

Article

A Forecasting Prognosis of the Monkeypox Outbreak Based on a Comprehensive Statistical and Regression Analysis

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Abstract: The uncommon illness known as monkeypox is brought on by the monkeypox virus. The Orthopoxvirus genus belongs to the family Poxviridae, which also contains the monkeypox virus. The variola virus, which causes smallpox; the vaccinia virus, which is used in the smallpox vaccine; and the cowpox virus are all members of the Orthopoxvirus genus. There is no relationship between chickenpox and monkeypox. After two outbreaks of a disorder resembling pox, monkeypox was first discovered in colonies of monkeys kept for research in 1958. The illness, also known as “monkeypox”, still has no known cause. However, non-human primates and African rodents can spread the disease to humans (such as monkeys). In 1970, a human was exposed to monkeypox for the first time. Several additional nations in central and western Africa currently have documented cases of monkeypox. Before the 2022 outbreak, almost all instances of monkeypox in people outside of Africa were connected to either imported animals or foreign travel to nations where the illness frequently occurs. In this work, the most recent monkeypox dataset was evaluated and the significant instances were visualized. Additionally, nine different forecasting models were also used, and the prophet model emerged as the most reliable one when compared with all nine models with an MSE value of 41,922.55, an R^2 score of 0.49, a MAPE value of 16.82, an MAE value of 146.29, and an RMSE value of 204.75, which could be considerable assistance to clinicians treating monkeypox patients and government agencies monitoring the origination and current state of the disease.

Keywords: human monkeypox; outbreak; geographical monkeypox analysis; machine learning; forecasting prediction



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1. Introduction

Although there are effective drugs to treat smallpox, there are no licensed treatments for monkeypox at this time. H. Adler et al.'s [1] investigation was the first to characterize the clinical course of monkeypox and look at viral dynamics and adverse effects from novel antiviral medications. They outlined the clinical features and virological results of seven patients with monkeypox who were diagnosed in the UK between 2018 and 2021. Clinical features included viremia, prolonged monkeypox viral DNA detection in upper respiratory tract swabs, and a deep tissue abscess. Five patients (range: 22–39 days) were isolated for longer than three weeks due to prolonged PCR positives. One patient who received tecovirimat (600 mg twice daily for two weeks orally) experienced viral shedding and sickness for a shorter period of time (10 days in the hospital).

F. Miura et al. [2] calculated the incubation times for 18 patients with exposure histories for monkeypox using a likelihood-based method, which permits exposure to be at either a single time point or a time interval. They looked at three different parametric distributions,

the lognormal, gamma, and Weibull, and selected the one that best fit the data. It was reported by the researchers that after a 21-day period has passed, symptoms were expected to appear in about 2% of the cases of monkeypox. The anticipated mean incubation period was in line with past findings for exposure to complicated and invasive monkeypox. Monkeypox typically takes 13 days to incubate in non-invasive exposures and 9 days in invasive exposures. In this outbreak, the estimated mean incubation time for monkeypox is 8.5 days, which is comparable with the typical values for difficult, invasive exposure. Direct contact with correspondingly broken skin or mucous membranes during sexual activity may be the most likely mechanism of infection.

A. K. Rao et al. [3] described how a man from Lagos, Nigeria, who visited Dallas, TX, USA, in July 2021 made history by becoming the seventh person to be diagnosed with monkeypox while traveling. In total, 144 (74%) of the 194 monitored encounters were flight contacts. The patient was given Tecovirimat, an antiviral medication used to treat orthopoxvirus infections. Postexposure Prophylaxis (PEP) was provided for those at high (no people) or intermediate risk (34 people), and 85% of the contacts (189) were classed as low risk.

The work of N. Bragazzi et al. [4], can aid practitioners, policymakers, and decision-makers in their efforts to contain and control the outbreak even if it is still in its early phases. Risk factors that can be identified include being male; having sex with other male; and engaging in risky behaviors and activities, including condomless sex, having HIV, and having a history of STIs such as syphilis. In total, 10 out of 34 (29.41%) participants in the US outbreak of 2003 were under the age of 18. Lesions from monkeypox often spread in a centrifugal, monomorphic pattern, focusing on the face and extremities. Clinical variables include subsequent infections and sequelae (OR 3, 95), rash size equal to or higher than 2 cm (OR 12.7), and genital ulcers (OR 1.94).

F. S. Minha et al. [5] stated that monkeypox is caused by the monkeypox virus, one of the orthopox viruses. UKHSA (UK Health Security Agency) announced a confirmed case of monkeypox in a visitor from Nigeria on 7 May 2022. As of 31 May, their investigation had uncovered 17 incidents in the US, the bulk of which involved males who identify as gay, bisexual, or who had intercourse with other men (MSM). Close contact with ill people or fomites is the main risk factor for monkeypox virus infection in human monkeypox epidemics. The large proportion of initial cases found in this outbreak among gay, bisexual, and other MSM individuals may simply be the result of the monkeypox's early introduction to related social networks. At sexual health clinics, UKHSA reported the discovery of a second unconnected cluster of two cases and a third clustered group of four cases.

This research evaluated and visualized the dataset and performed several forecasting models as follows.

- We evaluated and visualized the dataset by taking into account the current date as well as the daily growth in the disease infection rate.
- It was made clear to everyone in the region that which specific region had the largest number of confirmed cases.
- In addition to this, our study demonstrated the highest percentage of confirmed cases in a single day, the classification of confirmed cases according to symptoms and methods of confirmation, the percentage of confirmed cases with a history of hospitalization, the percentage of confirmed cases with a history of isolation, and the percentage of confirmed cases with travel history.
- In addition to this, we have provided information regarding the ages of those affected as well as the gender distribution of confirmed cases.
- The Polynomial Regression, SVR, Holt's Linear model, Holt-Winter's model, AR, MA, ARIMA, SARIMA, and Prophet forecasting prediction models were employed to predict the forecast of the confirmed cases. These models are considered to be the most common forecasting prediction models.
- Last, but certainly not least, the best forecasting models were identified by comparing the models' performance matrices, such as RMSE, MSE, MAE, MAPE, and the R^2 score.

2. Related Work

M. McCollum et al. [6] explained that from 2011 through August 2014, health officials investigated two suspected MPX cases in South Kivu and four suspected MPX cases in North Kivu. Only six of these instances were examined over the course of 3.5 years after diagnostic samples were delivered to the national laboratory. The study also mentioned the importance of healthcare workers remaining informed about disease risk, as well as having knowledge of the proper procedure of identification, care, and isolation for cases outside MPX-risk areas. In the Kivu region of the Democratic Republic of the Congo, there has been armed conflict and population displacement for almost 20 years (DRC). An increase in those who never developed vaccine-derived immunity to OPXVs has been linked to an increase in MPX incidence.

R. H. Doshi et al. [7], researchers in France, investigated 22 confirmed, probable, and possible cases of *Clostridium difficile* (C. diff) exposure in the French region of Guadeloupe. They looked into 43 possible cases in Betou, Enyelle, Impfondo, and Manfouété. Eleven home contacts who donated dried blood strips were also interviewed. All 18 patients had dried blood test strips accessible for the 22 instances we examined; all 18 (100%) were IgG-positive and 88.9% (16/18) were IgM-positive.

The work of E. M. Beer and V. B. Rao [8] on 71 documents, which include cases and outbreak data gathered between October 1970 and July 2018, was reviewed by the US National Library of Medicine. All of the documents were released or made available between 13 October 1972 and 27 July 2018. They include 23 situation reports, 11 reports on outbreak investigations, 9 case reports, 8 descriptions of surveillance data, 3 press reports, and 1 cross-sectional study.

D. Ogoina et al. [9] indicated, in their study, that there was insufficient evidence to support smallpox vaccination. Their analysis outlined some crucial elements, including that the face, trunk, arms, and legs were among the body parts that displayed skin rashes. Twenty-one of the forty cases (52.5%) had at least one complication. A polymerase chain reaction was used to diagnose concurrent chickenpox in a 21-year-old man. The attending physician's clinical judgment served as the basis for each diagnosis. Anxiety and depression symptoms in 11 of the 40 patients (27.5%) were noted, requiring psychological intervention.

M. R. Mauldin et al. [10] combined the analysis of genetic and epidemiologic data, showing no direct correlation between exportation-related cases. This conclusion is supported by the absence of mutational differences. The degree of genetic differentiation among these samples is lower than the average number of SNPs seen across all outbreak samples. Analysis shows they are closely related to one another and share an ancestor more recently than any other genomes sequenced too far. The first case in this cluster (BAY) was isolated from a medical professional at a hospital. Evidence suggests no direct links between the exportation-related cases, with the exception of UK2 and UK3. There was a lack of confirmed epidemiological links between the cases, timeline data, and increased level of genetic variation when compared with other epidemiologically linked clusters.

P.-Y. Nguyen et al. [11] stated that even though Nigeria's entire population rose from 55.98 million in 1970 to 195.87 million in 2018, the number of people who received vaccinations decreased from 43.22 million (77.2 percent of the total population) in 1970. The cross-immunity protection against monkeypox of 85% afforded by smallpox vaccination decreased to just 23.1% among those who received it.

R. Vivancos et al. [12] stated there has been one confirmed case of the virus in Scotland and 85 confirmed cases in England. The illnesses have not yet been linked to a single cause or exposure. It is known that 90% of patients are from London, of 38 years of age on average.

In the work of Y. Hammerschlag et al. [13], it was mentioned that an HIV-positive man in his 30s visited a primary care physician. He had an HIV viral load under 100 copies/mL and a CD4+ T-cell count of more than 700 cells/mm³. Results from tests utilizing real-time PCR (RT-PCR) from urine collection, rectal, and throat swabs for varicella zoster virus, herpes simplex virus, Chlamydia trachomatis, and Neisseria gonorrhoea were all negative.

This was a four-fold decrease in RPR from the time he received syphilis treatment in 2021, which was 8 months earlier.

M. P. Duque et al. [14] mentioned that the majority of cases occurred in the Lisbon and Tagus Valley (LVT) health region, with one case also occurring in the North Region and one in the Algarve. There were no more than 20 papules in total in two cases, although they had similar features on the trunk and limbs. Exanthema, inguinal lymphadenopathy, fever, and genital ulcers were the most prevalent symptoms. HIV infection was present in 14 distinct patients.

E. M. Bunge et al. [15] suggested the number of confirmed and suspected cases of monkeypox in Nigeria has risen from 3 in the 1970s to 181 in 2017–2019, according to this systematic review. The increase in instances from the 1990s ($n = 511$) through the years 2000–2019 ($>28,000$) is comparable in size to that of the current outbreak. Between 80 and 96 percent of cases were brought on by individuals who had not taken the vaccine. In 2016, only 10.1% of the populace of Nigeria had received immunizations.

A. Antinori et al. [16] carried out a study on four patients who underwent combined droplet and contact isolation measurements before being released from the hospital in excellent clinical standing. The ASM administered oral ciprofloxacin, acyclovir, and one dose of benzylpenicillin to patients for treatment. A patient in this case acquired numerous deep-seated lesions on the left leg, anterior, and posterior thorax. Patient 1 exhibited raised, itchy papules that were secreting serous; asthenia; inguinal lymphadenopathy; and fever. Multiple anal lesions were present in Patient 2, followed by isolated lesions on the back, legs, and the sole of one foot. Another patient with smallpox-like symptoms presented at the hospital with a history of fever and lesions on his head, chest, legs, arms, hands, and penis. The patient stated that he had received a smallpox vaccination as a youngster, 30 years earlier; he had never received a smallpox vaccination. A 30-year-old man referred to as Patient 4 was enrolled in an event-driven Pre-Exposure Prophylaxis (PrEP) program. After two days of myalgia, vesicular-papular vaginal lesions first appeared, followed by further skin lesions in the chest and suprapubic area six days later.

3. Methodology

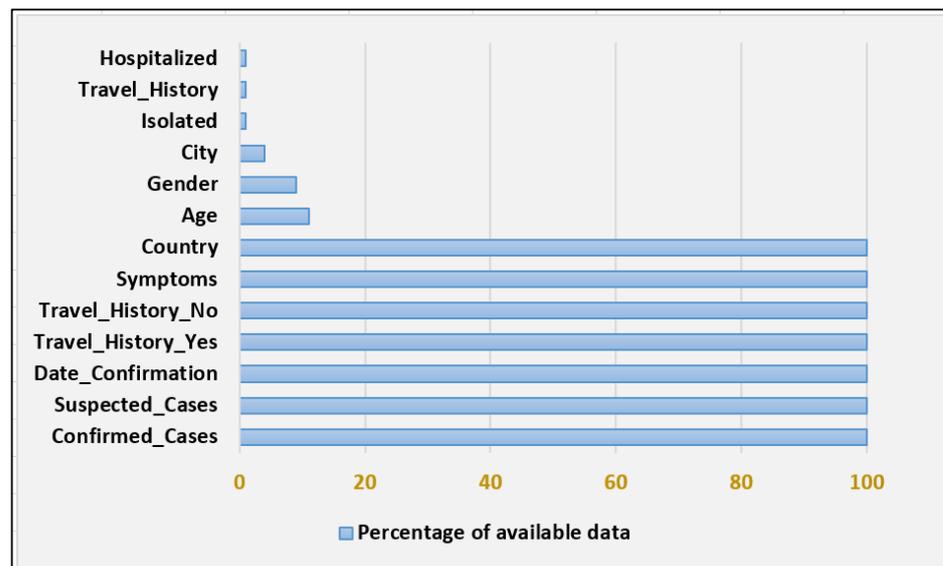
The section under “Dataset Collection” covers specifics regarding the dataset itself, as well as its origin. In this study, the Data Pre-Processing segment addressed steps required to prepare the data for additional analysis. Afterwards a comprehensive investigation through geographical analysis has been carried out and a quick overview of some of the findings from the statistical analysis have been included. In the following part, the “Train Test Split”, detailed out the policies undertaken for dataset division targeting the forecasting models. A description of the performance matrices that we used to assess the performance of the models has been provided in the section on performance matrices. After that, five time-series forecasting models and two machine learning prediction models were developed, and the prediction results were recorded for performance evaluation. The top performing models were then chosen after a thorough comparison of their performance. The working flow chart of this study is shown in Figure 1.



Figure 1. The complete working flow chart of this study.

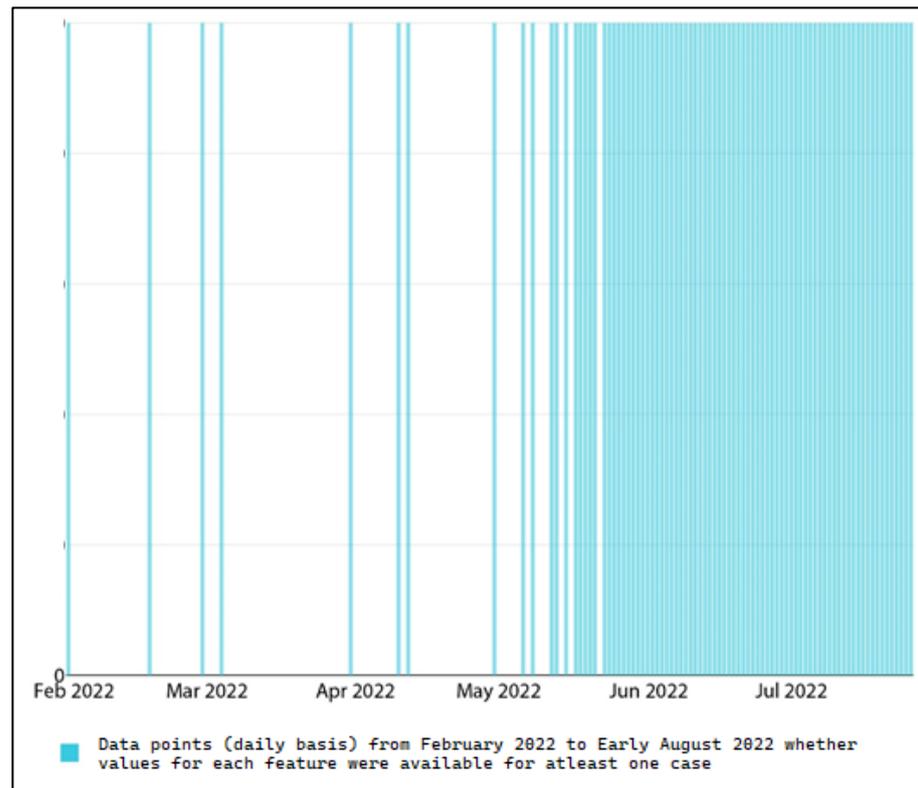
4. Dataset Collection

This study made use of the open-source Global Monkeypox Cases (updated daily) dataset from Kaggle [17]. It is an open source dataset. Figure 2a,b illustrate some key statistical characteristics of the dataset. Figure 2a depicts the percentage of Null values for each of the thirteen features while Figure 2b highlights data points (daily basis) from February 2022 to Early August 2022 whether values for each feature were available for atleast one case (if available, it the respective data point is marked in color Cyan).



(a)

Figure 2. Cont.



(b)

Figure 2. Few key Dataset statistics (a) the percentage of Null values for each of the thirteen features, (b) Feature completeness for cases on a daily basis from February 2022 to early August 2022.

We can observe that the Worldwide Case Detection Timeline in Figure 2a contains a lot of null values, which shows that the dataset is missing some information since it is not comprehensive. As a result, numerous data preprocessing techniques were used for the goals of the qualitative experiments, including null value replacement, necessary row and column insertion, grouping by selected features, uniqueness of instance for selected features, etc. The smoothness of the other two data frames is quite noticeable.

5. Data Pre-Processing

5.1. Replace Null Values

In order to simplify the process of numerical calculation, we substituted zero for the null values that were included in several columns in the dataset (a) Worldwide Case Detection Timeline.

5.2. Insert Necessary Columns

A new column with the name “ID” was added to the dataset (a) Worldwide Case Detection Timeline and (b) Monkeypox Cases Worldwide in order to keep track of the overall number of confirmed cases.

5.3. Grouped by Selected Features

We grouped the column in the dataset (a) Worldwide Case Detection Timeline with the name “Date_confirmation”, which allowed us to count the total number of confirmed cases according to the date.

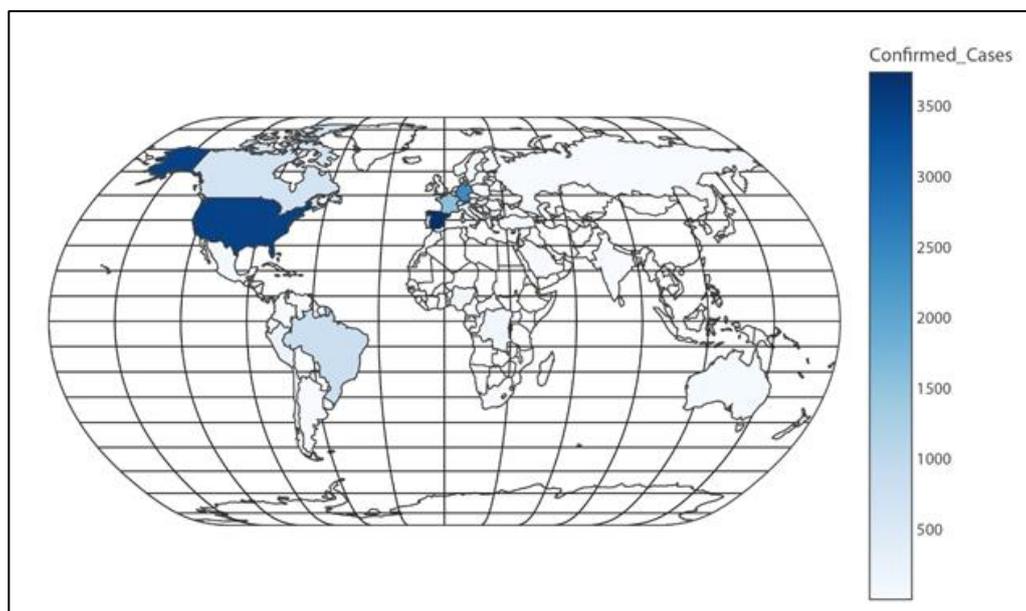
5.4. Uniqueness of Instance for Selected Features

In order to determine the true distribution of age and symptoms, we determined the uniqueness of instance for the columns “Age” and “Symptoms” in the dataset (a) Worldwide Case Detection Timeline.

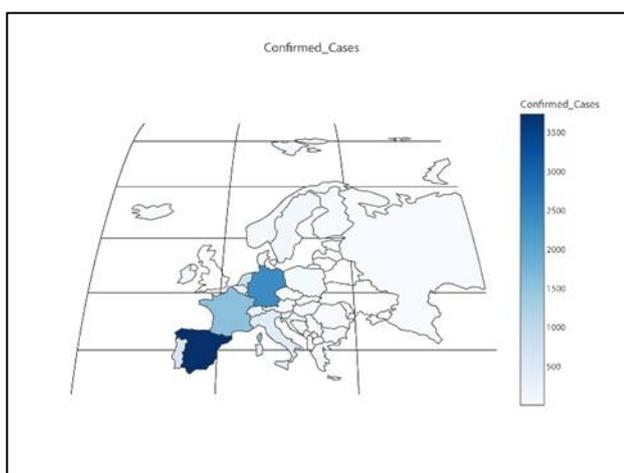
6. Geographical Analysis

6.1. Distribution of Confirmed Cases

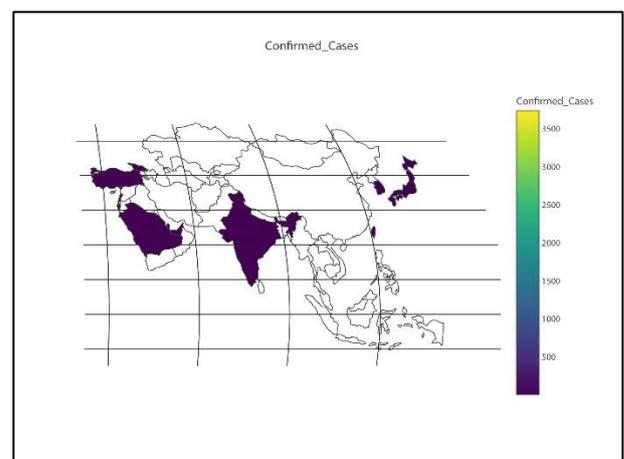
The majority of confirmed cases with travel histories included trips to Europe and North America. This is in contrast to West or Central Africa, where the monkeypox virus is commonplace. In order to conduct a geographical analysis, the data frame defined as (b) Monkeypox Cases Worldwide was utilized. Figure 3 shows (a) the worldwide distribution of confirmed cases, (b) the European distribution of confirmed cases, and (c) the Asian distribution of confirmed cases.



(a)



(b)



(c)

Figure 3. (a) Worldwide distribution of confirmed cases; (b) European distribution of confirmed cases; (c) Asian distribution of confirmed cases.

According to the information that we had available, this is the first time that a considerable number of cases and clusters of monkeypox have been recorded simultaneously in

endemic and non-endemic nations over a broad diversity of geographical areas. It would appear that the distribution in Europe is in a precarious situation, but the distribution in Asia is, in comparison, in a desirable state.

6.2. Country Wise Travel History

The travel history of each country was used to determine the number of instances that have traveled to another country or not. Only the cases that were confirmed were used for the measurement. Figure 4 shows the travel history based on nationality.

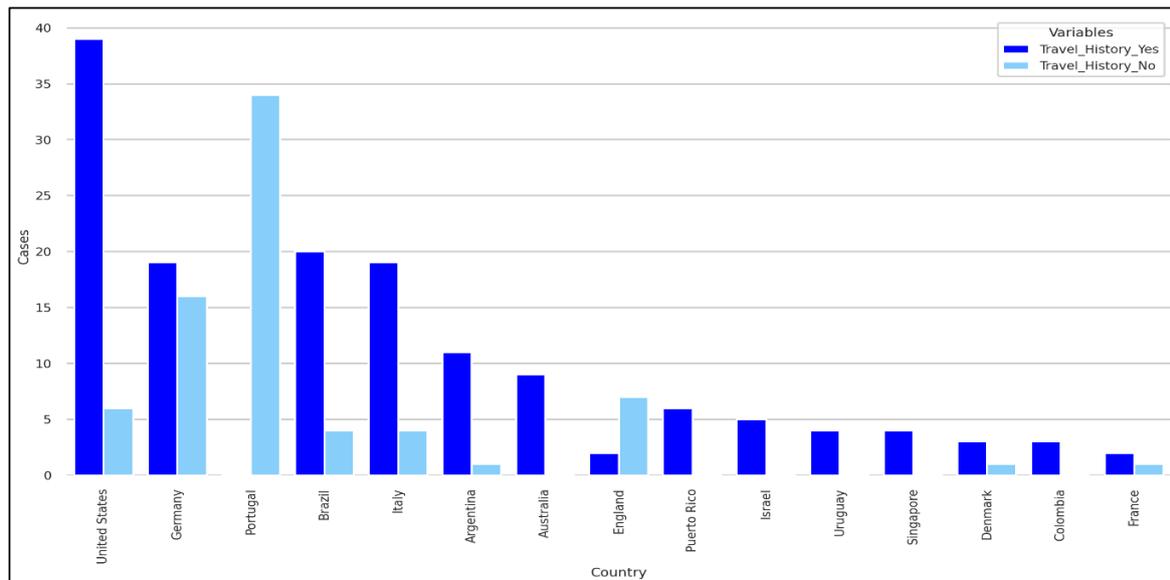


Figure 4. Travel history based on Nationality.

It is clear to us that the United States has a travel history with the highest percentage of confirmed cases who have visited other countries. When compared with other countries, the percentage of cases in Portugal who have never left the nation has the least extensive travel history.

6.3. Correlation among Confirmed, Suspected, and Hospitalized Cases

We made an effort to establish a connection between the confirmed cases, the suspected cases, and the hospitalized cases that have been reported throughout the world. The correlation between suspected cases, confirmed cases, and hospitalizations are illustrated in Figure 5.

6.4. Top 10 Countries According to Confirmed, Suspected, and Hospitalized Cases

The dataset demonstrates the cases that were recorded under three separate categories, including confirmed cases, suspected cases, and hospitalized patients. Whereas there were 18,903 confirmed instances, there were 1654 cases that were suspected and 111 cases that were hospitalized. The actual position of the top 10 countries according to the confirmed cases, suspected cases, and hospitalized cases are displayed in Figure 6: (a) confirmed cases, (b) suspected cases, and (c) hospitalized cases.

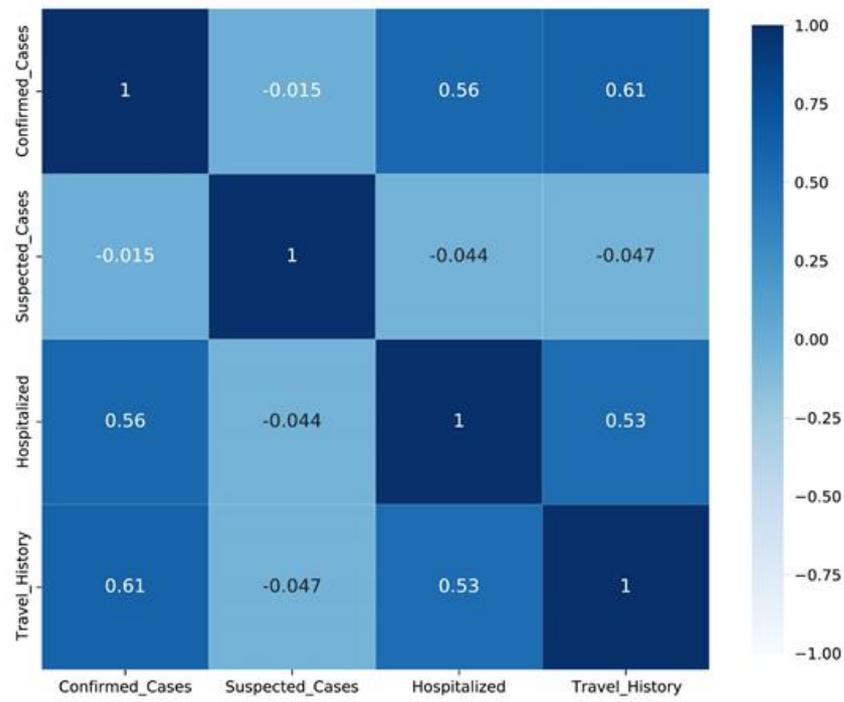
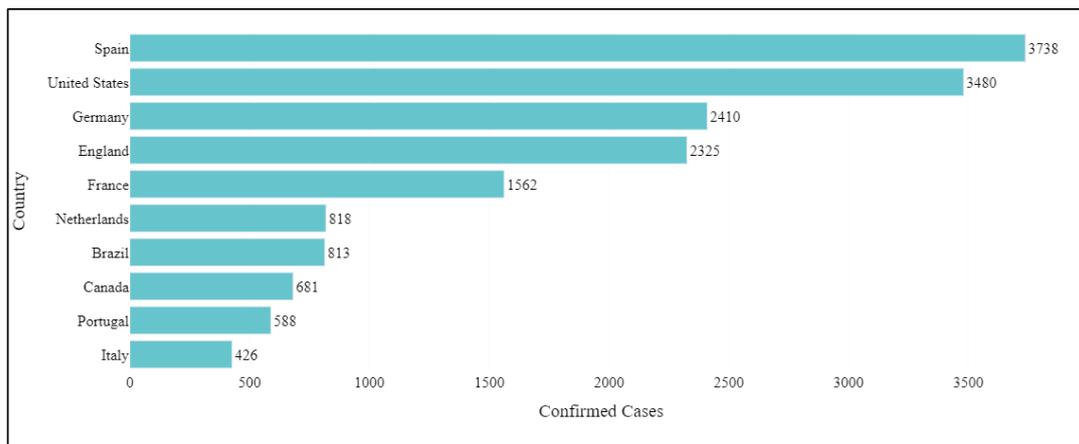
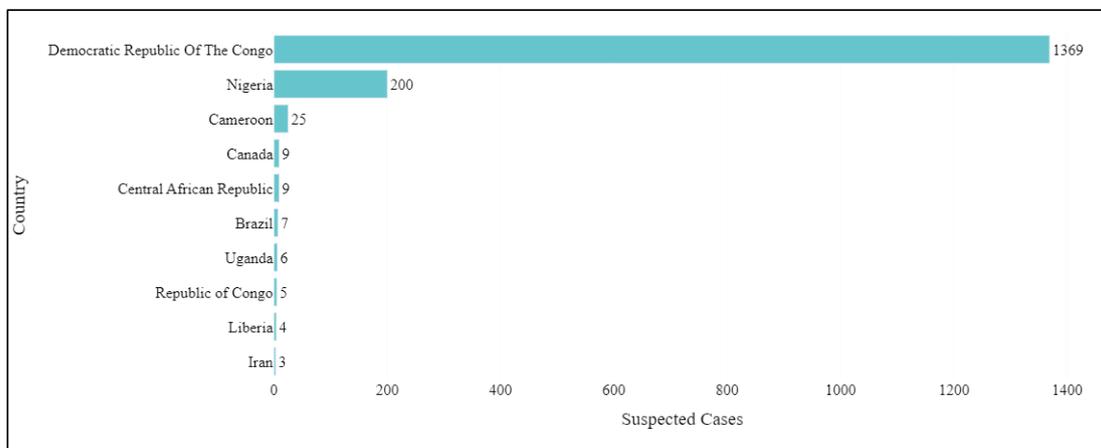


Figure 5. Correlation among confirmed, suspected, and hospitalized cases.

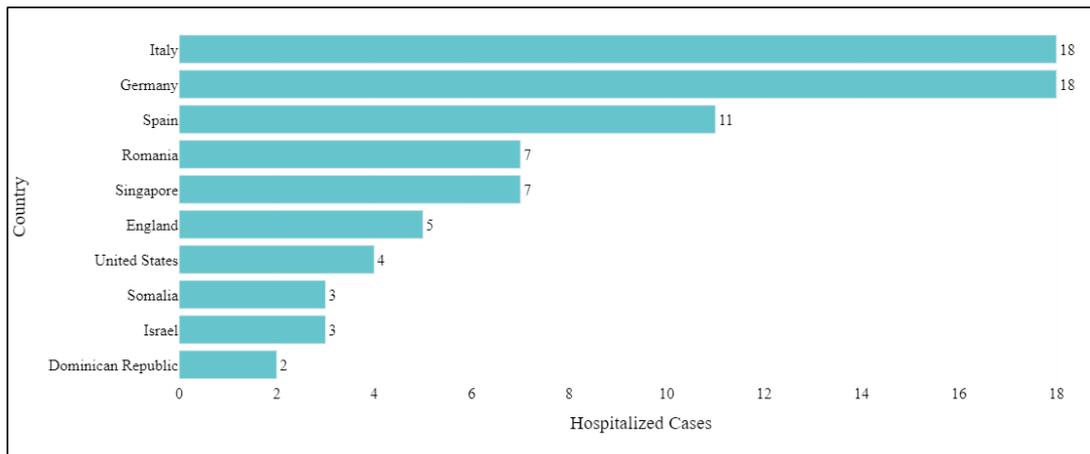


(a)



(b)

Figure 6. Cont.



(c)

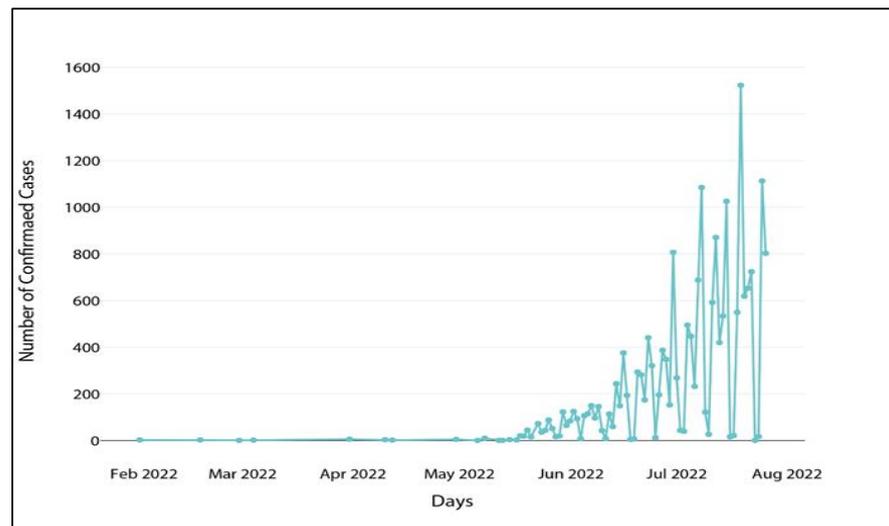
Figure 6. Top 10 countries according to the (a) confirmed cases, (b) suspected cases, and (c) hospitalized cases.

7. Statistical Analysis

For the statistical analysis, the data frame (a) Worldwide Case Detection Timeline was used.

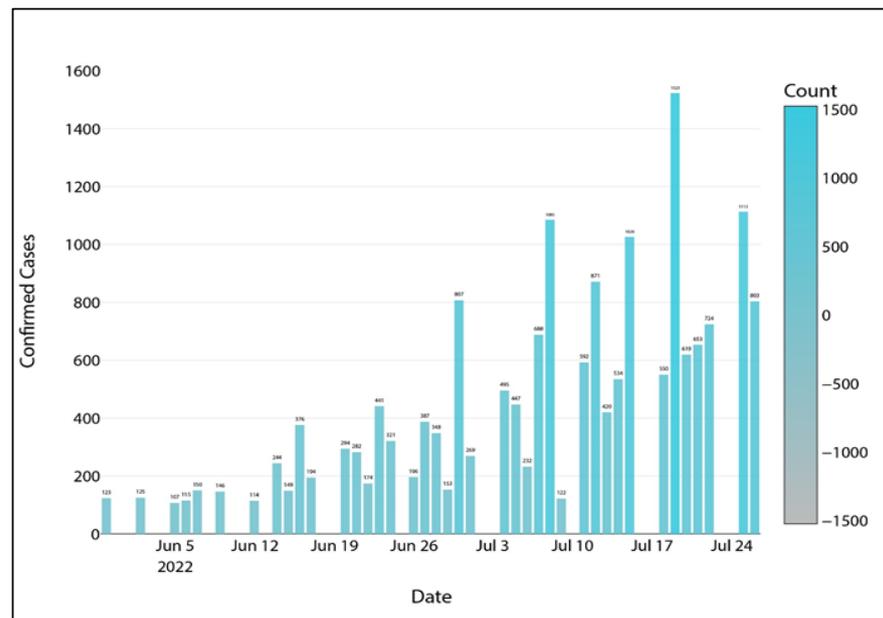
7.1. Global Confirmed Cases by Date

Cases of monkeypox have been documented in nations where the disease is not endemic since the end of January 2022, and they have continued to be reported in a number of countries where the disease is endemic. As of 31 January 2022 up until 26 July 2022, there have been a total of 19,140 confirmed cases across the globe. As the startling pace of new infections remains constant, the predicament is rapidly escalating into a crisis that threatens the entire population. The information presented in Figure 7 includes (a) global confirmed cases ordered by date and (b) global confirmed cases numbering more than 100 on any given day.



(a)

Figure 7. Cont.



(b)

Figure 7. (a) Global confirmed cases ordered by date and (b) global confirmed cases numbering more than 100 on any given day.

During the month of June 2022, a total of 5326 instances were reported. This represents an all-time high. In addition to this, each day, there are approximately 230.60 confirmed cases on average. There was a total of 1523 confirmed cases in a single day, which was the highest number ever seen.

7.2. Distribution of Confirmed Cases According to Age

A split operation was carried out on the age data, which allowed for the determination of each person’s age; counted independently afterwards. The distribution of confirmed cases in patients older than 15 years old is shown in Figure 8.

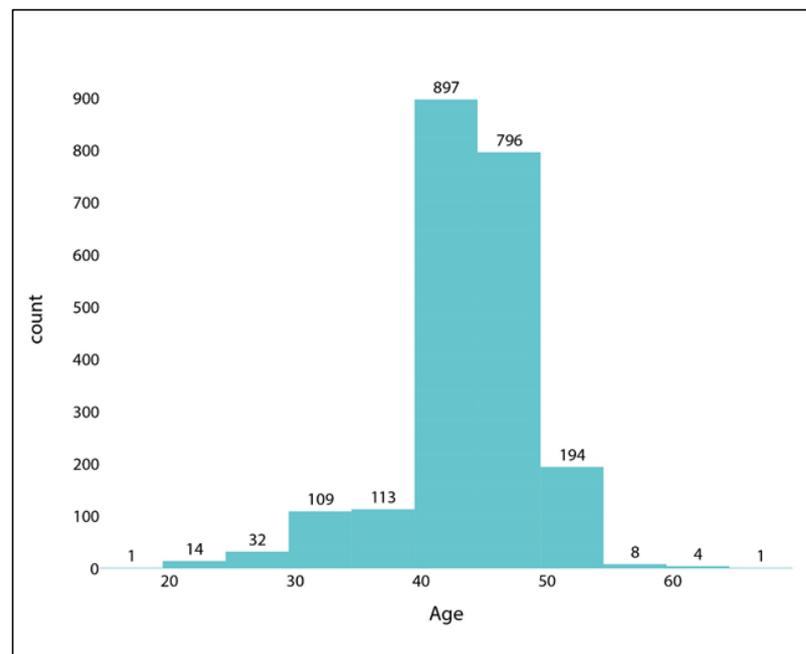


Figure 8. Distribution of confirmed cases where the Age is over 15.

There have been reports of infections occurring in adults aged 40 to 45 years old, with this age group accounting for the highest number of cases, 897, among confirmed cases. A sizable number of instances have been recorded for those between the ages of 40 and 55, with 796 cases reported for people between the ages of 45 and 50 and 194 cases reported for people between the ages of 50 and 55.

7.3. Categorization of Confirmed Cases According to Symptoms

Many symptoms, including bodily aches and pains, skin sores, weariness, fever, and chills, have been reported. It's also typical to experience fever, skin rashes, minor swallowing difficulties, and generalised heat. Some of the symptoms that may be present with this ailment are spots, vesiculated lesions, skin scabs, blisters, chills, muscle pain, pustule-like lesions, high fever, cough, skin lesions, muscle pain, and myalgia. Genital rash and genital ulcers are examples of lesions. Muscle aches, vascular rashes, and back and head pain are among the symptoms. Genital herpes symptoms include lesions, rash, inguinal adenopathy pustules, oral and genital ulcers, perianal papules, and fever. This condition's symptoms include skin lesions, ulceration sores, fever, swollen lymph nodes, headaches, and skin lesions. Inflammatory lesions manifest as a rash with vesicles. Figure 9 illustrates the (a) individual symptoms word cloud and (b) categorization of confirmed cases according to their respective symptoms.

We categorized each symptom in accordance with its individuality and ended up with 37 distinct symptoms. Fever is the symptom that has been observed the most frequently among all confirmed cases. Rash is the second most frequent symptom, and genital ulcer lesions are the third most frequent symptom.

7.4. Summary of Total Confirmed Cases according to Gender

There has been a total of 19,140 cases, and 1655 of those cases have had their sexual orientation confirmed, in which only 5 members the population were female while 1650 members of the population were male. The male gender has definitely reached the threshold for dangerous territory. Figure 10 presents a summary of the total confirmed cases according to gender.

7.5. Distribution of Confirmed Cases with Travel History

In total, 268 out of 19,140 people reported travel history data for confirmed cases. Whereas 77 people never traveled outside of their country, 191 did so. The distribution of confirmed cases that have a history of travel is presented in Figure 11.

7.6. Statistics of the Hospitalized Percentage of Confirmed Cases

The data relating to hospitalization were provided for 204 cases. In total, 115 of those cases resulted in hospital admissions, while the other 89 did not. The statistics regarding the percentage of confirmed cases that were hospitalized are shown in Figure 12.

7.7. Number of Confirmed Cases with Isolation Record

Only 320 people out of a total of 19,140 cases provided information about the quarantine of confirmed cases. They were in isolation due to their health condition. Figure 13 illustrates the number of confirmed cases that had a record of being isolated in some way.

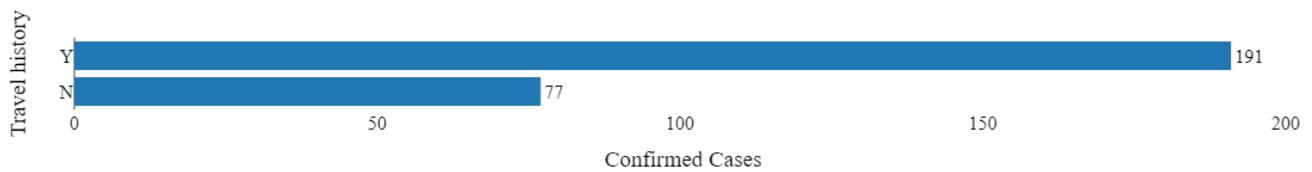


Figure 11. Distribution of confirmed cases with travel history.

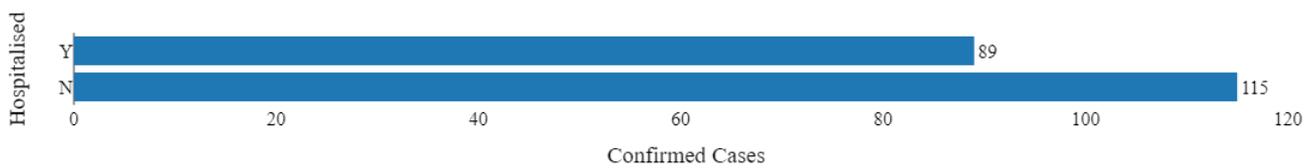


Figure 12. Statistics of the hospitalized percentage of confirmed cases.

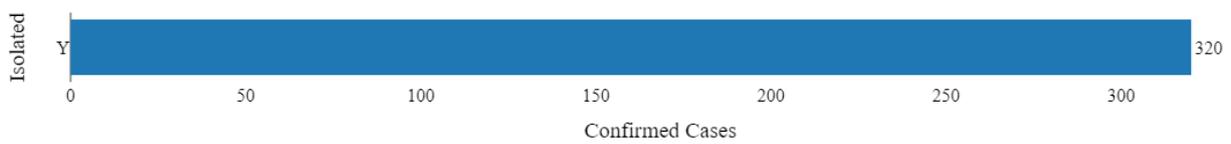


Figure 13. Number of confirmed cases with isolation record.

8. Train Test Split

By adding up daily cases of confirmed instances, we prepared the custom dataset for the forecasting prediction models. In addition to the total of daily confirmed cases we also created another column with the heading “Days_Since” to represent the nth day. Then, as indicated in Figure 14, we divided the dataset into 78 instances for training data and 5 instances for testing data.

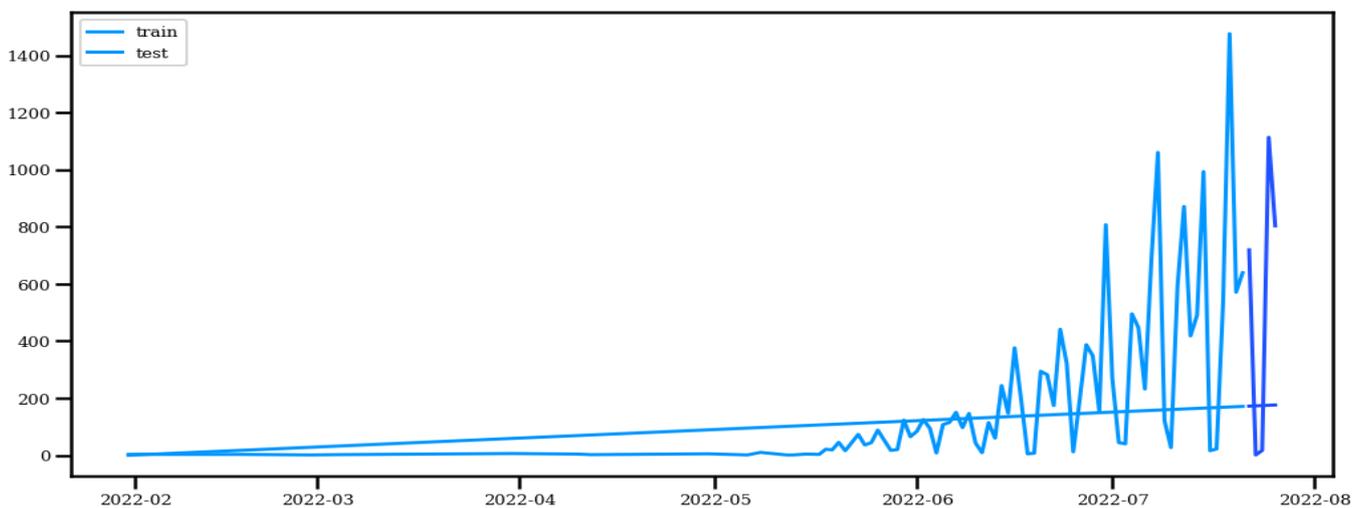


Figure 14. Train Test Split.

9. Performance Matrices

In this study, mean square error (MSE) [18], mean absolute error (MAE), root mean square error (RMSE) [18], mean absolute percentage error (MAPE), and crucial coefficient (R^2) were used to determine the accuracy of the model’s prediction. The specific formula for each statistic is described as follows:

$$MSE = \frac{1}{n} \sum_{t=1}^n (y_t - \hat{y}_t)^2 \tag{1}$$

$$MAE = \frac{1}{n} \sum_{t=1}^n |y_t - \hat{y}_t| \tag{2}$$

$$RMSE = \sqrt{\frac{1}{n} \sum_{t=1}^n (y_t - \hat{y}_t)^2} \tag{3}$$

$$MAPE = \frac{100\%}{n} \sum_{t=1}^n \left| \frac{y_t - \hat{y}_t}{y_t} \right| \tag{4}$$

$$R^2 = 1 - \frac{\sum_{t=1}^n (y_t - \hat{y}_t)^2}{\sum_{t=1}^n (y_t - \bar{y}_t)^2} \tag{5}$$

where n is the number of prediction points, y_t represents the actual load, the predicted load, and \bar{y}_t the average load [19].

10. Machine Learning Models for Forecasting Prediction

10.1. Polynomial Regression Model

A type of linear regression known as polynomial regression evaluates the connection between two variables using polynomials of the n th degree [20], which we set as the 8th degree for our prediction. Polynomial regression can be illustrated with the help of this particular instance of multiple linear regression. The performance of the polynomial regression may also be greatly impacted by the existence of one or two outliers. This is because polynomial regression is sensitive to the presence of outliers. Figure 15 illustrates the confirmed cases of polynomial regression model prediction.

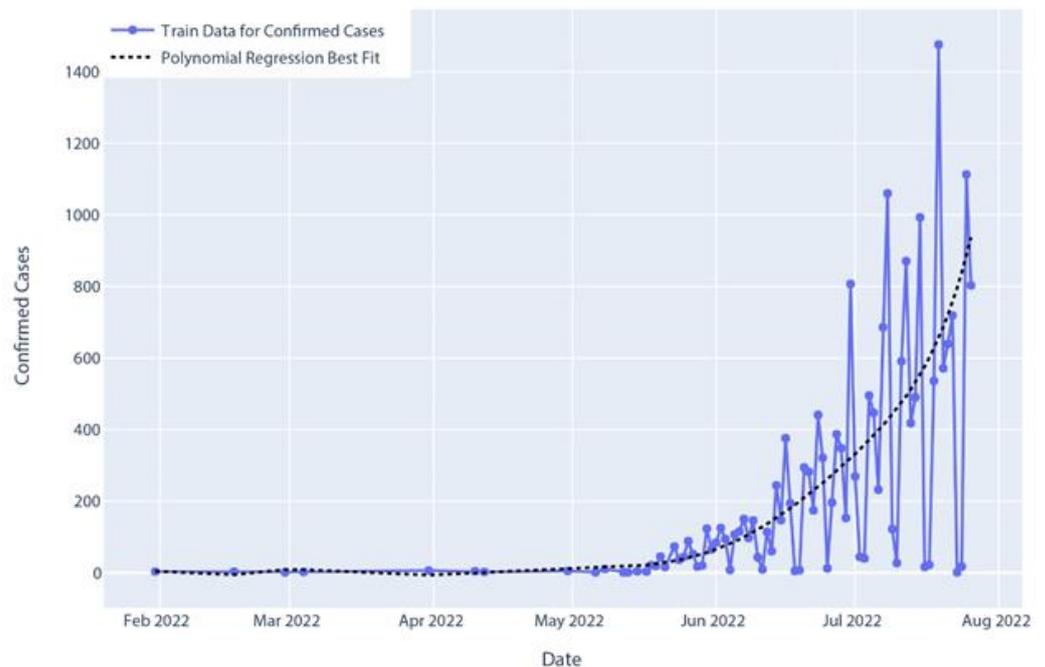


Figure 15. Confirmed cases of polynomial regression model prediction.

The following are the performance matrices obtained by the polynomial regression model: the MSE value is 275,449.04, the MAE value is 402.90, the RMSE value is 524.83, the MAPE value is 168.64, and the R^2 score is -0.39 . The prediction of the polynomial regression model’s confirmed monkeypox cases over five days from 22 July 2022 to 26 July 2022 is shown in Table 1.

Table 1. Polynomial regression model of confirmed case prediction over five days.

	Date	Polynomial Regression
0	22 July 2022	755
1	23 July 2022	795
2	24 July 2022	838
3	25 July 2022	885
4	26 July 2022	937

10.2. SVR (Support Vector Regression) Model

In order to make predictions regarding discrete values, a technique based on supervised learning known as support vector regression was utilized. Both support vector machines [21] and support vector regression are based on the same theoretical framework. Discovering the best possible fit line is one of the most basic aspects of SVR. In SVR, the line that provides the best fit is the hyperplane, which has the most points. The values for parameter C, degree and epsilon have been set to 1, 6 and 0.01 respectively. Figure 16 shows the confirmed cases of SVR (support vector regression) prediction.

The performance matrices derived from the SVR model are listed as follows, a situation where the MSE value is 217,897.28, the MAE value is 371.85, the RMSE value is 466.79, the MAPE value is 144.30, and the R² score is −0.10. Table 2 displays the forecast of the confirmed cases of monkeypox from the polynomial regression model over the five days from 22 July 2022 to 26 July 2022.

Table 2. SVR model confirmed case prediction for five days.

	Date	SVR
0	22 July 2022	657
1	23 July 2022	681
2	24 July 2022	705
3	25 July 2022	730
4	26 July 2022	756

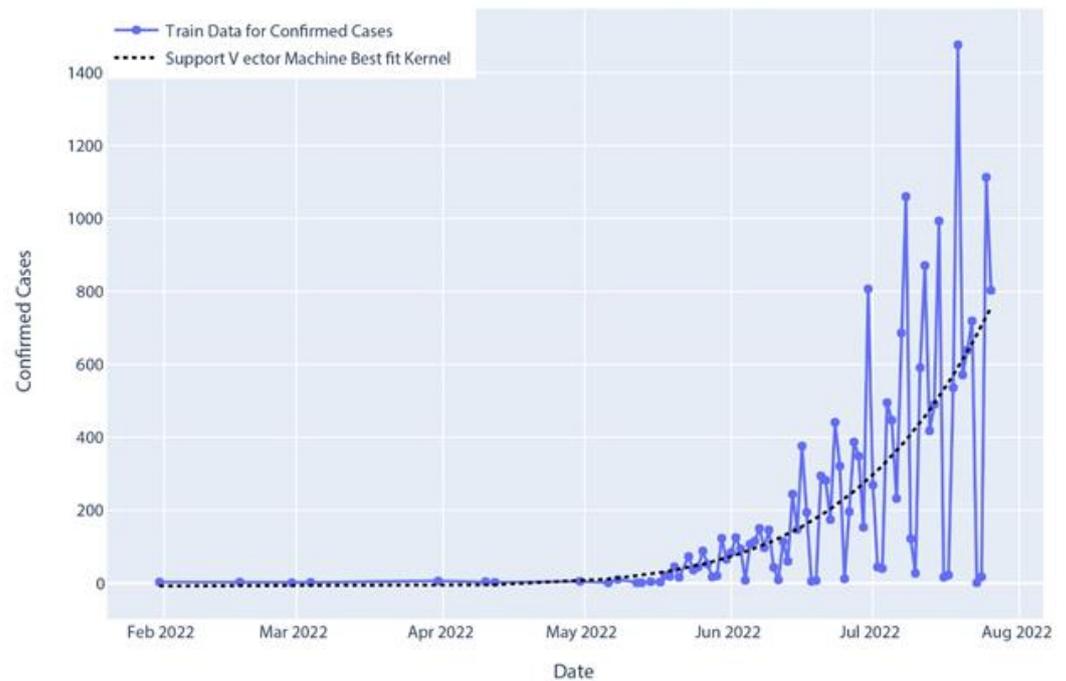


Figure 16. Confirmed cases of SVR (support vector regression) prediction.

11. Time Series Models for Forecasting Prediction

11.1. Holt’s Linear Model

The linear exponential smoothing approach is a popular tool for trend-driven data forecasting. Holt’s approach uses three methods to forecast. The first corrects the most recent smoothed number for the prior period’s trend. The second method refreshes the trend by comparing recent smoothed data. The third strategy yields the final forecast. Holt’s model uses two parameters for trend and overall smoothing. Trend-enhanced exponential smoothing is another name for it [22]. Both the smoothing level and smoothing slope were set to 0.4. The confirmed cases in Holt’s linear model prediction are displayed in Figure 17.

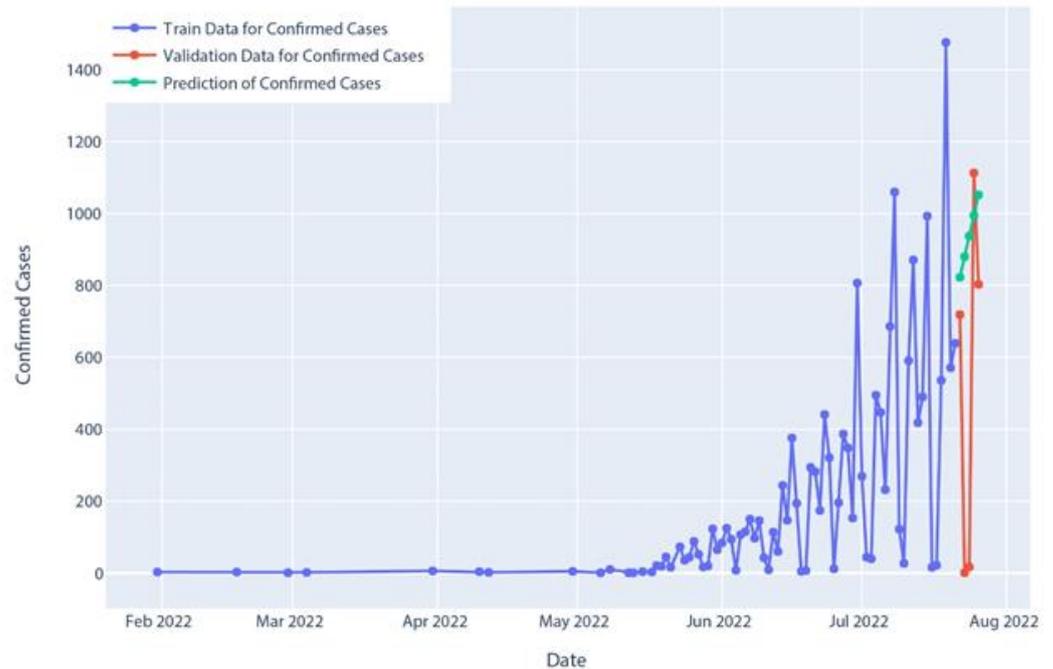


Figure 17. Confirmed cases in Holt’s linear model prediction.

These are the performance matrices that Holt’s linear model produced: the MSE score is 341,376.76, the MAE score is 454.14, the RMSE score is 584.27, the MAPE score is 186.77, and the R^2 score is -0.72 . Table 3 displays the forecast of the confirmed cases of monkeypox over the five days from 22 July 2022 to 26 July 2022, using Holt’s linear model.

Table 3. Holt’s linear model confirmed case prediction over five days.

	Date	Holt’s Linear Model
0	22 July 2022	822
1	23 July 2022	880
2	24 July 2022	937
3	25 July 2022	994
4	26 July 2022	1052

11.2. Holt–Winter’s Model

The approach of forecasting known as Holt–Winter’s model makes use of a smoothing that is mathematically comparable to a triple exponential. This smoothing takes into account all of the components, including those related to seasonality, levels, and trends. The three order parameters of Holt–Winter’s model are each given their own name and referred to by that name when used in the model [23]. These names are alpha, beta, and gamma. The value of the parameter that is known as alpha plays a role in determining the level smoothing coefficient. The beta value provides information on the coefficient that should be used to smooth out tendencies, and it can be found in the definition of beta. The

value of trending periods is set to add, the value of seasonal is set to multiply, and the value of seasonal periods is set to 14. The confirmed cases in Holt–Winter’s model prediction are presented in Figure 18.

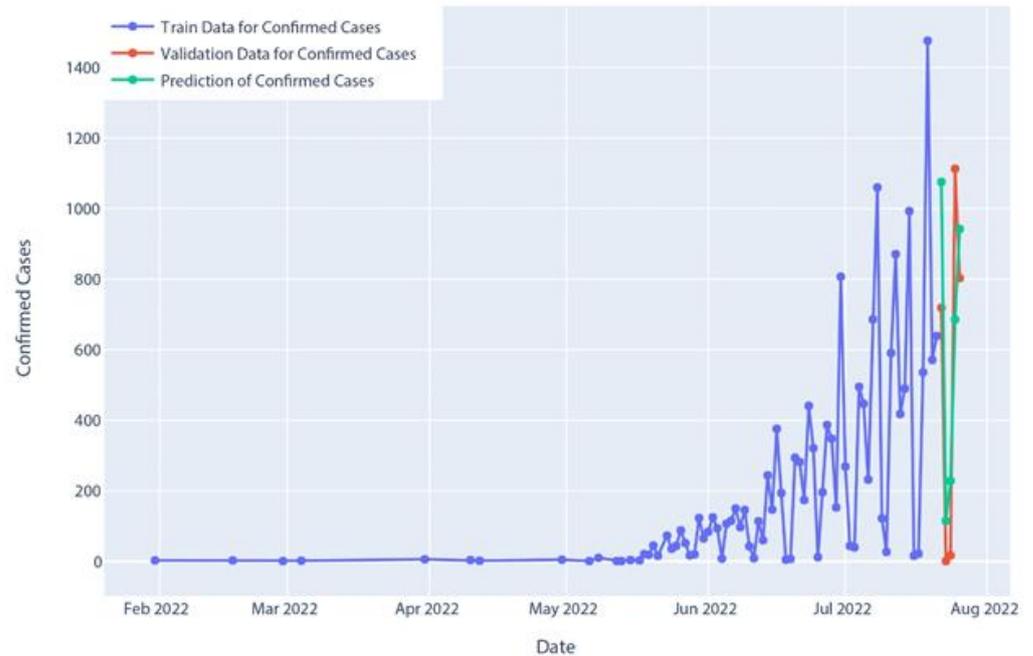


Figure 18. Confirmed cases in Holt–Winter’s model prediction.

The results of Holt–Winter’s model are shown in the performance matrices as follows. In this instance, the MSE value is 77,448.32, the MAE value is 249.81, the RMSE value is 278.30, the MAPE value is 25.43, and the R^2 score is 0.61. Table 4 displays the forecast of confirmed cases of monkeypox from 22 July 2022 to 26 July 2022 over five days.

Table 4. Holt–Winter’s model confirmed case prediction over five days.

	Date	Holt–Winter’s Model
0	22 July 2022	1075
1	23 July 2022	114
2	24 July 2022	228
3	25 July 2022	685
4	26 July 2022	942

11.3. AR (Autoregressive) Model

The Autoregressive model, which is also known as the *AR model*, makes projections about the values of the future solely on the basis of the values of earlier time periods. It is a linear model in which the values of the current period are calculated by first adding the results of the periods that came before it and then multiplying that total by a numerical factor [24]. In other words, the values of the current period are derived from the values of the periods that came before them. After adjusting the minimum p -value to zero, the minimum q -value to zero, the maximum p -value to four, and the maximum q -value to zero, the model order used was (4, 1, 0). Figure 19 shows the instances where the AR model prediction was confirmed.

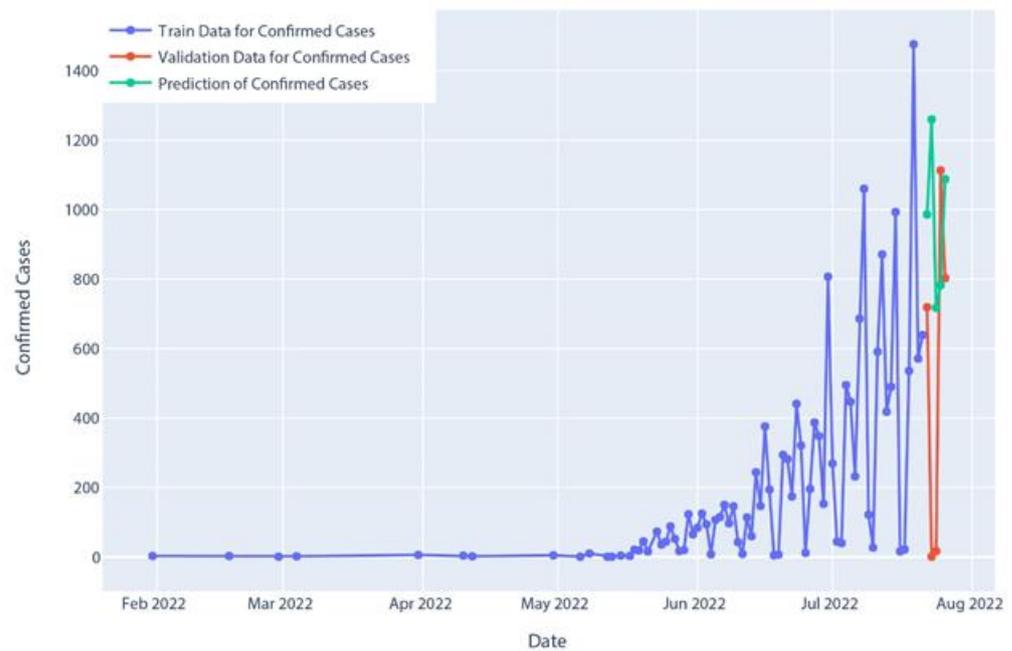


Figure 19. Confirmed cases of AR model prediction.

The output of the AR model is shown in the following performance matrices: the MSE score is 467,378.37, the MAE score is 568.36, the RMSE score is 683.65, the MAPE score is 260.19, and the R^2 score is -1.35 . As predicted by the AR model, there were five confirmed cases of monkeypox between 22 July 2022 and 26 July 2022 (Table 5).

Table 5. AR model confirmed case prediction over five days.

	Date	AR Model
0	22 July 2022	986
1	23 July 2022	1259
2	24 July 2022	717
3	25 July 2022	782
4	26 July 2022	1087

11.4. MA (Moving Average) Model

Using a predetermined number of variables at regular intervals, a moving average (MA) is a sort of average that is produced over time. The highest-ranking values from the most recently averaged group are discarded as the moving average advances through the series and are replaced by values from succeeding groups [25]. The moving average keeps going through this procedure until it reaches the start of the series. The model order utilized is as follows after making the appropriate modifications to make the minimum p -value equal to zero, the minimum q -value equal to zero, the maximum p -value equal to zero, and the maximum q -value equal to two: $(0, 1, 0)$. The cases where the MA model prediction was verified are shown in Figure 20.

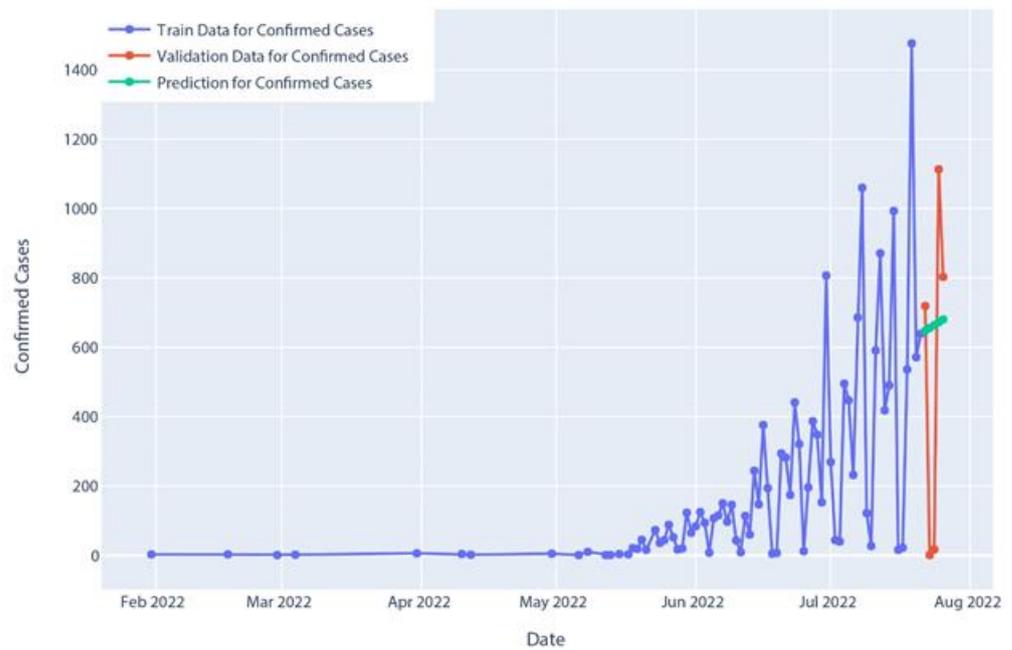


Figure 20. Confirmed cases of MA model prediction.

The performance matrices that the MA model produced are listed as follows, in which the R^2 score is -0.07 , the MSE value is 212,273.60, the MAE value is 387.34, the RMSE value is 460.73, and the MAPE value is 138.64. Table 6 displays the prediction of confirmed cases of monkeypox over the five days from 22 July 2022 to 26 July 2022.

Table 6. MA model confirmed case prediction over five days.

	Date	MA Model
0	22 July 2022	647
1	23 July 2022	655
2	24 July 2022	663
3	25 July 2022	672
4	26 July 2022	680

11.5. ARIMA (Autoregressive Integrated Moving Average) Model

Time series information was fed into a statistical analysis model known as an autoregressive integrated moving average, or ARIMA for short. This model’s purpose is to either improve one’s understanding of a dataset or to anticipate future trends [26]. It is asserted in a statistical model that it is autoregressive if it makes predictions about future values by using data from the past. After making the necessary adjustments, the order of the model that was used comes out as follows after making sure that the minimum p -value is equal to one, the minimum q -value is equal to one, the maximum p -value is equal to three, and the maximum q -value is equal to three: (2, 1, 3). Figure 21 illustrates the circumstances under which the ARIMA model’s forecast was shown to be accurate.

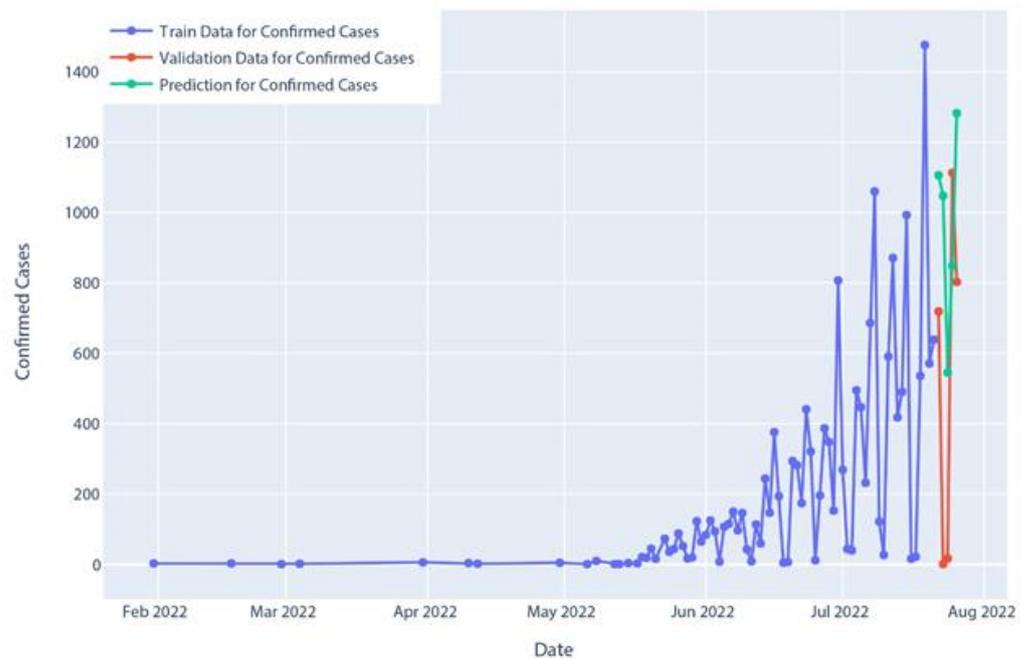


Figure 21. Confirmed cases of ARIMA model prediction.

The following is a list of the performance matrices that the ARIMA model generated, in which the MSE value is 364,778.86, the MAE value is 541.14, the RMSE value is 603.96, and the MAPE value is 215.81. The R^2 score is -0.84 . The forecast of confirmed cases of monkeypox over the five days from 22 July 2022 to 26 July 2022 is shown in Table 7.

Table 7. ARIMA model confirmed case prediction for five days.

	Date	ARIMA Model
0	22 July 2022	1105
1	23 July 2022	1047
2	24 July 2022	545
3	25 July 2022	848
4	26 July 2022	1282

11.6. SARIMA (Seasonal Autoregressive Integrated Moving Average) Model

A variation of ARIMA that explicitly accommodates univariate time series data with a seasonal component is called seasonal autoregressive integrated moving average, or seasonal ARIMA [27]. After making the necessary adjustments, the order and seasonal order of the model that were used come out as follows: (0, 1, 1) and (0, 1, 0, 7), respectively, after making sure that the minimum p -value is equal to zero, the minimum q -value is equal to zero, the maximum p -value is equal to two, the maximum q -value is equal to two, and m is equal to seven. Figure 22 illustrates the circumstances under which the SARIMA model’s forecast was shown to be accurate.

The SARIMA model produced the following list of performance matrices, in which the RMSE value is 442.12, the MAPE value is 23.18, the MAE value is 364.74, the MSE value is 195,471.08, and R^2 score is 0.02. In Table 8, the predicted number of confirmed monkeypox cases over the five days from 22 July 2022 to 26 July 2022 is presented.

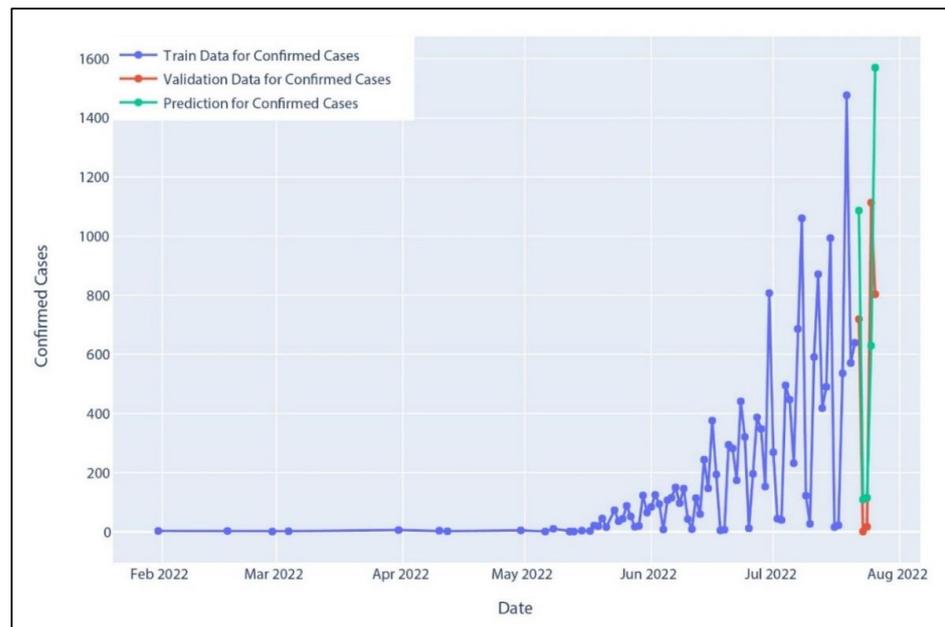


Figure 22. Confirmed cases of SARIMA model prediction.

Table 8. SARIMA model confirmed case prediction over five days.

	Date	SARIMA Model
0	22 July 2022	1086
1	23 July 2022	109
2	24 July 2022	115
3	25 July 2022	629
4	26 July 2022	1569

11.7. Prophet Model

Prophet is a technique for foreseeing time series data that uses an additive model to take into account non-linear patterns with seasonality that happen yearly, monthly, daily, on weekends, and during vacations [28]. Prophet also considers the possibility of seasonality occurring during the week in addition to on weekends and holidays. It is particularly effective with historical data that span multiple seasons and time series that are very seasonal. We set the weekly seasonality to true, the width interval to 0.95, and the periods to 5. The circumstances in which the Prophet model’s forecast was demonstrated to be accurate are depicted in Figure 23.

These performance matrices were generated by the Prophet model, in which the MSE value is 41,922.55, the R² score is 0.49, the MAPE value is 16.82, the MAE value is 146.29, and the RMSE value is 204.75. Table 9 shows the forecasted number of confirmed cases of monkeypox over the five days from 22 July 2022 to 26 July 2022.

Table 9. Prophet model confirmed case prediction for five days.

	Date	Prophet’s Model	Prophet’s Upper Bound
0	22 July 2022	499	870
1	23 July 2022	218	630
2	24 July 2022	272	672
3	25 July 2022	523	939
4	26 July 2022	572	982

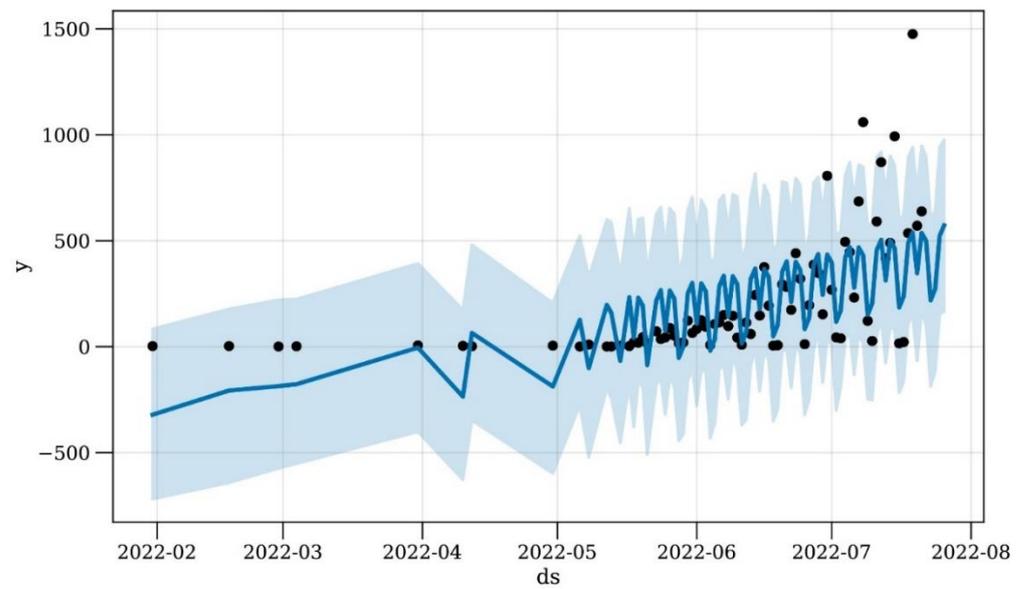


Figure 23. Confirmed cases of Prophet model prediction. Where ‘y’ represents the measurement of forecast and ‘ds’ represents date stamps. The original data are represented by black dots on the blue line, while the forecast error is shown by the shaded blue area.

12. Discussion

According to the data provided in Table 10, the Prophet model is superior to the other eight models because it has a lower RMSE value (204.75), a lower MSE value (41,922.55), a lower MAE value (146.29), a lower MAPE value (16.82), and a higher R² score (0.49). In contrast to the polynomial regression that was used in the machine learning model, the support vector machine (SVR) was able to achieve a score that was satisfactory. The SVR had an RMSE value of 466.79, an MSE value of 217,897.28, an MAE value of 371.85, a MAPE value of 144.3, and an R² score of −0.1. These values gave the SVR a satisfactory score. When comparing the two models developed by Holt, this is the situation that emerges: Holt–Winter’s model performs significantly better than Holt’s linear model, with an RMSE value of 278.3, an MSE value of 77,448.32, an MAE value of 454.14, a MAPE value of 25.43, and an R² score of 0.61. As compared with the performances of other models such as AR, MA, and ARIMA, the SARIMA’s results were significantly better than average, with an RMSE value of 442.12, an MSE value of 195,471.08, an MAE value of 364.74, a MAPE value of 23.18, and an R² score of 0.02.

Table 10. Summarized description of all models’ performance matrices.

	RMSE [18]	MSE [18]	MAE	MAPE	R ² Score
Polynomial Regression	524.83	275,449.04	402.9	168.64	−0.39
SVR	466.79	217,897.28	371.85	144.3	−0.1
Holt’s Linear Model	584.27	341,376.76	454.14	186.77	−0.72
Holt–Winter’s Model	278.3	77,448.32	249.81	25.43	0.61
AR Model	683.65	467,378.37	568.36	260.19	−1.35
MA Model	460.73	212,273.60	387.34	138.64	−0.07
ARIMA Model	603.97	364,778.86	541.14	215.81	−0.84
SARIMA Model	442.12	195,471.08	364.74	23.18	0.02
Prophet Model	204.75	41,922.55	146.29	16.82	0.49

13. Conclusions

In conclusion, we are able to state, based on the conversation that took place before, that the nation that causes the most concern is Spain. From a geographical standpoint, Europe is in a more precarious position than other regions. In addition, there is a much-increased likelihood that males, rather than females, will be impacted by the disease. This is a significant gender disparity. Furthermore, the severity of the epidemic is increasing on a daily basis, and the spread of the disease is also expanding in a cyclical manner. Therefore, if the respective management is unable to stop or reduce the transmission, the entire world may be faced with yet another catastrophe on the level of public health. More importantly, this study demonstrates nine different forecasting methods and found that the Prophet model is the most reliable forecasting model by comparing it with eight other models' performance. A comprehensive study of the monkeypox disease is still difficult to carry out as a result of the lack of data that are now available as well as the incompleteness of the dataset. In the future, we intend to continue our research by gathering datasets of images related to monkeypox in order to detect the monkeypox illness using a deep learning approach.

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Data Availability Statement: This research study is based on an open-source dataset. The dataset can be accessed from this link: <https://www.kaggle.com/datasets/andrewmvd/global-monkeypox-cases> (accessed on 12 April 2020).

Conflicts of Interest: The authors declare no conflict of interest.

Source Code Availability Statement:: The source code can be obtained from this link: <https://github.com/Farhana005/monkeyPoxPre.git> (accessed on 7 July 2022).

Abbreviations

MSE	Mean Square Error
MAE	Mean Absolute Error
RMSE	Root Mean Square Error
MAPE	Mean Absolute Percentage Error
SVR	Support Vector Regression
AR	Autoregressive
MA	Moving Average
ARIMA	Autoregressive Integrated Moving Average
SARIMA	Seasonal Autoregressive Integrated Moving Average

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