

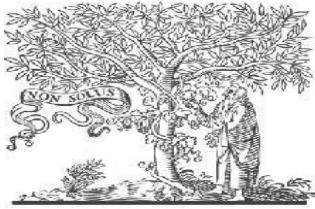


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## An automatic RBF ANN and PSO algorithm-based diabetes detection application

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### Abstract

Patients with diabetes mellitus have blood sugar levels that are consistently excessively high. This illness, which affects a broad variety of organs in the human body, targets blood vessels and nerves in particular. Many lives may be saved by early detection and treatment of diseases like these. In order to reach this aim, this study makes use of machine learning methodologies to analyze multiple risk indicators associated with this condition. 'Diabetes patients' diagnostic medical data sets may be utilized to develop prediction models for future outcomes, using machine learning techniques. Such data might be used to predict diabetes cases. Predicting diabetes using four well-known machine learning techniques based on adult population data: Support Vector Machine (SVM), Naive Bayes classifier (NBC), K-Nearest Neighbor classifier (KNN), decision tree (C4.5), neural network with cluster validity index (CVI), and genetic algorithm (GA)..

**Keywords:** Diabetes Mellitus, RBF Neural Network, Genetic Algorithm, Machine Learning

### 1. INTRODUCTION

The lack of insulin hormone in the human body is the root cause of diabetes, a metabolic and genetic illness. The hormone insulin is crucial in the process of converting food into usable energy. Excess sugar levels in the blood are caused by a deficiency of insulin. As a result, blood glucose levels in diabetics tend to be higher than normal. Diabetes Mellitus is the medical term for diabetes (DM). High blood sugar levels, frequent urination, and an increase in appetite and thirst are all signs that you may be suffering from this condition. Many

individuals throughout the world are being affected by diabetes, which is on the rise at an alarming rate. When blood sugar levels are too high, damage to blood vessels may occur and lead to a variety of health issues, including heart disease and stroke. Diabetes is a leading cause of Non-Communal Disease (NCD) fatalities in the global population, according to World Health Organization (WHO) data. More often known as "diabetes," which is a long-term condition in which blood sugar levels are unusually high. Diabetic symptoms may be caused by either a lack of insulin synthesis

(the hormone produced by the pancreas) or a lack of cell sensitivity to insulin.

Two of the most common types of diabetes that result in these two processes are insulin-dependent (type1) and non-insulin-dependent (type2).

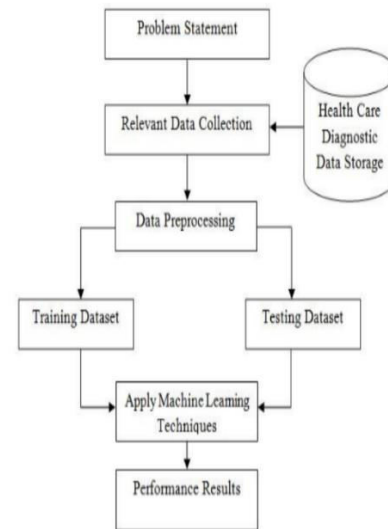
In type 1 diabetes, insulin levels are low or non-existent. Type 2 diabetics often have adequate insulin, but the cells on which it is supposed to work aren't always sensitive to it. Both types of diabetes have the same symptoms: increased urine output, a decreased appetite, and weariness. Glycosylated hemoglobin levels, blood glucose levels, and the glucose tolerance test are all used to diagnose diabetes (hemoglobin A1C). Depending on the type of diabetes, there are many treatment options. Diabetic consequences include dangerously high or abnormally low blood sugar, as well as blood vessel disease, which may cause damage to the heart, eyes, kidneys, nerves, and other parts of the body. In this work, multiple machine learning approaches are used in conjunction with numerous risk variables related with diabetes to predict the condition.

### Details of the software:

1. Python3 programming language
2. SQL, NLP and python libraries are used in this project (like Scipy, Sklearn)

### Specs about the hardware

1. To begin with, choose a device.
2. Keep an eye on the results.
3. In addition, a web browser is required.



**Fig.1: Block diagram for Predicting Diabetes Mellitus**

Many researchers have used machine learning approaches to extract information from accessible medical data in the study of diabetes. It was shown that the J48 machine learning algorithm gives superior performance and accuracy than other algorithms before preprocessing, according to a recent research. Because of cross-validation, classification methods were not more efficient. Data mining methods such as IB1, Naive Bayes, and C4.5 on an Ulster Community and Hospitals Trust dataset were used to predict and manage diabetes (UCHT). The performance of IB1 and Naive Bayes was improved by using the feature selection approach. It has been used to predict diabetes illnesses using real-world data sets collected by the distributed questioner (ANN, Logistic regression, and J48). Finally, J48 machine learning approaches were shown to be more effective and accurate than the competition.

## 2. RELATED WORK

Classifier Models for Predicting Diabetes Mellitus in 2015: A Performance Analysis:

Four prediction models for diabetes mellitus based on eight significant features are compared to each other in two separate scenarios. There are two stages in the data preparation process. According to the research, the decision tree J48 classifier is more accurate than the other three classifiers, with a precision rate of 73.82%. We get more accurate findings in subsequent studies that have been pre-processed, compared to the initial one. Compared to the other three classifiers, KNN (k=1) and Random Forest are the most accurate, with a classification accuracy of 100 percent. Models did not perform well with noisy data in this technique.

Classification Algorithms on the Diabetes Dataset-2016:

It is the kind of data we utilize as input that has the most impact on algorithm output and model creation time, but the data mining techniques we use are also impacted by the dataset's architecture.

Predicting outcomes is best done using classification approaches, according to a review of several methods. False alarms and poor detection rates plague the diagnosis of illness, despite the use of a variety of approaches.

Type-2 Diabetes Detection via Electronic Health Records in 2017: A Machine Learning-Based Framework A pilot research was conducted to identify patients with and

without type 2 diabetes (T2DM) based on EHR data, and this work suggested an accurate and efficient approach. T2DM patterns may be extracted using machine learning, which can then be boosted by overcoming the vast variety of examples and controls in expert methods, thereby enhancing the framework's prediction potential. It was shown that this system can identify people with and without T2DM with an average AUC of roughly 0.98, greatly surpassing the state-of-the art at an AUC of 0.71.

## 3. PROCEDURE AND METHODOLOGY

### Data Acquisition

The Pima Indians diabetes database has been used to predict diabetes. The data comprises 768 rows and 9 columns of characteristics such as glucose, BMI, age, pregnancies, insulin, skin thickness, and diabetes pedigree function, blood pressure.

### Data preprocessing

We use the term "preprocessing" to describe the process of turning raw data into something our system can comprehend and handle more quickly. It is common for real-world data to be inconclusive, inaccurate, and lacking in precise habits or trends. A proven solution to this problem is data preparation. It's common for preprocessing to include things like eliminating or replacing null values, encoding values, and deleting characteristics that are strongly linked or redundant. Before training the model, the work of standardization is accomplished by using the standard scalar as



Standard Scalar. The magnitude of variables in a dataset might vary widely. The AGE column in the Employee dataset, for example, will have values ranging from 20 to 70, whereas the SALARY column would have numbers ranging from 10,000 to 80,000. In order to develop a machine learning model with a consistent scale, the scales of these two columns are standardized. We use the term "preprocessing" to describe the process of turning raw data into something our system can comprehend and handle more quickly. It is common for real-world data to be inconclusive, inaccurate, and lacking in precise habits or trends. A proven solution to this problem is data preparation. It's common for preprocessing to include things like eliminating or replacing null values, encoding values, and deleting characteristics that are strongly linked or redundant. Before training the model, the work of standardization is accomplished by using the standard scalar as Standard Scalar. The magnitude of variables in a dataset might vary widely. The AGE column in the Employee dataset, for example, will have values ranging from 20 to 70, whereas the SALARY column would have numbers ranging from 10,000 to 80,000. In order to develop a machine learning model with a consistent scale, the scales of these two columns are standardized.

## Training the Data

Algorithms are trained using training data. Both the training and testing sets typically make up a specific proportion of the total dataset. Training and testing data sets are

separated. In order to make sure the algorithm used to train the machine is more precise and effective, training data is used. The algorithm or classifier often performs better when the training data is better. The activation function of the neuron processes the incoming signal to create an output. When a hidden neuron is activated by an input vector, its activation function is defined as  $(X)$ , which means that given an input vector  $X$ , its output will be  $(X)$ . 1-D input  $x$  generates a Gaussian neural activation function with centre (mean). Gaussian neural nodes divide the feature vector space into regions, each of which generates a signal corresponding to an input vector and whose strength is determined by the distance between its centre and the input vector. For inputs that are near in Euclidian vector space, the output signals must likewise be comparable. A neuron's reaction to  $X$  Gaussian neural nodes is referred to as a neuron's receptive field, and a neuron's receptive field is represented by the border of circles. There are 12 Gaussian nodes dividing up this 2-dimensional vector space. RBF may select how to react based on the combination of the activations of the collective system of neurons from each input vector. A and B will produce identical output signals from the neurons in the aforementioned setup, however C will provide very distinct output signals.

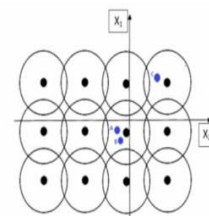


Fig 2.1(a): Gaussian Nodes

The center of each hidden neuron is represented by the weights linking the input vector to that neurons' hidden counterparts in RBF architecture. In order to train the network, weights linking hidden neurons to output neurons are set in advance such that the whole space is covered by their receptive field.

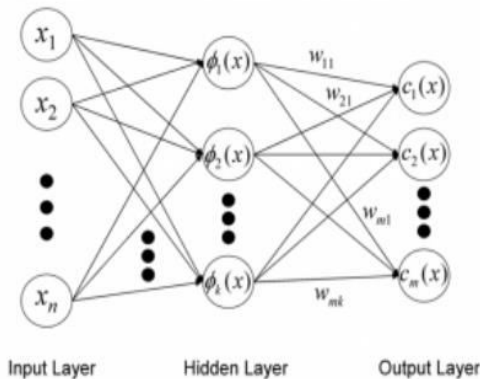


Fig 2.2(b): Radial Basis Neural Network Layers

- K Is for Select the number of cluster centers "K" in the clustering process.
- Randomly choose K locations from the dataset and designate them as the K centroids of the data.
- Find the centroid that is closest to each point in the dataset.
- For each centroid, compute the average of the points closest to the centroid.
- The associated centroids to their corresponding mean values, as seen in (4).
- Once you've made it to (3), keep going until you see a confluence.

In order to encompass the whole input vector, neurons have a receptive field that covers the complete range of their receptive fields. In other words, the greatest "d" distance between two hidden neurons is used to determine the value of sigma. Where M is the total number of hidden neurons, and d is their greatest distance from one others.

$$\sigma = \frac{d}{\sqrt{2M}}$$

### Analyzing Data from Various Machine Learning Classifiers Using Trained Data

Diabetes may be predicted using a variety of machine learning approaches. However, choosing the optimal method to forecast based on these characteristics is quite challenging. So we are using trained data on SVM, Naive Bayes, decision tree, and k-means and is made accessible for testing. However, we are also using an optimized radial basis neural function as it is not relevant to the model we are implementing the entire logic, preprocessed data is followed by making clusters of data using k-means clustering logic, then applying Gaussian function as kernel function to optimize the clusters formed, and to name clusters class by class we are using Dunn, Davies Bouldin, silhouette validity indexes and computing inverse-weight matrix to train the model. We are employing a genetic algorithm to know the correctness of the model when just the best features picked from the input are delivered to the output.

### Algorithm

- Use "K" to indicate the number of neurons that are concealed.

- K-means clustering was used to determine the locations of RBF centers.
- Use the equation to determine (2)
- Use the equation to determine the RBF node's actions (1)
- Equations may be used to train the output (3)
- Training the Data

The model's performance may be assessed using a set of performance measures, which are recorded in the test set. In this instance, we're focusing on precision.

## 4. IMPLEMENTATION AND RESULTS

### Dataset Pre – processing and Training the Data

In order to apply a model, you must first load the necessary libraries, import the dataset, deal with missing data, handle categorical data, divide the dataset into training and testing subsets, and then apply feature scaling to the dataset. The dataset for diabetes prediction has been processed and trained, as can be seen in the accompanying image.

```
suneera@suneera:~/Desktop/Inp15 python3 ga.py
Using TensorFlow backend.
2020-04-27 13:57:01.330551: W tensorflow/stream_executor/platform/default/dso_loader.cc:55] Could not load dynamic library 'libnvinfer.so.6': cannot open shared object file: No such file or directory
dlerror: libnvinfer.so.6: cannot open shared object file: No such file or directory
2020-04-27 13:57:01.330866: W tensorflow/stream_executor/platform/default/dso_loader.cc:55] Could not load dynamic library 'libnvinfer_plugin.so.6': dlerror: libnvinfer_plugin.so.6: cannot open shared object file: No such file or directory
2020-04-27 13:57:01.330884: W tensorflow/compiler/tf2tensorrt/utils/py_utils.cc:38] Cannot dlopen some TensorRT libraries. If you would
o use Nvidia GPU with TensorRT, please make sure the missing libraries mentioned above are installed properly.
Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI  DiabetesPedigreeFunction  Age  Outcome
0      6    148      72      35      0    33.6      0.627    58      1
1      1      85      66      29      0    26.6      0.351    31      0
2      8    183      64      0      0    23.3      0.672    32      1
3      1      89      66      23      94    28.1      0.167    21      0
4      0    137      40      35    168    43.1      2.288    33      1
Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin  BMI  DiabetesPedigreeFunction  Age  Outcome
count  768.000000  768.000000  768.000000  768.000000  768.000000  768.000000  768.000000  768.000000  768.000000
mean   3.845832  120.894531  69.105469  28.536458  79.799479  31.992578  0.471876  33.240885  0.348958
std    3.369578  31.972618  19.355987  15.952218  115.244092  7.081160  0.331339  11.760232  0.476951
min    0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.078008  21.000000  0.000000
25%    1.000000  99.000000  62.000000  0.000000  8.000000  27.300000  0.243758  24.000000  0.000000
50%    3.000000  117.000000  72.000000  23.000000  38.500000  32.000000  0.372500  29.000000  0.000000
75%    6.000000  140.250000  88.000000  32.000000  127.250000  36.600000  0.626258  41.000000  1.000000
max    17.000000  199.000000  122.000000  99.000000  846.000000  67.100000  2.420000  81.000000  1.000000
Pregnancies  0
Glucose      0
BloodPressure 0
SkinThickness 0
Insulin      0
BMI          0
DiabetesPedigreeFunction 0
Age          0
Outcome     0
dtype: int64
cluster list [array([[ 1., 85., 66., ..., 31., 0., 0.],
 [ 1., 89., 66., ..., 21., 0., 0.],
 [ 5., 116., 74., ..., 30., 0., 0.],
 ...,
 [ 2., 122., 70., ..., 27., 0., 0.],
 [ 5., 121., 72., ..., 30., 0., 0.],
 [ 1., 93., 70., ..., 23., 0., 0.]], array([[ 6., 148., 72., ..., 58., 1., 0.],
 [ 8., 183., 64., ..., 32., 1., 0.],
 [ 0., 137., 40., ..., 33., 1., 1.],
 ...,
 [ 6., 190., 92., ..., 66., 1., 0.],
 [ 9., 178., 74., ..., 43., 1., 0.],
 [ 1., 126., 60., ..., 47., 1., 0.]])]
```

Fig.3: Description of The Diabetes Dataset

### Applying Clustering Techniques

```
cluster list [array([[ 1., 85., 66., ..., 31., 0., 0.],
 [ 1., 89., 66., ..., 21., 0., 0.],
 [ 5., 116., 74., ..., 30., 0., 0.],
 ...,
 [ 2., 122., 70., ..., 27., 0., 0.],
 [ 5., 121., 72., ..., 30., 0., 0.],
 [ 1., 93., 70., ..., 23., 0., 0.]], array([[ 6., 148., 72., ..., 58., 1., 0.],
 [ 8., 183., 64., ..., 32., 1., 0.],
 [ 0., 137., 40., ..., 33., 1., 1.],
 ...,
 [ 6., 190., 92., ..., 66., 1., 0.],
 [ 9., 178., 74., ..., 43., 1., 0.],
 [ 1., 126., 60., ..., 47., 1., 0.]])]
```

Fig 4: Indexing To Clusters

Here, clustering is utilized to name the clusters for use in RBFN, an unsupervised machine learning task. K-Means is shown here. In order to reduce the variation within a cluster, clustering is used to allocate instances to certain clusters. The Dunn Index (DI) is a statistic that is used in conjunction with K-Means to assess clustering algorithms. Using the Davies–Bouldin index, clustering techniques may be evaluated. Using the dataset's intrinsic quantities and properties, this internal evaluation method evaluates how successfully the clustering was done..



## Constructing the RBFN and Predicting Its Accuracy

```
DUNN 0.0050613027829347745
DBb 0.713398516192508
SS 0.5687788342658853
RBFN accuracy: 0.7204724409448819
```

**Fig 5: Accuracy of RBFNN Model**

In this section, we would be predicting the RBFN accuracy by applying the K-means clustering technique implemented above.

## Computing Various Machine Learning Techniques

```
DecisionTree accuracy: 0.7857142857142857
/usr/local/lib/python3.6/dist-packages/sklearn/
Specify a solver to silence this warning.
FutureWarning)
logistic regression accuracy 0.8051948051948052
/usr/local/lib/python3.6/dist-packages/sklearn/s
n version 0.22 to account better for unscaled fe
"avoid this warning.", FutureWarning)
support vector machine accuracy 0.69480519480519
KNN accuracy 0.7597402597402597
Naive Bayes accuracy 0.7922077922077922
Gradient boosting accuracy 0.7857142857142857
```

**Fig 6: Accuracies of Various Machine Learning Algorithms**

A variety of machine learning accuracy measures, such as gradient Boosting and Naive Bayes, SVM, Decision Tree, and Logistic Regression, are computed.

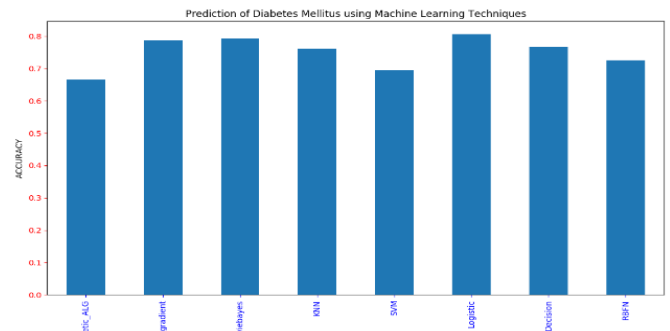
## Predicting Genetic Algorithm Accuracy Using SVM Classifier as RBF kernel Function

```
Genetic Algorithm accuracy:0.67
Available features:['Pregnancies', 'Glucose', 'BloodPressure', 'Insulin', 'DiabetesPedigreeFunction', 'Age', 'SkinThickness']
supported features:[False True False False False True True True]
```

**Fig 7: Accuracy of Genetic Algorithm Model**

The following output predicts the Genetic Algorithm's accuracy using SVM Classifier as RBF kernel Function with gamma and cost as hyper-parameters by selecting the key features trained in the dataset.

## Performance Analysis of Computed Models as a Bar Plot



**Fig 8: Bar Plot of Performance Analysis**

## Comparative Difference of All Computed Models

On the same dataset, different models were run, and each model produced different performance metrics. The accuracy achieved by the models is summarized in the table below.

**Table 9: Performance Analysis of Various Models on Dataset**



MODEL	ACCURACY
Radial Basis Neural Network Function	72%
Genetic Algorithm	67%
DUNN Index	5%
Davies Bouldin Index	71%
Silhouette Index	56.8%
Decision Tree	78.5%
Logistic Regression	80.5%
Support Vector Machine	69%
K-Nearest Neighbors	75.9%
Naive Bayes	79%
Gradient Boosting	78.5%

## 5. CONCLUSION AND FUTURE SCOPE

A novel categorization model for diabetic patients was suggested in this study, which took into consideration a variety of characteristics connected to the condition. Cluster validity index and k-means clustering technique are integrated into the proposed model in Radial Basis Neural Network. For the prediction of diabetes mellitus, we have also carried out our tests on adult population data using machine learning techniques, notably Support Vector Machine (SVM), Naive Bayes (NB), K-Nearest Neighbor (KNN), and decision tree (DT). Although Naive Bayes has the best accuracy (79.2%), it presupposes class conditional independence and hence loses accuracy. Using an SVM classifier as a kernel function and an RBFNN neural model, we achieved accuracies of 67% and 72%, respectively. Diabetes patients were categorized into one of two groups (positive or negative) using our approach. K-means algorithm incorporates a cluster validity index to ensure the best possible cluster placements. The categorization process was sped up by optimizing cluster centers, which reduced network complexity. As a result, the Genetic Algorithm model used in this study

is helpful in predicting diabetes with more accuracy and minimizing the likelihood of false alarms. A hybrid particle swarm optimization algorithm may be used to determine the weights of objects in the future. As a further option, we may use kernel functions like polyharmonicspline and inverse quadratic for classification.

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