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Efficient classification of kidney disease detection using Heterogeneous Modified Artificial Neural Network and Fruit Fly Optimization Algorithm

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Chronic kidney disease (CKD), a significant issue for public health, affects millions of individuals globally. The course of end-stage renal disease must be stopped or reversed, hence it is crucial to find chronic kidney disease early in order to receive therapy. Prediction of CKD is a second source of treatment, as machine learning techniques, with their high classification accuracy, are becoming increasingly significant in medical diagnosis. To learn about CKD and associated issues in this situation, deep learning is used. The sole inputs used to construct the three distinct types of models were the retinal fundus image alone (test model), the covariate only (the reference model), and the retinal fundus image plus covariate (hybrid model). To maintain the accuracy of contemporary classification systems, feature selection techniques must be applied correctly in order to reduce data size. Here, recommend the Fruit fly optimisation algorithm (FFOA) and the heterogeneous artificial neural network (HMANN) in this paper for efficient disease categorization. An Internet of Medical Things (IoMT) platform is presented for the early detection, segmentation, and diagnosis of chronic renal failure using a heterogeneous modified artificial neural network (HMANN). The Multilayer Perceptron (MLP) and Support Vector Machine (SVM) algorithms are used to classify the suggested HMANN. The ideal feature is chosen using an FFOA from a large pool of candidate features. The proposed method uses ultrasound pictures as its foundation and, as a first step in processing, slices a region of interest in the kidney in the ultrasound image. The accuracy, sensitivity, specificity, positive predictive power, negative predictive power, false positive rate, and false negative rate of the suggested CKD classification system were all taken into consideration when evaluating its performance.

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1. Introduction

Patient morbidity, mortality, and hospitalisation are all dramatically elevated by chronic kidney disease (CKD), a noncommunicable illness, across the globe [1]. The rate of its spread is accelerating and it is one of the main causes of death worldwide. According to reports, CKD is now the 13th biggest cause of mortality worldwide, with an annual death toll owing to the condition rising by 90% between 1990 and 2013 [2]. There are 850 million potential renal disease patients worldwide [3] as a result of different circumstances. At least 2.4 million individuals lose their lives to kidney-related illnesses each year, according to the 2019 World Kidney Day study. In terms of death causes worldwide, CKD is currently the sixth fastest rising. With lower levels of identification, prevention, and treatment, the burden is significantly greater in low-income nations [3]. Kidney In Ethiopia, sickness affects thousands of individuals of all ages and genders and is a significant public health issue [4]. The cause is thought to be a lack of clean water to drink, a healthy diet, and physical activity. The prevalence of CKD is also poorly understood in rural communities.

Health information classification is the process of using classifier models with datasets to enhance the definition of healthcare. Identify and predict targets by creating clinical records. How to forecast the results of the extraction is significantly impacted by this. In the course of a particular diagnostic, these technologies aid medical personnel in reaching reliable analytical results. Combining several tree topologies for classification is simple [5], and decision trees continue to be a popular classification method in decision making. Information retrieval systems can be made to particularly look for cases, themes, frameworks, or decision-making components that are concealed in health information and are reliable, instructive, and logical [6]. Chronic kidney disease (CKD), which causes a steady deterioration in kidney function, can affect both children and adults [7].

Machine learning is an intriguing area of research since it focuses on examining vast amounts of data with various features. The fundamentals of machine learning can be traced back to studies in pattern recognition and computational learning theory for artificial intelligence. Analytical techniques, computational methods, and algorithms are employed. Medical professionals and doctors can benefit from machine learning by being able to detect high-risk patients, pick the best course of therapy for patients, and, most significantly, make challenging and accurate diagnoses. health of the body. moderate cost. Speaking recognition, computer vision, medical diagnostics, and engineering are only a few of the fields where machine learning (ML) has been impressively shown to be effective [8].

Disease classification is just one application for classifiers; they are also employed in machine learning, the categorization of mocap data, and many other areas. For instance, Bayesian Networks (BNs) are quickly emerging as a significant advancement in connected AI. BN is a robust and adaptable technique for taking into account and utilising motion capture databases in atypical circumstances by integrating stochastic hypotheses and graphical depictions of conditions between items with effective derivation algorithms. Information must be divided into subsets as the initial stage in creating an artistic sequencing and recovery approach. The motion capture data classification issue is used as an analogy to show it. These enlightening anomalies need to be resolved by robust classification techniques [9].

The excessive amount of data present in real-time issues, on the other hand, is superfluous and makes data analysis challenging because of data duplication. FS is a preprocessing procedure that eliminates pointless repeated features and pinpoints the final set of most informative features to deliver reliable results in a data mining model (i.e. classification). To make it easier for our classification model to use the characteristics we require, we want to reduce the amount of features in the search space. It is believed that employing bio-inspired algorithms, this optimisation problem

can be resolved. This paper uses the FFOA (Fruit Fly Optimisation Algorithm) algorithm of FS in light of the foregoing.

The main contributions of the paper as follows:

- We suggest using a machine learning-based heterogeneous modified artificial neural network (HMANN) and a super-optimization technique for the prediction and diagnosis of chronic kidney disease (CKD).
- The classification model in this case is HMANN, and the FS method is FFOA.
- Computer vision and machine learning include the development of algorithms to extract meaningful meaning from digital images.
- To start, a collection of features is defined using the FFOA, and the best one is chosen. In order to use HMANN for classifying medical data, a subset of the CKD dataset's features are processed and sent into the programme. The suggested CKD classification method's effectiveness was assessed in terms of accuracy, sensitivity, specificity, positive predictive power, negative predictive power, false positive rate, and false negative rate.

2. Literature Survey

The authors suggested a hybrid model that incorporates both LR and RF to forecast CKD [10]]. LR, RF, SVM, KNN, Naive Bayes (NB), and Feedforward Neural Network (FNN) are six machine learning (ML) approaches that we examined with the suggested model. The model suggested by their produced a 99.83% accuracy rate. Jongbo *et al.*, [11] have employed the J48, K-Star, SVM, and NB classifiers to predict CKD. Use WEKA software to compare performances. The J48 algorithm outperforms other algorithms with an accuracy of 99%.

Jena *et al.*, [12] have categorised recent advancements in imaging technology, including terahertz (THz) pulse imaging and dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI). from a summary of biological image analysis. Examine the fundamental elements. Assume the following preprocessing guidelines apply to spatial signals that are repeated in time and space. Release of sound, examination of the spectrum, ripple variation, and principal component analysis [13]. We present the procedure for extracting and classifying characters from vectors using the aforementioned modification method. These incorporate extreme learning machine classification, SVM, and Mahalanobis distance. There aren't many situations that can be successfully divided between TPI and DCE-MRI [14]. As a result, the created complex classification model improves the entire dataset integration of continuous spatial pictures employed at various time intervals. The need for multi-channel biomedical imaging modalities and biomedical signal processing is therefore crucial [15].

The Adaptive Neural Clearance Inference System (ANFIS) was developed by Shi *et al.*, [16] to forecast chronic renal failure. In this case, the quantity of membership functions for the input variables and the quantity of fuzzy bases are both equal. To differentiate glomerular filtration rate and compare systems, an ANFIS neural network was deployed [17,18].

Clinical characteristics such serum creatinine, renal proteinuria on biopsy, chronic kidney disease (CKD), renal survival at 1-3 and 5 years, and patient-specific histology are deeply integrated with a learning method [18]. In classification tasks, the suggested CNN model performs better than PEFS, and it more reliably diagnoses CKD stages than does PEFS that is systematic.

In order to forecast chronic kidney illness, Hosseinzadeh *et al.*, [19] developed support vector machines and artificial neural networks (ANN-SVMs). The mean value for each attribute is used in

studies to fill in any missing data values. Following that, utilising ANN (Artificial Neural Network) and SVM, the ideal parameters are determined based on numerical analysis [20].

Problem description:

Because renal disease poses a serious risk to life, early identification of kidney stones is crucial. Finding the kidney's location is necessary in order to do surgery to remove kidney stones. Renal disorders are difficult to discern on ultrasound because the kidney pictures are low contrast and composed of plaque. Because of this, diagnosing small kidney types and absences might be challenging for medical professionals. We extract and resolve stone energy levels by utilising the proposed wavelet subscale and HMANN classification methods for SVM and MLP-BP.

3. Proposed Method

Another procedure that uses different conditions and techniques to arrange information in a database or repository is data classification. This is primarily accomplished through database programming or business knowledge programming, which offers the capacity to look up, find, and isolate information. The field of medicine values classification highly. It is possible to translate treatment choices and procedure descriptions into a thorough, universal medical code using medical classification or medical coding. Decisions and plans are frequently obtained from numerous medical service records, such as doctors' notes, researchers' findings, imaging, and conclusions from various sources. The best feature extraction techniques are currently used in hybrid classifiers for medical classification algorithms. Current classification models' poor performance and problems with temporal complexity are their key drawbacks. FFOA and multi-core SVM are integrated in the suggested model to get over these issues. Preprocessing is used in this case to filter the input dataset. The preprocessed data is then used to perform FS using FFOA. To classify clinical data into normal and pathological data (CKD or non-CKD), the HMANN technique is used as the final step. Figure 1 depicts the strategy for classifying scattered CKDs overall.

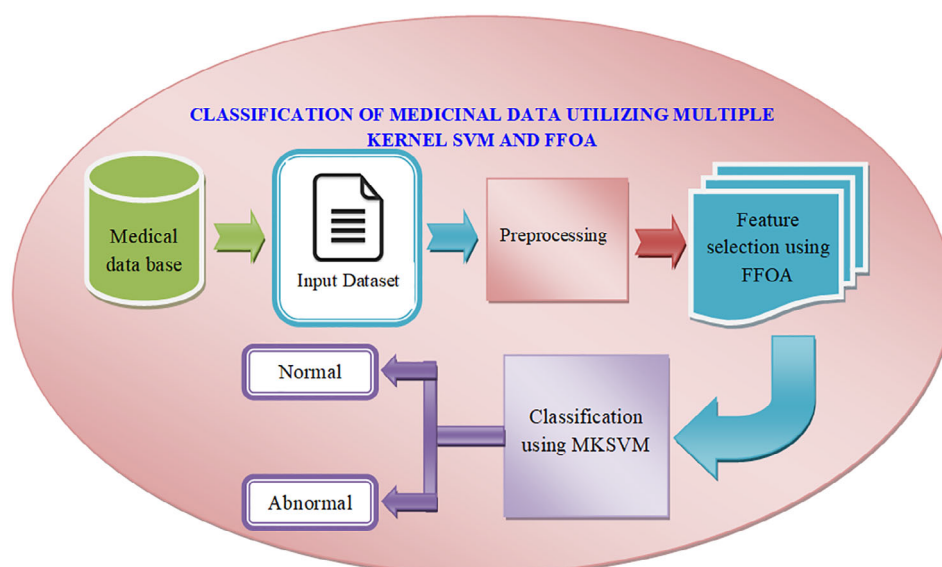


Fig. 1. The general structure of the proposed chronic kidney disease (CKD) classification and prediction method

Imaging models:

Inception v3 serves as the deep learning architecture. For the purpose of predicting CV risk factors as SBP, DBP, BMI, age, and HbA1c, ImageNet's Inception v3 architecture underwent pre-training. Following the pretrained model's transfer learning approach, the model was trained on the UK Biobank retinal fundus imaging dataset to forecast CKD disease and biomarkers. Each biomarker and comorbidity is used to train a model on the risk of existing and future diseases. An Adam gradient-based optimisation technique is used to train the model with a learning rate of $3e-4$ and to optimise the loss function.

Covariates-only model and hybrid models

The random forest model architecture, with 100 estimators and a `max_depth` of 10, was selected for the covariate-only and mixed models. These model architectures were scored out-of-bag. Compute feature importances for each covariate in a trained random forest model. When predicting the dependent variable, feature importance analyses how each covariate is influenced. Higher levels indicate more significance; the value ranges from 0 to 1. For every feature in a specific model, the total feature importances always equal 1. In order to visualise the additional influence of the retinal fundus picture, the relative predictive relevance of the variables and features included to the model were also displayed in the reference vs. mixed model. Factors that are common.

Statistical methods

The patient characteristics (demographics, medical history, and biomarkers) present in each dataset are interpreted by an interpretive analysis. The number of patients, the mean SD and median at the 25th and 75th percentiles, the minimum and maximum values, the frequencies and proportions for categorical variables, and the missing rates for all different types of variables are described. To evaluate model performance, consider its sensitivity, specificity, and AUC when predicting categorical outcomes. Other measures to consider include R^2 , the percentage of outcome variance that can be explained by all of the model's predictors, MAE, models for predicting continuous outcomes, and a confusion matrix that shows which predictions are accurate and which are not. A Bland-Altman plot is also used to compare the actual and anticipated values.

Pre-processing:

Outliers and noise are present in the dataset. The pretreatment stage should therefore start with it being clean and free of scratches. The preprocessing stage involves noise reduction techniques like outlier checking, normalisation, and pooling to remove unbalanced data because certain measurements and missing values may be lost when examining patients. It also contains missing value estimate. The remaining items in the collection have missing values, and the dataset has 158 completed cases. The simplest method for handling missing values is to ignore records, although tiny datasets do not benefit from this approach. Using algorithms to infer missing data is a different option from deleting records. Fill in the blanks for each mode's nominal features. The mean is used to fill up the gaps in numerical features.

Fruit fly optimization algorithm for FS:

In comparison to different species, smell and vision analyses are superior. The olfactory system of the fruit fly has the capacity to recognise pleasant smells in a larger surroundings. Moreover, it alludes to food supplies that can be reached even from far away. Therefore, the foraging chopper is characterised as (b) or approaching the food spot while utilising a sensitive look; and (c) ultimately, switching places while flying in the opposite direction of the butterfly swarm.

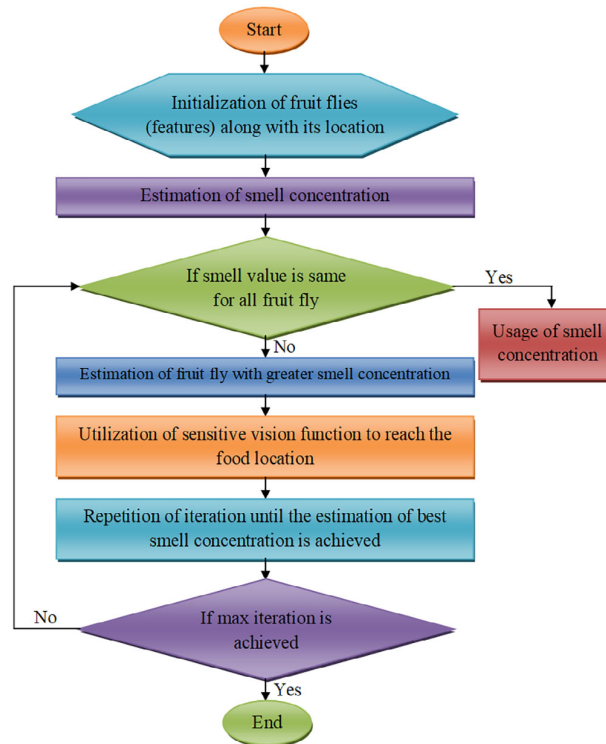


Fig. 2. Flowchart of Fruit fly optimization algorithm (FFOA)

Steps of fruit fly optimization algorithm:

Step 1: Initialization of the parameters: The primary characteristics of FFOA include evolutionary value, population size, and the position of the main chocolate group. The functional index in this study is represented by the Drosophila optimisation method. Drosophila (FUaxis, FVaxis) arbitrary position initialization.

Step 2: Using arbitrary path application and olfactory bioseparation.

where Rand is a randomly chosen variable that produces random integers and (FU_m, FV_m) is an arbitrary position.

Step 3: Since we don't know where the food is, we first estimate the distance D and the concentration SC, also known as the reciprocal, to get the distance as follows.

Step 4: In order to estimate the odour concentration for each fly location, involves replacing the odour concentration value (SC) with a fitness function.

Step 5: Decide where the best odour concentration (highest value) will be.

Step 6: Hold the value with the highest odour concentration and combine (FU, FV), after which the butterfly group flies to the location of the maximum odour concentration indication. To grow in a certain direction, use visualisation.

Step 7: A continuous optimisation process seems to carry out steps 2 through 5, after which it assesses whether the odour concentration is greater than the standard continuous odour concentration and, if so, carries out task 6.

Classification:

The suggested HMANN approach proposes three alternative structures for classifying data: support vector machine (SVM), layered perceptron, and backpropagation method. A method for classifying images that combines backpropagation, multi-layer perceptrons, and support vector machines (SVM).

Support Vector Machine:

Support vector machines (SVMs) are a group of map learning techniques for locating, regressing, and spotting outliers. When classification is facilitated by a large feature space, we select the maximal-margin hyperplane to produce in that space in order to minimise the distance between the hyperplane and the support vectors that are closer to it on each side. The interior result of the functional space influences the design. Calculations that are too massive may become unstable. SVM aims to develop a model that more accurately captures the traits of two distinct groups during training. When defining the W_j , S_j , and biases for SVM, an optimisation technique is used. The Y vector is classified using the vector in the following image.

$$x = \sum_j S_j L(W_j, Y) + A \quad (1)$$

where L is the kernel function. Radial, polynomial, linear, and layer realisation are just a few of the numerous kernel functions that SVM classifiers might utilise. L represents the linear kernel's dot product. Y is categorised as belonging to the first group if X is high; otherwise, it is categorised as belonging to the second group. SVM classifiers can be of the following varieties:

a. Linear support vector machine:

It can identify the format if C is the training data for normal and abnormal image consisting of m photos.

$$C = \left((y_j, x_j) \mid y_j \in T^q, x_j \in (-1,1) \right)_{j=1}^m \quad (2)$$

As the formula demonstrates (18), the class to which y_j belongs is indicated by x_j , where x_j is either 1 or -1. The datasets for normal and aberrant images are represented by the two-dimensional matrix y_j , respectively.

b. Polynomial kernel

Described as follows is the polynomial kernel

$$l(y, x) = (y^R x + b)^c \quad (3)$$

Formula (19), where y and x are two vectors in the input space. With c set to 3 and b set to 0, a homogeneous kernel backpropagation model with test and training sample evaluations is employed to create feature vectors.

c. Radial basis function kernel

In the Gaussian kernel, which is a radial function kernel, an image vector is represented by two y and y' samples.

$$l(y, y') = \exp\left(\frac{\|y - y'\|^2}{2\sigma^2}\right) \quad (4)$$

Equation (4) is used to calculate the squared Euclidean distance between feature vectors. shows that the kernel Gaussian variance is set to 1.

Multilayer Perceptron:

Tangent kernel hyperbolic multilayer perceptrons are a kind of multilayer neural network. One layer should combine several recognitions. For all single-layer perceptrons, sigmoid transfer functions—such as tangent hyperbolic or logistic functions—are employed and are denoted by

$$l(y, y') = \tanh(\rho(y, y'), \beta) \quad (5)$$

Chronic kidney disease detection, segmentation, and diagnosis using HMANN (Heterogeneous Modified Artificial Neural Network). The existence of kidney cysts or stones can be classified using SVM, a multi-layer perceptron (MLP) classifier with extracted characteristics.

To lessen noise in ultrasound images and enhance image quality, the suggested solution employs level set partitioning. Kidney photos are classified as normal or pathological using machine learning methods. Automated learning and intelligent inference are the main goals of machine learning algorithms. The classification process results in the creation of a weak classifier, which lowers the classifier's accuracy. By adding weights, this technique fixes samples that were incorrectly classified. Consequently, we employed a supervised learning technique to construct a reliable classifier. In order to map the energy values obtained from the subband wavelets, the artificial neural network method is sent to a multi-layer perceptron. Three or more hidden layers' backpropagation of the non-linear activation process is amplified by this energy value before being transmitted to the input layer. The MLP-BP (Multilayer Backpropagation Perceptron) algorithm is the main one. The MLP-BP method

that is being proposed outperforms existing algorithms in terms of accuracy, speed, and performance. IoMTs can also be used to monitor data from the intensive care unit (ICU), electrocardiograms, abnormal renal tests, cancer treatment, and other sensing devices such implants pill heart rate sensors.

3. Results and Discussion

Investigating the applicability of the ordering system will be aided by the planning task's outcomes. The four datasets' results are organised into categories in Table 1 below. For the time being, we are organising medical data using multi-core distributions. Alternately, improve the evaluation of the correctness of sequence estimate. Each of the following sections makes up Table 1. For the four records in the dataset, Table 3 displays the estimated values. Models for computationally classifying medical data can be predicted to perform well using these metrics. 98.50746%, 96.0396%, 93.19728%, and 95.12195% are the accuracy percentages for the four datasets. Accordingly, the four datasets' sensitivity levels are 0.976%, 0.987805%, 0.914894%, and 1%. 1%, 0.928058%, 0.962264%, and 0.947826% are the respective specificity values for the four datasets. For both the Renal Chronic and Swiss datasets, the inserted HMANN's positive and negative predictive values settle at an ideal level of 1%. A false positive rate of 0.071942% was found for the established method on the Cleveland dataset and a false positive rate of 0.135593% for the predicted method on the Hungarian dataset.

Table 1
 Performance of the proposed method utilizing various dataset

Name of the dataset	Accuracy	Sensitivity	Specificity	PPV	NPV	FPR	FNR
Kidney chronic (CKD; own and original data set)	98.7	0.984	1	1	0.9735	0	0.041278
Non-CKD	97.5	0.9765	0.9514	0.9621	0.9847	0.08471	0.025647
Cleveland data	96.2	0.9882	0.9364	0.9523	0.9916	0.08641	0.024879
Hungarian data	93.4	0.9265	0.9746	0.9843	0.8734	0.46242	0.246572
Switzerland data	95.5	1	0.9534	0.5874	1	0.06486	0

Efficiency of the classification:

In this section, the effectiveness of applying the HMANN classification to categorise medical data is covered. Through precise FS processes, the technology can be used to divide medical data. Our Drosophila-optimized system has the best choice of the current function. By contrasting the suggested CKD categorization approach with existing research, we are able to attest to its effectiveness. The model can also be used with hybrid kernel SVMs and current SVMs in addition to fuzzy min-max GSO neural network (FMMGNN). For classifying medical data, this study makes use of the most precise FS programme. CKD data from our own raw dataset is referred to as "medical." The

accuracy of the research reported in this paper is shown through its usage as evidence. Use of HMANN is part of the suggested classification approach.

Table 2
 Comparison result for time complexity

Name of the dataset	Proposed HMANN	HKSVM	FMMGNN	SVM
Kidney chronic (CKD; own and original data set)	508	558	682	614
Non-CKD	489	497	565	536
Cleveland data	473	490	536	504
Hungarian data	509	531	604	589
Switzerland data	538	588	693	651

Furthermore, employing all of the available datasets, the current methods take longer to finish the procedure overall. Conventional methods are compared to the system created to illustrate the energy of the FS model. Here, the current system chooses a non-FS input function. In this case, the classifier serves as the simple input function. FFOA is used for FS in the newly proposed approach, which also offers specific features for classification algorithms.

In terms of accuracy, Table 3 offers a thorough comparison of the outcomes produced with and without the feature selection method. As a result of the results above, we discovered that the multi-kernel SVM classifier performs better than conventional approaches. The entire process also takes very little time to finish. The proposed FS technique, used to all four datasets, achieves the highest level of classification accuracy when compared to the standard methods. In this study, we thereby show that the suggested HMANN classifier-oriented technique for classifying medical data beats the state-of-the-art.

Table 3 Comparison result for accuracy value with and without feature selection method

Name of the dataset	Accuracy value of proposed method with feature selection (%)	Accuracy value of existing method without feature selection (%)
Kidney chronic (CKD; own and original data set)	99.50	98.245
Non-CKD	98.487	94.657
Cleveland data	97.245	91.354
Hungarian data	96.185	87.345
Switzerland data	94.321	90.157

4. Conclusion

A new FS-based classification model for CKD is presented in this research. This task's utilisation of FFOA for effective FS and HMANN for categorization is what makes it novel. HMANN is used to classify the data after FFOA has been completed and a chosen set of features has been supplied. The anticipated effort will result in the estimation of PPV, NPV, FPR, and FNR using four scale datasets: Rice Field, Kidney Chronic, Cleveland Dataset, and Hungarian Dataset. On the renal chronicity dataset, the suggested method outperforms the existing HKSVM, FMMGNN, and SVM algorithms with a classification accuracy value of up to 98.7%. While preserving the lowest FNR and FPR when compared with the conventional technique, note the PPV and NPV values. For better categorization in the future, clustering strategies will be used, along with a reduction in cases that are incorrectly classified.

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