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Design of Monkeypox Disease Diagnosis Model Using Classical Machine Learning Algorithm

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ABSTRACT

Monkeypox is a zoonotic viral disease that the World Health Organization (WHO) reported as an epidemic in 2022. In most nations, the rate of these illness infections started to rise over time. Monkeypox can be caught directly from an infected person or via animal contact. In this study, an artificial intelligence-based diagnostic model for early monkeypox infection detection is developed. The proposed method is based on building a model based on K-Nearest Neighbors, Support Vector Classification, Random Forest, Naive Bayes and Gradient Boosting for the classification problem. A voting method was also used to determine the final diagnosis of the proposed model. The system was trained and evaluated using a dataset that represented the clinical signs of monkeypox infection. The dataset comprises one hundred twenty infected patients and 120 typical cases out of 240 probable cases. The suggested model attained 75% accuracy.

1. Introduction

The monkeypox virus (MPXV) spread in 2022, alarming the public and raising experts' concerns due to its quick spread [1]. Between 1 to 11% of cases result in mortality [2]. According to the World Health Organization (WHO), more than 318,000 persons contracted this virus in August 2022, a considerable increase in the number of affected individuals [3]. Figure. 1. according to the World Health Organization, shows the number of monkeypox infections in each country (May 26, 2022). This virus is comparable to zoonotic smallpox and is a member of the corticovirus genus [4]. It affects humans and is brought on by the orthopoxvirus, a hazardous member of the poxviridae family [5].

For the first time, the illness was discovered in Africa, more specifically in the Republic of the Congo [4]. After that, it expanded throughout the world's nations. More than 1,256 cases of monkeypox had been documented as of June 2022 in various parts of Spain. The majority of cases were male. The average age was approximately 36 years at the time [6]. Direct contact with an infected person, animal, or object is the only way to contract monkeypox. It can also spread via mucous from the mouth, nose, or eyes [7]. Transmission of the monkeypox is focused, though not solely, during sex [5].

Smallpox and monkeypox have fairly similar clinical presentations, as shown in Figure. 2. however, the symptoms that develop after infection vary from case to case. Yet, in addition to anogenital lesions, sluggishness, and muscle pain, skin rash is the most typical indicator of infection [7]. Symptoms of monkeypox can last up to four weeks. Also, children are the most at risk [8]. The illness's adverse effects can include bronchiolitis, hypothermia, bacterial infections, and respiratory failure in patients [9]. The illness is challenging to diagnose based on a variety of clinical symptoms.

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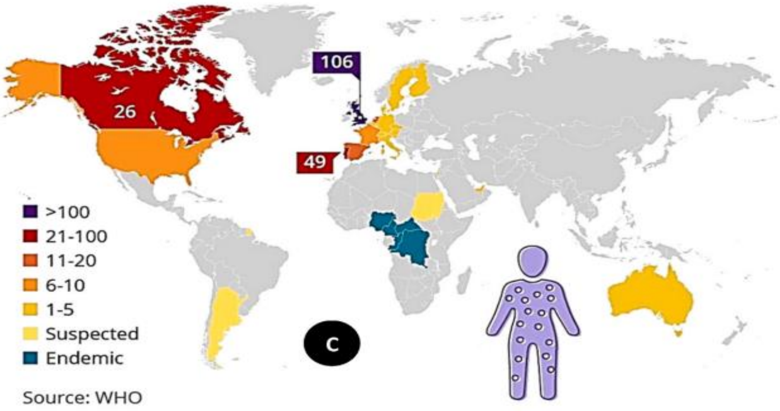


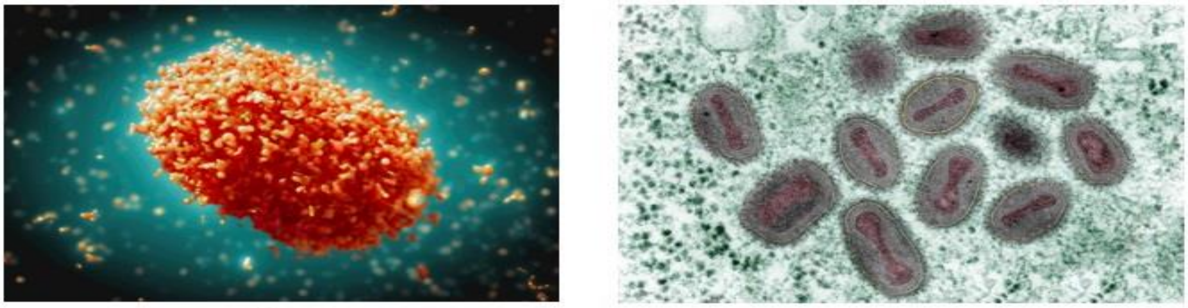
Figure 1 Number of monkeypox infections in each country [10]

It can take a while to learn the findings of laboratory tests before making an appropriate diagnosis of monkeypox since it must be distinguished from other diseases using a molecular test [10].[11].

Researchers have resorted to using artificial intelligence in medical and biological applications to diagnose illness problems as a result of the proliferation of AI applications [12]. Depending on the dataset gathered from the photographs of the lesions or the clinical signs of the infected, they utilised it in a variety of ways. [2] employ several techniques for gathering data. Skin lesion photographs make up the data. gathered manually and by contact with sick people. The study's main objective was to distinguish monkeypox from cases of related smallpox of other forms. Using VGG16 Deep Transfer Learning was the method used. It uses a neural network after three layers of convolutional filters to extract information from the photos. It had the ideal idea to employ transfer learning. The results' degree of accuracy was 86%.

The research conducted by [13] was split into three distinct investigations. These were all carried out using the suggested methodology. Generalization and Regularization are used in Multiclass Classification by Transfer Learning Approaches (GRA-TLA). Skin lesion photos make up the training dataset. It was created to aid the hospital in making decisions. According to computational findings, the first and second investigations could discriminate between those who had monkeypox and those who hadn't with an accuracy of 77% to 88% using the suggested method. In the third research, the residual network (ResNet), with accuracy ranging from 84% to 99%, performed the best for multiclass classification.

In this paper, we present a predictive model to enable the early detection of monkeypox. The proposed model is designed based on the combination of Gradient Boosting, SVC, KNN, Naïve Bayes and Random Forest algorithms. In addition to a voting system to determine the output of predictive filters. The method's performance was tested on clinical data from the bmj centre in London and compared with machine learning algorithms. The results provide that the proposed method could be used for early diagnosis of monkeypox disease.



(a)

(b)

Figure 2 Difference between (a)- monkeypox virus and (b)- smallpox virus [10]

The structure of this paper is organized as follows: Section 2 theoretically describes the applied algorithms and the mechanism of creating the Model. Section 3 presents Experimental Study. Findings and discussions are presented in Section 4. Section 5 reports on the conclusion.

2. Methodology

This section describes a proposed approach for the early detection of monkeypox patients. Attempts to quickly and accurately diagnose patients with monkeypox. This approach consists of five classifiers and a voting system, as shown in Figure. 3. Thus, the detection model of monkeypox will be recognized by dataset based on the clinical symptoms that the patient presents with during the infection period to give the desired results. The proposed model was built using five techniques: Naive Bayes, KNN, SVC, Random Forest, and Gradient Boosting, combined with a voting method to provide the best diagnostic results. Following sections, the mechanism of action of each classification algorithm will be explained separately, as well as how to diagnose the disease based on the voting system in detail.

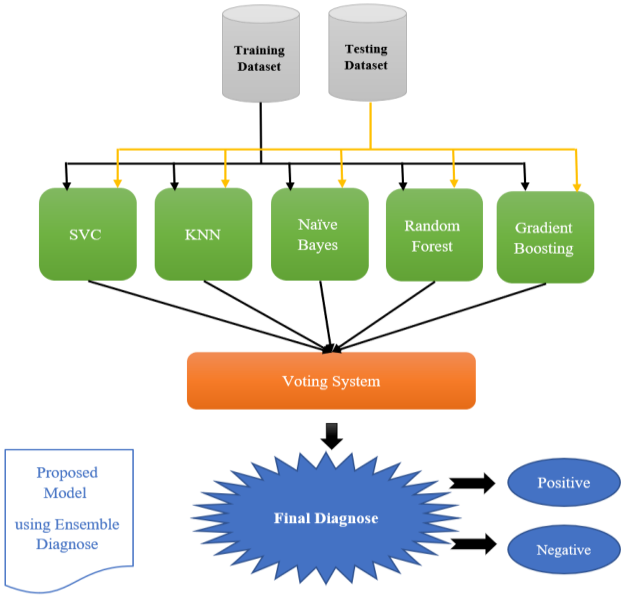


Figure 3 Proposed Diagnose Model

2.1. Naïve Bayes (NB) Algorithm

In this section, the working mechanism of the NB algorithm is explained. In fact, NB is one of the traditional machine learning algorithms (Figure. 4.). It is characterized by simplicity, and it has many uses in recognizing images and shapes, and it can also handle real-time problems, and it also gives high efficiency in early detection of diseases in medical systems [14].

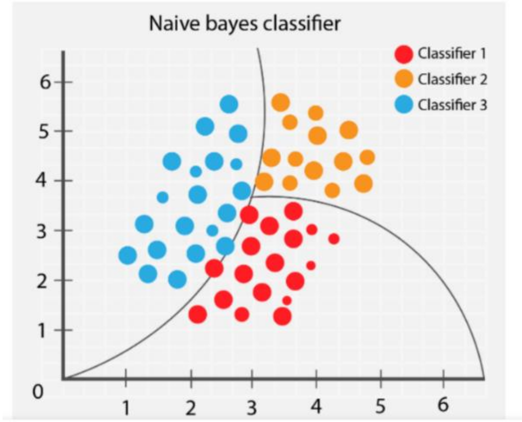


Figure 4 Naïve Bayes Classifier

This algorithm can handle large and small dataset. And it can give quick diagnosis instead of other models. It is also distinguished that it is not affected by noise in the data sets, that is, it is less sensitive to missing data. Bayes' theorem states that the probability of a hypothesis is determined after prior knowledge has been determined. This theory is related to conditional probabilities. As Eq. 1. given below states:

$$P(A|B) = \frac{P(B|A) * P(A)}{P(B)} \qquad (1)$$

In fact, although NB is an effective algorithm for real-time applications such as medical diagnostics, one of its disadvantages is that all features are considered equal and independent during training.

2.2. K-Nearest Neighbors (KNN) Algorithm

KNN is one of the most popular and easy machine learning algorithms. It is used in many applications such as controlling electrical circuits and driving loads. In its learning, this algorithm depends on the value of K, which determines the number of samples that affect the classification process. In fact, there is no fixed value for the K factor, but it is set experimentally. This depends on the nature of the problem to be solved, as it differs from one unit to another. As shown in Figure. 5.

In this paper, KNN is introduced as a diagnostic model for monkeypox disease. It is based on the optimal value of K to obtain the best possible accuracy.

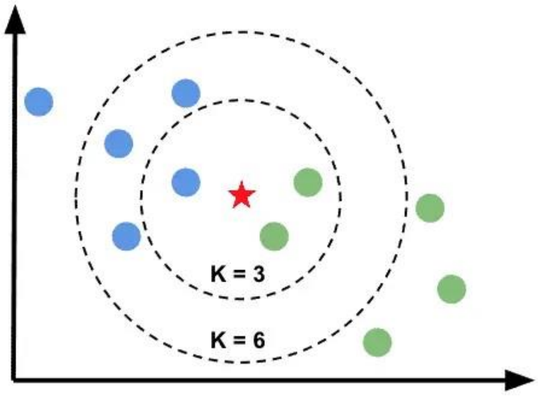


Figure 5 KNN algorithm

The KNN algorithm is based on the Cartesian distance function to measure the distance between samples [14]. The work of this algorithm can be summarized in three steps: In step 1, the distance between each testing sample and each training samples is calculated using the Euclidean distance, mentioned in Eq. 2.

$$d = \sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2} \tag{2}$$

In step 2, the value of k is set to give the minimum distance between the test sample and the training samples. In step 3, the final test sample is classified depending on the k-neighbor’s diagnoses.

2.3. Support Vector Classification (SVC) Algorithm

SVC falls under traditional machine learning algorithms. It is easy and simple. Data points are classified into two categories. This algorithm is based on tracing the line between the two data types. Always strives to find the best positioning of the dividing line between the two categories [15].

This algorithm can solve classification and regression problems, and it works with both linear and nonlinear arithmetic operations. Therefore, this algorithm can be applied to Classification of images and text categorization, in addition to its use in medical engineering. As shown in Figure. 6.

The logic that the algorithm will use to separate points into different groups and categorize them can be set to one of the following techniques: - Linear: The line separating the two sets of data is a straight line. - Polynomial: This pattern allows the separation of data using polynomials of degrees, which contributes to increasing classification accuracy when using complex data. - RBF: It is an acronym for Gaussian Radial Basis.

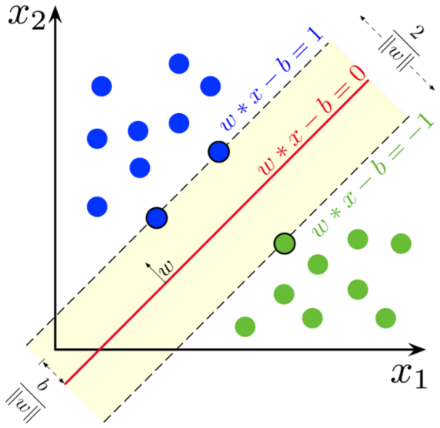


Figure 6 SVC algorithm

This principle works to create Gaussian distributions for each set of data in a way that determines the best distribution for the data. - sigmoid: uses the logic of logistic regression [16].

2.4. Random Forest Algorithm

Random Forest is one of the most used algorithms in machine learning and data science. This algorithm is considered moderated and is widely used in classification problems. One of the advantages of this algorithm is its ability to deal with continuous data, whether in regression problems or classification problems [17].

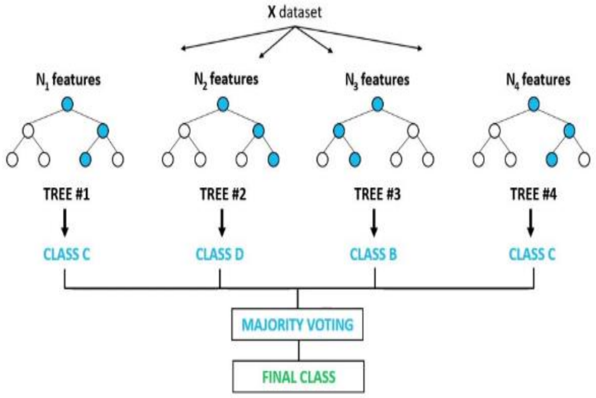


Figure 7 Random Forest algorithm

It can reach high accuracy during data training. This algorithm falls under the name of Ensemble Method. You create a subset of the training data, and the final output depends on the majority vote. The Random Forest model is a set of decision trees that have been used in machine learning problems. All internal nodes and branches in decision trees are associated with the test result. The internal nodes are the result of a specific feature test, while the branch represents the overall test result, and the leaf nodes are the expected result [18]. Its working mechanism consists of the following stages:

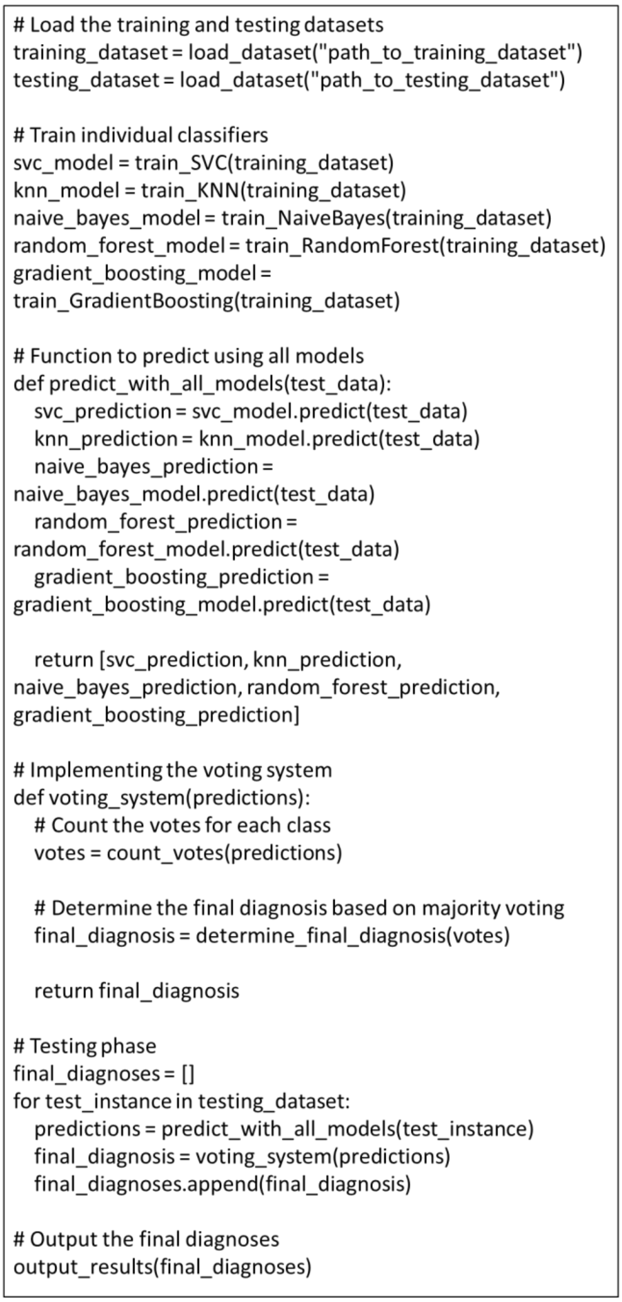
Stage 1: A subset of data points and a subset of features are selected to create each decision tree. Stage 2: Individual decision trees are generated for each sample. Stage 3: Each decision tree will generate an output. Stage 4: The final output is considered on the basis of majority vote or average rating and regression, respectively (Figure 7).

2.5. Gradient Boosting Algorithm

Gradient Boost is one of the most powerful algorithms in machine learning. It is well known that errors in machine learning are divided into bias errors and variance errors [19]. Therefore, the Gradient Boost algorithm is used to reduce the bias error in the model. Unlike the Adaboosting algorithm, we cannot mention the base estimator in the Gradient Boost algorithm [20]. This algorithm can handle both continuous data and categorical data. When this algorithm is used in regression problems, the error function is MSE. While Log Loss is in classification problems. Elements on which the algorithm depends: (a)- Loss Function: In this case, it aims to maximize the loss, which is not fixed and changes according to the nature of the problems. (b)- Weak Learners: These are mainly used for predictions. Decision tree is an example of poor learners. For the required real output values of the divisions, specific regression trees are applied. (c)-Additive Model: Adding more trees at a time. Thus, reducing losses at each addition.

3. Voting Method

In this section, the output of the five classifiers is voted on, as a way to determine the final output of model. The method of voting depends on giving all workbooks the same weight, which is the value 1. Classification cases are collected into two ‘Normal’ or ‘infection’ cases. Then he decides the outcome of the vote according to the largest number determined by the classifiers. That is, based on the majority vote, if the category “Normal” gets three votes and the category “infection” gets two votes, then vote will decide “Normal”. According to this mechanism, the voting system works.



```
# Load the training and testing datasets
training_dataset = load_dataset("path_to_training_dataset")
testing_dataset = load_dataset("path_to_testing_dataset")

# Train individual classifiers
svc_model = train_SVC(training_dataset)
knn_model = train_KNN(training_dataset)
naive_bayes_model = train_NaiveBayes(training_dataset)
random_forest_model = train_RandomForest(training_dataset)
gradient_boosting_model =
train_GradientBoosting(training_dataset)

# Function to predict using all models
def predict_with_all_models(test_data):
   svc_prediction = svc_model.predict(test_data)
   knn_prediction = knn_model.predict(test_data)
   naive_bayes_prediction =
naive_bayes_model.predict(test_data)
   random_forest_prediction =
random_forest_model.predict(test_data)
   gradient_boosting_prediction =
gradient_boosting_model.predict(test_data)

   return [svc_prediction, knn_prediction,
naive_bayes_prediction, random_forest_prediction,
gradient_boosting_prediction]

# Implementing the voting system
def voting_system(predictions):
   # Count the votes for each class
   votes = count_votes(predictions)

   # Determine the final diagnosis based on majority voting
   final_diagnosis = determine_final_diagnosis(votes)

   return final_diagnosis

# Testing phase
final_diagnoses = []
for test_instance in testing_dataset:
   predictions = predict_with_all_models(test_instance)
   final_diagnosis = voting_system(predictions)
   final_diagnoses.append(final_diagnosis)

# Output the final diagnoses
output_results(final_diagnoses)
```

Figure 8 Pseudo Code of Proposal Model.

Figure. 8. shows us the pseudocode outlines a method for building an ensemble learning model to improve diagnostic accuracy. First, it loads the training and testing datasets. Then, it trains five different machine learning models: Support Vector Classifier (SVC), K-Nearest Neighbors (KNN), Naive Bayes, Random Forest, and Gradient Boosting. Each model makes its own predictions for the test data. These predictions are combined using a voting system that decides the final diagnosis based on the majority vote. During testing, each data point is evaluated by this ensemble of models, and the final diagnoses are recorded. This approach combines the strengths of various classifiers, making the diagnostic process more accurate and reliable.

4. Experimental Study

This section gives an overview of the training dataset's processing as well as a summary of some of its features. Together with the suggested model's performance metrics, which have equations to determine each value.

4.1. Dataset

The database provided for the study was obtained from Kaggle [21]. This dataset was based on patients with monkeypox, and other suspected cases. This data is published according to thebmj center in London. This data contains 240 diagnosed cases with 11 features which are described in Table 1.

Table 1 Detail of Dataset

SN	*Attribute*	*Type*	*Value*
1	Patient_ID	Numerical	[1 - 240]
2	Systemic Illness	Nominal	Fever, None, Swollen Lymph Nodes, Muscle Aches and Pain
3	Rectal Pain	Nominal	True, False
4	Sore Throat	Nominal	True, False
5	Penile Oedema	Nominal	True, False
6	Oral Lesions	Nominal	True, False
7	Solitary Lesion	Nominal	True, False
8	Swollen Tonsils	Nominal	True, False
9	HIV Infection	Nominal	True, False
10	Sexually Transmitted Infection	Nominal	True, False
11	MonkeyPox	Nominal	Positive, Negative

A retrospective observational study was performed on individuals with polymerase chain reaction (PCR) confirmed monkeypox virus, who were evaluated and managed at a south London HCID center. This center, one of five HCID centers in the UK, serves the population of inner city central and south London. Diagnostic swabs were taken from lesions at affiliated community sexual health and HIV medicine services, upon hospital admission (either in inpatient wards or emergency departments), or upon transfer of patients suspected of having monkeypox from neighboring NHS trusts. These samples were processed at the Rare and Imported Pathogens Laboratory in Porton Down, UK.21 Individuals suspected or confirmed to have monkeypox were stratified by risk according to disease severity, immune status, and their ability to self-isolate, and were managed accordingly. As part of standard clinical care, individuals were clinically assessed prior to testing. All individuals with a positive PCR test result for monkeypox virus participated in a telephone consultation to receive counseling about their result and to undergo a risk assessment.

This dataset contains newly infected patients who show symptoms of monkeypox. From the 240 data set we have 120 cases of monkeypox, and 120 healthy cases. Patients with monkeypox are considered positive cases, whilst healthy individuals are considered negative instances. A negative case does not always imply that the person is healthy and free from monkeypox. But, based on this information, we can tell if he merely had monkeypox. There are 11 characteristics in this dataset, including the patient's clinical symptoms like fever and inflammation. These characteristics are used to describe the symptoms that a patient experiences in order to convey the patient's condition.

We computed the linear correlation coefficient between the features and observed varying degrees of correlation among the data. Additionally, the dataset contains no null values. We encoded the binary variables as follows: True as 1 and False as 0. The dataset was then divided into two subsets, with 80% allocated for training and 20% for testing. Overall, the proportions of infected and non-infected cases were evenly distributed across these subsets.

In actuality, the dataset for monkeypox was split into two sets of data: 168 cases for the training set and 72 cases for the test set. There are 120 positive instances and 120 negative cases total. Initial instances often contain noisy and missing values. Therefore, it is necessary to pre-process the raw data to achieve good results. All data set used has been verified. In (Systemic Illness) we converted the categorical attribute to numeric. The dataset does not have any missing values. Furthermore, we performed correlation analysis on these datasets, when two attributes are closely related, one of them needs to be omitted to achieve better results.

4.2. Performance Evaluation

Algorithms for classifying data are measured for accuracy using statistical techniques. These techniques help establish the accuracy, precision, F1-score, and sensitivity standards for the used algorithm (They are shown in Table. 2.). If the individuals have been correctly categorized, monkeypox in our dataset can be classed as True Positive or True Negative. If misdiagnosed, it may be labelled as a False Positive or False Negative. Figure. 9. illustrates these properties. As a result, the following estimated values are provided:

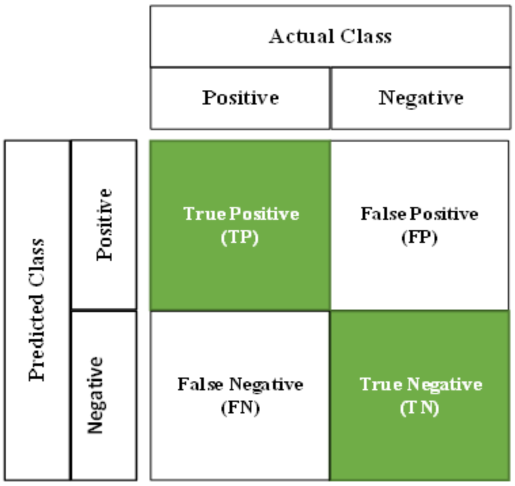


Figure 9 Confusion Matrix

- *True Positive (TP):* It predicts positive values when its true values are positive.
- *True Negative (TN):* It predicts negative values when its true values are negative.
- *False Positive (FP):* It predicts positive values when its true values are negative.
- *False Negative (FN):* It predicts negative values when its true values are positive.

Tools by which algorithm accuracy is measured depending on Confusion Matrix are:

Table 2 Statistical methods for measuring the accuracy of a machine learning model.

Method Name	*Equation*
Accuracy	$\frac{T_p + F_p}{T_p + T_n + F_p + F_n}$
Precision	$\frac{T_p}{T_p + F_p}$
Sensitivity	$\frac{T_p}{T_p + F_n}$
F1-score	$2 * \frac{Recall * Precision}{Recall + Precision}$

4.2.1. Accuracy

This way is used to describe the performance of a classifier based on the correctly predicted states versus the overall states. As in Eq. 3.

$$Accuracy = \frac{T_p + F_p}{T_p + T_n + F_p + F_n} \tag{3}$$

This measure is not considered sufficient to be considered the best model, if the data set is not balanced.

4.2.2. Precision

It determines the ratio between actual positive values and all projections that are positive. When the model assumes more false positives, the accuracy value drops. As in Eq. 4.

$$Precision = \frac{T_p}{T_p + F_p} \tag{4}$$

4.2.3. Sensitivity

The percentage of positive diagnostics that were diagnosed as positive. As in Eq. 5.

$$Sensitivity = \frac{T_p}{T_p + F_n} \tag{5}$$

4.2.4. F1-score

The F1-Score runs from 0 to 1, and it is a harmonic mean of precision and recall. Low false negative and false positive readings produce this metric's higher value. As in Eq. 6.

$$F1 - score = 2 * \frac{Recall * Precision}{Recall + Precision} \tag{6}$$

5. Result and Discussion

A sample dataset of 72 values from the dataset, which is a combination of monkeypox cases gathered at thebmj center in London, is used to evaluate the proposed model.

The only instances of monkeypox with a variety of symptoms were included in the sample data. This also addresses how many positive and negative instances there are with various symptoms, and therefore it suggests a five-classifier model diagnostic approach: Gradient boosting, SVC, KNN, Naïve Bayes and Random Forest.

Table 3 Performance of proposed model

phase	*Performance*			
	Accuracy	*F1-Score*	*Precision*	*Sensitivity*
Training	87 %	87 %	87 %	88 %
Testing	75 %	75 %	69 %	81 %

Table. 3. presents the results of the proposed model during training and testing. The performance of the model was measured by several criteria. They appear as follows: in the training period accuracy, F1-score, precision and sensitivity take the values 87%, 87%, 87%, 88%. Respectively. When testing, accuracy, F1-score, precision, and sensitivity standards were taken as 75%, 75%, 69%, 81%. Respectively. Figure. 10. presents the confusion matrix of the proposed model during training and testing.

Table 4 Performance of RF, SVC, KNN, NB, GB

Algorithms	*Performance*			
	Accuracy	*F1-Score*	*Precision*	*Sensitivity*
RF	52 %	51 %	53 %	52 %
SVC	58 %	58 %	60 %	58 %
KNN	60 %	60 %	60 %	60 %
NB	61 %	60 %	62 %	61 %
GB	63 %	62 %	63 %	61 %

Table. 4. reveals that Gradient Boosting (GB) outperformed other algorithms across all metrics, demonstrating superior accuracy, F1-Score, precision, and sensitivity. Naive Bayes (NB) and K-Nearest Neighbors (KNN) also performed well, particularly in precision and sensitivity. Support Vector Classifier (SVC) showed moderate performance, while Random Forest (RF) had the lowest scores in all evaluated metrics. These results suggest that Gradient Boosting is the most effective model among those tested for this dataset, offering a balanced performance in both identifying and accurately predicting positive cases.

6. Conclusion

The study briefly overviews the origin of the zoonotic illness monkeypox, which is spread from animals to people. The very virulent Orthopoxvirus family includes this virus. Many people are alarmed by the disease's societal proliferation. As a result, society needs an automated system for early detection that aids in diagnosing this illness infection, should it arise. Early diagnosis can save lives by preventing complications for those with the condition. This work aims to develop a model for identifying monkeypox infection based on the clinical symptoms of the illness that manifest in the infected person. There are five machine-learning algorithms in the suggested model. A 75% accuracy rate was reached using the proposed model. As the current strategy to develop a diagnostic mechanism for monkeypox illness is backed by several published literature that uses an AI-based diagnostic model, we hope that this paper will assist future researchers and practitioners gain from the presented approach.

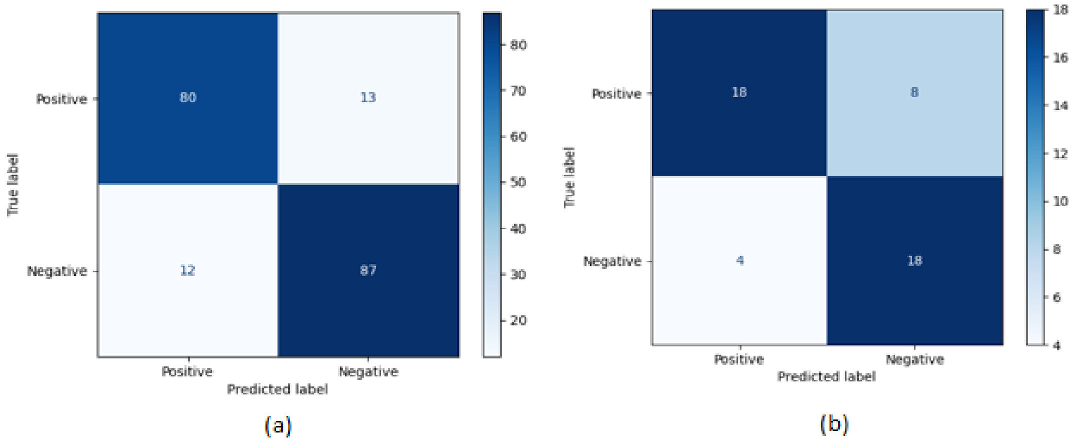


Figure 10 (a) Confusion matrix of training phase for the proposed model. (b) Confusion matrix for testing

The proposed model is substantiated by numerous scholarly publications that utilize AI-based diagnostic models. It is our aspiration that this article will aid future researchers and practitioners in leveraging the outlined approach to create a diagnostic framework for monkeypox disease. In subsequent research, we intend to develop an AI methodology capable of extracting features for monkeypox using real-time data and achieving higher classification accuracy.

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