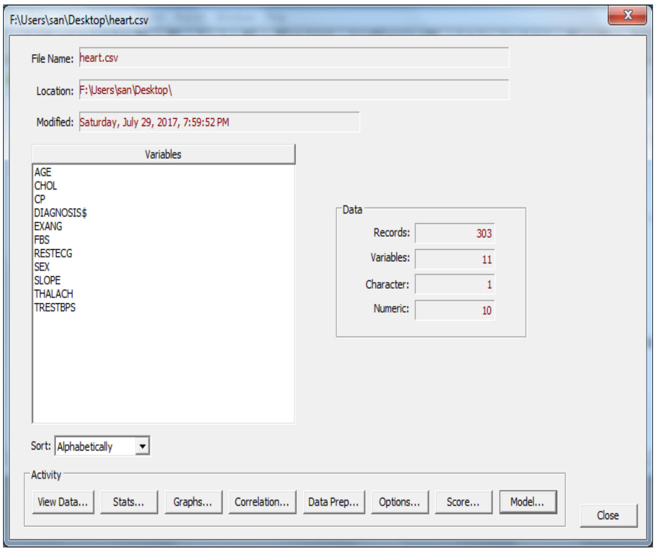
We can implement this system for uploading the heart datasets from UCI Repository from this link http://archive.ics.uci.edu/ml/datasets/Heart+Disease.

And we can perform regression analysis using tool named as Salford Predictive modeler for WINDOWS OS with any configuration. The imported datasets and variables are shown in Table 1. Data used for present work is obtained from UCI (University of California, Irvine C.A) Centre for machine learning and intelligent systems. The data have been collected from 303 patients are used for proposed work. This database contains 76 attributes, 13 of them are available for experiments but we have used only 11 of them which are required for coronary heart disease. The attributes that we have considered in this proposed work are:

Table 1. Dataset description

S.No	**Attribute**	**Description**
1	Age	age in years
2	Sex	Sex (1 = Male, 0 = Female)
3	Cp	Chest pain type 1= typical Angina 2 = Atypical angina 3 = Non-Anginal Pain 4 = Asymptomatic
4	Trestbps	Resting Blood pressure
5	Chol	Serum Cholestoral
6	Fbs	Fasting Blood sugar
7	Restecg	Resting Electrocardiographic results 0= Normal 1= Abnormality 2 = Ventricular hypertrophy
8	Thalach	Maximum Heart rate achieved
9	Exang	Exercise induced angina 1= yes 0=no
10	Slope	The slope of the peak exercise ST segment 1 = Upsloping 2 = Flat 3 = Downsloping
11	Diag	Diagnosis 0 = Normal 1 = Heart Disease

Then we can choose target and predictive information. From the above table, we can set target variable as Diag and Predictive variable as Age and Gender.



F:\Users\san\Desktop\heart.csv

File Name: heart.csv

Location: F:\Users\san\Desktop\

Modified: Saturday, July 29, 2017, 7:59:52 PM

Variables: AGE, CHOL, CP, DIAGNOSIS$, EXANG, FBS, RESTECG, SEX, SLOPE, THALACH, TRESTBPS

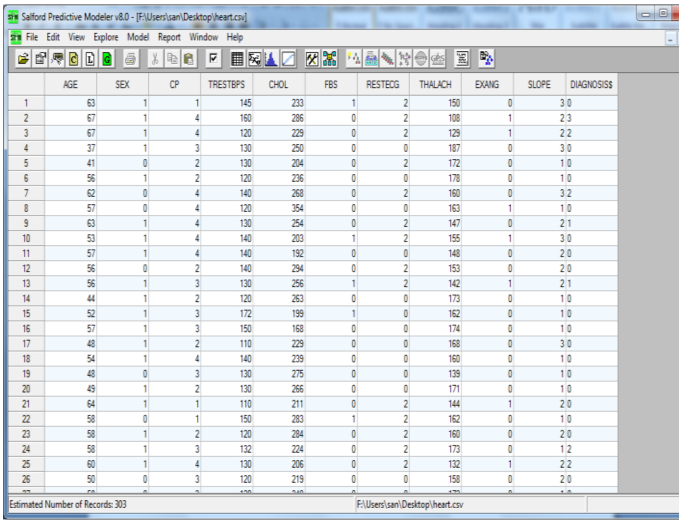
Data

Records:	303
Variables:	11
Character:	1
Numeric:	10

Sort: Alphabetically

Figure 5. Upload dataset

The overall variables, records, numeric values are shown in figure 5 and view all records in figure 6



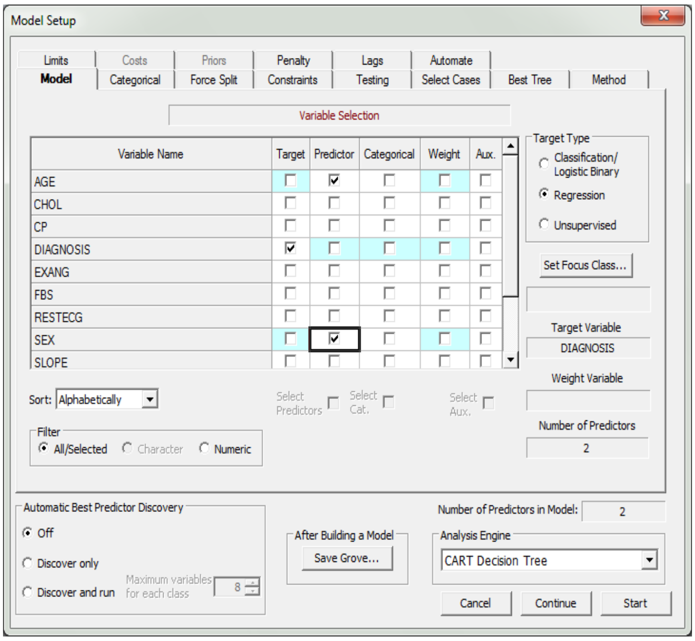
Salford Predictive Modeler v8.0 - [F:\Users\san\Desktop\heart.csv]

	AGE	SEX	CP	TRESTBPS	CHOL	FBS	RESTECG	THALACH	EXANG	SLOPE	DIAGNOSIS$
1	63	1	1	145	233	1	2	150	0	3	0
2	67	1	4	160	286	0	2	108	1	2	3
3	67	1	4	120	229	0	2	129	1	2	2
4	37	1	3	130	250	0	0	187	0	3	0
5	41	0	2	130	204	0	2	172	0	1	0
6	56	1	2	120	236	0	0	178	0	1	0
7	62	0	4	140	268	0	2	160	0	3	2
8	57	0	4	120	354	0	0	163	1	1	0
9	63	1	4	130	254	0	2	147	0	2	1
10	53	1	4	140	203	1	2	155	1	3	0
11	57	1	4	140	192	0	0	148	0	2	0
12	56	0	2	140	294	0	2	153	0	2	0
13	56	1	3	130	256	1	2	142	1	2	1
14	44	1	2	120	263	0	0	173	0	1	0
15	52	1	3	172	199	1	0	162	0	1	0
16	57	1	3	150	168	0	0	174	0	1	0
17	48	1	2	110	229	0	0	168	0	3	0
18	54	1	4	140	239	0	0	160	0	1	0
19	48	0	3	130	275	0	0	139	0	1	0
20	49	1	2	130	266	0	0	171	0	1	0
21	64	1	1	110	211	0	2	144	1	2	0
22	58	0	1	150	283	1	2	162	0	1	0
23	58	1	2	120	284	0	2	160	0	2	0
24	58	1	3	132	224	0	2	173	0	1	2
25	60	1	4	130	206	0	2	132	1	2	2
26	50	0	3	120	219	0	0	158	0	2	0

Estimated Number of Records: 303 F:\Users\san\Desktop\heart.csv

Figure 6. View All Records

Target and predictive variable settings can be shown in figure 7



Model Setup

Variable Selection

Variable Name	Target	Predictor	Categorical	Weight	Aux.
AGE	□	☑	□	□	□
CHOL	□	□	□	□	□
CP	□	□	□	□	□
DIAGNOSIS	☑	□	□	□	□
EXANG	□	□	□	□	□
FBS	□	□	□	□	□
RESTECG	□	□	□	□	□
SEX	□	☑	□	□	□
SLOPE	□	□	□	□	□

Sort: Alphabetically

Select Predictors □ Select Cat. □ Select Aux. □

Filter: ● All/Selected ○ Character ○ Numeric

Target Type: ○ Classification/ Logistic Binary ● Regression ○ Unsupervised

Set Focus Class...

Target Variable: DIAGNOSIS

Weight Variable

Number of Predictors: 2

Automatic Best Predictor Discovery: ● Off ○ Discover only ○ Discover and run

Maximum variables for each class: 8

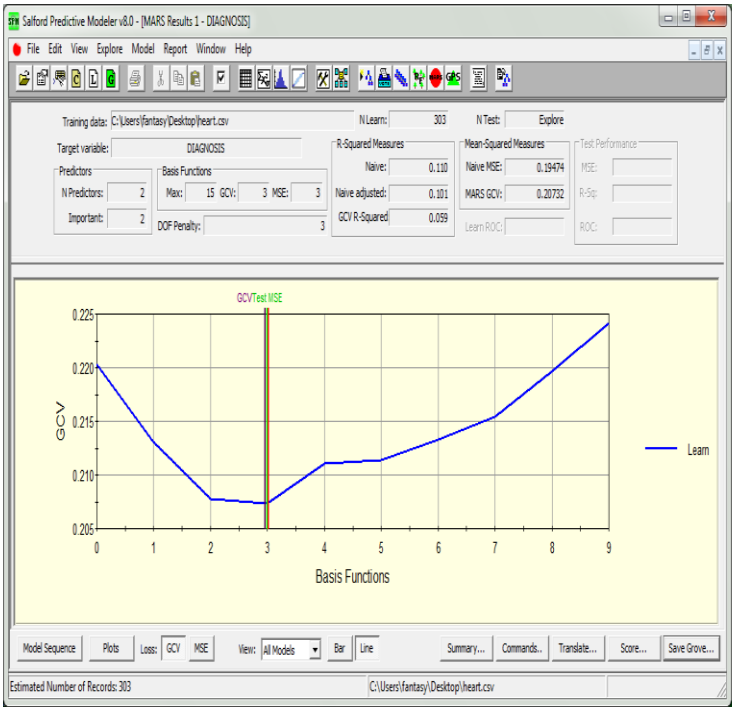
After Building a Model: Save Grove...

Number of Predictors in Model: 2

Analysis Engine: CART Decision Tree

Figure 7. Target and Predictive variable settings

Then perform various regression model MARS. The results of all algorithms are shown in the figure 8



Salford Predictive Modeler v8.0 - [MARS Results 1 - DIAGNOSIS]

Training data: C:\Users\fantasy\Desktop\heart.csv N Learn: 303 N Test: Explore

Target variable: DIAGNOSIS

Predictors: N Predictors: 2 Important: 2

Basis Functions: Max: 15 GCV: 3 MSE: 3

DOF Penalty: 3

R-Squared Measures: Naive: 0.110 Naive adjusted: 0.101 GCV R-Squared 0.059

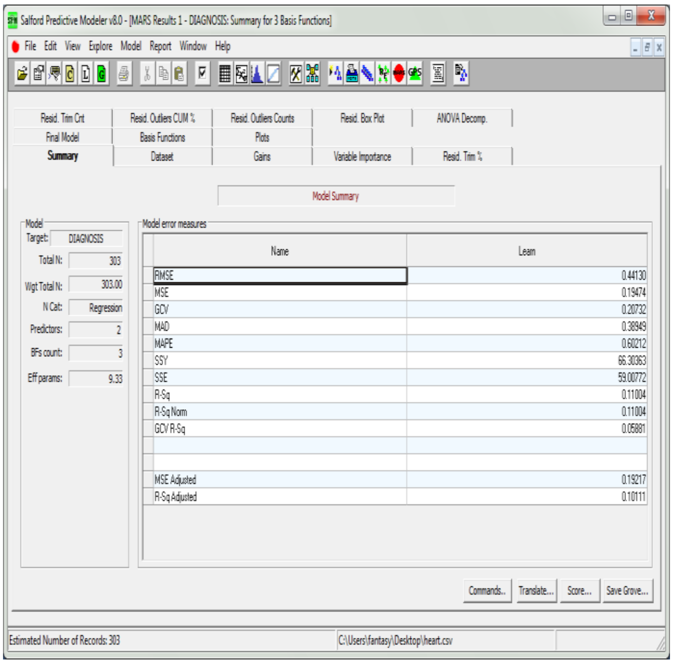
Mean-Squared Measures: Naive MSE: 0.19474 MARS GCV: 0.20732

Learn ROC:

Test Performance: MSE: R-Sq: ROC:

Estimated Number of Records: 303 C:\Users\fantasy\Desktop\heart.csv

Figure 8. MARS performance



Model Summary

Model

Target: DIAGNOSIS

Total N: 303

Wgt Total N: 303.00

N Cat: Regression

Predictors: 2

BFs count: 3

Eff params: 9.33

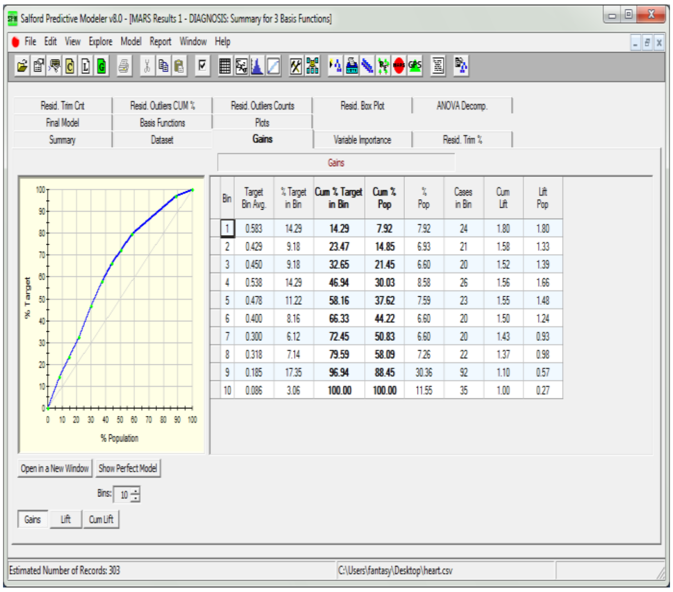
Model error measures

Name	Learn
RMSE	0.44130
MSE	0.19474
GCV	0.20732
MAD	0.38949
MAPE	0.60212
SSY	66.30363
SSE	59.00772
R-Sq	0.11004
R-Sq Norm	0.11004
GCV R-Sq	0.05881
MSE Adjusted	0.19217
R-Sq Adjusted	0.10111

Estimated Number of Records: 303

C:\Users\fantasy\Desktop\heart.csv

Figure 9. Measurements of MARS



Gains

Bin	Target Bin Avg.	% Target in Bin	Cum % Target in Bin	Cum % Pop	% Pop	Cases in Bin	Cum Lift	Lift Pop
1	0.583	14.29	14.29	7.92	7.92	24	1.80	1.80
2	0.429	9.18	23.47	14.85	6.93	21	1.58	1.33
3	0.450	9.18	32.65	21.45	6.60	20	1.52	1.39
4	0.538	14.29	46.94	30.03	8.58	26	1.56	1.66
5	0.478	11.22	58.16	37.62	7.59	23	1.55	1.48
6	0.400	8.16	66.33	44.22	6.60	20	1.50	1.24
7	0.300	6.12	72.45	50.83	6.60	20	1.43	0.93
8	0.318	7.14	79.59	58.09	7.26	22	1.37	0.98
9	0.185	17.35	96.94	88.45	30.36	92	1.10	0.57
10	0.086	3.06	100.00	100.00	11.55	35	1.00	0.27

Estimated Number of Records: 303

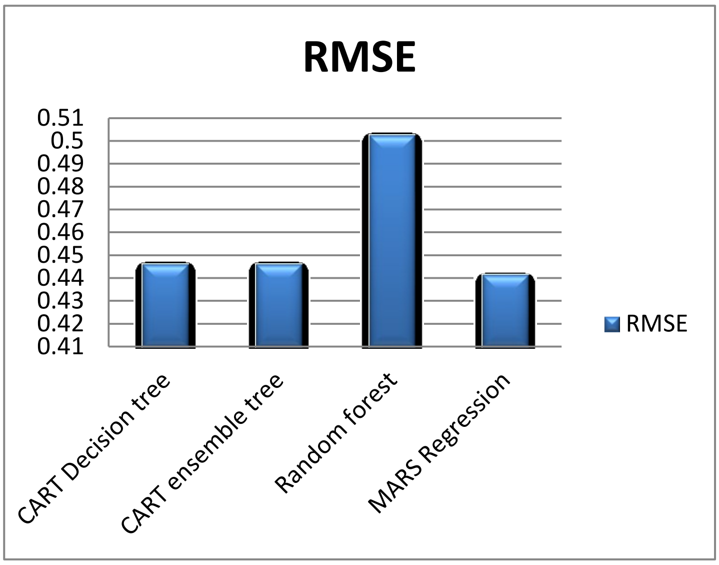
C:\Users\fantasy\Desktop\heart.csv

Figure 10. Gain values for MARS

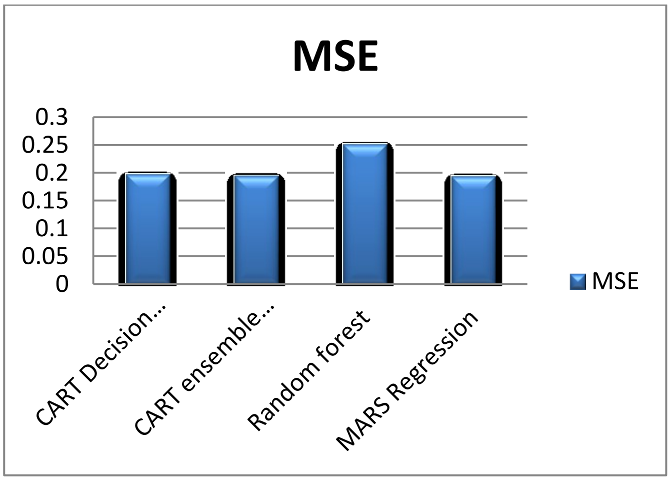
From above model construction we can evaluate the performance of each algorithm and compare the performance based on test regression measurements and shown in table and performance graph. The performance is listed in table 2

Table 2. Performance of various algorithms

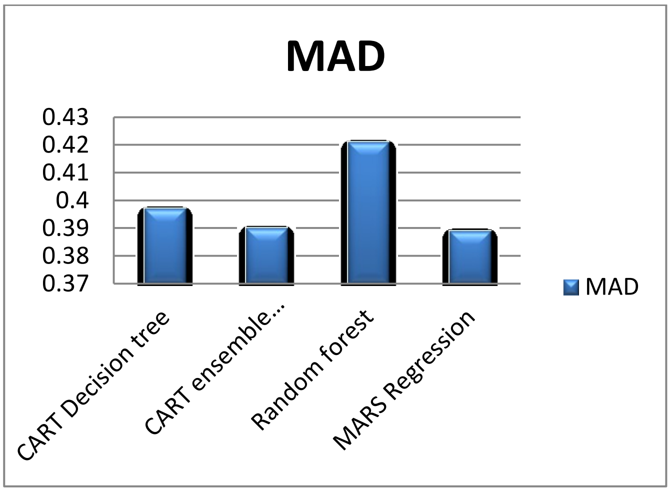
Algorithms	**RMSE**	**MSE**	**MAD**
CART Decision tree	0.44604	0.198	0.397
CART ensemble tree	0.44603	0.195	0.39
Random forest	0.50248	0.252	0.421
MARS Regression	0.4413	0.194	0.389



A. RMSE performance



B. MSE performance



C. MAD performance

Figure 11. Performance Graph of RMSE, MSE and MAD measurements

From the above comparison, can be shown in fig 11, MARS outperforms than the existing algorithms and provides reduce number of RMSE, MAE and MAD values and Provide GCV rate is 0.207 for 303 patients datasets.

IV. Conclusion

Using data mining technology for disease prediction and diagnosis has become the focus of attention. Data mining technology provides an important means for extracting valuable medical rules hidden in medical data and acts as an important role in disease prediction and clinical diagnosis. There is an increasing interest in using regression trees to identify subgroups of heart patients at increased risk for adverse events and outcomes. In the current study, have demonstrated, using a large sample of patients hospitalized with regression. But regression tree methods did not predict the patients as accurately as did conventional logistic regression. Furthermore, demonstrated that the predictive performance of conventional logistic regression was comparable to that of modern flexible regression method such as MARS models. This study is a comparison analysis between various integrated and enhanced regression methods. Then aimed at using the SPM tool for regression analysis of various regression algorithms in the tool by setting the target and predictive attributes from the data set and conclude the best by the various performance measures such as RMSE, MSE and MAD values. The performance measures are taken as the deviation and error rate of the various regression algorithms. Among them MARS proves to the best of all which is concluded by the minimum error value and minimum deviation. In future extend the framework to implement neural network algorithms for prediction target variables for classification with improved accuracy results.

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