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Software engineering health data prediction: Application of health Systems using machine learning

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Abstract

Recently, machine learning has become a hot research topic. Therefore, this study investigates the interaction between software engineering and machine learning within the context of health systems. We proposed a novel framework for health informatics: the framework and methodology of software engineering for machine learning in health informatics (SEMLHI). The SEMLHI framework includes four modules (software, machine learning, machine learning algorithms, and health informatics data) that organize the tasks in the framework using a SEMLHI methodology, thereby enabling researchers and developers to analyze health informatics software from an engineering perspective and providing developers with a new road map for designing health applications with system functions and software implementations. The SEMLHI approach utilizes the principal component analysis (PCA) for feature extraction and feature reduction. Further, SEMLHI model also utilizes the extreme learning machine (ELM) for prediction problems. The SEMLHI approach considers the Indian Diabetes dataset to perform the simulations, and proposed ELM is outperformed as compared to state of art approaches.

Keywords: Software engineering, Machine learning, health informatic, Indian Diabetes dataset, extreme learning machine.

1. Introduction

Human body needs energy for activation. The carbohydrates are broken down to glucose, which is the important energy source for human body cells. Insulin is needed to transport the glucose into body cells. The blood glucose is supplied with insulin and glucagon hormones produced by pancreas. Insulin hormones produced by the beta cells of the islets of Langerhans and glucagon hormones are produced by the alpha cells of the islets of Langerhans in the pancreas. When the blood glucose increases, beta cells are stimulated, and insulin is given to the blood. Insulin enables blood glucose to get into the cells and this glucose is used for energy. So, blood glucose is kept in a narrow range. Diabetes is a chronic disease with the potential to cause a worldwide health care crisis. According to International Diabetes Federation 382 million people are living with diabetes across the whole world. By 2035, this will be doubled as 592 million [1]. However, early prediction of diabetes is quite challenging task for medical practitioners due to complex interdependence on various factors. Diabetes affects human organs such as kidney, eye, heart, nerves, foot etc. Data mining is a process to extract useful information from large database, as there are very large and enormous data available in hospitals and medical related diabetes. It is a multidisciplinary field of computer science which involves computational process, machine learning, statistical techniques, classification, clustering and discovering patterns. Recently, Data mining techniques have been widely used in predicting the data like time-series [2, 3]. A number of data mining algorithms have been proposed for early prediction of disease with higher accuracy in order to save human life and reduce the treatment cost [4]. Thus, applying these algorithms to predict diabetes should be done. In our work, we used five different supervised learning methods to conduct our experiment.

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The field of health informatics (HI) aims to provide a largescale linkage among disparate ideas. Normally, a healthcare dataset is found to be incomplete and noisy; as a result, reading data from dataset linkage traditionally fails within the discipline of software engineering. Machine learning (ML) is a rapidly maturing branch of computer science since it can store data on a large scale. Many ML tools can be used to analyze data and yield knowledge that can improve the quality of work for both staff and doctors; however, for developers, there is currently no methodology that can be used. Regarding software engineering, there has been a lack of approaches to evaluating which software engineering tasks are better performed by automation and which require human involvement or human-in-the-loop approaches [1]. Big data has many challenges regarding analysis challenges for real-world big data [2], including OLAP mass data, mass data protection, mass data survey and mass data dissemination. Recently, a set of frameworks have been used to develop data analysis tools such as Win-CASE [3] and SAM [4]. The market has vast data analysis tools that can discover interesting patterns and hidden relationships to support decision makers [5]. BKMR used the R package as a statistical approach on health effects to estimate the multivariable exposure-response function [6]. Augmentor included the Python image library for augmentation [7], while for the visualization of medical treatment plans and patient data, CareVis was used [8], as it was designed for this task. Other applications require a visual interface using COQUITO [9]. For health-care data analytics, the widely known 3P tools [10] were used. Many simple applications, such as WEKA, which provided a GUI for many machine learning algorithms [11], while Apache Spark was used for the cluster computing framework [12], are powerful systems that can used in various applications for solving problems using big data and machine learning [13]. Software engineering for machine learning applications (SEMLA) discusses the challenges, new insights, and practical ideas regarding the engineering of ML and artificial engineering (AI) [14]. NSGA-II proposed algorithms for real-world applications that include more than one objective function for enhancing performance in terms of both diversity and convergence [15]. ML algorithms in clinical genomics generally come in three main forms: supervised, unsupervised and semi-supervised [16]. Interflow system requirement analysis (ISRA) has been used to determine the system requirements.

2. Literature survey

K.Vijiya Kumar et al. [17] proposed random Forest algorithm for the Prediction of diabetes develop a system which can perform early prediction of diabetes for a patient with a higher accuracy by using Random Forest algorithm in ma- chine learning technique. The proposed model gives the best results for diabetic prediction and the result showed that the prediction system is capable of predicting the diabetes disease effectively, efficiently and most importantly, instantly.

Muhammad Azeem Sarwar et al. [18] proposed study on prediction of diabetes using machine learning algorithms in healthcare they applied six different machine learning algorithms Performance and accuracy of the applied algorithms is discussed and compared. Comparison of the different machine learning techniques used in this study reveals which algorithm is best suited for prediction of diabetes. Diabetes Prediction is becoming the area of interest for researchers in order to train the program to identify the patient are diabetic or not by applying proper classifier on the dataset. Based on previous research work, it has been observed that the classification process is not much improved. Hence a system is required as Diabetes Prediction is important area in computers, to handle the issues identified based on previous research.

Tejas N. Joshi et al. [19] presented Diabetes Prediction Using Machine Learning Techniques aims to predict diabetes via three different supervised machine learning methods including: SVM, Logistic

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regression, ANN. This project pro- poses an effective technique for earlier detection of the diabetes disease.

Nonso Nnamoko et al. [20] presented predicting diabetes onset: an ensemble supervised learning approach they used five widely used classifiers are employed for the ensembles and a meta-classifier is used to aggregate their outputs. The results are presented and compared with simi- lar studies that used the same dataset within the literature. It is shown that by using the proposed method, diabetes onset prediction can be done with higher accuracy.

Deeraj Shetty et al. [21] proposed diabetes disease prediction using data mining assemble Intelligent Diabetes Disease Prediction System that gives analysis of diabetes malady utilizing diabetes patient's database. In this system, they propose the use of algorithms like Bayesian and KNN (K-Nearest Neighbor) to apply on diabetes patient's database and analyze them by taking various attributes of diabetes for prediction of diabetes disease.

3. Proposed Method

In proposed system the combining Software Engineering and Machine Learning algorithms to improve disease prediction in health care systems and to minimize time taken to predict disease as we don't have enough hospitals or bed to accommodate growing number of patients and we can solve this problem of predicting disease with less time by employing software and machine learning algorithms. Proposed method concept is known as SEMLHI Software Engineering with Machine Learning for Health Data).

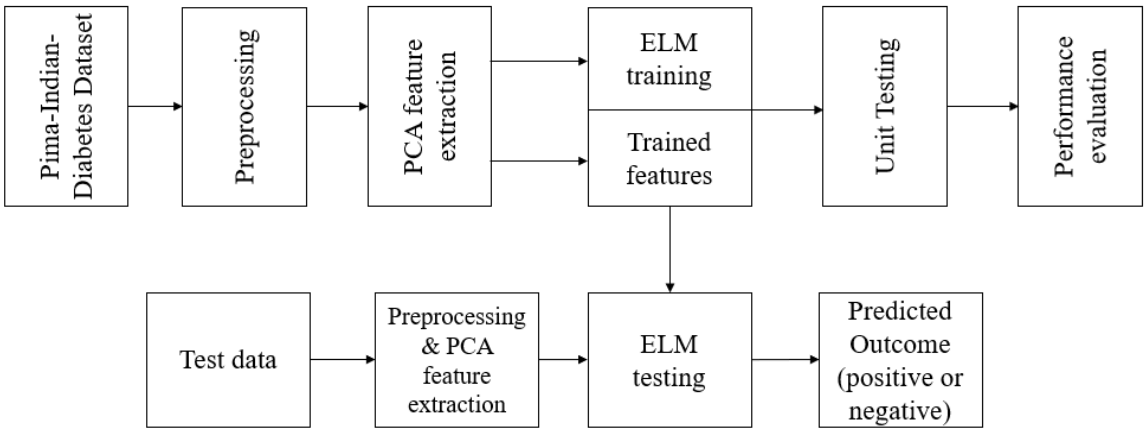

Fig. 1: Proposed framework.

Fig 1 shows the proposed framework. Propose SEMLHI consists of 4 components

- Health Informatics Data: To predict any disease we need to build Machine Learning models by using datasets and this dataset often contains missing data, null and non-numeric data and this type of data could degrade ML prediction accuracy and to overcome from this problem this work is applying PREPROCESSING on health care data to remove all missing and null values and then convert non-numeric data to numeric data by applying python SKLEARN PREPROCESSING classes. Often this dataset may contain unnecessary columns or attributes and to remove this attribute here applying dimensionality reduction algorithm called PCA. The PCA (principal component analysis) remove unnecessary attributes from dataset and maintain only important attributes necessary to make correct prediction.

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- ML Algorithms: In this module we are using various machine learning algorithms such as Linear SVC, Multinomial Naïve Bayes, Random Forest, Logistic Regression, KNN and Extreme Learning Machine (ELM). This algorithm train itself with available datasets and then generate a train model and then this train model will be applied on new test data to perform prediction. By using above algorithms, we can make machine to learn and perform prediction without any human supports.
- Machine Algorithm Model: Once after building above models then we can apply new test data on this model to predict whether patient lab reports are positive or negative.
- Software: This module used by developers to check reliability of above modules by applying software quality check, UNIT TESTING and software verification.

In proposed work by using various size of dataset we are applying classification, clustering ore regression and to implement this concept is using Palestine Hospital dataset and this dataset not available on internet and also not publish this dataset on internet so using INDIAN DIABETES dataset. we will use this dataset to train above ML algorithms and then perform UNITTESTING to check all ML algorithms are giving accurate accuracy values.

3.1 Dataset

This data set contains 416 liver patient records and 167 non liver patient records collected from Northeast of Andhra Pradesh, India. The "Dataset" column is a class label used to divide groups into liver patient (liver disease) or not (no disease). This data set contains 441 male patient records and 142 female patient records. Any patient whose age exceeded 89 is listed as being of age "90".

Columns**:**

- Age of the patient
- Gender of the patient
- Total Bilirubin
- Direct Bilirubin
- Alkaline Phosphotase
- Alamine Aminotransferase
- Aspartate Aminotransferase
- Total Protiens
- Albumin
- Albumin and Globulin Ratio

Dataset: field used to split the data into two sets (patient with liver disease, or no disease)

3.2 Preprocessing

Data preprocessing is a process of preparing the raw data and making it suitable for a machine learning model. It is the first and crucial step while creating a machine learning model. When creating a machine learning project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean it and put in a formatted way. So, for this, we use data preprocessing task.

Need of Data Preprocessing: A real-world data generally contains noises, missing values, and maybe in an unusable format which cannot be directly used for machine learning models. Data preprocessing is required tasks for cleaning the data and making it suitable for a machine learning model which also increases the accuracy and efficiency of a machine learning model.

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3.3 Splitting the Dataset

In machine learning data preprocessing, we divide our dataset into a training set and test set. This is one of the crucial steps of data preprocessing as by doing this, we can enhance the performance of our machine learning model. Suppose if we have given training to our machine learning model by a dataset and we test it by a completely different dataset. Then, it will create difficulties for our model to understand the correlations between the models. If we train our model very well and its training accuracy is also very high, but we provide a new dataset to it, then it will decrease the performance. So we always try to make a machine learning model which performs well with the training set and also with the test dataset.

3.4 PCA feature reduction

The Principal Component Analysis is a popular unsupervised learning technique for reducing the dimensionality of data. It increases interpretability yet, at the same time, it minimizes information loss. It helps to find the most significant features in a dataset and makes the data easy for plotting in 2D and 3D. PCA helps in finding a sequence of linear combinations of variables.

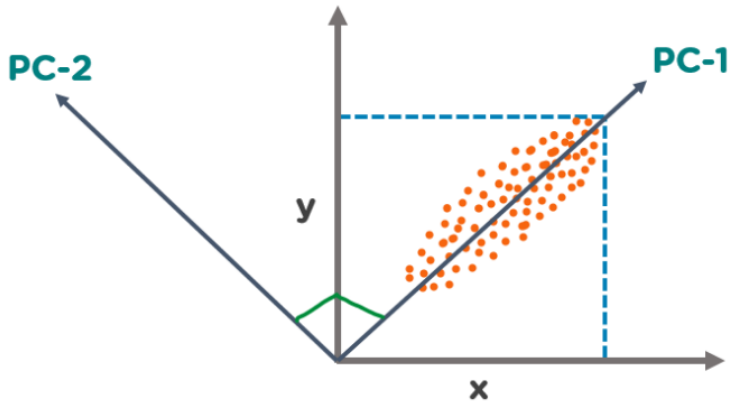

Fig. 2: PCA analysis.

In the above figure, we have several points plotted on a 2-D plane. There are two principal components. PC1 is the primary principal component that explains the maximum variance in the data. PC2 is another principal component that is orthogonal to PC1.

Fig. 3: Applications of PCA in Machine Learning.

- PCA is used to visualize multidimensional data.
- It is used to reduce the number of dimensions in healthcare data.
- PCA can help resize an image.
- It can be used in finance to analyze stock data and forecast returns.
- PCA helps to find patterns in the high-dimensional datasets.

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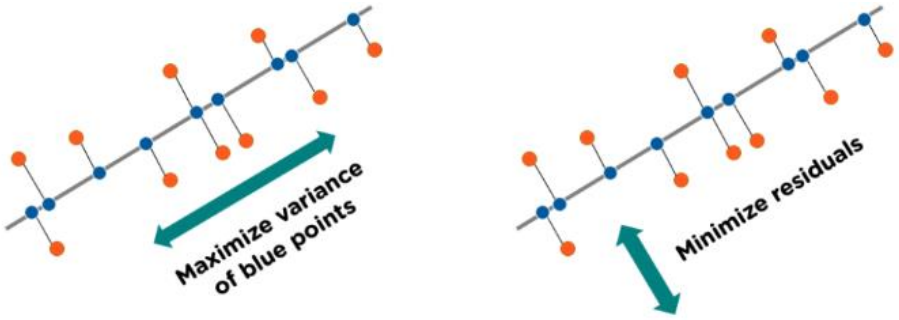

Fig. 4: PCA working.

Step 1: Normalize the data: Standardize the data before performing PCA. This will ensure that each feature has a mean = 0 and variance = 1.

$$Z = \frac{x - \mu}{\sigma}$$

Step 2: Build the covariance matrix: Construct a square matrix to express the correlation between two or more features in a multidimensional dataset.

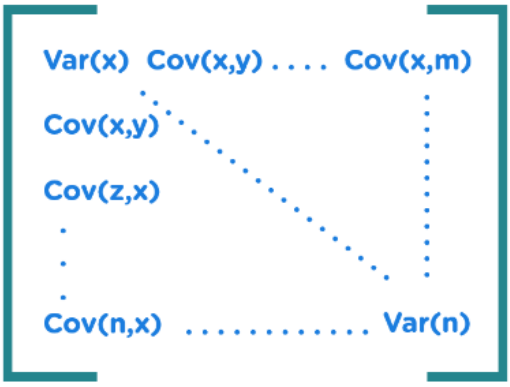

Fig. 5: Covariance matrix formulation.

Step 3: Find the Eigenvectors and Eigenvalues: Calculate the eigenvectors/unit vectors and eigenvalues. Eigenvalues are scalars by which we multiply the eigenvector of the covariance matrix.

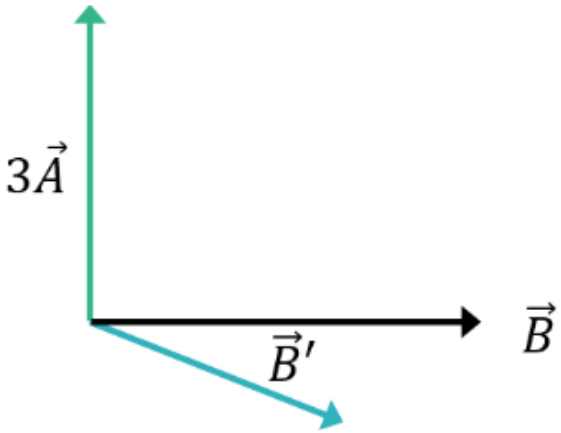

Fig. 6: PCA dimension reduction.

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Step 4: Sort the eigenvectors in highest to lowest order and select the number of principal components.

3.5 ELM Prediction

ELM is a kind of advanced neural network, consists of three layers such as input layer, hidden layer (number of neurons) and an output layer. The input layer captures the input variable, hidden layers make a linear relationship among the variables and the output layer presents the predicted value. The following principle that differentiates ELM from other traditional NN is based on the parameters of the feed-forward network, inputs weights and biases provided to the hidden layer. In ELM, the bias of the hidden layer and input weight are randomly generated, and the output is calculated by the Moore–Penrose generalized inverse of the hidden layer output matrix. The randomly chosen input weight and hidden layer biases learn the training samples with minimum error. After randomly choosing the input weights and the hidden layer biases, SLFNs can be simply considered as a linear system. The main advantage of ELM, its structure does not depend on network parameters which produce stability. Hence it is useful for classification, regression, and clustering.

Therefore, we adopted ELM as a classification model in predicting the software quality. Figure 2 shows the architecture of ELM with four input layers, ten hidden layers, and three output layers. The process of training and testing the ELM contains a network with two vectors of input vector and target output vector. The ELM prediction model used for classification form a function FðxÞ, considering ða1; a2;:::; anÞ attributes as input vector and ðzjÞ as output classification label target vector. In this proposed work, the attributes ISC, BICM, SCCR, and SCCP are considered as input metrics to predict software quality in terms of Maintainability, Independency and Portability. The classification labels zj vector denotes this software quality factors. Each of the input vector attributes describes the software components in the JavaBean software system. The objective consider is, to design an optimal input weight in SLFN with minimum error rate. Therefore, the evaluation of function FðxÞ is performed on the given dataset (S), where S is grouped into two parts of the training set ðSTrainÞ and testing set ðSTestÞ. The learning process uses a back propagation algorithm for SLFN. Finally, the output classification label is evaluated on STest. Consider L training samples be aj;zj , where aj ¼ aj1; aj2; ...; ajm T 2 Rm aj ¼ aj1; aj2; ::; ajm T 2 Rm indicates the input vector of jth samples with m-dimensional attributes and zj ¼ zj1;zj2; ...zjn T 2 Rn indicates the jth output (target) vector with n-dimension. In ELM, the bias to the hidden layer and input weights are generated randomly instead of tuning the network parameter. Therefore, the nonlinear system is transformed into linear system. The output function of SLFN is defined in mathematically as follows,

$$F(x) = \sum_{j=1}^{N} \beta_j G(\alpha_j x_j + c_j) = o_j \quad j = 1, 2, 3, \ldots, L \qquad (1)$$

where oj denotes the jth sample output value, bj ¼ ðbj1; bj2; ...; bjmÞ bj ¼ ðbj1; bj2; ...; bjmÞ denotes the output weight vector connection between the jth hidden neurons to the output neurons, cj 2 R denotes the randomly assigned bias vector to the hidden neurons and the output neurons, and aj 2 R denotes the random input weight vector assigned between the input neurons and hidden neurons. The whole representation of Gðajxj þ cjÞ indicates the output of jth hidden neurons with xj input samples.

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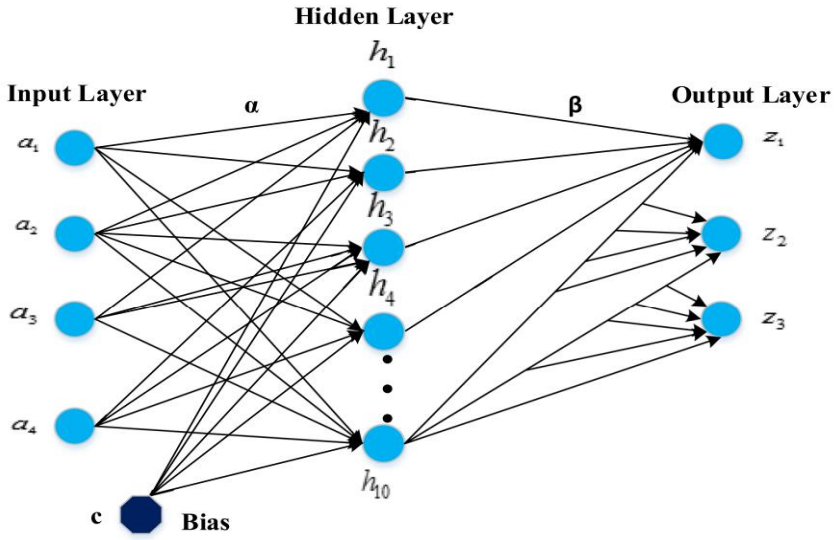

Fig. 7: The architecture of the extreme learning machine.

4. Results

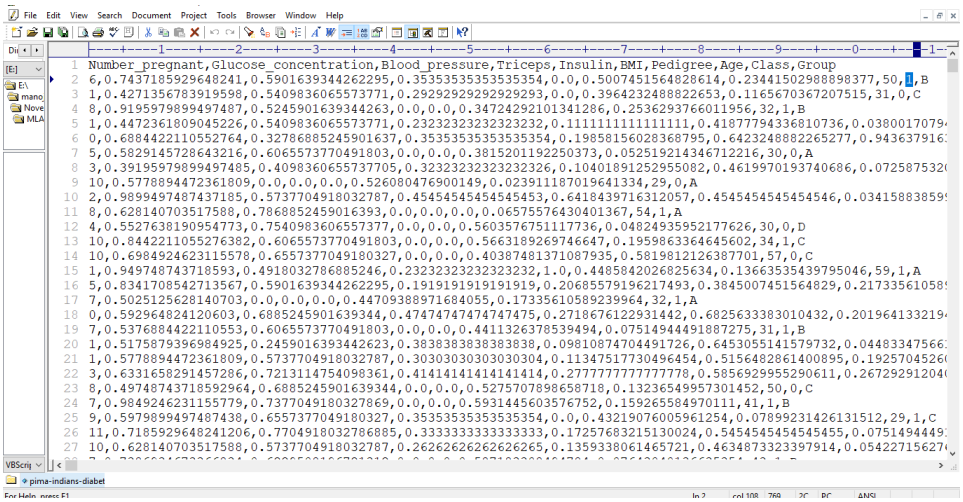

Fig. 8: Sample Dataset.

In Fig 8 dataset screen all values are the lab report values and ‘Class’ value contains 0 or 1 and ML algorithm will train with above lab report values and Class Value and then generate a model. Generated train model we will apply on below test data to predict class label. In below test dataset we can see there is no Class label column and ML will predict Class label by using alone lab values.

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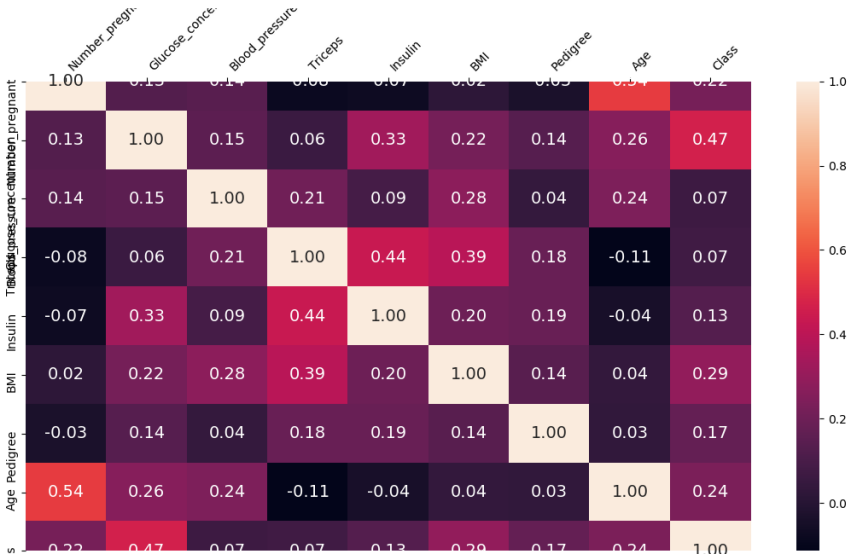

Fig. 9: Skewness Matrix.

In Fig 9, we can see names of columns and in boxes values with minus symbols are not important and only positive column values are important and ML algorithm will train only with positive values. In Fig 10, green colour dots are the records which contains no disease and red colour dots are the records which contains disease and this graph generated for all 154 test records. Now close above graph to see all ML prediction accuracy

Table 1. Performance comparation

Model	KNN	Naïve Bayes	Random Forest	Logistic Regression	Linear SVC	Proposed ELM
Accuracy	63.6363	70.1298	74.6753	75.3246	59.0909	92.8571

In Table 1, we can see prediction accuracy of each algorithm and from all algorithm's proposed ELM is giving good prediction accuracy and now all ML algorithms.

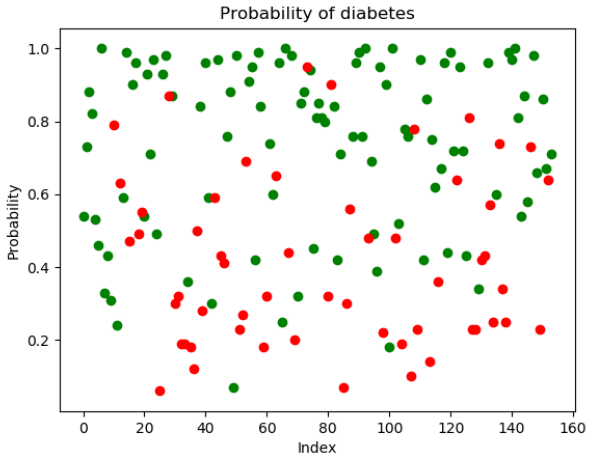

Fig. 10: Probability of diabetes.

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```
[ 6.        0.74371859  0.59016393  0.35353535  0.        0.50074516
  0.23441503 50.       ] DISEASE PREDICTION RESULT : POSITIVE

[ 1.        0.42713568  0.54098361  0.29292929  0.        0.39642325
  0.11656704 31.       ] DISEASE PREDICTION RESULT : NEGATIVE

[ 8.        0.91959799  0.52459016  0.          0.        0.34724292
  0.25362938 32.       ] DISEASE PREDICTION RESULT : POSITIVE

[ 1.        0.44723618  0.54098361  0.23232323  0.11111111  0.41877794
  0.03800171 21.       ] DISEASE PREDICTION RESULT : NEGATIVE

[ 0.        0.68844221  0.32786885  0.35353535  0.19858156  0.64232489
  0.94363792 33.       ] DISEASE PREDICTION RESULT : POSITIVE

[ 5.        0.58291457  0.60655738  0.          0.        0.38152012
  0.05251921 30.       ] DISEASE PREDICTION RESULT : NEGATIVE
```

Fig. 11: Prediction from test data.

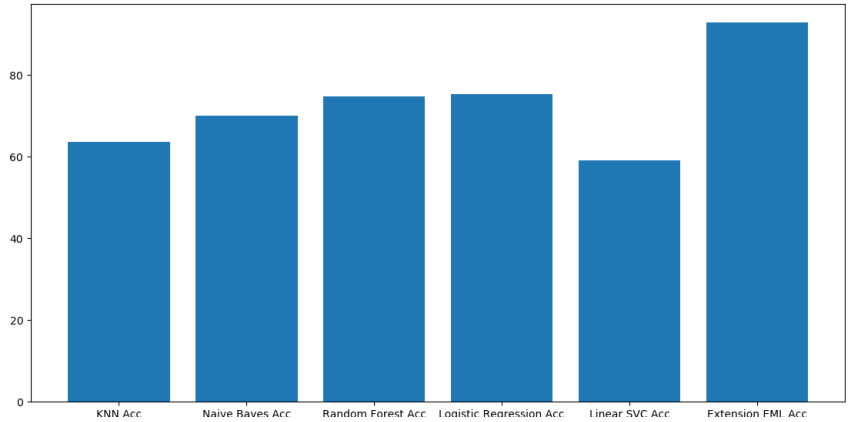

Fig. 12: Graphical Representation of comparation.

In Fig 11 for each test lab record ML predict whether disease is positive or negative. Fig 12 represents ML algorithm names and y-axis represents accuracy of all those algorithms and from above graph we can conclude that proposed EML is giving better accuracy.

5.Conclusion

This research introduced a new methodology, that can develop health informatics application using machine learning. Our methodology used the grounded theory methodology to develop SEMLHI framework. Developers use SEMLHI methodology to analyse and developing software for the HI model and create a space in which SE and ML experts could work on the ML model lifecycle. Proposed framework includes a theoretical framework to support research and design activities that incorporates existing knowledge. Our work introduces a new approach form clustering and classification for ML in HI. SEMLHI methodology includes seven-phase, designing (encode data and Define outlier and cleaning up the data), implementing (Verification & Validation), maintaining and defined Workflows, structured Information, security and privacy, testing and performance, and reusing software applications. SEMLHI framework includes four modules that organize the tasks for each module and introduce a SEMLHI Methodological that enable researchers and developer to analyze health informatics software from an engineering perspective. The ultimate goal from a SEMLHI Methodological is to define a standardized methodology for software development in the Health area and include all stages from defining the problem until developing the application and get the result with the test stage.

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