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Research Article

Predictive Modeling and Analysis of Monkeypox Outbreaks Using Machine Learning Techniques

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ABSTRACT

As Monkeypox becomes a prevalent public health issue, it is important to develop advanced detection and prediction methods that will inform public health strategies that govern Monkeypox prevention. This study employs machine learning methods to analyze and predict Monkeypox case trends. In particular, features on new cases and deaths were applied to regression and classification models to predict the total number of Monkeypox cases and new case probablity. The regression models that were applied included Linear regression (LR), Decision Tree Regression (DT), Random Forest Regression (RF), Support Vector Regression (SVR), and K-Nearest Neighbor Regression (KNN), with total cases as the outcome. Among regression methods, the Random Forest Regression model performed the best with a Mean Squared Error (MSE) of 92,425,437.81 and R-squared of 0.06, indeicating moderate predictive ability. The methods were also similar to predict new cases, and once again the same algorithms were applied to classification methods, including Decision Tree (DT), Random Forest (RF), and K-Nearest Neighbor (KNN) classification, and each model achieved an accuracy score of one (1.00), indicating no new cases would be missed. These results provide evidence that these are effective machine learning methods, and random forests in particular provides the best predictive capability for Monkeypox case trend analysis. The results illustrate how these models can assist data-driven decisions in public health, and evidence-based preparedness and response for future Monkeypox outbreaks.

1. INTRODUCTION

Artificial Intelligence (AI) has established itself as one of the most powerful technologies of the present time, generating innovation throughout multiple sectors [1]–[3], including finance, transportation, education, and manufacturing [4]–[7]. By simulating human cognitive functions such as learning, reasoning, and problem-solving, AI systems have the capability to process and analyze huge amounts of data more rapidly and with greater complexity than a human could [8]–[11]. Of the many applications for AI, its impact in the healthcare sector has been particularly significant. Disease diagnosis and treatment plans, medical imaging, outbreak prediction, and care delivery have all contributed to the evolving relationshipon how medical care is provided. In particular, AI-based solutions, especially those that leverage machine learning, are increasingly being used to support the public health response to the epidemic of infectious disease outbreaks by investigating patterns, modeling disease spread, and giving early warnings of potential outbreaks [12]–[14]. These capabilities are increasingly more vital to public health as infectious diseases emerge, such as monkeypox [15]. The availability of real-time data can help respond to public health threats and significantly reduce transmission while improving global health.

Monkeypox resurfaced again in recent months as sporadic outbreaks, central and west Africa being the new onset, have become an increasing public health threat in the last months of the year [16]. This virus was mostly rural in the past years, confined mostly to central and west Africa, but now the distribution has been increased on other parts of the globe, and any possible outbreak may be bigger than before. It has become easier for the virus to infect since the evidence of vaccination

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was recently eliminated and, therefore, casting the shadow of a disease similar to smallpox. It has become important, therefore, to improve prevention and predictive measures [15]. Monkeypox, the other zoonotic disease, similar to smallpox belonging to the orthopoxvirus family, but generally it is mild and in many cases mortality is low, or there could even be a zero mortality rate [17]. The most dangerous thing is that it is a serious threat to resource-limited areas where, if the infections get out of control, such places would not be able to deal with them because their health-care systems would have already been overwhelmed. Considering the increased global travel and migration networks, monkeypox poses a novel level of risk that needs urgent attention to set up and implement the international health interventions. [18].

ML recently used in epidemiology for early warning and predictions of disease outbreaks [19]. The usefulness of ML algorithms is primarily derived from the fact that they analyze large amounts of complex information and make sense of these patterns in forecasting outbreaks [20], [21]. Starting with influenza to COVID-19, infectious diseases have had their respective predictions, risk regions, and even the allocation of healthcare services done by machine-learning models [22], [23]. When it comes to monkeypox, ML would entirely change how we anticipate and deal with the outbreaks by utilizing historical data from cases and deaths to estimate future case numbers and the onset of new outbreaks, thus feeding critical information to health authorities and policymakers [24].

The research aims to analyze various machine learning techniques for prediction of monkeypox and virus transmission dynamics. To realize this objective both regression and classification methods will be involved to complete two objectives: forecasting the total number of monkeypox cases and the probability of new case events occurring. Regression models will allow for longer term insight into the change of cases over attempts to predict how monkeypox will spread and how many cases overall there will be over time. Classification models will give a more immediate estimation concerning the likelihood that that new outbreaks will happen, and therefore identify areas at greater risk for future cases [25]. Therefore, these two approaches would work together to build a more integrated framework for understanding and forecasting the transmission patterns of monkeypox. The machine-learning techniques applied in this research include, linear regression, decision trees, random forests, support vector machines, and K-nearest neighbors. Each of these models is selected based on previous studies that validated their robust and reasonable performance for both forecasting COVID-19 regressions and classifying expected future COVID-19 cases. For regression analysis, the models will rely on historical data of new cases and deaths to make predictions about an overall total new case. For classification purposes, these models would be used in similar data in order to predict the chances of new cases in monkeypox will happen. The two experiments allow for both continuous (regression) and categorical (classification) in monkeypox data and higher-level insight into the dynamics of transmission among cases.

Notwithstanding the expanding literature on monkeypox, there has been near exclusive emphasis on the clinical disease presentation, transmissibility, and measures to contain or mitigate future outbreaks; there is a notable absence of the use of predictive analytics to derive anticipation of future outbreaks [26]. This study fills that absence through the application of machine learning algorithms to publicly available health datasets, with the intent to present actionable findings to inform future public health responses. In utilizing regression and classification types of models, we are able to present a more detailed understanding of the expansion of monkeypox through providing consideration of the overall magnitude of monkeypox outbreaks in addition to penetrating understanding of the probability of new cases occurring.

In addition to its contribution to the academic literature, this work provides practitioners the tools to monitor and manage outbreaks of monkeypox. Accurate predictive models are crucial in allowing public health officials to enact effective preventive measures such as vaccination campaigns, resource allocation, and public health messaging [27]. Machine learning techniques provides a flexible model that is capable of updated predictions as a new variant emerges or a transmission route change. Thus, machine learning provides a scalable and flexible approach to accurate predictive models as new data become available.

Research related to monkeypox is quickly increasing in number; however, only a few reports have examined the differing clinical features, routes of transmission, and containment processes for the virus. This significant gap is in predictive modeling to prepare for future outbreaks [26]. Using machine learning methods on monkeypox public health data, this study seeks to fill the gap in knowledge by providing useful information for public health responses. Both regression and classification models will enhance our understanding of how monkeypox transmits between cases, addressing both total outbreak size and probability of new cases.

The implications of this disaster bring both academic and operational benefits in the detection and management of monkeypox outbreaks. If the appropriate predictions are available, health authorities can react accordingly in relation to vaccination campaigns, resource allocation, and public health notifications [27]. The power of this model is dependent on its ability to adapt: as variants of the virus emerge or modes of transmission change, machine learning will be a suitable prediction about outbreaks. Scaling up with data growth provide assurance for the capability of modeling that can continue to be utilized to predict future instances in the most agile manner with an expanding dataset.

2. ARTIFICIAL INTELLIGENCE AND HEALTHCARE: AN OVERVIEW

In contemporary healthcare, artificial intelligence (AI) is an incredibly disruptive force that allows for the most innovative response to some of health care's most complex challenges. AI technologies provide the ability for machines to perform such human-like tasks as reasoning, learning, and decision-making. That may be applied to reshaping some areas of diagnosis, treatment, patient monitoring, and administrative work. This chapter discusses the components of AI in health care to include applications, benefits, and ethical considerations with the dynamic context of AI developments.

2.1. The Evolution of AI in Healthcare

Over the past several decades, artificial intelligence (AI) has changed considerably in healthcare [28], [29], from rule-based expert systems (which were groundbreaking but struggled with adaptability and scalability) to machine learning (ML) and deep learning (DL) based approaches much happier to find patterns in large datasets and enhance their performance more autonomously without programming [2], [30], [31]. AI applications in modern practice are numerous and diverse and can be found across different specialties. For instance, in the field of radiology, AI-based algorithms are used to analyze and interpret medical imaging, leading to more accurate diagnostic decisions and more efficient workstreams [32], [33]. In genomics, AI is used to analyze complex genomic data, enabling personalized and targeted interventions. Surgical robots, with AI, are meant to provide precision and control beyond what a human can offer, leading to fewer surgical complications and improved patient safety [29]. Finally, virtual health assistants powered by AI and natural language processing engage with patients and provide timely medical information, which aids in follow-up care and adherence to treatment plans [34].

2.2. Applications of AI in Medical Diagnostics

A primary area of advancement in the use of artificial intelligence in healthcare is medical diagnostics. In recent years, development in machine learning [35], specifically convolutional neural networks (CNNs) [36] has enabled artificial intelligence systems to evaluate medical images at an unparalleled level of accuracy. By training models on amounts of labeled images, researchers have been able to create systems that detect minute patterns and anomalies that a human observer may overlook [37]. Many CNN-based tools have shown to have comparable or greater diagnostic accuracy than experienced clinicians. With the widespread use of artificial intelligence tools in radiology for analyzing and evaluating X-rays, MRIs, and CT scans, materialization of artificial intelligence in this subfield has now occurred [38]. Movement to detect a breadth of conditions, from lung diseases to bone fractures, or tumors, or vascular abnormalities, is feasible. The artificial intelligence interprets complex data in a fraction of the time a radiologist would take, resulting in not only expedited and accurate diagnoses for the radiologist, but also aids in the prioritization of pathways to care for acute patients [39]. Others have mentioned this is especially critical when individuals do not have access to a radiologist, where a timely diagnosis could save lives. Artificial intelligence integration is occurring outside of radiology, with some important examples being in pathology and dermatology [40]. For example, in pathology, artificial intelligence algorithms are used to evaluate digital slides of tissue, identifying cancerous cells while simultaneously quantifying characteristics in the tissue, all of which are performed with accuracy that increases confidence in the diagnosis [41], [42]. The applications of this technology can be used in a primary diagnosis, or supporting a secondary review of the diagnosis, where it provides definitive evidence reducing variability between pathologists, thus reducing variability across institutions. In dermatology, particularly involving melanoma, identification and classification of skin lesions by deep learning models has been developed to a level of accuracy similar to dermatologists [43]. The work of designing artificial intelligence algorithms do not stop with creating the diagnosis, but have worked rapid processing times into smart phone apps and tele dermatology, allowing early detection and triaging for care, especially in remote locations. Another example of what we can do with artificial intelligence in healthcare is eye pathology—specifically diagnostic criteria such as ages related macular degeneration, glaucoma, and diabetic retinopathy, where retinal scans are analyzed [44]. Early detection of common causes of vision loss through diagnostic imaging with artificial intelligence is critical. In summary, artificial intelligence in medical diagnostic tools continue to improve accuracy, efficiency, but also increase availability of enhanced healthcare treatment systems. Development of algorithms using diverse, representative datasets will aid in continued dependability and fairness in diagnostics and generalize clinical practice of individuals at a population level transitioning from providers to patients to a more systematic, data-based delivery of care.

2.3. AI in Treatment and Personalized Medicine

The emergence of artificial intelligence has been disruptive in the transformation from a singular standard of care approach to personalized medicine. The combination of massive and varied datasets (evidence-based literature, genetic/genomic, social/health risk factors, electronic health records, etc.) and AI technologies has enabled personalized treatment recommendations that fit a patient's biology, environment, and health history [45]–[47]. The personalized approach will increase the precision, outcomes, and safety of care for patients, especially those with complex and chronic disease. One of the most powerful areas where AI has contributed is the analysis of genomic data [48]–[50]. AI, particularly machine learning (ML), can analyze genomic data and identify mutations through the analysis of millions of genetic variants associated with disease risk, potential response to treatment, and prognosis. The results are used to better guide therapy for patients, especially in oncology, where significant/inconsistent genetic variability exists between tumors.

AI has the potential to maximize the effectiveness of treatment while minimizing exposure to ineffective and/or potentially toxic therapies [51]. In addition to oncology, personalized care driven by AI is being used in treating cardiology, neurology, and metabolic disease [52]. A practical example is within diabetes management, where patients use continuously monitoring of glucose observed devices [53], [54]. The AI algorithm rapidly predicts likely shifts in blood sugar levels and recommends personalized doses of insulin and/or dietary recommendations to treat the condition [55]. Within the same framework of behavioral analytics model, we see AI potentially managing aspects of mental health. The ML model can analyze behavior patterns and treatment histories, and recommend individualized treatment modalities [56]. Based on the analysis the patient and therapeutic relationship can be continuously optimized through AI recommendations and as severe or early signs of relapse appears.AI will also influence the dynamic iteration of the treatment protocol [57]. In real-time, the AI will learn from observation of patients within the framework of their environment and modify therapy strategies that efficiently reflect the patient's clinical status and changing health parameters [29], [58]. The AI learning does not only rely on real-time data but can include patient profiles based on the existing medical literature [59]. AI will also assist in predicting patient-reported side effects for medications and avoid bad effects before they occur [60]. As AI increasingly is relied upon to assist in clinical decision-making, we are seeing the framework for treatment to be designed, managed, and implemented shaped by AI. The natural partnership of AI analytics and personalized medicine, will ultimately advance better clinical outcomes for patients [47], and will be considered in improving efficiency within the allocation of resources and reducing healthcare costs. In conclusion, AI will eventually incorporate continuous oversight of the data and ethics that allow data-driven, individualized predictions to be the standard of care in medical practice.

2.4. Challenges and Ethical Considerations

Artificial Intelligence (AI) holds great promise to create transformative improvements in healthcare outcomes [61], however, the implementation of AI technologies into clinical healthcare settings presents a multitude of unique challenges and ethical issues requiring consideration toward ensuring fair and ethical use [62]–[64]. One of the primary challenges involves the quality, availability and representativeness of the data used to train AI systems [65], [66]. Medical AI technologies typically rely on massive amounts of patient data, including electronic health records, medical images, and genomic sequences [48], [67]. On the downside, these data-sets can be problematic due to inconsistencies, incomplete data, and a lack of standardization across different healthcare institutions. Additionally, many AI models are trained using data from specific populations such as patients from a well-resourced institution or geographic location [68]. This leads to algorithmic bias where the AI performs well with the majority population, but not well with patients that are represented less well [69], [70] (e.g., racial minorities, and patients with special conditions), perpetuating inequities in healthcare. Privacy and data security are also paramount. Patient data is sensitive, and misuse could result in discrimination and/or stigmatization and guarantee confidentiality of the data must be ensured [71], [72]. AI use in healthcare requires a rigorous framework to safeguard patient data, anonymize it, and protect against hacking and cyber security threats. Patients have a host of concerns related to how their information is used once it enters the AI ecosystem. It is important to facilitate patient control over their own information [73], [74]. Even anonymized databases could be unsafe, if combined with patient data from other sources, indicating that patient population's privacy may be violated. Transparency and explainability are also ethical challenges in implementing medical AI. Many high-performance AI models (e.g., deep learning systems) are opaque, or "black boxes", in the sense that the model may provide useful output without providing reason for the decision [75]. In the clinical space, outcome decisions can be life or death, and so this lack of explainability represents a serious concern. Clinicians need to be able to interpret AI recommendations and trust outputs before with integrating the AI into their decision-making processes [76]. As a result, there are increased calls for explainable Artificial Intelligence (XAI) methods to promote useful understanding of how algorithms interface with their models allowing for accountability, trust, and supporting clinical validation [19], [77]. Regulatory and legal standards have struggled to keep pace with the rapid development of AI technologies. In many regions, no consensus exists regarding how AI-based medical tools or algorithms should be defined, validated, and monitored.

An additional challenge on the ethical use of AI in healthcare is the susceptibility of AI models to adversarial attacks [78]. Adversarial attacks are intentional modifications of the input data in subtle ways that mislead an AI model into making a wrong prediction or classification with little to no indication of the tampering to the unaided human observer [79]. In a clinical context, this erroneous forecasting or misclassification could lead to dangerously wrong diagnostic information or treatment recommendations [78]. For example, the AI model could misclassify a malignant tumor as benign (and vice versa) in a medical imaging study if an imperceptible change to the image were applied that a radiologist could not detect. The concern of adversarial attacks assumes particular urgency and situational awareness of potential meddling when relying on AI models shows the need for AI models to be developed to demonstrate robustness to adversarial attacks. The potential constraining effect of adversarial vulnerabilities adds further legislative, legal, and social significance to the implementation of AI into healthcare settings where medical practitioners are required to place trust not only in the AI system's performance being correct, but also its safety and security from adversarial attack [80]. As healthcare shifts more towards AI-driven modalities of being practice, it becomes not only reasonable but essential to add adversarial robustness to the burgeoning conversations and discussions regarding explainability and fairness in AI to aid in the preservation as need of integrity in decision making within clinical fields of practice, and public trust with the use of AI technologies in healthcare settings [81]. The consideration of adversarial attacks shouldn't be overlooked as well, and easily should be regarded as a contextual concern that is included in discussions of AI governance, patient safety, equity, and ethical treatment in healthcare settings [19], [75].

Ultimately, ethical alignment and public trust are essential for the successful integration of AI in healthcare. AI systems need to be designed and implemented in ways that respect human dignity, uphold professional medical standards, and facilitate opportunities to engage in shared decision-making regarding patients' treatments with their healthcare providers [82], [83]. This should include the avoidance of AI processes that would dehumanize care and undermine the relationship between patients and providers [84], [85]. Participant stakeholders, including but not limited to patients, healthcare providers, ethicists, and policymakers, throughout the design and implementation stages of the technological development process can be beneficial for ensuring appropriate alignment between the technology and community values. Governance, education, and ongoing conversations will be important in ensuring that a multidisciplinary approach to managing an increasingly AI-enabled healthcare environment. If we actively engage in the challenges presented by AI usage in healthcare, these systems will be able to realize their potential to improve health outcomes, as long as ethical principles, as well as rights to care, are guaranteed for all patients.

As illustrated throughout this chapter, artificial intelligence has notably improved healthcare delivery from early detection to personalized treatment and real-time monitoring using sophisticated models such as deep learning. This capacity is especially important for emerging infectious diseases where time is of the essence in detecting and intervening to contain outbreaks and preserve life. One infectious disease is monkeypox. The next chapter discusses works related to the methodology and results with discussion and conclusion utilized in this research, that predictive modeling and analysis of Monkeypox outbreaks using machine learning techniques. This practical application highlights AI's role in responding to a health emergency, as well as offers an innovative way for intelligent systems to respond to future outbreaks.

3. RELATED WORKS

A study by [86] compared 13 pre-trained deep learning models to determine early detection of the Monkeypox virus, with the intention of curbing its spread. The models were fine-tuned and then ensemble and had great performance where average Precision, Recall, F1-score, and Accuracy scores of 85.44%, 85.47%, 85.40%, and 87.13% achieved, outperforming the previous methods. Another study [87] used optimized Long Short-Term Memory (LSTM) model with BER (Al-Biruni Earth Radius) optimization algorithm fine-tuning it to a low Mean Bias Error of 0.06. The BER-LSTM model was more powerful than six machine learning models and four optimization algorithms, validated by ANOVA and Wilcoxon tests.

In [88], authors proposed the "Monkeypox Skin Lesion Dataset (MSLD)" for early diagnosis of Monkeypox, the virus which has some similarities with chickenpox and measles. The data consisted of images of Monkeypox, chickenpox, and measles, and various pre-trained deep learning models were utilized in the study. The ResNet50 model achieved an accuracy of 82.96%. The prototype web application for online screening was built; yet, this requires larger datasets for good generalization. The other study [89] evaluated the application of machine learning models compared to the traditional time series models in the forecast of Monkeypox cases. The comparison showed that MLP achieved an RMSE of 54.40, as opposed to 150.78 from ARIMA, proving the merits of machine learning for case predictions.

Lastly, a study [90] analyzed public sentiment regarding Monkeypox using a hybrid CNN-LSTM model to classify Twitter posts with the hashtag #Monkeypox. The model achieved 83% accuracy, with specificity, recall, and F1-scores of 99%, 85%, and 88%, respectively. The analysis revealed that 45.42% of users expressed neutral sentiments, while 19.45% expressed negative or fearful feelings, contributing to raising public awareness about the Monkeypox outbreak.

These studies demonstrate the growing reliance on AI, deep learning, and social media analytics in tackling public health crises like Monkeypox.

4. METHODOLOGY

This chapter outlines the research methodology used in the study. This chapter describes the systematic procedures carried out to realize the study's aims, including data collection, data preprocessing, data analysis, and model development. The selected research method was determined to maximally guarantee the reliability and validity, and scientific rigor of the research outcome, providing the researcher with an ordered and organized methodology to realize meaningful and practical contributions (outcomes) to the study area. Figure 1 below depicts the research study process taken in a flow chart to visualise the sequence implemented in the study including the key steps. This chapter describes the effects of each stage in more detail below:

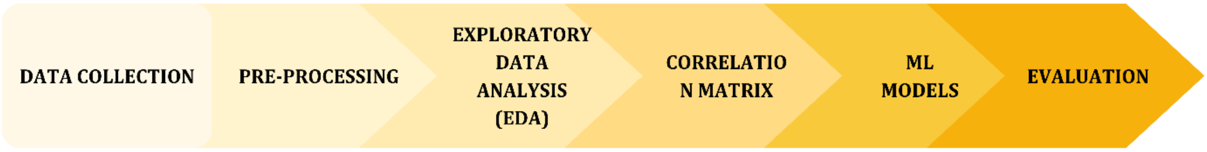


Fig. 1. Methodology steps

4.1. Data collection

The data were gathered from [91] based on the cases of reported monkeypox that occurred in different areas. In total, the data set consists of 79,045 entries: this means the dataset represents a number of reports about confirmed or suspected monkeypox cases. This data set ranges widely both in time and space, and some critical characteristics of the disease were registered. The key features of the dataset will include: date of reporting, location of occurrence, demographic details about patients, and a binary classification: confirmed or suspected. The dataset was constructed to allow applying machine learning algorithms by serving as a good platform for training algorithms aimed at future outbreaks prediction, risk group identification, and key factors for spread understanding. The supervised learning models rely on the fact that there is a clear difference between confirmed and suspected cases: thus, the algorithm is capable of detecting patterns in these cases, differentiating between true outbreaks and cases flagged as false positives or suspected cases.

4.2. Preprocessing

The dataset underwent many trials, exercises, and processing before the model ran. This helped in making sure data quality for regression and classification was satisfied on the dataset. The features taken from the dataset were very well selected. Features such as `new_cases` and `new_deaths` were taken as predictors (input features). Additionally, `total_cases` is a regression target, while another target of the binary classification is derived based on `if new_cases > 0`, then 1, otherwise 0`. The cleaning and standardization were confirmed done in a manner to assure that there would be no considerable variability in records that may introduce a bias or distortion in later analyses of the data. Also, duplicates and incomplete records were also removed to avoid bias and distortion in subsequent analyses. A graphical description of features is provided in Figure 2. Every single record should be carefully reviewed and checked in respect of inclusion into the study bounds.

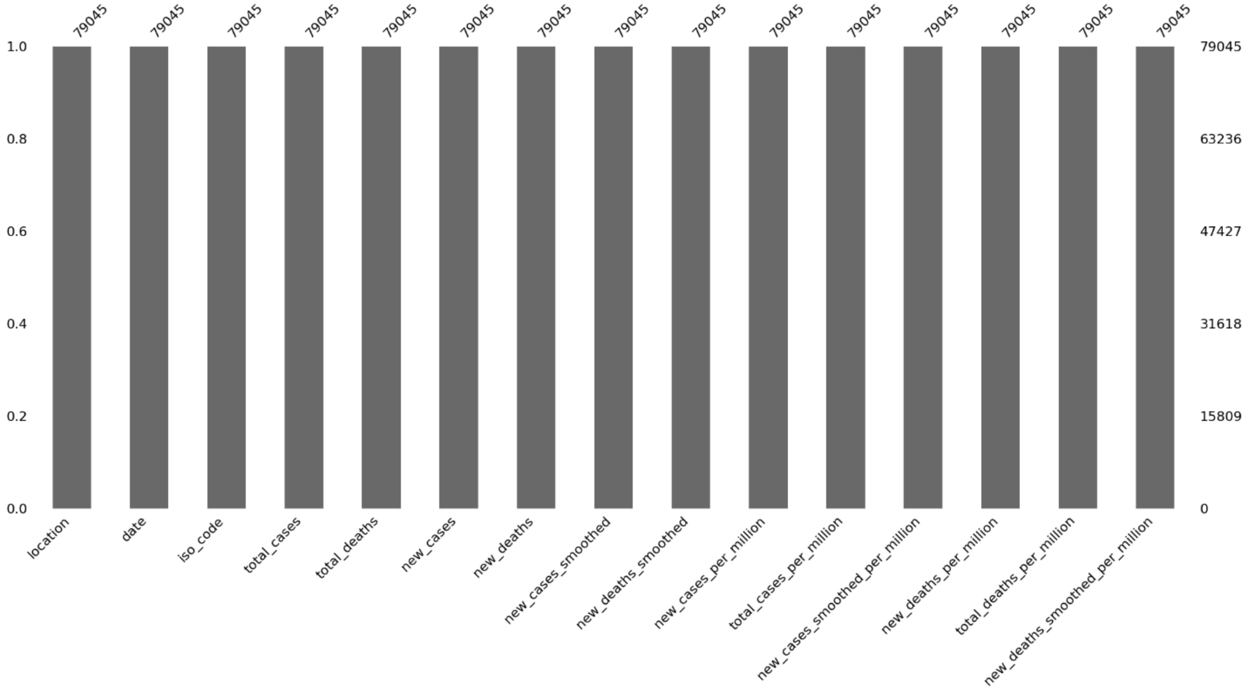


Fig. 2. Main features with total entries

The dataset was split into training and testing sets using an 80/20 split to evaluate the model's performance accurately. For both regression and classification tasks, 80% of the data was used to train the models, while the remaining 20% was reserved for testing. This split was done using the `train_test_split` function [92], ensuring a consistent random state for reproducibility. To improve model performance and ensure comparability across different algorithms, feature scaling was applied. Standardization was performed using the `StandardScaler` function, which scales the features to have zero mean and unit variance. This step was crucial for algorithms like SVM [93] and KNN [4], which are sensitive to the scale of input features. The scaling transformation was fitted on the training set and then applied to both the training and testing sets to prevent data leakage. These preprocessing steps laid the foundation for the subsequent modelling process, ensuring the data was clean, well-structured, and appropriately scaled for machine learning models.

4.3. Exploratory Data Analysis (EDA)

The following analysis focuses on several visualizations that provide insights into monkeypox cases and deaths over time, by country, and by location. Figure 3 presents two side-by-side time series plots: one for daily new cases (in blue) and the other for daily new deaths (in red) due to monkeypox. The epidemic appears to have peaked around August 2022, with daily new cases exceeding 14,000 at the height of the outbreak. Following the peak, there was a sharp decline in cases by late 2022, with sporadic and minimal case reports extending into 2024. The death toll followed a similar trajectory, with the highest number of daily deaths (about 30) occurring in the same period. However, the number of deaths consistently remained much lower compared to cases, and by 2024, both new cases and deaths had significantly decreased, indicating effective containment and management of the outbreak.

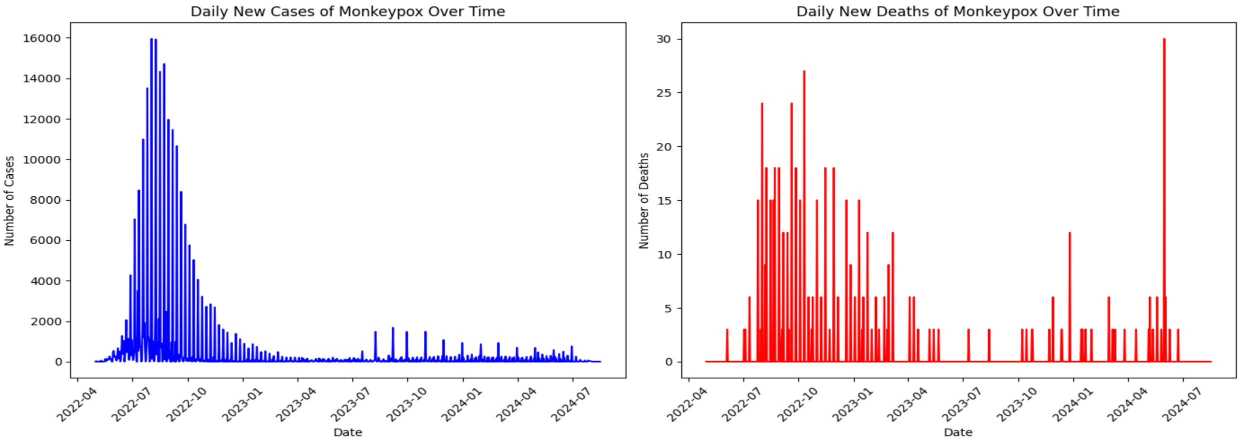


Fig. 3. daily new cases and daily new deaths due to monkeypox

Figure 4 expands the scope of analysis to larger geographical locations, grouping cases by continents or regions. North America leads with the highest number of total cases, followed by Europe. South America also shows a considerable number of cases, while Africa and Asia report significantly fewer cases. The global distribution indicates that the outbreak was more concentrated in the Western Hemisphere, particularly in North America and Europe. This could reflect differences in travel patterns, healthcare systems, and public health interventions.

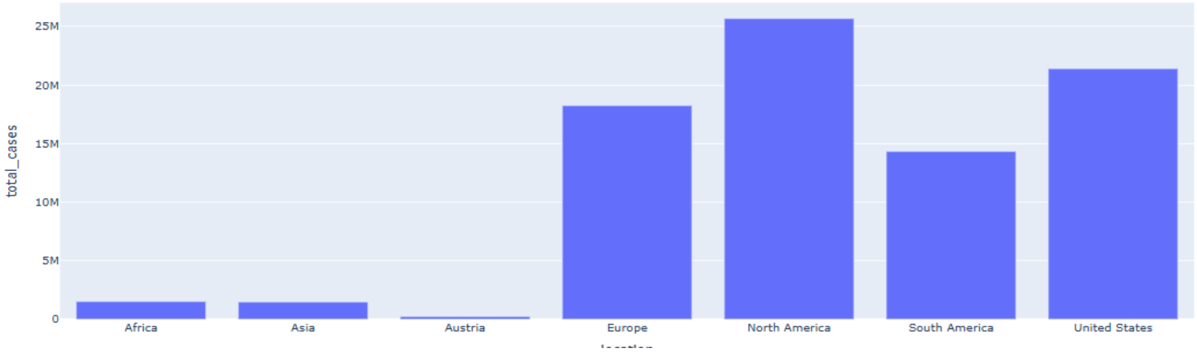


Fig. 4. The scope of analysis to larger geographical locations

Figure 5 highlights the distribution of monkeypox cases across various countries. The United States experienced the highest number of cases, with over 20 million reported. Brazil follows with a substantial number, above 5 million cases. Other countries like Spain, Germany, and France show comparatively lower case counts, with Canada having the least in this dataset. This graph suggests that North America, especially the U.S., was heavily impacted by monkeypox, possibly due to various factors such as population density, healthcare access, or response measures.

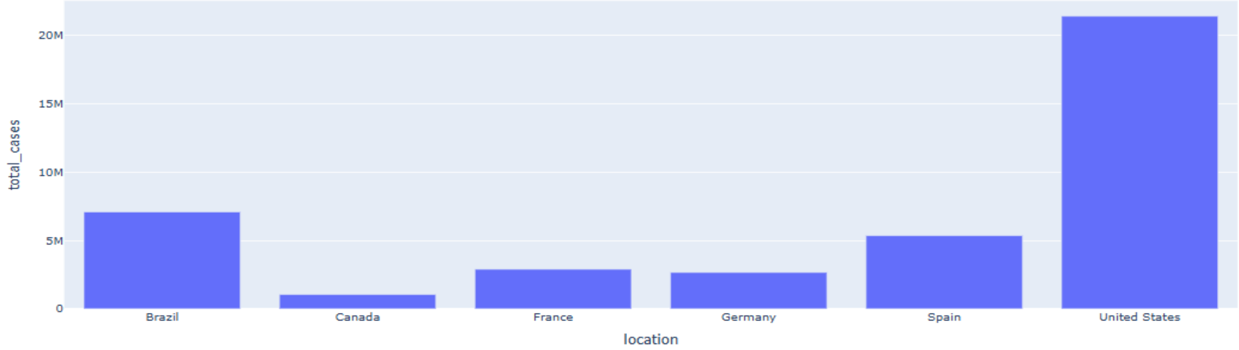


Fig. 5. The distribution of monkeypox cases across various countries

Figure 6 provides insights into the total number of deaths by location. North America has the highest death toll, with over 60,000 fatalities, while the United States also has a significant number of deaths, close to 40,000. Africa and South America follow, though with much lower death counts compared to North America. The distribution of deaths somewhat mirrors the case distribution, with North America bearing the brunt of both cases and fatalities. However, it's notable that Africa, despite having relatively fewer cases, still experienced a substantial number of deaths, possibly pointing to challenges in healthcare infrastructure or disease management.

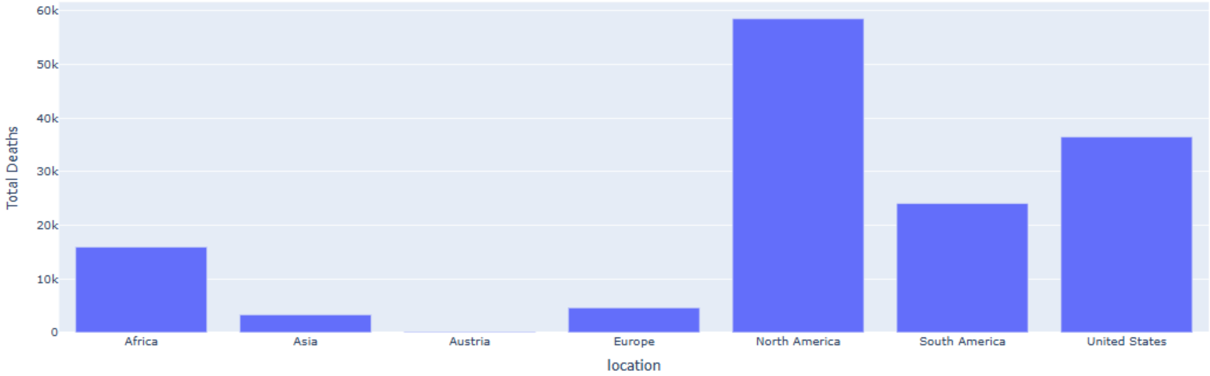


Fig. 6. The total number of deaths by location

Figure 7 illustrates the total number of deaths across various countries. The x-axis lists different countries, while the y-axis represents the total number of deaths. The red line shows the death toll for each location, with the height of the peaks corresponding to the number of deaths. Most locations show relatively low death counts, as indicated by the flat portions of the line. However, several countries experience noticeable peaks. Notable spikes include locations like the United States and Vietnam, which show significantly higher death totals, particularly the United States with a sharp rise nearing 100,000 deaths. Other smaller peaks can be observed in regions like Morocco and Russia.

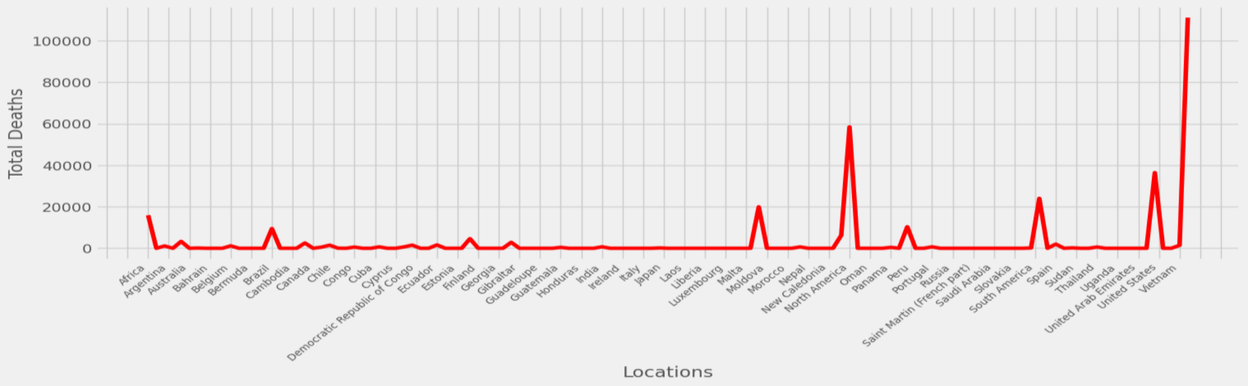


Fig. 7. The total number of deaths across various countries

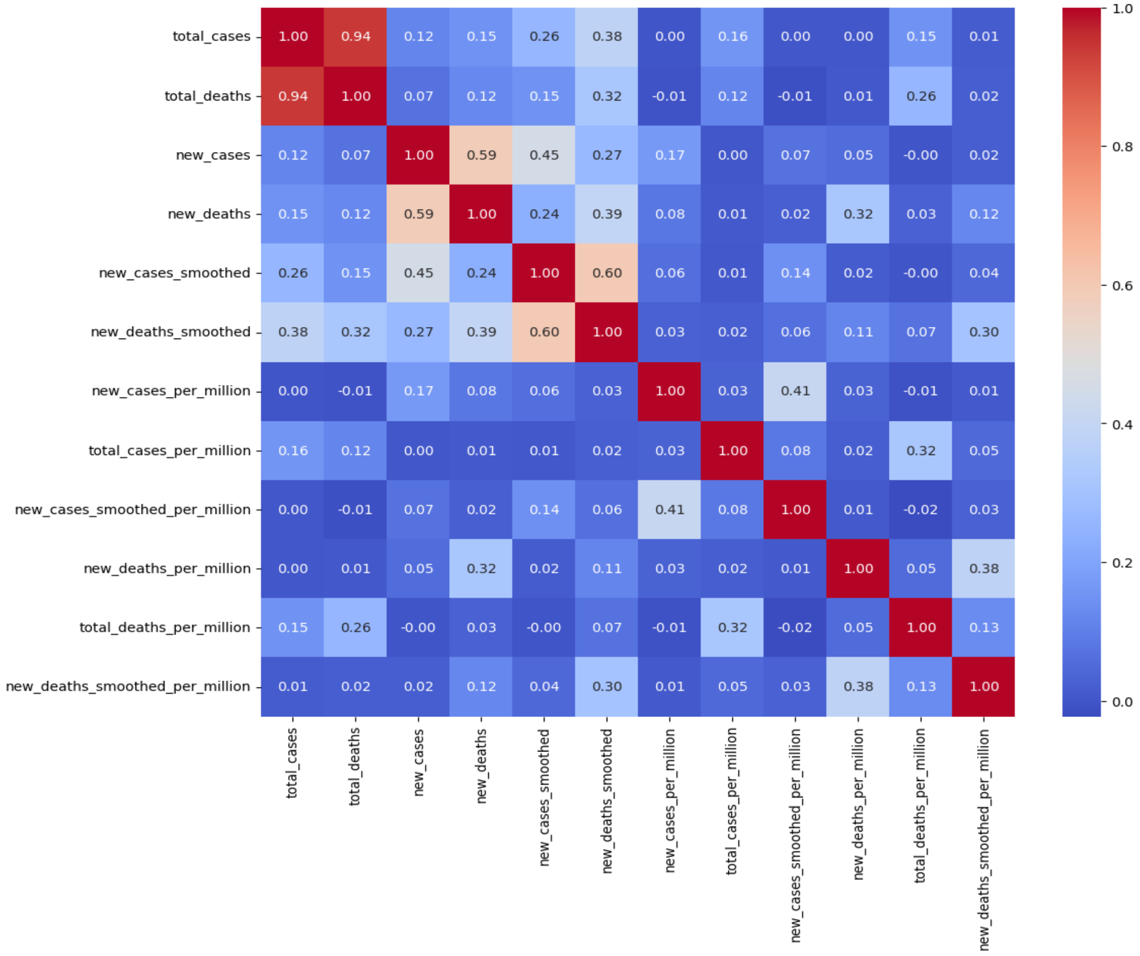
The visual data suggests that the monkeypox outbreak had a significant global impact, with the U.S. and North America being the most affected in terms of both cases and deaths. The trend over time shows a rapid increase and subsequent decline in both new cases and deaths, suggesting that public health measures eventually curbed the spread of the virus. However, regional disparities in case and death counts highlight the different ways the disease affected various parts of the world.

4.4. Correlation Matrix

To better understand the relationships between the features in the dataset, a correlation matrix was computed for all numeric variables. This matrix presents a statistical indicator summarizing the strength and directionality of the linear relationship between pairs of features, within the range of -1 to 1. Values of 1 correlate to positive relationship strength while values of -1 correlate to negative relationship strength. As the value approaches 1, a stronger positive relationship can interpretation or analysis support, values would indicate a more negative linear correlation. A value of zero indicates that no linear relationship is found between the respective features.

A data processing stage was conducted before performing the correlation coefficient matrix analysis. During the data processing stage, it was determined that all of the features were numeric. String-based data in columns was excluded (or when possible, converted to numeric using the appropriate method). Mainly, this was being done to avoid data type issues throughout the analysis process.

Once the dataset was formatted numerically, the Pearson correlation coefficient [94] was calculated for all pairs of features. The data were represented in a matrix and visualized in a heat map, which provides a good intuitive representation of the variables' relationships. This heat map employed color gradients (for example red was used for a strong positive correlation and blue was used for a strong negative correlation). The heatmap for the heat map is presented in figure 8.



	total_cases	total_deaths	new_cases	new_deaths	new_cases_smoothed	new_deaths_smoothed	new_cases_per_million	total_cases_per_million	new_cases_smoothed_per_million	new_deaths_per_million	total_deaths_per_million	new_deaths_smoothed_per_million
total_cases	1.00	0.94	0.12	0.15	0.26	0.38	0.00	0.16	0.00	0.00	0.15	0.01
total_deaths	0.94	1.00	0.07	0.12	0.15	0.32	-0.01	0.12	-0.01	0.01	0.26	0.02
new_cases	0.12	0.07	1.00	0.59	0.45	0.27	0.17	0.00	0.07	0.05	-0.00	0.02
new_deaths	0.15	0.12	0.59	1.00	0.24	0.39	0.08	0.01	0.02	0.32	0.03	0.12
new_cases_smoothed	0.26	0.15	0.45	0.24	1.00	0.60	0.06	0.01	0.14	0.02	-0.00	0.04
new_deaths_smoothed	0.38	0.32	0.27	0.39	0.60	1.00	0.03	0.02	0.06	0.11	0.07	0.30
new_cases_per_million	0.00	-0.01	0.17	0.08	0.06	0.03	1.00	0.03	0.41	0.03	-0.01	0.01
total_cases_per_million	0.16	0.12	0.00	0.01	0.01	0.02	0.03	1.00	0.08	0.02	0.32	0.05
new_cases_smoothed_per_million	0.00	-0.01	0.07	0.02	0.14	0.06	0.41	0.08	1.00	0.01	-0.02	0.03
new_deaths_per_million	0.00	0.01	0.05	0.32	0.02	0.11	0.03	0.02	0.01	1.00	0.05	0.38
total_deaths_per_million	0.15	0.26	-0.00	0.03	-0.00	0.07	-0.01	0.32	-0.02	0.05	1.00	0.13
new_deaths_smoothed_per_million	0.01	0.02	0.02	0.12	0.04	0.30	0.01	0.05	0.03	0.38	0.13	1.00

Fig. 8. Correlation matrix

The correlation matrix was helpful to understand how the different features behaved. This then informed the feature selection and model building choices made. For example, feature with high correlation were analyzed carefully to consider whether multicollinearity was affecting the regression models.

4.5. ML models

When investigating the use of machine learning to forecast monkeypox cases or investigate the spread of the disease by risk factors, many different machine learning models may be utilized. Each model has its advantages but may be more suited to the properties of the dataset variables and the types of predictions.

- **Linear Regression (LR):** is one of the most straightforward and interpretable models which assumes a linear relationship between the independent variables (features) and resulting variable (target). It tries to model the target as a weighted sum of input features. For predicting the number of monkeypox cases, linear regression would indicate how particular variables such as population density and mobility rates would provide a linear increase or decrease in case counts. Its simplistic structure may not allow for appropriate predictive performance in more complex datasets, especially if the relationship between variables is non-linear [95].
- **Decision Tree Regression (DT Regression):** is a non-linear model which utilizes a tree-like structure to partition the data into decision nodes based on each feature's value, producing predictions at the leaves. This type of model is highly interpretable and continues to reliably learn non-linear relationships making it an appropriate choice when predicting monkeypox case counts when the underlying interactions are complex. Decision trees are able to obtain local patterns in the data but can run the risk of overfitting, especially with the existence of noise [96].
- **Random forest regression (RF regression):** is a technique that utilizes the practice of ensemble learning; building decision trees, then combining their outcomes for a more stable output. As an ensemble model, the random forest is less prone to overfitting than would be the case for the single decision tree used to build the forest, and it often performs better overall than the latter. Random forests work well with large amounts of data and many features, such as can be found when predicting monkeypox outbreaks across diverse geographic areas. This model, by average of several trees, can better account for non-linear relationships and interactions between variables than can models based on linear assumptions [97].
- **Support vector regression (SVR):** is an effective method that attempts to fit the best hyperplane, based on a threshold of error. In comparison to linear regression, SVR can fit non-linear relationships by employing kernel functions to map out the data into higher dimension space. In the context of monkeypox case prediction, SVR can model complex trends particularly well when using non-linear kernel approach such as radial basis function (RBF). However, SVR can be excessively computationally intensive and may need fine tuning of parameters to limit overfitting or underfitting the data [98].
- **K-Nearest Neighbors Regression (KNN):** is non-parametric, predicting the value of a target variable by averaging the value of the outcome in the k nearest neighbors in feature space. This model works very well for target variables when the relationship between the features and the target outcome is extremely non-linear, and for data modeling patterns highly dependent on distance in the data. In terms of monkeypox predictions, KNN will be able to react well to local shifts in case counts based on historical data of adjacent regions or similar time periods. Some issues with KNN classifications are the sensitivity to the number of neighbors (k), and a strong reliance on a distance metric and distance metrics can have issues in high-dimensional or large datasets [98].

All models have unique advantages for predicting monkeypox cases or interpreting the underlying spread of the infection. The model choice refers to data complexity and relationships, data size, and prediction objectives. Often, it would be appropriate to explore several models and tune hyperparameters concurrently to gain a more complete picture of the best-performing model for any one task.

4.6. Evaluation

The process of evaluating machine learning models involve putting forth a number of metrics that report the predictive power of the models. For the purpose of predicting monkeypox cases, it is important to consider both regression and classification evaluation metrics depending on what task was completed. Below is a brief overview of how the different evaluation metrics such as Mean Squared Error (MSE), R-squared, Accuracy, Precision, Recall, the F1 Score, and ROC Curve applies to the models.

- **Mean Squared Error (MSE):** is a frequently used metric for evaluating regression models, such as linear, decision tree, random forest, support vector, and k-nearest neighbor regression models. MSE computes the average of the squares of the errors, or deviations between predicted and actual values. A lower MSE indicates that the model predicted values that are close to the actual target values. In predicting cases of monkeypox, random forests and support vector regression models experienced comparatively lower MSE because these models capture non-linear patterns, while linear regression had higher MSE when the functional relationship between features and target was not linear [99].
- **R-squared (R^2):** is another key metric for regression models, indicating the proportion of variance in the target variable explained by the model. An R-squared value closer to 1 signifies that the model is explaining a larger portion of the variance in monkeypox cases, thus making better predictions. Linear models like Linear Regression typically yield straightforward R-squared values, but non-linear models such as Decision Tree and Random Forest

may achieve higher R-squared values, especially when the relationships between input features and the target are more complex [99].

- **Accuracy:** Although accuracy is typically used for classification problems, it can be applied in regression tasks by setting threshold values for prediction correctness. In classification tasks, accuracy measures the proportion of correct predictions out of the total number of cases. However, in highly imbalanced datasets, such as those with a large number of non-infected individuals compared to infected ones, accuracy may not provide meaningful insights. For instance, in monkeypox case detection, high accuracy may still occur even if the model fails to predict the minority class (i.e., infected individuals) [100], [101].
- **Precision:** measures the proportion of true positive predictions out of all the positive predictions made by the model [22], [101]. In the context of predicting monkeypox outbreaks (when framed as a classification problem: outbreak vs. no outbreak), precision tells us how many of the predicted outbreaks were actually true outbreaks. Models like Random Forest and SVR, which are typically strong classifiers, often achieve high precision because they minimize false positives. High precision is essential when predicting events like disease outbreaks where false alarms could cause unnecessary panic.
- **Recall:** also known as sensitivity, measures the proportion of true positives out of all actual positives [9], [102]. In other words, it tells us how many actual monkeypox outbreaks were correctly predicted. In cases where it is critical to detect all possible outbreaks (even at the expense of some false positives), models with higher recall are preferable. Decision Tree Regression and Random Forests often perform well in this regard, as they are designed to capture complex patterns in the data.
- **F1-score:** is the harmonic mean of precision and recall, yielding a single measure to balance both concerns. A high F1-score means a model will score highly for both correctly predicting positive cases (outbreaks) and suffering from a low false positive rate [79], [102]. This metric is particularly useful when dealing with imbalanced datasets, as is often the case with datasets which deal with disease outbreaks, where both precision and recall are important. Random Forests and Support Vector Regression usually give a higher F1-score in comparison with simpler models such as Linear Regression on imbalanced data.
- **The ROC curve:** A graphical representation of a model’s ability to discriminate between classes is the receiver operating characteristic (ROC) curve. The ROC curve plots the true positive rate (i.e., recall) against the false positive rate, at different threshold levels. The area under the ROC curve (AUC) is a scalar metric of a model’s classification capacity. A model that produces a larger AUC has a higher classification capacity. In classification tasks like predicting whether a monkeypox outbreak will occur in a given region, Random Forest models or support vector machines (SVM) will often produce larger AUCs than simpler models with linear regression or KNN because they have greater capability to model complex boundaries. Therefore, a larger AUC represents the model’s ability to discriminate between outbreaks vs. non outbreaks [103].

5. RESULTS AND DISCUSSION

The effectiveness of the five machine learning models—Linear Regression (LR), Decision Trees (DT), Random Forest (RF), Support Vector Regressor (SVR), and K-Nearest Neighbors (KNN)—was assessed through their respective metrics of Mean Squared Error (MSE) and R-squared values. According to the evaluations, the models exhibited mixed performance in terms of predicting monkeypox, with some functioning more effectively than others. Table 5 displays the performance indicators of the machine learning models with respect to both the MSE and R-squared components or metrics. Of the models tested, it was revealed that the LR did not perform particularly well, with an MSE of 95,412,067 and an R-squared of 0.03, meaning that the model predicts 3% of the variance of the target variable. The model’s interpretation suggests that it struggled to find any sort of relationship between the features and the complex data. Any sort of linear regression will not work or accurately describe this set of data due to a high MSE value and no discernable linearity within the data. As for the DT, there was a small improvement over LR, yielding an MSE of 94,419,145.38 and an R-squared of 0.04, accounting for 4% of the variance. While the MSE value was fairly small and the numbers were reduced by only a little here, it might potentially point to a situation in which an algorithm has captured a few more non-linear relationships within this complex dataset. The fact that the Clean Green start to show only a little improvement in the R-squared value may imply that this model encumbered overfitting or that it lacked the depth necessary to understand or generalize future predictions on the unseen data. Overall, the Random Forest established itself as the best performing of the five models in terms of the MSE value at 92,252,507.97, and the R-squared value at 0.07, now accounting for 7% of the variance of the target variable. While this is not great, there is fairly little over here, and a variation improvement simply implies that Random Forests can aggregate multiple decision trees and better capture interaction effects in terms of predicting new cases while reducing the negative impact of overfitting. The MSE here indicates Random Forest produced more accurate predictions when it comes to predicting nominal values as set up when compared to the other models, enacting it as the most promising machine learning approach at this moment in time.Finally, in terms of poor performing on the models in terms of the goal of the piece, was the Support Vector Regressor (SVR), coming in with an MSE of 103,735,945.68, and most troubling, a negative R-squared of -0.05, a sign that this model performed even lower than the baseline models or simple conjunction of baseline data as the model did not even capture enough of a repeated measure to even account for the simple mean data. Overall, this indicates that SVR struggled even more with the basis of tuning hyperparameters associated with the scale and size of this problem not being approached in a way that could masquerade as the problem without more enhancements or adjustments to this problem.

Lastly, KNN had an MSE of 98,466,734.59 and an R-squared value of 0.00, showing that it failed to explain any variance in the data. While KNN can be effective in capturing local relationships, its performance may have been hindered by the high dimensionality or noise in the dataset, which could have limited its ability to generalize effectively. As a result, KNN's predictions were not significantly better than a baseline model.

While RF demonstrated the best performance in this analysis, none of the other models were able to explain a large portion of the variance in the data as that presented in table 1.

TABLE I. RESULTS OF PREDICATION FOR FIVE MODELS

ML method	MSE	R-squared
LR	95412067.00	0.03
DT	94419145.38	0.04
RF	92252507.97	0.07
SVR	103735945.68	-0.05
KNN	98466734.59	0.00

Figure 9 displays scatter plots comparing actual values against predicted values for five regression models that used in this study. Each plot includes a dashed line representing the ideal case where predicted values match the actual values perfectly. In all cases, the data points are dispersed around the diagonal line, indicating some error in the predictions. The Linear Regression and Support Vector Regression plots show more scattered data, especially for higher actual values, suggesting larger errors. The DT and RF models show better performance in capturing some patterns but still exhibit a wide range of prediction inaccuracies.

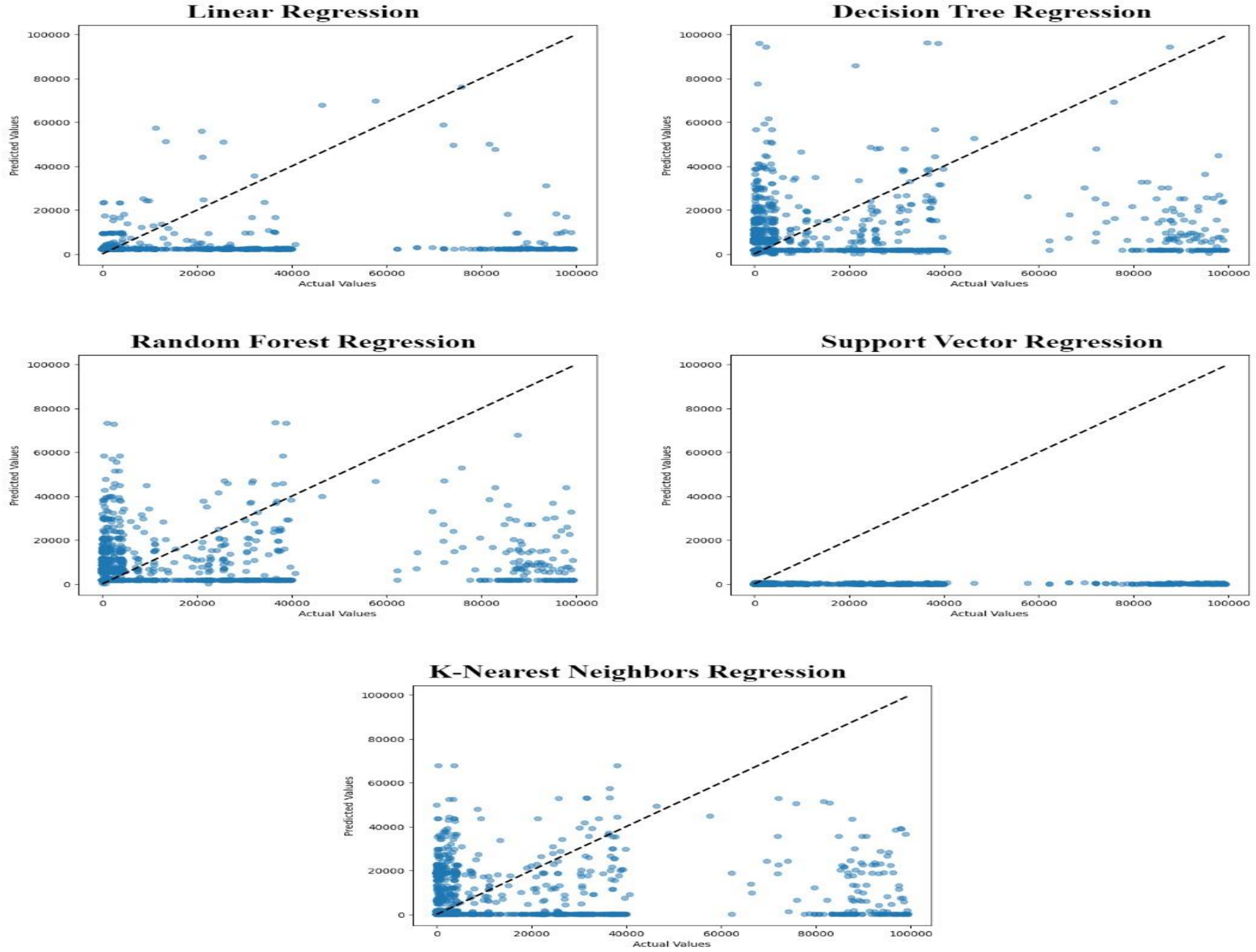


Fig. 9. Comparing actual values against predicted values for five regression models

The classification performance of the five models (LR, DT, RF, SVC, and KNN) was evaluated using Accuracy, Precision, Recall, and F1-score metrics. Overall, the results demonstrate strong predictive power across all models, with most achieving near-perfect or perfect scores in all evaluation metrics.

LR achieved an accuracy of 0.97, showing a high degree of correct predictions. Its precision was 1.00, meaning that all predicted positives were true positives, but its recall was lower at 0.53, indicating that only 53% of the actual positives were correctly identified. This imbalance between precision and recall is reflected in the F1-score of 0.69, which is a harmonic mean of the two. Logistic Regression, while highly precise, struggled to detect all true cases, possibly due to its limitations in handling non-linear decision boundaries.

DT delivered perfect results, with an accuracy, precision, recall, and F1-score of 1.00 across the board. This indicates that the model correctly predicted every instance without any errors, making it highly effective for this dataset. The ability of decision trees to fully capture both linear and non-linear patterns in the data likely contributed to this flawless performance. However, such perfect scores can sometimes indicate potential overfitting, where the model performs exceptionally well on the training data but might generalize poorly to unseen data.

Similarly, RF also achieved perfect performance, with 1.00 for all metrics. RF, which is an ensemble of decision trees, provides robust predictions by reducing overfitting and variance through averaging across multiple trees. The model's ability to capture complex relationships while avoiding the pitfalls of single decision trees contributed to its perfect performance on this dataset.

SVC performed slightly below Decision Tree and Random Forest, with an accuracy of 0.99 and a precision of 1.00, indicating it perfectly identified all positive instances. However, its recall was 0.78, meaning that 78% of actual positives were detected. The F1-score of 0.87 indicates a good balance between precision and recall, but the model struggled to identify all true cases, suggesting some limitations in its decision boundary or tuning of the margin.

Finally, KNN) also achieved perfect scores across all metrics, with 1.00 for accuracy, precision, recall**, and F1-score. KNN’s performance, like DT and RF, was flawless, meaning it made no incorrect predictions on the dataset. KNN's simplicity and effectiveness in capturing local patterns might have contributed to its strong performance in this case. These results suggest that tree-based models and KNN are highly effective for this classification task as that shown in table 2.

TABLE 2. RESULTS OF CLASSIFICATION FOR FIVE MODELS

ML method	Accuracy	Precision	Recall	F1-score
LR	0. 97	1.00	0.53	0.69
DT	1.00	1.00	1.00	1.00
RF	1.00	1.00	1.00	1.00
SVR	0.99	1.00	0.78	0.87
KNN	1.00	1.00	1.00	1.00

These results underscore the superior performance of DT and KNN for the classification task at hand, as illustrated in the accompanying ROC curve in Figure 10, which demonstrates the models' ability to achieve high true positive rates with minimal false positives.

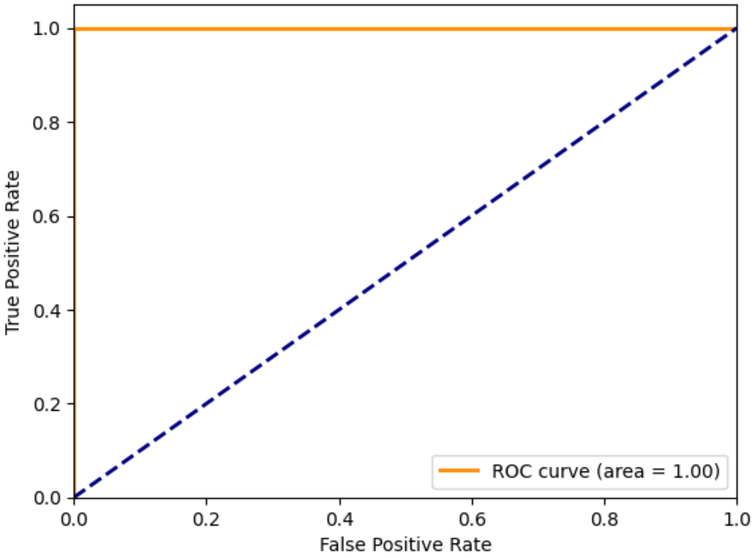


Fig. 10. The ROC curve

6. CONCLUSION AND FUTURE WORKS

This research underscores the remarkable promise of machine learning methods to forecast and examine monkeypox outbreaks. We showed that Random Forest was the most effective approach for forecasting total cases, while DT and KNN were best for classifying new cases. Our study contributes a vital proof-of-concept for the importance of advanced predictive analytics in health care and public health by providing useful knowledge on one pathology to inform decision making for improved and timely interventions and resource allocation. Monkeypox will continue to present challenges to public health even after the current outbreak concludes, one avenue to improve our understanding of outbreaks and improve response is to utilize ML models. Future directions for additional research would include refining these models by considering other variables that contribute to important dynamics of monkeypox transmission, i.e. environmental factors, vaccination rates, and demographic shifts. Another future direction could include the use of real-time data for model training which could make the models timelier and more accurate. Additionally, applying ML techniques to other diseases could provide a more comprehensive understanding of how ML may assist in outbreak prediction across various conditions. Finally, development of a user-friendly interface for public health officials to visualize and utilize the data to inform decision making would be beneficial, as would decisions made in developing these technologies, with respect to resources to assist, and improve, public health decision making.

Conflicts of Interest

The author declares that there is no conflict of interest regarding the publication of this paper.

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