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An Effective Analytics using Machine Learning Integrated Approaches for Diagnosis, Severity Estimation and Prediction of Heart Disease

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Abstract. Heart Disease is one of the precarious issues in the medial domain whereby the number of cases is huge in the global scenario. The instances of heart transplants increase a lot every year even in the developed countries. Heart disorder identifies a number of heart disease disorders with the cardiac disorders including illnesses of the blood stream, coronary artery disease, cardiovascular rhythms and related cardiac defects. Cardiovascular disease commonly implies disorders requiring restricted or blocked blood pathways that can lead to cardiac attack, chest pressure (angina) or a stroke. Some cardiac disorders including key causes of heart disease are often regarded as influencing the cardiac muscle, valves and rhythms. Many cases of cardiac illness can be reversed or managed with a safe lifestyle. Heart Failure (HF) is not a disorder but a complex health illness. The rise in costs in health care, the increasing occurrence, the decreased quality of life, frequent hospitalizations and early mortality have turned HF into a global and Indian crisis and have emphasized the need to diagnose HF and determine its magnitude and efficacy. The principal goal of this research manuscript is to find a machine-based learning approach to diagnoses, intensity predictions and heart disease prediction. In this manuscript, we present the regression as well as ensemble learning based analysis on the benchmark dataset of Cleveland from UCI repository for the estimation of cardiac diseases. A further aspect is that 303 records are scheduled for this review. The knowledge from Cleveland consists of approximately 13 features and we have intended to group it in five groups in this report. The presented outcomes on the assorted algorithmic approaches are quite effective and ensemble-based approach is quite performance aware.

1. Introduction

In recent days, ICT applications are not confined to the sharing of data, cloud activity, social media, web servers and mobile applications. Informatics has influenced every field of social and corporate sector since last decade, including the health and the medical sciences [1]. Most health laboratories today have specialized computer-based instruments for the effective detection and selection of parameters for the human body, such as Magnetic Resonance Imaging (MRI), CT, Electroencephalography (EEG), ECG, ultrasound, mammography, Laparoscopy, X-Ray, and several more. It is having greater specificity in examining the human body that assists the surgeon or specialist in detecting the disease. Such approaches are used by the physicians to prescribe adequate care for the patients [2].



The software approaches and libraries are not only implemented in the vast testing devices of medical study but to test biological data obtained from diagnostic machines by computational approaches for multiple diseases [3][27]. The definition of bioinformatics is used in this sense to explain biological and medical data using analytical techniques and applications. These software suites use high-performance programming languages to process and analyze the biological data collection with the aims of discovering the conditions of the human body for successful implementations [4].

The high incidence of cardiac failure in adults is around 2%, and in patients older than 75 years of age it varies over 8% [25]. Heart disease events in hospitals are very regular and 3–5 percent of hospital admissions are mostly focused on cases of heart disease [31]. In terms of clinical experience, it is a heart disease that triggers most hospital admissions [30]. The treatment for cardiac failure is substantially high and cannot be afforded by ordinary civilians and induces about 2% of overall health costs in many developing countries [27]. If we want to develop an efficient disease control plan, we need to carry out research on a wide spectrum of results, including disease diagnosis as soon as possible, severity-based evaluation and efficient prediction of adverse events[5][32].

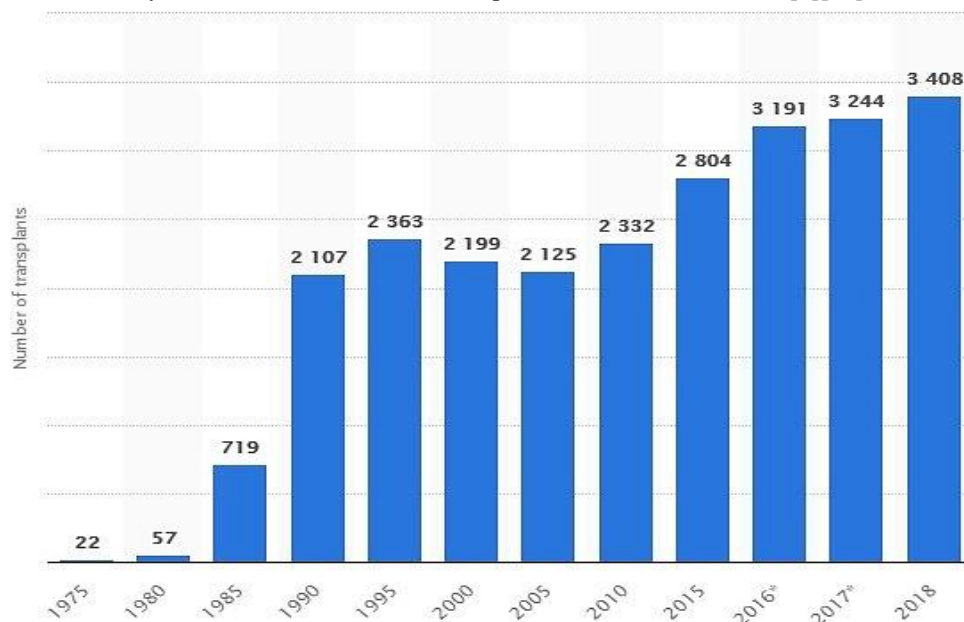


Figure 1 : Heart Transplants in USA (1975-2018 Source : Statista)

Artificial intelligence (AI) is the key domain of research that is implemented to replicate cognitive processes for human beings. It introduces a paradigm change into the health industry, assisted by improved access to health data and rapid advances in analytics [6]. Two big groups are primarily AI. Machine learning (ML) techniques that examine organized data such as graphic, genetic and electrophysiological data are part of the first group[24]. ML attempts to analyze the characteristics of the patient in medical procedures or predict the risk of the results of the illness. The second group involves Natural Language Processing (NLP) for the incorporation and refinement of organized medical data from unstructured data, such as medical notes and journals. The NLP procedures are aimed at translating text to structured data which are readable from computer and can be analyzed using ML techniques[7][29].

Machine learning should be viewed as an artificial intelligence subset involving the design and creation of algorithms, and functions like a container. These designing algorithms will improve the subject's actions on the basis of empirical evidence. Examples of observational results are used to demonstrate the interactions between variables identified. The emphasis of machine learning is on automated learning and pattern recognition of the given examples and on making machines smart judgments or decisions[8].

In classification based predictive analysis [28], a sample is categorized in this protocol as one of many pre-defined groups, according to the methodology used to undertake testing of machine learning. The regression requires several computer tools and technique, which can be used successfully in the regression and classification process. For inputs and a single output variable to draw the final product, they use different input variables. Such examples of regression and classification activities are, Classification and Regression Vector Machines (SVM)[27], Naive classification bays, K-Nearest Neighbors (KNNs), Classification and Regression Tree (CART), Adaptive Regression Multivariate Splines (MARSplines) etc. [9].

2. Related Work and Review of Literature

New developments in science are structured to rely on a more precise and focused analysis of prediction models to assess the magnitude of cardiovascular disease based on clinical outcomes and computational methods [10].

The findings of Liu Q et al., work [11] suggested a conventional paradigm for Chinese medical practice based on a Bayesian approach for computer diagnostics. Study was also carried out in order to develop expert programmed for forecasting and diagnosing cardiac diseases in the context of general programming [12]. Assanelli et.al, [13] has recommended the use of ECG data for cardiac diseaseprediction.

In 1999 Carven [14] employed techniques such as text classification, together with the Naive Bayes algorithm classification and relational algorithms further. In 2001, Craven used the Hidden Markov models that are similar to the 2004 model of Rosario and Hearst, which primarily concentrated on object identification. In the sense of discrimination between two variables, namely diseases and medicines, Srinivasan et.al [15] used a history approach [16]. A lot of work has been performed on construction codes in order to extractposition.

In 2002 Feldman et al. used a rule-based method to isolate and explain interactions dependent on DNA, proteins, medications and diseases. In order to consider a number of biological and molecular relations, Friedman et al. intensify the construction of a rules-based structure by handcrafting a semantic grammar and collection of semanticconstraints [32][17]. Regulatory methods were commonly used in biomedical literature for the resolution of interaction extraction tasks. Either syntactic (POS) and syntactic (similarly) structures; or semantic knowledge in form of set patterns containing terms that cause a certain interaction is a key source of information used in this method

One of the disadvantages of using rule-based approaches is that more specialist commitment is needed than data-driven methodologies. The better regulatory systems are those with rules manually or semi-automatically constructed, manually refined and automatically removed. The fact that they yield decent outcomes for accuracy, though reclamation levels are also poor is a successful feature of rules-based systems. Syntactic rule-driven extraction schemes are dynamic frameworks driven on tools used for the allocation of POS tags or the extraction of syntactic parses. It is understood that such resources are not yet up to date in the biomedical literature, as they are for general English texts, so their success on phrases is not necessarily the greatest.

Polat et al. [18] suggested this definition and an AIRS based on blurry weighted pre- processing, which displays 92.59 per cent precision. The algorithms of SMO, Bagging, ANN and the use of Z-Alizadeh Sani data were suggested by Roohallah et.al [19], with 303 patients with 54 features. This analysis then showed that "Chest Pain and Age" had the greatest efficiency effect as the remaining characteristics and their reported accuracy was as high as 94.08%. ANN-ANFIS contrasting with MATLAB applications is dealt with in Abushariah et.al. [20].

The accuracy of the ANFIS 100% and ANN 90.74% training results have been determined. However, the precision of the experimental results has been obtained for ANN 87.04% and ANFIS 75.93%. Negar Ziasabounchi et.al [21] addressed ANFIS technique's precision. The UCI data with seven features is treated as an input in their analysis. The analysis findings indicate 92.30 percent accuracy. The accuracy obtained was 72.5% by five classes, but when analyzing it for two classes, which include patients and stable persons, the accuracy achieved was 90.57%.

3. Methodology and Implementation

Inferring the Cleveland data set can be described as a classification issue where cardiac disease data have been used. This problem is known to be a regression problem because we take any data part as vector, of which the time-series data are obtained. In fact, we hope that all components can be modified, so it can be considered a problem with regression in this experiment [23]. Traditional approach uses a node's regression predictor and takes little account of the association between time-nodes. Even with the exception of the first time we added goal to the feature set to boost prediction accuracy.

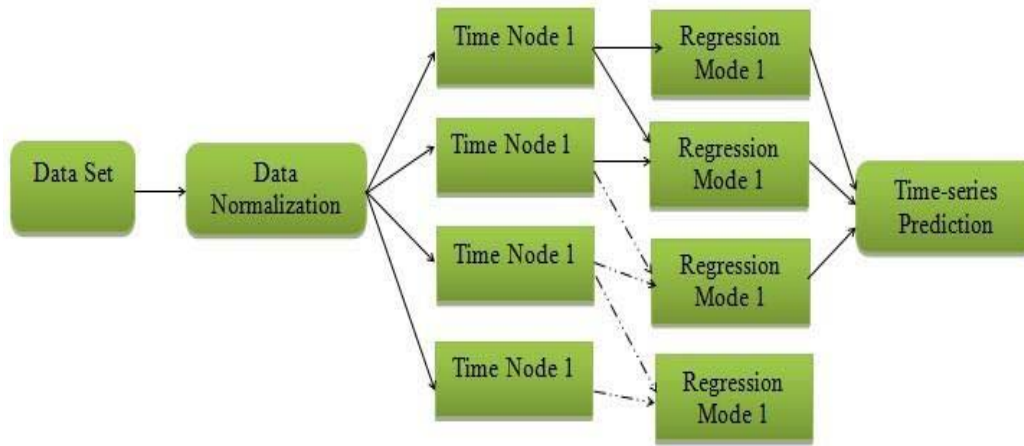


Figure 2: Proposed System Architecture

3.1 Polynomial Regression Based on Multi-Target

The role of multi-target polynomial regression is to induce data from the given polynomial equation, and it is capable of predicting the value of the multiple variables considered. As a simple platform for polynomial regression, based on multiple objectives, the principle of general linear model is used. The following is described in this strategy:

$$P = \beta_0 + \sum_{i=1}^m \beta_i \cdot T_i$$

$$T_i = \prod_{j=1}^n X_j^{a_{ij}} \quad \text{is denoted as terms.}$$

In the above equation β_i , $i = 1, \dots, m$ and β_0 are the constant vectors and they are no constants. The number of targets that has to be predicted is based upon the dimensions of these three vectors.

An example for this is given below,

$$P = (2, 5, 7) \cdot X_1^2 X_2 + (1, 3, 5) \cdot X_1 X_2^3 + (3, 2, 7).$$

This equation model is used in predicting the three targets brought under consideration and this is equivalent to the three single target polynomial equations given below,

$$\text{i.e., } P = (P_1, P_2, P_3),$$

where

$$P_1 = 2 \cdot X_1^2 X_2 + 1 \cdot X_1 X_2^3 + 3$$

$$P_2 = 5 \cdot X_1^2 X_2 + 3 \cdot X_1 X_2^3 + 2$$

$$P_3 = 7 \cdot X_1^2 X_2 + 5 \cdot X_1 X_2^3 + 7$$

Though the three equations P_1 , P_2 , and P_3 have same structure they have different coefficients for each target variable.

3.2 Algorithmic Approach

Step 1: Input: Tr (x, y) and Ts procedure evaluation

Step 2: datasets Exit: Fault test E0

Step 3: Use regression algorithm to train the model L to the training set Tr with the initial node and measure the training error.

Step 4: Move 2: Apply to the feature set the estimation value of the previous goal and use the regression algorithm to forecast the new aim and compute training errors.

Step 5: Iteratively execute step 2 before the final goal is specified. Combine and execute the test results with all the parameters.

Step 6: Close

The study provided statistics on Cleveland cardiac disease provides datasets at the following (<https://archive.ics.uci.edu/ml/datasets/heart+disease>).

This including 303 reports of 13 characters, as shown in Table. The results separated into 5 groups indicating loss of cardiac disease, and Grades 1 to 4 reflect a rise of heart disease incidence respectively. The features of these data are:

Table 1. Benchmark Dataset of Heart Disease for Prediction

Data Set Characteristics	Multivirat0065	Number of instances	303	Area	Life
Attribute Characteristics	Categorical, Integer, Real	Number of Attributes	75	Date Donated	01-07-1988
Associated Tasks	Classification	Missing Vales	Yes	Number of Web Hits	1309737

3.3 Benchmark Dataset for Analytics: Cleveland Heart Disease Dataset

Table 2 : Cleveland Heart Disease Dataset

Attribute	Description	Domain of Value
Age	Age in years	29 to 77
Sex	Sex	Male (1) Female (0)
Cp	Chest Pain type	TypicalAngina(1) Atypical Angina(2) Non-angina(3) Asymptomatic(4)
Trestbps	Resting blood sugar	94 to 200 mm Hg
Chol	Serum Cholesterol	126 to 564 mg/dl
Fbs	Fasting blood sugar	>120 mg/dl True (1) False(0)
Restecg	Resting ECG Result	Normal (0) ST-Twave Abnormality (1) LVhyper Trophy(2)
Thalach	Max heart Rate	71 to 202
Exang	Exercise include angina	Yes(1) No(0)
Old peak	ST depression induced by exercise relative to rest	0 to 6.2
Slope	slope of peak exercise ST segment	Up Sloping (1) Flat (2)
Ca	No.of. major vessels colored by fluoroscopy	Download sloping(3) 0-3
Thal	Defect type	Normal(3) Fixed Defect (6) Reversible defect (7)
Num	Heart Disease	0-4

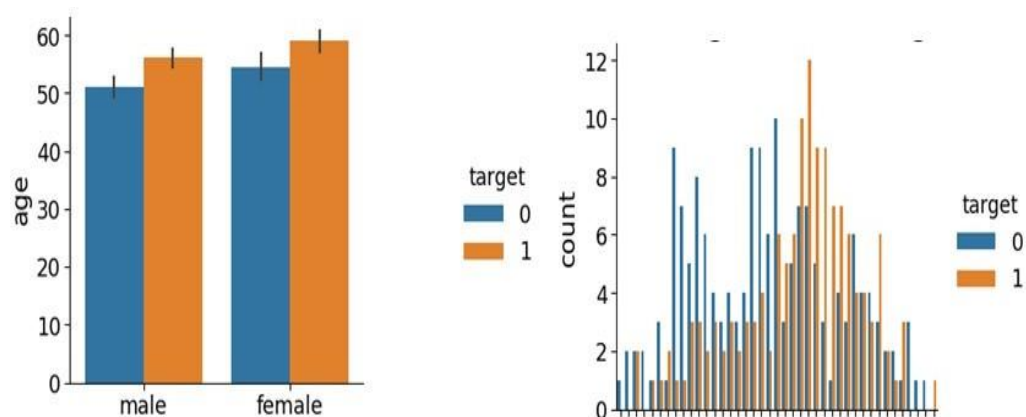


Figure 3: Distribution Patterns of Variation in Cleveland Benchmark Dataset

4. Experimental Results and EvaluationMetric

The estimation of results from the polynomial regression multi-target model results in an optimized and functional model. The classification methods are determined in conjunction with the following 1 to 4 formula with multiple Criteria, such as specificity, sensitivity, precision and accuracy to test. To calculate the indexes, we will use the uncertainty matrix. This matrix is a valuable tool to evaluate classification system output in the identification of data or evaluation in different groups. Ideally, the main diagonal of the matrix needs to contain a significant number of observe results, with the remaining matrix values being zero or equivalent to zero.

PP = Truly Classified Positive data labels

NF = Falsely Classified Negative data labels

PF = Falsely Classified positive data labels

NP = Truly Classified negative data labels

$$\text{Specificity} = NP / NP + NF \quad (1)$$

$$\text{Sensitivity} = PP / PP + PF \quad (2)$$

$$\text{Precision} = PP / PP + NF \quad (3)$$

$$\text{Accuracy} = PP + NP / PP + NP + NF + PF \quad (4)$$

Table shows the values of four indices for each class labels. The values have been calculated for C5.0 algorithm using the confusion matrix. The error rate or misclassification rate can also be calculated based on accuracy (formula 5) index.

$$\text{Error Rate} = 1 - \text{accuracy} \quad (5)$$

Table 3: Evaluation Analysis

Category (Class) Label	Accuracy (%)	Specificity (%)	Precision (%)	Sensitivity (%)
0	79	65	77	72
1	78	67	76	75
2	78	68	78	76
3	77	66	78	78
4	78	68	79	77

The plot shows about the different categories specificity, sensitivity, precision and accuracy

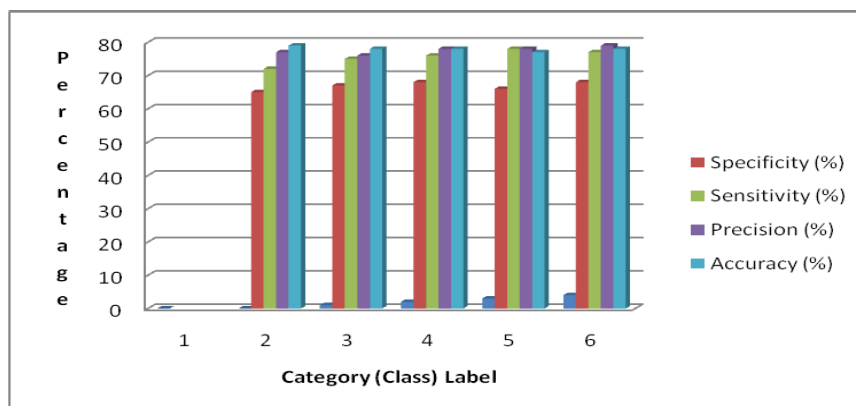


Figure 4: Assorted Patterns on Sensitivity, Specificity, Precision and Accuracy

The table shows the overall comparison of existing system with proposed system. AUC (Area Under Curve)-ROC is a performance metric for classification problems based on the different Threshold values. ROC is a likelihood curve and AUC measure the separability. In simple terms, we will learn from AUC-ROC metric how model can differentiate between classes. More AUC, better model, the better model is generated with the outputs

Table 4: Overall comparison of proposed system with existing system

Different algorithms	Performance in Percentage
Projected algorithm	92
Naïve Bayes Approach	90
Neural Network Based Implementation	91
CART Algorithm	83
ID3 Approach	65
J48 Approach	84

The cumulative performance level of proposed implementation with existing system is given

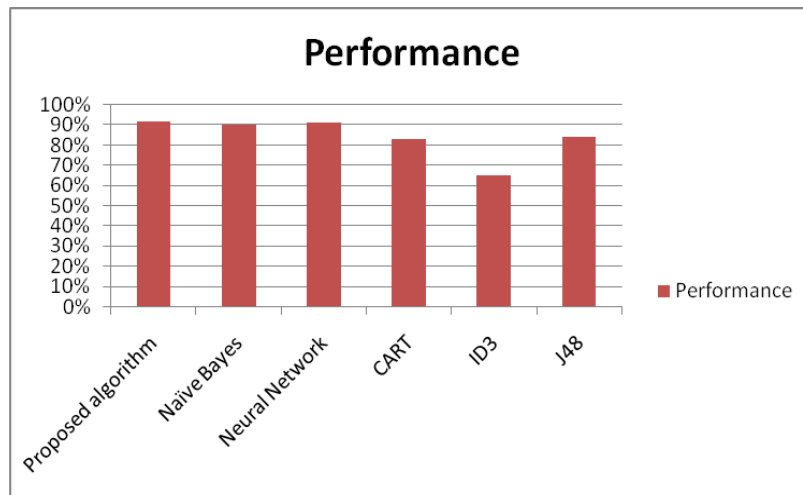


Figure 5: Overall performance

4.1 Integration with Assorted Ensemble Based for Effectual Learning

Different models of machine learning are used to build a hybrid ensemble learning models as weak learners in this role. These models may be Logistic Regression Model, Decision Tree, Support Vector Machine, K-Nearest Neighbor Model, Naive Bayes Model or other. The term hybrid is used here since a homogenous set of weak students is used in other ensemble models, but a heterogeneous selection of weak learners is used for this assignment.

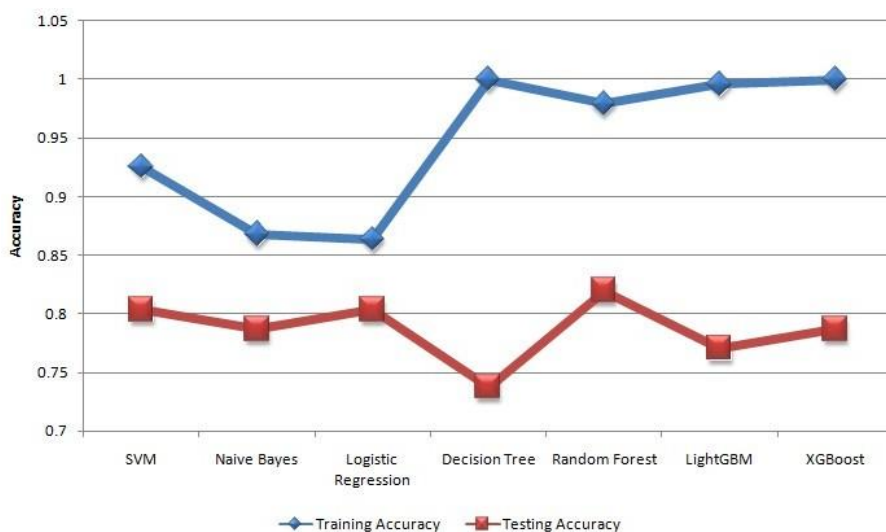


Figure :6 Evaluation process of Accuracy

Table 5: Models of Accuracy in Training and Testing

Models	Training Accuracy	Testing Accuracy
SVM	0.9256198347107438	0.8032786885245902
Naive Bayes	0.8677685950413223	0.7868852459016393
Logistic Regression	0.8636363636363636	0.8032786885245902
Decision Tree	1.0	0.7377049180327869
Random Forest	0.9793388429752066	0.819672131147541
LightGBM	0.9958677685950413	0.7704918032786885
XGBoos	1.0	0.7868852459016393

5. Conclusion

Bioinformatics based data analytics include the biological data's mathematical representations and are mostly used to provide statistical information through computational methods. Machine learning is a prominent domain of research for the bioinformatics and related segments which involves the development of algorithms to improve or create the actions involved in a given task by integrating new data in it. In the last few decades, the very large number of genetic sequence data generates large data banks which defy human researchers' ability to analyze and process these things effectively and without using computer methods. In addition to the ever more advanced application, other areas in medicine and biology are rapidly protected by machine learning.

For example, images from neuro-imaging methods such as CT and MRI are now being studied by machine-learning so that scientists can gain insight into the signs and characteristics of early diseases. This is especially helpful for brain and heart disease, as systems can dig through several thousands of findings in order to locate commonalities. Thus, the work of polynomial regression, i.e. the use of data in polynomial regression models, is discussed in this manuscript along with the tree-based approaches in association of ensemble learning. Polynomial structures have been commonly used in the past, but many people thought about it until the endorsement of machine learning. The presented work is having the integration patterns of assorted approaches on the base of ensemble learning so that the higher degree of accuracy can beachieved.

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References

- [1] Rana, H. K., Akhtar, M. R., Islam, M. B., Ahmed, M. B., Lió, P., Huq, F., & Moni, M. A. (2020). *Machine Learning and Bioinformatics Models to identify Pathways that Mediate Influences of Welding Fumes on Cancer progression*. *Scientific Reports*, 10(1), 1-15.
- [2] Wood, A., Najarian, K., & Kahrobaei, D. (2020). *Homomorphic Encryption for Machine Learning in Medicine and Bioinformatics*. *ACM Computing Surveys (CSUR)*, 53(4), 1-35.
- [3] Li, H., Tian, S., Li, Y., Fang, Q., Tan, R., Pan, Y., & Gao, X. (2020). *Modern Deep Learning in Bioinformatics*. *Journal of molecular cellbiology*.
- [4] Pikula, K., Zakharenko, A., Chaika, V., Kirichenko, K., Tsatsakis, A., & Golokhvast, K. (2020). *Risk assessments in nanotoxicology: Bioinformatics and computational approaches*. *Current Opinion in Toxicology*, 19, 1-6.
- [5] Nowbar, A. N., Gitto, M., Howard, J. P., Francis, D. P., & Al-Lamee, R. (2019). *Mortality from ischemic heart disease: Analysis of data from the World Health Organization and coronary artery disease risk factors From NCD Risk Factor Collaboration*. *Circulation: Cardiovascular Quality and Outcomes*, 12(6), e005375.
- [6] Chicco, D., Heider, D., & Facchiano, A. (2020). *Artificial Intelligence Bioinformatics: Development and Application of Tools for Omics and Inter-Omics Studies*. *Frontiers in Genetics*, 11.
- [7] Chen, C., Hou, J., Tanner, J. J., & Cheng, J. (2020). *Bioinformatics methods for mass spectrometry-based proteomics data analysis*. *International Journal of Molecular Sciences*, 21(8), 2873.
- [8] Parvizpour, S., Pourseif, M. M., Razmara, J., Rafi, M. A., & Omid, Y. (2020). *Epitope-based vaccine design: a comprehensive overview of bioinformatics approaches*. *Drug Discovery Today*.
- [9] Liu, G., Zeng, H., Mueller, J., Carter, B., Wang, Z., Schilz, J., & Gifford, D. K. (2020). *Antibody complementarity determining region design using high-capacity machine learning*. *Bioinformatics*, 36(7), 2126-2133.
- [10] I. H. Witten, E. Frank. (2005). *"Data Mining: Practical machine learning tools and techniques"*. 2nd Edition, Morgan Kaufmann, San Francisco.
- [11] Luo Y, Liu Q, Du CF, Long HX, Wang F, Zhu W, Zhou M, Xi J, Liu SD, Wen Y. (2014). *"Quality assessment for Chinese Meta-analysis on prevention and treatment of coronary heart disease"*. *Chinese Circulation Journal*. Dec, 29 (12): pp.979-982
- [12] J. Han and M. Kamber. (2001). *"Data Mining: Concepts and Techniques"*. San Francisco, MorganKauffmannPublishers
- [13] Deodato Assanelli, L. Cazzamalli, M. Stambini, M.L. Poeta. (1993). *"Correct diagnosis of chest pain by an integrated expert system"*, *IEEE Xplore Conference: Computers in Cardiology*.
- [14] Jennifer G. Dy. (2004). *"Feature Selection for Unsupervised Learning"*, *Journal of Machine Learning*, pp.845-889.
- [15] Srinivasan, P., Rindfleisch, T. (2002). *"Exploring text mining from Medline"*. In: *Proceedings of the AMIA Symposium*.
- [16] M.A. Jayaram, Asha Gowda Karegowda. (2007). *"Integrating Decision Tree and ANN for Categorization of Diabetics Data"*. *International Conference on Computer Aided Engineering*, December 13-15, 2007, IIT Madras, Chennai, India.
- [17] Mark A. Hall, *"Correlation-based Feature Selection for Machine Learning"*, Department of Computer science, University of Waikato. <http://www.cs.waikato.ac.nz/~mhall/thesis.pdf>.
- [18] K. Polat and Salih Güneş, (2007). *"A hybrid approach to medical decision support systems: Combining feature selection, fuzzy weighted preprocessing and AIRS"*, *computer methods and programs in biomedicine*, Vol. 88, No. 2, pp.164-174.

- [19] R. Alizadehsani, J. Habibi, M. J. Hosseini, H. Mashayekhi, R. Boghrati, A. Ghandeharioun, B. Bahadorian and Z. A. Sani., (2013), "A data mining approach for diagnosis of coronary artery disease", *Computer methods and programs in biomedicine*, Vol. 111, No. 1, pp.52-61.
- [20] M. A. M. Abushariah, A. A. M. Alqudah, O. Y. Adwan and R. M. M. Yousef, (2014). "Automatic Heart Disease Diagnosis System Based on Artificial Neural Network (ANN) and Adaptive Neuro-Fuzzy Inference Systems (ANFIS) Approaches." *Journal of Software Engineering and Applications*, 7, No.12.
- [21] N. Ziasabounchi and I. Askerzade, (2014). "ANFIS Based Classification Model for Heart Disease Prediction", *International Journal of Electrical & CS IJECS-IJENS*, Vol. 14, No. 02, pp.7-12.
- [22] S. Bhatia, P. Prakash and G.N. Pillai, (2008). "SVM based decision support system for heart disease classification with integer-coded genetic algorithm to select critical features", In *Proceedings of the World Congress on Engineering and Computer Science, WCECS, San Francisco, USA*, pp.22-24.
- [23] P. Palanikumar, S. Geofrin Shirly, S. Balakrishnan, (2015). "An Effective Two Way Classification of Breast Cancer Images", *International Journal of Applied Engineering Research*, ISSN 0973-4562, Volume 10, Number 21, pp.42472-42475.
- [24] Masetic Z, Subasi A. Congestive heart failure detection using random forest classifier. *Comput Methods Programs Biomed* 2016; 130:54–64.
- [25] Yang G, Ren Y, Pan Q, Ning G, Gong S, Cai G, (2010), "A heart failure diagnosis model based on support vector machine". *2010 3rd international conference on biomedical engineering and informatics (BMEI)*, vol. 3; 2010. p. 1105–8.
- [26] Zheng Y., Guo X., Qin J., Xiao S. (2015), "Computer-assisted diagnosis for chronic heart failure by the analysis of their cardiac reserve and heart sound characteristics." *Comput Methods Programs Biomed*. 2015; 122: pp.372–383.
- [27] Balakrishnan S, K. Aravind, A. Jebaraj Ratnakumar, A Novel Approach For Tumor Image Set Classification Based On Multi-Manifold Deep Metric Learning", *International Journal of Pure and Applied Mathematics*, Vol. 119, No. 10c, 2018, pp.553-562.
- [28] A. Jebaraj Rathnakumar, S. Balakrishnan, "Machine Learning based Grape Leaf Disease Detection", *Jour of Adv Research in Dynamical & Control Systems*, Vol. 10, 08-Special Issue, 2018. Pp.775-780.
- [29] N Satyanandam, Ch Satyanarayana, "Heart Disease Detection Using Predictive Optimization Techniques", *International Journal of Image, Graphics and Signal Processing (IJIGSP)*, Vol.11, No.9, pp. 18-24, 2019. DOI:10.5815/ijigsp.2019.09.02
- [30] N Satyanandam, Dr. Ch Satyanarayana, A New Multilayer Perceptron Model to Detect Heart Disease Severity, *International Journal of Scientific & Engineering Research*, Volume 7, Issue 12, December-2016 ISSN 2229-5518
- [31] N Satyanandam, Dr. Ch Satyanarayana, Detection of Heart Disease Severity using A Novel Multilayer Perceptron Model: Validation through Major Datasets, *Advances in Fuzzy Mathematics*. ISSN 0973-533X Volume 12, Number 3 (2017), pp. 333-345 © Research India Publications