Review

A review on the use of machine learning techniques in monkeypox disease prediction

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A B S T R A C T

Infectious diseases have posed a global threat recently, progressing from endemic to pandemic. Early detection and finding a better cure are methods for curbing the disease and its transmission. Machine learning (ML) has demonstrated to be an ideal approach for early disease diagnosis. This review highlights the use of ML algorithms for monkeypox (MP). Various models, such as CNN, DL, NLP, Naïve Bayes, GRA-TLA, HMD, ARIMA, SEL, Regression analysis, and Twitter posts were built to extract useful information from the dataset. These findings show that detection, classification, forecasting, and sentiment analysis are primarily analyzed. Furthermore, this review will assist researchers in understanding the latest implementations of ML in MP and further progress in the field to discover potent therapeutics.

1. Introduction

1.1. Monkeypox and machine learning (ML)

Human monkeypox (MP) is a zoonotic disease caused by monkeypox virus (MPV) [1,2]. This *Orthopoxvirus* displays similarities to smallpox [1,3]. In humans, MPV infections are acknowledged to be highly significant after smallpox [4,5]. This virus, initially discovered in monkeys in a Danish laboratory in 1958, has since been given the name of monkeypox [6].

MP was first recorded in 1970 [7] and observed in a 9-month-old boy with fever, followed by a centrifugal rash after two days [8]. Initially, this disease was endemic to the Democratic Republic of the Congo and spread throughout Africa, particularly in Central and West Africa. The first case of MP outside Africa was reported in 2003 [6].

The genome of MPV, which belongs to the *Poxviridae* family, is approximately ≈200 kb long and contains conserved regions at the center that code for replication and machinery required for assembly [9]. The terminal ends of MPV contain genes that play a role in pathogenesis and host-range determination [9]. They contain linear DNA [9]. Typically, MPV is characterized by a pleomorphic, enveloped virus with a dumbbell-shaped core and lateral bodies [10].

MPV has two clades: the West Africa and Congo Basin [11–14]. The fatality rate associated with the Congo Basin strain is 10%, while that of West Africa strain is about 1% [15]. The West Africa strains are generally less pathogenic [9] due to the presence of open reading frames containing fragmentations and deletions that promote reduced virulence [10]. In infected individuals, MPV typically manifests as a maculopapular rash on the soles and palms, accompanied by fever and swollen lymph nodes [5,12]. The rash progresses through stages, evolving from macules and papules to vesicles and pustules, eventually forming scabs and undergoing desquamation [16,17].

The spread and transmission of the disease may occur through contact with skin lesions, respiratory droplets, and bodily fluids. It might also spread because of fomite contamination [18]. The animal hosts for MP are monkeys, rats, pigs, prairie dogs [19], squirrels [19], hedgehogs, primates, and mice; therefore, MP can be transmitted from animals to humans [18]. The transmission has also been observed in humans [20]. To alleviate MP, it is essential to curb disease transmission [21].

Artificial intelligence (AI) is a fascinating and interesting approach among current analytical tools [22]. ML and AI have been increasingly recognized for their ability to diagnose diseases [23]. Machine learning-based disease diagnosis (MLBDD) is gaining importance because of its advantages, such as low economic burden and less time consumption. The MLBDD comprises data obtained from X-rays, MRI and patient information [23].

The ML process generally consists of supervised [24] and unsupervised [25] models, depending on the presence or absence of the label to be predicted. The most commonly employed supervised learning methods are the naïve Bayes, support vector machine, and decision trees [26]. Principal component analysis and k-means clustering are commonly employed in unsupervised learning [26].

1.2. Artificial intelligence and machine learning

ML and AI assist healthcare professionals in finding rapid solutions [27]. AI is an approach to representing the intelligent behaviour of humans. ML is a subset of AI that enables studying algorithms for executing particular tasks [28,29]. AI can facilitate various patient-care processes and provide intelligent health systems [30]. Researchers can use a large amount of data obtained from hospitals to apply AI to understand certain medical conditions, such as the prediction of disease stage, hospital stay, diagnosis, and death prediction [31,32]. The term "artificial intelligence" was first coined in 1956 [33]. AI and ML play significant roles in healthcare [34]. They are essential for accurately predicting diseases [35–37] and are used in decision-making [38–40]. Precision medicine is one of the most widely used applications [27]. Several algorithms have successfully identified malignant tumors in the field of cancer, thereby directing researchers further [27]. In addition, various other applications include drug discovery and development [41], transcription of medical documents, enhancement of patient-physician communication, and remote treatment of patients [33]. Another report described the use and development of AI and global tendencies of heart diseases and stroke, identified research gaps, and recommended future guidelines and directions [32]. Samuel defined ML as the capacity of computers to learn without programming [26]. ML approaches involve supervised and unsupervised learning algorithms and reinforcement learning.

1.3. Supervised learning

In supervised learning methods, data contain labels or classes. These data can be divided into training and test datasets [26,28,42–44]. The algorithm was trained using the training dataset and was applied to the test dataset for classification or prediction (Fig. 1A) [26,28]. These types of prediction are referred to as classification models [42,44]. Conversely, when the output has a continuous value, it is called the supervised regression model [44]. Here, a few common supervised learning methods are discussed, such as random forest (RF), decision tree, support vector machine (SVM), naïve Bayes, linear regression, and logistic regression [42].

1.3.1. Random forest

In 2001, Breiman suggested a highly successful algorithm called the RF [45,46]. Predictions were made by merging numerous decision trees and averaging their results [45,47]. Because many randomly generated decision trees are employed to build the final model (Fig. 1B), this is

called RF [42]. This is a beneficial method when the variables are greater than the observations [45]. It is non-parametric, competent, and easy to interpret. It can accurately predict the outcomes when used with different data types [48].

1.3.2. Decision tree

This can be adapted for classification and regression methods to build a model to predict target values using the basic decision rules available from the data features (scikit-learn). This is similar to a graph that records outcome based on choices [26]. A decision tree typically contains a root, internal nodes, branches, and leaves (Fig. 2A) [53]. The attribute is checked in the internal node, and the result is passed on to a branch [42, 44]. The root node, which is also referred to as the decision node, contains choices that are further divided. Internal or chance nodes correspond to a particular chance obtainable in the tree at a given point. The parent node is linked to the top edge of the node, and the bottom edge is joined to the child or leaf node. Braches are possible results arising from roots and internal roots [54]. The end outcome was labelled at the leaf node. Correspondingly, the paths in a decision tree are governed by specific rules [42].

1.3.3. Support vector machine

It is a widely used ML algorithm suitable for complex data classification [55] and imbalanced data of small to medium size [47]. The SVM approach provides superior classification accuracy [56]. A hyperplane dividing the data into two classes in an n-dimensional vector space was plotted [47]. This division was enlarged by expanding the margins on both sides of the hyperplane [42]. The area bound to the hyperplane with the maximum possible margin was used in this investigation (Fig. 2B) [42]. SVM approaches can be employed for linear or non-linear classification [26,47]. Non-linear classification was executed using a kernel trick, and the inputs were mapped to high-dimensional feature spaces [26]. Before starting the SVM method, it was essential to correctly label the input data [56].

1.3.4. Naïve Bayes

This is an easy-to-build algorithm that depends on Bayes' theorem [26,57]. When the data to be analyzed have numerous data points and features, naïve Bayes swiftly trains the data and builds a model to obtain the prediction (Fig. 3A) [57]. Typically, the naïve Bayes method assumes that the existence of a specific feature in a class is unrelated to another feature [26]. The naïve Bayes method produces good results for simple predictions [42].
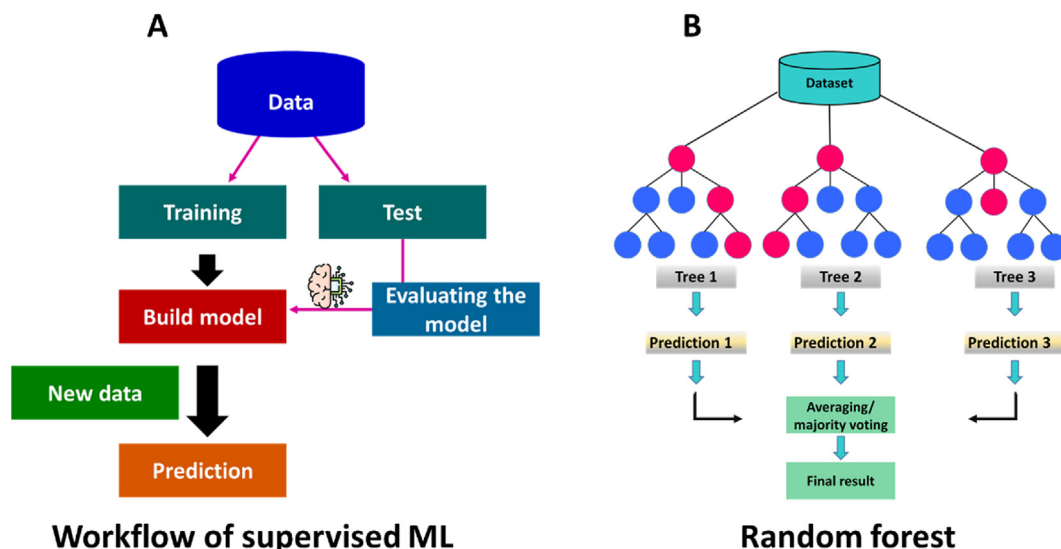

Fig. 1. Methods of supervised learning. A) Workflow of supervised learning approach. B) Depiction of random forest.
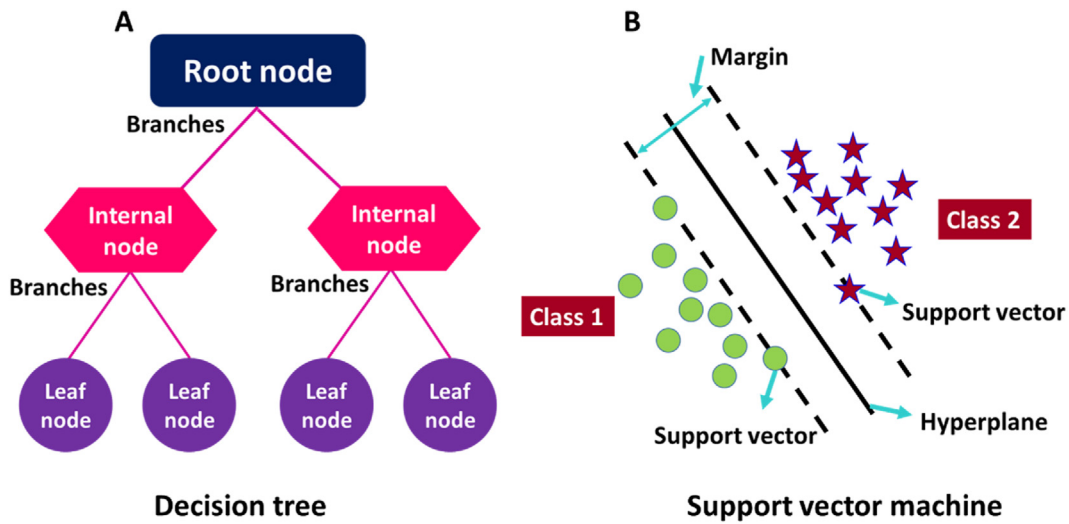
Fig. 2. Different supervised learning models A) Decision tree approach. B) Support vector machine method.

1.3.5. Linear regression

In 1894, Galton first proposed the idea of linear regression. This method helps assess the correlation between predictors [49]. Correspondingly, the target variable is identified by plotting the straight line called the "least squares regression line'. This best-fit line is plotted between the features or independent variables and the target or dependent variables [42]. The dependent variables are plotted on *y,* and the independent variables are plotted on *X*. The independent variables are also called input variables, observations, data points, features, attributes, dimensions, or observed data (Fig. 3B). The regression model aims to predict a continuous target variable. The objective of the classification approach is to predict the labels. The model is trained using the training dataset and employed to predict the unlabeled test dataset [44]. If one independent variable must be analysed for prediction, it is called a simple linear regression. If more than one is involved, it is known as multiple linear regression [50–52].

1.3.6. Logistic regression

Logistic regression makes predictions by fitting data to a logistic function [44]. This is a typical classification method [58,59]. The logistic regression model infers that the result variable Y is categorical and is established on the probabilities connected to Y, which adapts the value 1 for positive or success and 0 for negative or failure [42,60]. This depends on the association between the dependent variables or target and the independent input variables or features [42]. Here, an 'S'- shaped logistic function (sigmoid function) predicts between 0 and 1 [61,62]. The threshold value indicates the probability that the model could be separated into classes (Fig. 3C) [42,63].

1.4. Reinforcement learning

The algorithm learns from an environment responsive to trial and error [44]. The learning algorithm is directed by the feedback provided
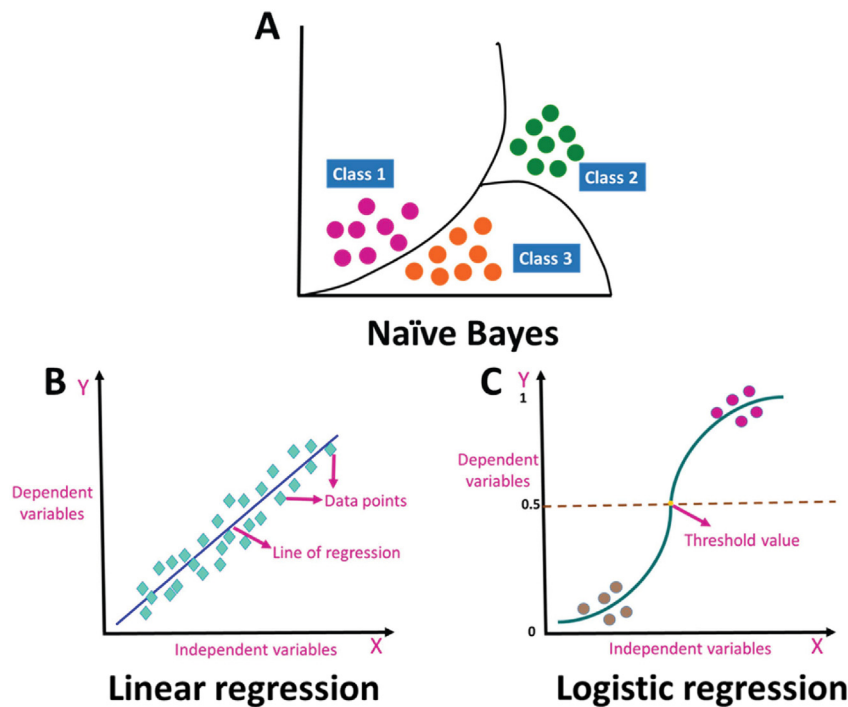

Fig. 3. Various supervised learning models. A) Naïve Bayes. B) Linear regression. C) Logistic regression.
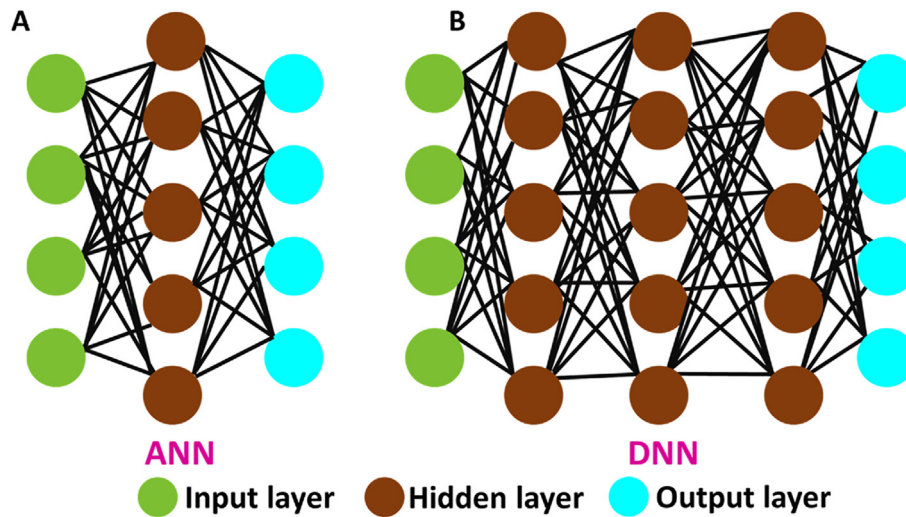
Fig. 4. Neural network approaches. A) Artificial neural network (ANN). B) Deep neural network (DNN).

by the environment [44]. There are four elements in reinforcement learning: policy, reward, value, and model [64]. The policy function refers to mapping possible states to the actions to be performed. Typically, this is the performance of a learning agent over a particular period. The reward function describes the goal to be solved (the problem) in reinforcement learning. This is feedback obtained from the environment. These rewards are scalar or integer variables [65]. Unpleasant events are referred to as punishments [66]. The value function explains the existing mapping of probable states. It describes what is good, as it predicts rewards [64,65]. The model is a demonstration of a learning environment that is employed for learning [65].

1.5. Artificial neural networks (ANNs)

ANNs are motivated by mechanisms in the human brain. ANNs can adapt to variations in the input, producing the best output without remodeling the output conditions. ANNs have extremely interconnected components referred to as neurons. These neurons execute functions such as input collection from neurons or an exterior source and produce an output [67]. The neurons in an ANN are nodes [68]. Neural networks can adapt to changing input; therefore, the network generates the best possible results without redesigning the output criteria [26]. Generally, an ANN has three layers: the input layer to accept the input, the hidden layer known as the black box [68], where the input is processed; and the output layer to convey the output result (Fig. 4A) [26].

If many nodes are present inside the hidden layer, it is referred to as a deep neural network (DNN) (Fig. 4B). Classically, convolutional neural networks (CNNs) belong to the DNN class and are appropriate for exploring highly complex data [42]. One promising aspect of a CNN is

that it automatically identifies important features without human intervention [69].

1.6. Unsupervised learning

Unsupervised algorithms (also called clustering algorithms) use unlabeled data. The results (new data to be analyzed) can be obtained in clusters or groups based on their similarity to the given data [42]. Here, the algorithm tries to match in the form of patterns [28]. The most common unsupervised ML algorithms are K-Means clustering and principal component analysis (PCA) [26,42].

1.6.1. K-Means clustering

This is a simple yet powerful approach for understanding data without labels. Here, the input data were categorised into clusters. Typically, a cluster refers to an assembly of points in the given data accumulated together owing to specific similarities. In this method, the 'k' centres (Fig. 5) are to be defined for every cluster and are to be placed at varied positions and distances from each other to obtain vivid results. Subsequently, each point in a given data set is connected to the closest centre [26]. This algorithm was described in detail by Hartigan [70].

1.6.2. Principal component analysis

PCA is a statistical method that facilitates dimensionality reduction [71]. The features required to build a model can be reduced because this approach can emphasise the influence of different features of a given dataset via the principal components [42]. In 1901, Karl Pearson first proposed this method [72–74]. The primary aim of this approach is to identify the condensed features that depict the original data in reduced
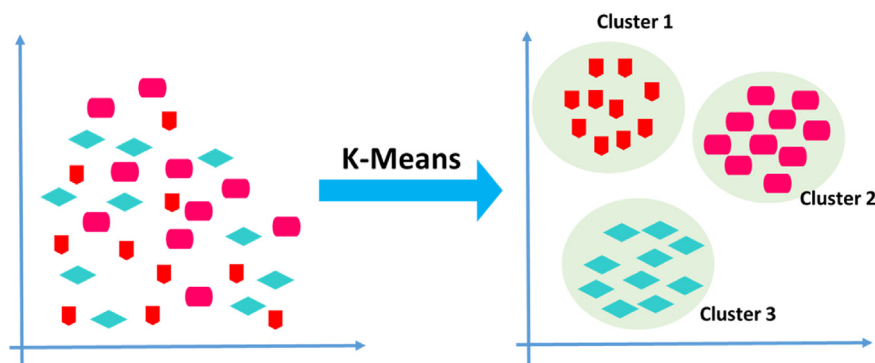

Fig. 5. Unsupervised learning model, K-means clustering.

subspace dimensions with less information loss. PCA models are useful for large amounts of data with multiple variables, big data with various observations for a given variable, and highly correlated data. The reduced size offers several benefits, including less space for storage, elimination of collinearity, two-dimensional (2D) or three-dimensional (3D) visualisation, and reduction of noise [72].

1.7. Applications of AI/ML in MP

1.7.1. Diagnosis/prediction

Sitaula et al. used publicly available data to detect MPV by adapting pre-trained deep learning methods. To accomplish this, 13 different pre-trained deep learning models were compared. Universal custom layers were added after fine-tuning. The results were examined regarding precision, recall, F1-score, and accuracy. The best model was selected, and majority voting over the probabilistic outputs was used to improve the overall performance. According to the evaluated findings, the ensemble approach performed best with a precision of 85.44%, recall of 85.47%, F1-score of 85.40%, and accuracy of 87.13% [75].

An MP classification method was developed from images of skin lesions. Classification can be performed using a Deep Pre-trained Network and Mobile Application. For this purpose, publicly available datasets and a deep transfer learning approach were used, and MATLAB was used for training and testing. The network with the highest accuracy was trained and created and using the TensorFlow software. This model was used in mobile devices after being transformed into the TensorFlow Lite model. The test results showed that the system can accurately classify images with an accuracy of 91.11% [76].

Abdelhamid et al. used publicly available images to classify MP. This was performed using transfer learning and the Al-Biruni Earth Radius optimization algorithm with a publicly available dataset. The obtained average accuracy of classification was 98.8% [77].

Ozsahin et al. used publicly retrievable data (images) for the classification and detection of MP and chickenpox lesions by adapting a deep learning framework [78]. A 2D CNN with four convolutional layers was used; three max-pooling layers were added after the second, third, and fourth convolutional layers. The CNN test accuracy was observed to be 99.60% and a weighted average precision recall score was observed to be as 99.00% [78].

A study reported the development of an MP model for diagnosis with Generalization and Regularization-based Transfer Learning approaches (GRA-TLA). This model can be used for classification which includes binary and multiclass classifications, and was evaluated on 10 CNN models conducted in three individual studies. The findings have shown that, in studies one and two, the model could differentiate between the individuals with MP and without MP accuracy, ranging from 77% to 88% when executed with Extreme Inception (Xception). In the third study, the Residual Network (ResNet)-101 outperformed multiclass classification, with an accuracy score between 84% and 99% [79]. Because of the limited data availability during the experiment, the authors pooled the data with images of patients' with MP [79].

A recent study reported using Particle Swarm Optimization (PSO) to select digital images to predict MP and its corresponding prevention. The images were collected from the International Skin Imaging Collaboration (ISIC), and the PSO model was compared with pre-trained deep learning models such as VGG16 ResNet50, InceptionV3, and Ensemble for MPV identification. The results obtained by the PSOMPX model were significantly superior, with an accuracy of 90.01% [80].

In one study, various deep CNN models were used with different multiple machine learning classifiers on skin images to predict MP diagnosis. Three CNN models, GoogleNet, Vgg16Net, and AlexNet, were utilized with naïve Bayes, K-Nearest Neighbors (KNN), Decision Tree, Random Forest, SVM classifiers. The results have shown that the Vgg16Net features and naïve Bayes classification model have given the best results, with an accuracy of 91.11% [81].

Ali et al. initially developed a dataset of skin lesions called the 'Monkeypox Skin Lesion Dataset (MSLD)'. This dataset contained images of chickenpox, measles, and monkeypox. Different pre-trained deep learning models were used to classify MP, followed by the additional development of a model which is an ensemble of the three. ResNet50 obtained the best overall accuracy of 82.96 ($\pm$4.57) % [82].

Another image-based classification of MP was conducted using integrated deep transfer-learning-based methods and a convolutional block attention module (CBAM). The aim was to deduce significant parts of the features to execute the image-based classification of MP. Here, five deep learning models, namely, Xception, VGG19, EfficientNetB3, DenseNet121, and MobileNetV2, were used together with integrated channel and spatial attention mechanisms. The results showed that Xception-CBAM-Dense layers had better results, with an accuracy of 83.89% [83].

One study reported using data-mining and AI methods to detect MP at an early stage. This approach is called Human Monkeypox Detection (HMD) and has a Selection Phase (SP) and a Detection Phase (DP) as the major phases. The SP attempts to select the best features, from which the DP can detect MP precisely and swiftly. The accuracy, precision, and recall values equal 98.48%, 91.1% and 88.91%, respectively for HMD approach [84].

A new method that could predict MP cases was developed by Eid et al. and was established on a Long Short-Term Memory (LSTM) deep network. The Al-Biruni Earth Radius (BER) optimization algorithm was used to fine-tune the hyper-parameters. A publicly accessible dataset was used for this investigation. The proposed model demonstrated a greater value when subjected to the evaluation criteria, including a Mean Bias Error of 0.06 [85].

MP was detected using a CNN on publicly available open-source image data. Correspondingly, the images were preprocessed, and 6 investigations were conducted using MiniGoggleNe with varied epoch numbers. The best model had 50 epochs and demonstrated an accuracy of 0.9708 [86].

The detection of MP was also examined using a CNN with a Transfer Learning approach [87]. In the CNN model, a function model for learning was incorporated by modifying the transfer-learning model and the hyperparameters. Among the various custom models used, the hybrid MobileNetV3-s model demonstrated an accuracy of 0.96. The image data were obtained from open sources and assembled as positive and negative [87].

In a previous study, a deep-learning approach was used to analyze photos of skin lesions from a public dataset. Five pre-trained deep neural networks, including AlexNet, SqueezeNet, GoogLeNet, ResNet-18, and Places365-GoogLeNet, were utilised to find the best model; among them, ResNet18 showed a 99.49% accuracy rate [88].

The early detection of MPV was achieved using a deep convolutional neural network (named MPXV-CNN) with images of skin lesions. A dataset of different photographic images of skin diseases (n = 139,198) were curated from various sources. The test dataset showed a specificity of 0.898 and sensitivity of 0.91 [89].

Different models have demonstrated a good accuracy from the above studies, ranging from 84% to 99.49% when applied to different datasets. Overall, the DL-ResNet18 method exhibits an accuracy of 99.49%.

1.7.2. Time-series forecast

One study predicted the transmission rate of the disease using Stacking Ensemble Learning (SEL) and ML techniques. The data from all reported MP cases were used in this study. The results showed that the SEL could be helpful in predicting MP with a root mean square error (RMSE) of 33.1075, MSE of 1096.1068, and mean absolute error of 22.4214 [90].

Researchers have conducted investigations to predict models and outbreaks and visualize them using time-series data. They used a decision tree, linear regression, random forest, AutoRegressive Integrated Moving Average (ARIMA) and elasticNet. The results showed that the ARIMA was best, with an R^2 of 0.9267 [91].

A study was conducted to assess the global spread of MPV using ML methods such as decision trees, ANN, RF, linear regression, CNNs and elastic net regression. Furthermore, events over time was assessed by a time-series motivated study adapting seasonal auto-regressive integrated moving averages (SARIMA) and ARIMA. Here, we analyzed the global spread of MP [92].

A report was published on the prediction of the MP occurrence by using regression analysis and a comprehensive statistical approach. This approach used a public dataset from Kaggle [93].

MP forecasting has also been studied using stochastic models. For this investigation, the multilayer perceptron (MLP) model was compared with the traditional method (the Box–Jenkins methodology, called the ARIMA model). These methods were employed on the MP dataset that is available worldwide and examined according to mean absolute error, mean absolute percentage error, and root mean square error. The MP adapts the ARIMA model (7, 1, 7) with the root mean square error of 150.78, while the MLP demonstrated a root mean square error 54.40. The MLP uses a sigmoid activation function with a single input and ten hidden neurons [94].

One group investigated the future probability of MP by using ARIMA and ANNs. The prediction showed that, for MP cases and deaths, ARIMA (5,2,3) and ARIMA (0,2,1) were more effective [95].

A tool that forecasts the MP experiment with 5 models: LSTM, ARIMA, stacking model, Prophet, and NeuralProphet on the data available from the CDC official website. The results demonstrated that the NeuralProphet performance was better, with an R2 of 0.76 and RMSE of 49.27 with an accuracy of 95% [96].

1.7.3. Sentiment analysis

Sentiment analysis was performed using Twitter posts with unsupervised ML methods [97]. Bidirectional Encoder Representations from Transformers (BERT) were used. Subsequently, topic modelling was conducted, particularly BERTopic and physical thematic exploration. The results showed that 5 topics were grouped into 3 themes [97].

Sentimental analysis was conducted to understand people's approaches to MP using natural language processing (NLP). Twitter posts have been analyzed that were posted from June 1, 2022, to June 25, 2022. The

Table 1
Artificial intelligence/machine learning techniques on monkeypox.

| Disease name	Type	Dataset	Method	Reference
MonkeyPox	Detection	Publicly available data	Deep learning	[75]
	Classification	Publicly available skin lesions images	Deep transfer learning approach	[76]
	Classification	Publicly available images	Transfer Learning and the Al-Biruni Earth Radius	[77]
	Classification and detection	Publicly retrievable images	CNN	[78]
	Classification	Patients images	Generalization and Regularization-based Transfer Learning approaches (GRA-TLA) for binary and multiclass classification	[79]
	Prediction and Diagnosis	Images from ISIC	Particle Swarm Optimization	[80]
	Classification	Skin images	Vgg16Net features, Naïve Bayes	[81]
	Classification	MSLD	Deep Learning	[82]
	Classification	MSLD	Xception-CBAM-Dense layers	[83]
	Detection	Data mining	HMD	[84]
	Prediction	Publicly accessible dataset	LSTM-BER	[85]
	Detection	Publicly accessible images	CNN	[86]
	Detection	Image data open sources	Hybrid MobileNetV3-s	[87]
	Detection	Image data open sources	DNN	[88]
	Detection	Image data curated from different sources	MPXV-CNN	[89]
	Transmission rate	All the reported data	Stacking Ensemble Learning (SEL)	[90]
	Prediction, Outbreak Forecasting, Visualization	–	ARIMA	[91]
	Time Series Analysis	–	ARIMA and SARIMA	[92]
	Forecasting MP prognosis	Public dataset	Regression analysis and comprehensive statistical approach.	[93]
	Forecast	Our World in Data	MLP	[94]
	Forecast	Literature	ARIMA	[95]
	Forecast	CDC official website	NeuralProphet	[96]
	Sentiment analysis	Twitter posts	BERT	[97]
	Sentiment analysis	Twitter posts	NLP	[98]
	Sentiment analysis	Multilingual Twitter posts	TextBlob annotation- Lemmatization-CountVectorizer -SVM	[99]
	Sentiment analysis	Twitter posts	Hybrid CNN-LSTM model	[100]
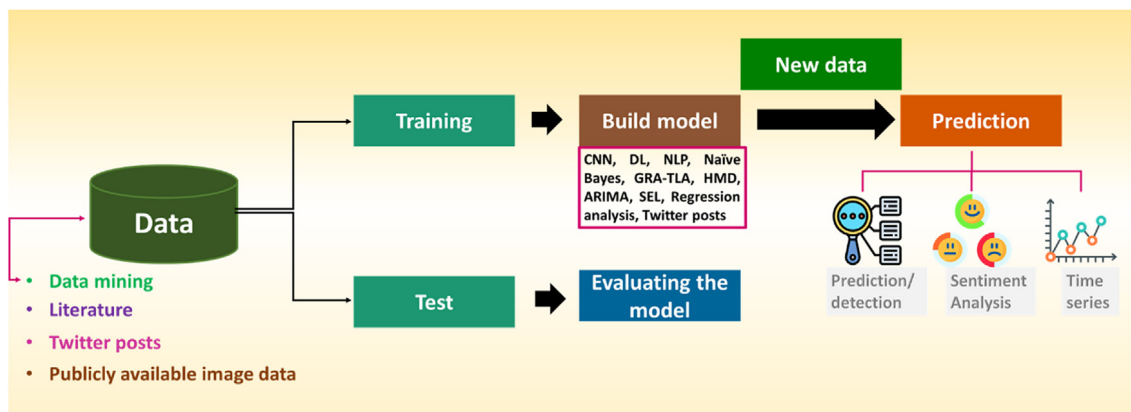
Fig. 6. General workflow for the detection of monkeypox using machine learning.

analysis was executed in two parts: in Part 1, sentiment analysis was conducted to understand the people's views, and in Part 2, Latent Dirichlet Allocation (LDA) topic modeling was conducted to capture the noteworthy aspects during the discussion. The results showed that 48.16% of the tweets displayed neutral sentiments, 28.82% showed positive sentiments, and 23.01% demonstrated negative sentiments. Upon topic modelling from negative sentiments tweets, concerns were about death, severity, lesions, airborne MPV, and MP vaccines. [98].

Sentiment analysis was conducted on multilingual MP tweets with TextBlob and VADER. Subsequently, 56 classifier models were used with lemmatization and stemming approaches for vocabulary normalization, and CountVectorizer and TF-IDF were employed for vectorization. Learning algorithms, such as SVM, KNN, naïve Bayes, RF, XGBoost, Logistic Regression, and MLP, were used. The findings with TextBlob annotation, Lemmatization, CountVectorizer, and SVM showcased an excellent accuracy of 0.9348 [99].

Sentimental analysis was conducted on Twitter posts using hybrid models, including LSTM and CNN. The hybrid CNN-LSTM model was predicted with an accuracy of 83% [100]. Comprehensive applications of AI/ML in MP are presented in Table 1 and Fig. 6.

These results will help researchers and healthcare professionals to understand and diagnose the disease with greater accuracy. Furthermore, the sentimental analysis results demonstrated public opinion and views on the disease. Most importantly, models that predict early disease detection plays an important role in curbing its spread.

2. Limitations of the study

The primary limitation of the study is limited resources available for the data to perform the training and test analyses. Most investigations have been conducted using open-source images of skin lesions. Investigations and analyses with other data, such as blood samples, gene perturbations, and biomarkers, may further strengthen this study. A comprehensive method can be developed to overcome and reduce errors and false-positive results. Further studies should be conducted to address strains with mutations to reduce the number of positive cases.

3. Conclusion

Recently, AI/ML has become popular in healthcare and disease diagnosis. Rapid results were obtained with greater accuracy. The present review focuses on various AI/ML approaches for understanding MP. This review shows that the sentiment analysis is most widely used method. Furthermore, a forecast of the MP disease was conducted. Through these studies, we can prepare to counter this disease.

Compliance with ethical standards

Conflict of interest

The author declares no conflict of interest.

Ethical approval

This article contains no studies involving human participants or animals.

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