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Integrating Genetic algorithm and Leverage the slap swarm algorithm to optimize the Multi-Objective Random Forest model to predict cerebrovascular disease

B.Venkatesh [1], Dr. N.Sandhya [2], Neelima Gogineni [3], K.Mouneswari [4], Susanna Sreshta Joshi [5], Dr S Rama Sree [6]

[1,2] Department of CSE-AIML&IoT, Vallurupalli Nageswara Rao Vignana Jyothi Institute of Engineering &Technology, Hyderabad, India. venkycaptain@gmail.com [1], sandhyanadela@gmail.com [2]

[3] Gokaraju Rangaraju Institute of Engineering and Technology, Bachupally Hyderabad,India. neelima1689@grietcollege.com

[4,5] Department of CSE, CMR Institute of Technology, Hyderabad, India. mouni13bmouneshwari@gmail.com [4], sreshtajoshi@gmail.com [5]

[6] Department of Computer Science and Engineering, Aditya University, Surampalem, India. ramasree_s@adityauniversity.in

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ABSTRACT

Heart disease is now a big health worry for many people because it is the top cause of death in the world. Finding heart problems such as heart diseases, valve problems, and so on is one of the most important jobs and regular medical study. Heart problems may save numerous lives if it is found early. A lot of progress has been made in using machine learning methods in the medical field. In the suggested work, a new SSO-MORF (Slap Swarm Optimised Multi-Objective Random Forest) method for predicting heart disease was shown. For this proposed study, data on heart disease from many Universities was mined using data mining techniques such as categorisation and individual customer recognition. For getting the data ready and pulling out features, min–max normalisation along with principal component analysis, or PCA, had been used. So, a pretty simple guided machine learning method could be used to very correctly identify heart problems, which would be very useful. The RF method was used in this study to make a classification that had 99.46% accuracy, 98.4% memory, 98.7% precision, along with a 98.8% f1 score. The system is better at predicting heart disease compared to other cutting-edge methods, as shown by this result.

INTRODUCTION

Cardiovascular illnesses include a range of problems affecting the heart. Global Medicine estimates that cardiac diseases result in 17.8 million fatalities each year, establishing them as the foremost cause of mortality worldwide [1]. Numerous factors, including plaque accumulation, diabetes, increased triglycerides, and hypertension, augment the risk of myocardial infarction and cerebrovascular accident. The International Heart Organisation lists many indicators, including sleeplessness, irregular heart rhythm, swollen arms, and obesity, which manifests as a weight gain of 1-2 kg each week [2-5]. The volume of information gathered is growing, providing physicians with a renewed opportunity to enhance patient diagnosis. To enhance decision-making support, practitioners have improved the utilisation of computer technology. Various health management diseases, genetic expression, and medical imaging are defined by a concise set of characteristics. Cardiac failure is a prevalent condition that may be lethal for adolescents and persists into later life stages. Cardiovascular disease is more common in men than in females. Approximately twenty-four percent of global fatalities are ascribed to heart failure. Cardiovascular disease will be the leading cause of mortality globally.

Some states and developed nations. In many states and wealthy countries, heart disease is a leading killer [6-7]. Cardiovascular disease is a leading cause of death worldwide. Age, body type, gender as well, cholesterol, rhythm of the heart, gastro-oesophageal reflux, overweight or obese status, & food all contribute to heart attacks. Traditional cardiovascular disease risk assessments include a doctor reviewing a patient's medical history. Early detection may reduce heart disease quickly [8-10]. Thus, early cardiovascular disease detection reduces mortality and improves survival. Heart disease is linked to life satisfaction and vitality, two key psychological well-being factors. Life satisfaction may lower mortality from all causes in healthy people, protecting against sickness. Patients' well-being and happiness suffer. Additionally, alcohol usage and a family history of cardiac attacks were linked to a worse standard of life. Medical groups worldwide are collecting cardiovascular disease data [11-13]. Despite their complexity and distribution, hospitals rely on various technology. Since providers use different standards for comparable or identical networks, medical information and execution inefficiencies, inaccuracies, and mistakes occur more often. In several states, 14% of deaths are caused by coronary heart disease (CHD), which which is the most common type of heart failure. Early detection of cardiovascular disease reduces health risks and prevents heart failure. Cardiac disease includes cardiovascular problems. A common cardiovascular disease, heart disease reduces heart circulation. Circulation decreases may cause cardiac events. Smoking, vascular problems, and high lipids also cause heart disease [14-16]. Nearly half of some state people had warning signs. Resistance to insulin, obesity, poor nutrition, inactivity, and alcohol abuse increase risks. The most prevalent congenital defect is CHD, impacting 7 per one thousand live births. It accounts for most congenital defects that need heart surgery or catheterisation. Medical advances have greatly reduced mortality.

In addition to improving weak classification techniques, researchers utilised a health care dataset to demonstrate that the system might identify illnesses early. Labelling and growth may stabilise small groups and forecast stroke and heart attack risk, according to the research. Researchers investigated smart healthcare systems that may integrate elements and recommended ensemble deep learning for heart attack prediction. At initially, the attribute synthetic technique merges device features with digital health information to create relevant health data [17-18]. By replacing extraneous features with the most critical ones, a learning technique reduces computer stress and improves reliability. An SVM-based performance improvement method was proposed. This strategy is used by genomic algorithms and generalisations to identify heart disease-prone characteristics. specifics and a comfort-selected sample compare genuine (GA-SVM) outcomes for income, integrity, beta quadratic, just the one profiles produced, filtered behaviour, benefit %, and other chosen features techniques to their tests. Important features and information mining technologies that might improve bypass graft projections are of considerable interest to researchers. Classification techniques included SVM, decision trees, stupid beads, logistical regression, and logistic regression. People utilise Neural Networks & Integrate to forecast. The research found that the structure used to forecast coronary artery diseases, which was first constructed utilising the best attributes found, such as a superior data processing approach, had an 87% success rate. The major purpose is to raise awareness of heart disease by using multiple models to anticipate and improve outcomes [19]. Comparing those forecasting approaches based on their effectiveness lays the groundwork for additional research, improved findings, and a diabetes diagnosis. More input-based systems were tested for heart disease prediction. Health variables include blood pressure, cholesterol, & sex. Some researchers investigated if modelling temporal links between incidents in medical records, or EHRs may improve the structure for predicting the initial diagnosis of HF (heart failure) compared to other techniques. Due to these electronic health data, researchers were capable of to link test findings and determine illness diagnosis. The medical records are challenging to recover since most of the information was missing or incorrect. It thoroughly examines all relevant machine learning (ML) is computer-assisted design detection (also called CAD research papers from 1993 to 2020. Multivariable impacts are properly assessed. Collection factors (location, sample selections, and number of stenos in each coronary artery) and machine learning techniques (feature recruitment, assessment measures, and processing) are important. Finally, the public understands about ML computer-aided design diagnostics' major shortcomings. Different artificial intelligence approaches were used to forecast. Omi, ANN, and KNN test forecast system accuracy. We found that a learning algorithm-made sign can predict a child's weight after the first birthday. Instead, then merely considering sugar, weight (BMI), and other hormones, a diabetes prediction algorithm ought to consider many key parameters. The latest dataset improves analysis [20]. Diabetic projections were changed to be process-based to improve classification. ECGs include various properties; hence this research proposed an ML approach for categorisation. A cardiac ECG measures coronary artery electrical activity. The recommended solution was implemented in Apache Spark using a large log code editor and ML-limbs, a versatile neural network tool. The most crucial part of grouping ECG data is discovering anomalies, which helps diagnose a person.

2. Methods and Material:

Random forest is an effective way to learn as a group that can be used to solve problems like regression, categorisation, and more. It might help reach more than one goal at the same time when used with optimisation with multiple objectives. For example, it might help improve accuracy while lowering the number of false positives along with false negatives in predicting cardiovascular disease. The suggested way is shown in Figure 1.

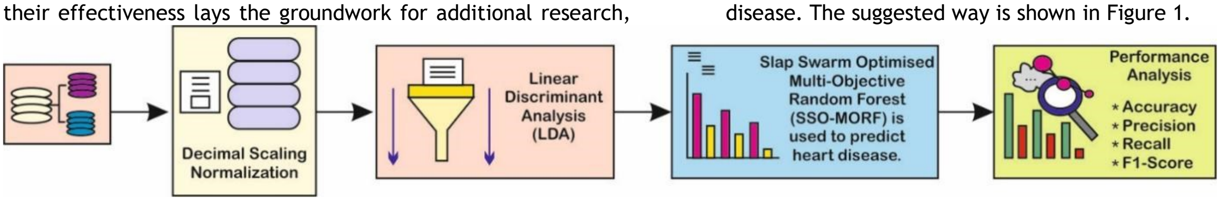

Figure 1. Flowchart Illustrating the Suggested Methodology

2.1. Dataset:

Heart disease progression data is available from several sources. At least 305 medical records in the database of records were incomplete. These six were removed from the database, leaving 297 medical files for processing. Multiple-class variables having binary categorisation were introduced based on the database properties. This multiclass factor detects cardiac failure. Heart attack victims choose this number. The score is 1 if there are no cardiac issues and 0 otherwise. Diagnostic numbers of health data are transformed to prepare information. An initial analysis of 297 private data reveals 139 items with several criteria confirming a diagnosis of CVD. Meanwhile, 165 showed no cardiac failure.

2.2. Data preparation with min-max normalisation:

This strategy minimises the variance between the maximum and minimum values by aggregating the information from the lowest value. The formula for Y is Y $[Ymin(Y)]/range(Y)$ $[Ymin(Y)]/[max(Y)\ min(Y)]$, where $min(Y)$ specifies the least value, $max(Y)$ indicates the maximum value, and the range (Y) represents the span across the power source. The extent of the horizontal area among [0, 1] as well as a region j.

$$Y^* = [Y - \min(Y)] \,/\, range\ (Y) = [Y - \min(Y)] \,/\, [\max(Y) - \min(Y)] \quad (1)$$

2.3. Utilising Linear Discriminate Analysis (LDA), which for Feature Extraction:

Classification, dimensionality reduction, & feature extraction are all areas where linear discriminate analysis (LDA), a machine learning method, finds use in pattern classification issues. The first linear discriminator was created by the researcher as a two-class method. Using Byes' rule equation and conditional class densities fitted to the data, LDA, a supervised classification approach, provides a class prediction using a linear decision surface (1). In a scenario with two classes, i and b, the presumed probabilities, $li(y)$, are given by bb in Equation (2). These predicted probabilities are based on the beginning probabilities (prior probabilities) of all classes in the original dataset of a machine learning technique known as classified works, which involves extracting characteristics, reducing dimensions, and making categories in pattern classification problems. The expected probability of y for class i is denoted by $li\ (y)$. If there are two groups, i and a, bb, the basic frequency (prior frequency) of each group is shown from its original input.

$$B(x = j \mid y) = \frac{B(y \mid x = j)b(x = j)}{\sum i \sum b_{ij*} l_j(y)} \quad (2)$$

The differentiate rule looks at the odds of each class along with the odds that the data in each class belongs to that class. While the Gaussian distribution functional is used on the data, its mean (μ) and covariance (o) show how the ₑ is distributed, and the equation's classification method is found.

$$T_j(y) = log l_j(y) + log B_{ij} \quad (3)$$

The distinguish function figures out how likely it is that data y belongs to each class. The choice surface between types i and i is made up of sets y. The two functions that separate the two groups had the same value, along with any data that falls on the choice surface is equally likely to belong to both groups (unknown). LDA happens when we think that classes i along with j have the same correlation matrix, which means that they are equally likely to be related to each other. Eq. (3) shows the equal correlation distinguish function of LDA. The training data are used to predict the mean, correlation, as well as previous probability given in Equations (3). The result estimate is based on the likelihood of the class via the highest value.

$$T_j(y) = y^D \mu_j \Sigma^{-1} - \frac{1}{2}\mu_j^D \mu_j \Sigma^{-1} + logB_{ij} \quad (4)$$

Shrinkage is a punishment term, like using $L1$ or $L2$ regularisation on the optimiser to stop the LDA method from overfitting. It is possible to get a better estimate of the range when shrinking is used instead of the original raw estimate. To get the shrinking, the gamma function has been added to the estimate. Any function that makes something smaller is called a gamma function.

2.4. A Multi-Objective Random Forest Slap Swarm Optimisation (SSO-MORF):

2.4.1. Random forest with many objectives:

Using the equation $b(n,\ m)$, a produced forest classifies a collection of dispersed random carriers (n). Each branch chooses a category to emphasise at intake m together. Generate Odata for the intake trial, whose O is similar to the original specimens. Calculate f characteristics using l attributes using columnar testing. Several practice packages (numbered $g1$, $g2$,..., gr) were in use. The matched lesson sets may form a decision tree ($d1$, $d2$,..., dr). Jungle foliage is full and lush save for pruning. In classification, several chosen trees form a random forest. The number of selected forests or canopy nodes and plant length (T) are key factors for categorisation. This work used a thorough search approach to identify optimal A and T for improved random forest model accuracy. We build a random forest architecture and add a new dataset. If the new example's samples are selected by a choice forest, overall identification may be possible. Voting is the forest's last option. Bootstrapping generates a random forest of building stems via replication, returning the beginning input. Bootstrapping makes replacement-based modelling and interaction easy. Randomised cascades choose a certain number of instances from the initial batch. After sampling, some of the measured amount is added to the database. Researcher produce bootstrap samples from the collected numbers. Samples from the classroom group may be analysed after receipt. Reviewing early data without retaining them may be beneficial, similar to choosing from a separate population. Consider randomly selecting k samples from a case study. We can calculate the chances of samples whether they are collected on every occasion using 1 and (1 1). If random selection is repeated K times, the probability of the sample being picked is (1 1k) K, wherein K convergence occurs to fa = 0.369. Additionally, an optical specimens will be offered. The case will also vanish in fresh specimens. Out-of-bag items are forgotten after recovery. Open-ended bag issues exist. It may be analysed as mean.

$$OE = \frac{W}{MA} \quad (5)$$

If you check a certain amount of material, this first equation shows that V is the degree of error, and MA is the percentage of files that are recognised within a set with any data. Utilising the CART method and the Gini coefficient, a list of options is made that talks about the amount of pollution in the framework. Unclean substances are present when the Gini ratio is high. There are fewer pollutants when the Euler grade is lower. When there is a problem with categorising things, the Gini score equation says that the chance of the I^J group is om for the $theM$ group.

$$Gini(C) = \sum_{m=1}^{m} om(1 - om) = 1 - \sum_{m=1}^{m} Om^2 \quad (6)$$

People use the Gina index to choose which traits to use in decision chains. The equation is used in the math.

$$\Delta Gini(B) = Gini(C) - Gini_B(C') \quad (7)$$

If the Gini score is at its highest level, this can be picked for divide quality via divide circumstances. Most of the time, choice trees are too good. Techniques used before or after surgery can lower the rates of response. This might cause decision trees to get too big, but it might lead to better results in the end. Also, unlike cutting, picking grows all the way through. They put some of the features into the RF process along with classification to pick out a single set of data and the best choice of all the $N - 1$ attribute units (or groups) that were made by Ke. RF categorisation was used to choose the best set of data among the N −1 attribute vector (or subgroup) produced by Ke. This combination of qualities is employed using a grid-search methodology to find the ideal RF hyperparameters. Additional attributes are subsequently added to the RF method, as well as the grid's search engine searches again for the optimal hyperparameters. An analogous approach is conducted for the created section of attributes. Finally, the most reliable heart failure risk predictors were presented.

2.5. Slap Swarm Improvement:

The size Swarming algorithms are very important. This method is based on the hitting family for underwater critters that are small, clear, and barrel-shaped. To figure out the safest way to find food sources and ascertain what parts of this sample work together. Putting two of these strange bugs on top of each other makes a line. It's the main link in the road that looks into how to use the algorithm to make the search method work better for modelling what it does. The leader of the team decides where to go and where to eat on new roads within the area. His position moves to take care of the food source and is the best choice for it. The first letter L stands for the food supply, which is currently the best answer. Each part in a T-dimensional search area is symbolised by a vector with 3 dimensions named X. The position of this dimension's boss is changed by a later code.

$$y_i^1 = \begin{cases} L_i + v_1((up_i - fp_i)v_2 + fp_i), v_3 \geq 0.5 \\ L_i - v_1((up_i - fp_i)v_2 + fp_i), v_3 \geq 0.5 \end{cases} \quad (8)$$

The president is denoted by $y1$, and the top along with bottom searching limits with a $j - th$ dimensions are given the names wpia and FBI. The numbers v1, v2, and v3 are chosen at random from the range [0, 1]. The symbol Fj shows where the best answer is located (food supply). The choices v2 and v3 control the number of stages along with the point where a new answer can be made that is close to zero or infinity. However, v1 is thought to be the the most important variable because it affects how well hunting and mining work together and is one of the most important factors that affects how well the finding method works. The module v1 is set by.

$$v_1 = 2a^{-(\frac{4f}{F})^2} \quad 2 \quad (9)$$

The formula that shows Newton's concept of progress changes the order of viewers. The number of repetitions via the cycle that is shown as f is the most, and the number of repetitions that are shown as f is the last.

$$y_i^j = \frac{1}{2}ed^2 + C_0 d \quad (10)$$

Where y_i^j stands for the j^{th} follower in the ij^{th}dimension and j is greater than or equal to 2. Time is represented by the annotation d, which is equal to $\frac{C_{final}}{C_0}$, where $C = \frac{y - y_0}{d}$, and C_0 is the beginning speed. The third issue may be phrased as follows: with each optimisation technique being represented as a single attempt, the difference among repeats is the one for $c0$ = 0 at the start.

$$y_i^j = \frac{1}{2}(y_i^j + y_i^{j-1}) \quad (11)$$

3. Results:

3.1. Accuracy:

The correctness of the estimates is measured by a scientific indicator. The percentage of accurate predictions compared to other projects is used to measure accuracy. This is done by comparing guesses made by a program to real numbers. Figure 2 along with Figure 3 show how the results of this method are similar and different. While the suggested method is 0.96% accurate, modern methods like the LR, RF, GBM, and SVM methods get 0.86%, 0.89%, 0.85%, as well as 0.87%, respectively. These show the general benefit of the way we suggest you do things now. The plan can help you guess how heart disease will turn out.

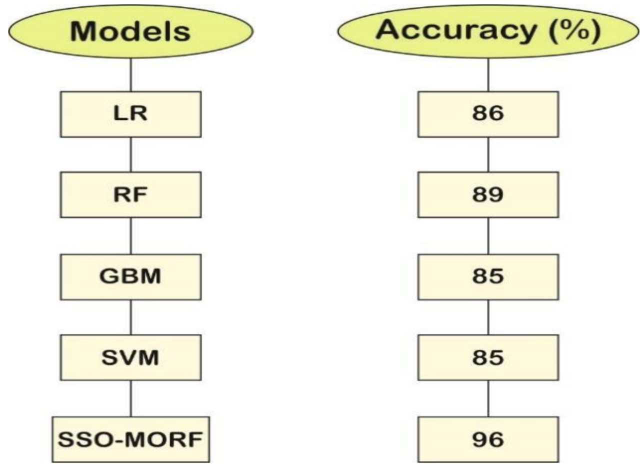

Figure 2. Accuracy Numerical Outcome

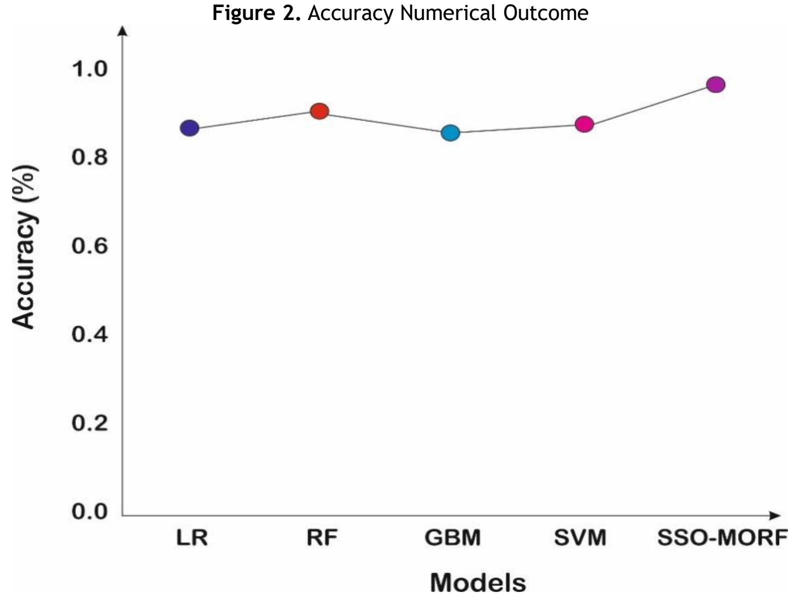

Figure 3. Outcome of Accuracy

3.2. Precision:

How exactly accuracy is stated is based on the number of times that positive information is compared to all negative information.

$$precision = \frac{TP}{TP + FP} \qquad (13)$$

Figure 4 and Figure 5 show how the suggested methods are similar and different from the current ones. A separate test of these two methods showed that the suggested method is accurate 0.94% of the time, just like other methods like the LR (0.86%), Radio Frequency (0.88%), GBM (0.85%), along with SVM (0.88%). This shows how the strategy we offer is different from the present method. So, our system has been able to correctly identify heart problems.

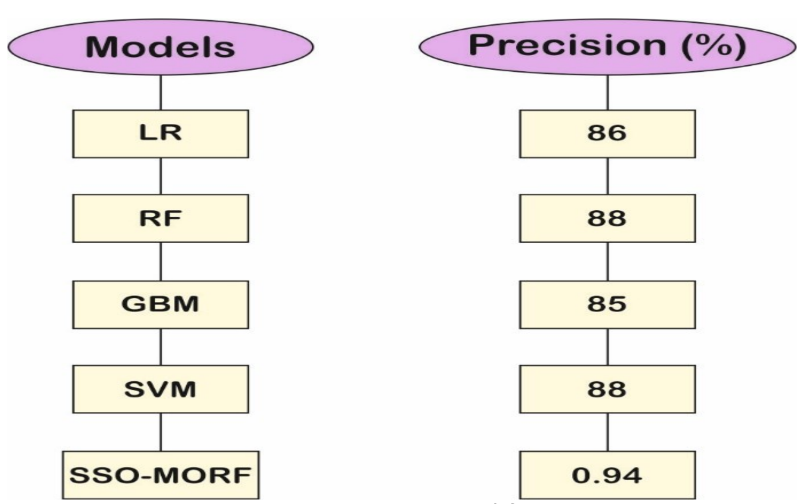

Figure 4. Precision Numerical Outcome

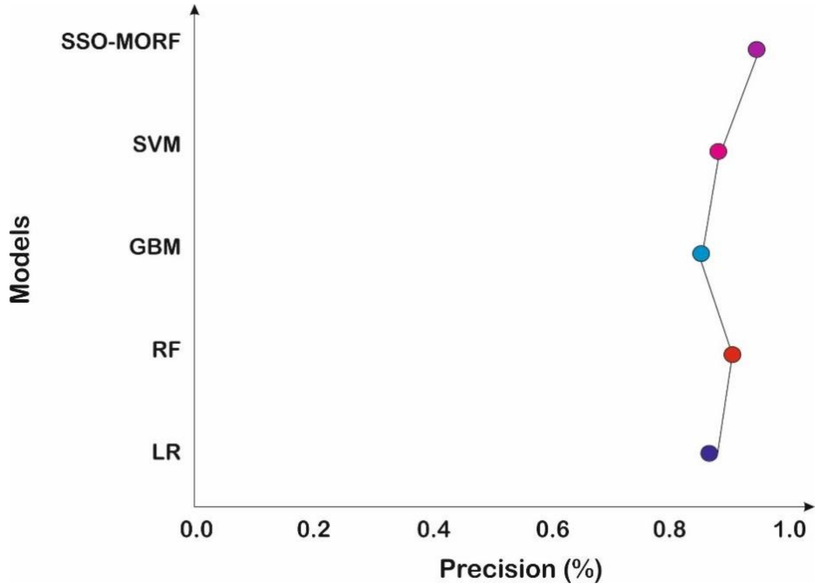

Figure 5. Outcome of Precision

3.3. Recall:

Relevance meant being able to find or guess every important case in the information gathered. A categorisation strategy's ability to tell the difference between real negatives and negatives when there are three cases of positives is measured by memory. The memory is also known as the vulnerability or the real positive rate.

$$recall = \frac{FN}{FN + TP} \qquad (13)$$

Figure 6 along with Figure 7 show how the current methods are similar and different. We suggested a method that worked 0.95% of the time, while existing methods like LR, RF, GBM, and SVM only worked 0.87%, 0.88%, 0.85%, as well as 0.88% of the time, showing the difference. The current method will be compared to the plan we offer. This meant that our technology was able to correctly identify heart problems.

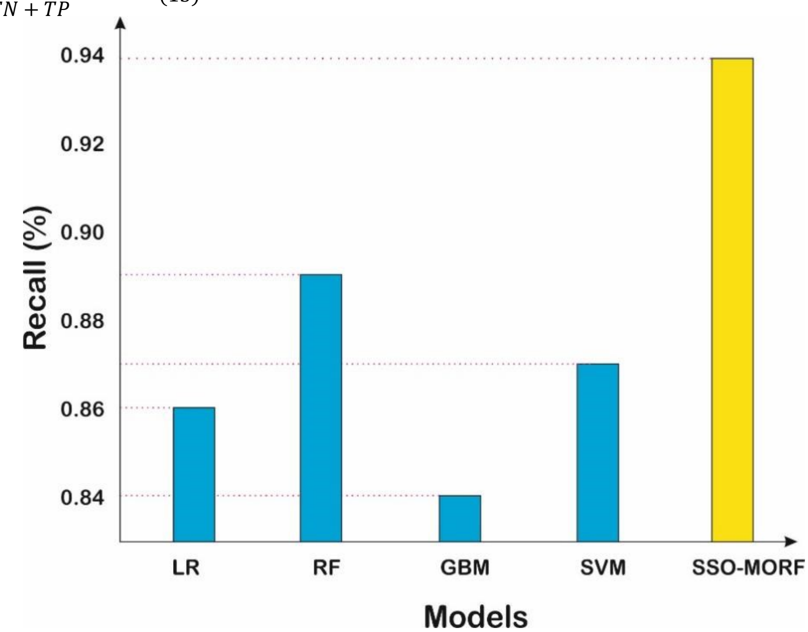

Figure 6. Outcome of Recall Test

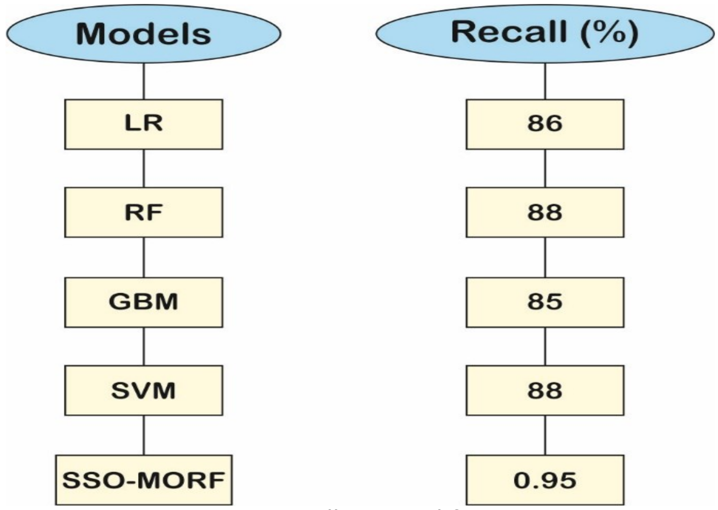

Figure 7. Recall Numerical Outcome

3.4. F1 score:

The memory and accuracy parts of an example's F1 score are used to judge how well it does on tasks that need binary classification. These factors are added together to get a single number that gives a fair picture of how well the plan works. This method figures out the harmonic ratio by blending "recall along with precise" into a single number, which is called the f1-score.

$$F1 - Score = \frac{(precision) \times (recall) \times 2}{precision + recall} \quad (14)$$

Figure 8 and Figure 9 show how the suggested methods are similar and different from the current ones. If we compared our suggested method to old ones like LR, RF, GBM, along with SVM, which only got to 86%, 88%, 85%, and 87%, respectively, it got to 0.96%. This shows that the difference between our plan and the present way of doing things is about the same. As an example, our system has been able to accurately identify heart problems.

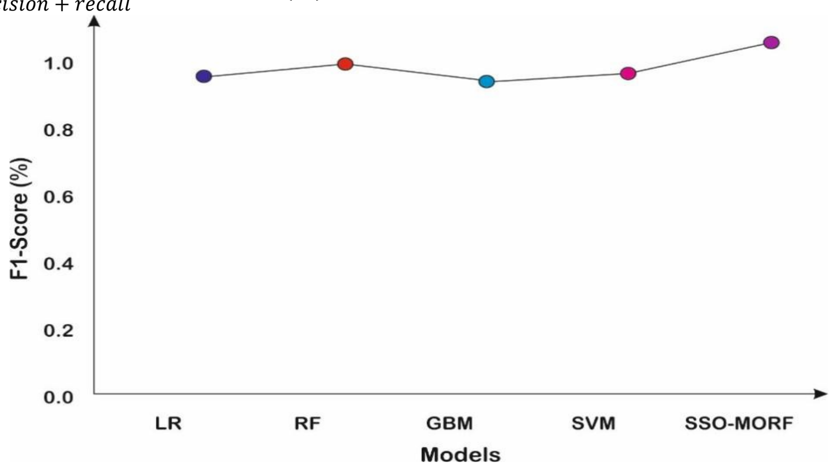

Figure 8. F1-Scores

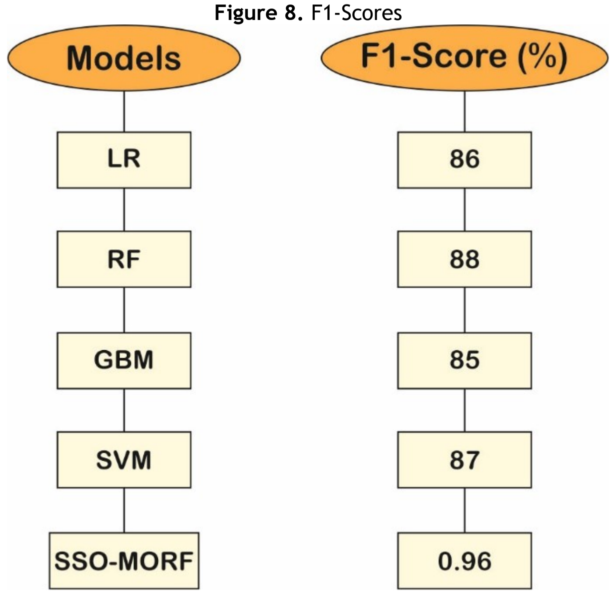

Figure 9. F1-Score Numerical Outcome

DISCUSSION

LR doesn't take into account any odd connections between these two types of factors that might appear in real life. When it comes to complex relationships, these models are better at handling them. RF needs a lot of store space because a lot of them change during training, especially when huge databases and complicated topologies are used. Random forests are called "black box" algorithms because they can make accurate predictions. People find it hard to understand the GBM system, even when they are trying to figure out what factors affect the outlook of heart disease. In healthcare situations, doctors need to be willing to look at data to figure out what's going on and make smart decisions. People think of SVM as a "black box," which makes it hard to understand the results, especially when it's used for making medical decisions. Trying to figure out the factors that affect the chance of getting heart disease may be hard. Based on this result, the "SSO MORF" may not be connected to any well-known training technique or method used to predict heart disease.

CONCLUSION

Finding ways to deal with new medical data about heart function will help make sure people live longer and find problems with heart disease more quickly. A new way of thinking about heart disease was created by using machine learning methods to look at the original data and come up with new ideas. It is hard and very important in medical care to be able to predict heart problems. Death rates will go down, though, if the disease is found early and measures are taken as soon as possible. It would be best to keep doing this study and turn the results into real information instead of just ideas on computer models. Several types of ML strategy blends could be used in this kind of study to improve results. In the same way, new component decisions have been made to find important traits that make heart disease forecast more accurate. Several types of machine learning techniques could be used in this study to make prediction methods better. To get a better sense of important traits and make heart attack estimates more accurate, new ways of picking features could be created. Because of this, they made the SSO MORF to identify heart disease. This method got good scores for F1-score (0.96%), accuracy (0.96%), precision (0.94%), and memory (0.95%). This is the best way to learn about the scope, features, and possible uses for "SSO-MORF" in predicting heart diseases: read up on current research papers, magazines, or reliable sources in the heart along with machine learning fields.

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