

Forecasting the Spread of Viral Diseases in Jordan Using the SARIMA Statistical Model

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Abstract: Time series models can help predict disease. Incidence data can be used to predict future disease outbreaks. Advances in modeling techniques allow us to compare the predictive capabilities of different time series models. Public health monitoring systems give essential data for accurate forecasting of future epidemics. This paper describes a study that used two types of infectious disease data, namely Mumps and Chickenpox, collected from a department of statistics open source data in mainland Jordan, to assess the performance of time series methods, specifically seasonal autoregressive integrated moving-average with exogenous regressors. The data collected from 2000 to 2023 were used as modeling and forecasting samples, respectively. The performance was evaluated using two metrics: mean absolute error and mean squared error. The statistical models' accuracy in predicting future epidemic illnesses established their use in epidemiological monitoring. The seasonal autoregressive integrated moving average with exogenous regressors model, which was used to estimate total mumps cases in Jordan, was applied to a real dataset over the years 2000 to 2023. The dataset was separated into three groups: 78% training, 9% validation, and 13% testing. The results showed a mean squared error of 26629 and a mean absolute error of 152. The model predicted that Jordan will have 2341 cases of mumps by 2028.

Keywords: Time series model, Jordan, prediction, diseases, forecasting model, sarimax, seasonal autoregressive integrated moving-average with exogenous regressors.

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1. Introduction

Global epidemics of deadly diseases are caused by viral infections that are emerging and resurrecting. There have been apparent gaps in preventative efforts following the COVID-19 pandemic. The healthcare industry is facing extra challenges due to emerging illnesses including smallpox, Zika, Ebola, Marburg, Hantavirus, and Nipah viruses, which increase the load on therapeutic and diagnostic limits [25].

The COVID-19 [3] pandemic surfaced and quickly became widespread, killing millions of people worldwide. When vaccines were subsequently developed, the disease's severe symptoms could be effectively avoided. Some people are still vulnerable to serious symptoms like chest discomfort and dyspnea, though.

The communicable diseases directorate in the Jordanian ministry of health [18] aims to provide preventive health services related to health and safety with high quality promptly through a highly efficient national vaccination program and through monitoring and controlling the occurrence of communicable diseases and diseases in the Kingdom of Jordan and implementing programs to prevent and control these diseases. The health sector in Jordan generates income for Jordanian domestic production regularly [2]. Artificial Intelligence's (AI) impact on medical

surveillance, outcome prediction, patient monitoring, genetic tracking, clinical help, therapeutic screening, drug and vaccine development, and other studies was recognized [25]. AI technology can anticipate disease transmission, evaluate the efficacy of therapies, and efficiently manage public health policy. These models help to make evidence-based decisions and allocate resources by evaluating massive volumes of epidemiological data and adding real-time updates [9].

Digital healthcare has several chances to minimize time and human error while improving therapeutic results [21]. A wide range of businesses are embracing the culture of hiring machine learning-based decision-making. Machine Learning (ML) is one of several learning strategies used in AI [22]. The medical and healthcare sectors are among the most vital and helpful. In the realm of healthcare. Predicting and detecting complicated diseases as rapidly as feasible is one of the essential features now being used with data-driven techniques, demonstrating that machine learning plays an important role in making a genuine impact in efforts to save human lives. Although illness prediction and detection are significant and one of the most important roles that machine learning adaptation performs in the health business, they may be challenging and time-consuming because of the complexities of diseases and their behaviors [22].

Deep Learning (DL) has emerged as a fast-emerging

medical specialty. It facilitates the detection of Infectious Diseases (IDs), which is critical for disease management and forecasting future outbreaks. Many scientists and researchers have used distance learning techniques to detect and forecast epidemiological and other healthcare-related issues, however, the results contain limitations and study gaps [1].

During an active outbreak or epidemic, accurate prediction of transmission risks and dissemination patterns is crucial for informing public health initiatives. Projections of an increase or drop in transmission among at-risk groups can help enhance treatments, especially when resources are limited [23].

The study was divided into the following categories:

1. An overview of the subject.
2. An overview of previous studies on the use of statistical models, machine learning, and deep learning approaches to predict the development of different diseases across many nations.
3. Thorough methodology and dataset analysis of viral disease.
4. Using SARIMAX on viral data, doing various implementation experiments, and recording the results.
5. An overview of the research and a discussion of the results.
6. A list of research references.

2. Literature Review

This portion of the study examines several previous works on disease spread prediction using AI approaches, ML, and DL.

Researchers investigated the prospect of predicting infections in food-borne illnesses using ensemble learning approaches, which surpassed previous machine learning models with 97.26% accuracy [15]. Ibrahim *et al.* [10] suggest a late fusion model based on machine learning for detecting beta-thalassemia carriers using red blood cell analysis. This work used the delayed fusion approach to implement four machine learning algorithms. The total accuracy for identifying beta-thalassemia carriers was 96%.

Support Vector Machines (SVM), Convulsion Neural Networks (CNN), and Artificial Neural Networks (ANN) are commonly utilized in cancer research to create prediction models that allow for accurate and effective decision-making [5]. Iwendi *et al.* [11] employ open-source data comprising geographic, social, and economic circumstances, clinical risk factors, symptom reports, and demographic data of COVID-19 patients in the region of nations impacted by the illness in Latin America to forecast survival and death.

Differences across nations and illnesses (e.g., economic circumstances, modes of transmission, etc.) make it difficult to develop models with cross-country prediction skills [27].

Sun *et al.* [23] offer the DeepDynaForecast model, a

cutting-edge deep learning system for predicting pathogen transmission dynamics. DeepDynaForecast was trained on detailed simulation data, identifying samples with an accuracy of 91.6%. Model performance and applicability were tested using outbreak data from Florida's HIV pandemic from 2012 to 2020 [23].

The study presents a comparative examination of four machine learning algorithms: k-Nearest Neighbor (K-NN), Naive Bayes (NB), Decision Tree (DT), and Random Forest (RF). These supervised classifiers predict widely specified illnesses based on an individual's visible symptoms. RF had the greatest accuracy, 99.5% [7]. Researchers developed a mixed deep learning model for clinical Non-Contrast Computed Tomography (NCCT) to predict early Hematoma Expansion (HE) following ischemic hemorrhage (sICH). The clinical NCCT deep learning multi-layer perception model has an accuracy score of 0.921 [26].

In research comparing time series models, a comparison analysis was done with established approaches such as ARIMA and ARIMAX, indicating that the intelligent ARIMAXS model outperforms them by obtaining the lowest error rates [12].

Every year, a life-threatening tick-borne viral infectious disease called Kyasanur Forest Disease (KFD) breaks out and kills many people in South Asia. In the present Majumdar *et al.* [17], the authors propose a novel e-healthcare architecture based on fog computing to monitor KFD patients at an early stage of infection and control the epidemic. To achieve a high prediction rate, a novel technique called Extreme Optimization-tuned Neural Network (EO-NN) is constructed by combining extreme optimization and feed-forward neural network. In addition, a location-based alerting system is suggested to deliver GPS-based position information for each KFD-affected user and sensitive locations as soon as feasible to avoid an epidemic. The EO-NN provides an average accuracy of 91.56%.

Colubri *et al.* [6] present a ML pipeline for Ebola Virus Disease (EVD) prognosis prediction, that incorporates the best models into a mobile app for use in clinical care settings. The pipeline was trained using a public EVD clinical dataset from Sierra Leone, which included 106 cases. The tiny sample size and high rate of missing records presented considerable obstacles. Researchers used multiple imputation and bootstrap sampling to rectify missing data and assess overfitting. This approach explains how to deal with limited sample sizes and missing data.

In a study conducted in China [28], nine different types of disease data collected through the national public health surveillance system in China were used to evaluate the effectiveness of four-time series techniques. Two decomposition methods (exponential regression and smoothing), ARIMA, and SVM. Data from 2005 to 2011 and 2012 were used as samples for modeling and forecasting. Performance was measured using three

metrics: Mean Absolute Error (MAE), Mean Absolute Relative Error (MAPE), and Mean Squared Error (MSE). The accuracy of statistical models in predicting future epidemic diseases has proven useful in epidemic surveillance.

ARIMA and Random Forest (RF) models were used to forecast infectious disease outbreaks, in particular the Highly virulent avian Influenza (H5N1) epidemic. The Kane *et al.* [13] discovered that the RF model performed better in terms of prediction than the ARIMA model. Moreover, researchers discovered that the Random Forest model performed well in anticipating the H5N1 breakout in Egypt. The correlation between epidemics in birds and humans has surfaced as a novel method for forecasting these catastrophic events [13].

Table 1 contains a collection of prior research that dealt with the application of ML and DL techniques to forecast the expansion of dangerous illnesses in people.

Table 1. Cluster of previous studies.

Ref.	Year	Method	Dataset	Accuracy
[15]	2024	DT, RF, k-NN, stochastic gradient descent, extremely randomized trees, and Ensemble modeling	Food-borne diseases	Ensemble model outperformed all other classifiers, with 97.26% accuracy
[10]	2024	The late fusion-based ML model	Thalassemia reports from the Internet of Medical Things (IoMT) enabled devices in a feature-based dataset.	96%
[3]	2024	Explainable AI (XAI)	Two Manipal hospitals' COVID-19 data	95%
[27]	2024	Neural Network XGBoost, Logistic Boost, RF, and Kernel SVM	Statistics on outbreaks of 43 illnesses in 206 nations	80%–90%
[23]	2024	DeepDynaForecast [16]	Data from the HIV epidemic in Florida between 2012 and 2020.	91.6%
[7]	2024	KNN, Naive Bayes, DT, and RF.	Dataset containing frequent symptoms	RF (99.5%), DT (95.8%), KNN (93.4%), and Naive Bayes (87.7%).

3. Methodology

This portion of the study explains the research methodologies used to attain the research aim.

3.1. Overall Methodology

This section of the study outlines the general procedure. First, reliable data on a range of illnesses spread by air pollution in Jordan is obtained from the official website of the Jordanian Department of Statistics. The obtained dataset is then assessed, and following that, a statistical model is used to the data to determine the diseases that will spread in the upcoming years based on the number of instances, and finally, the results are obtained. Figure 1 shows the methodology used in the research.

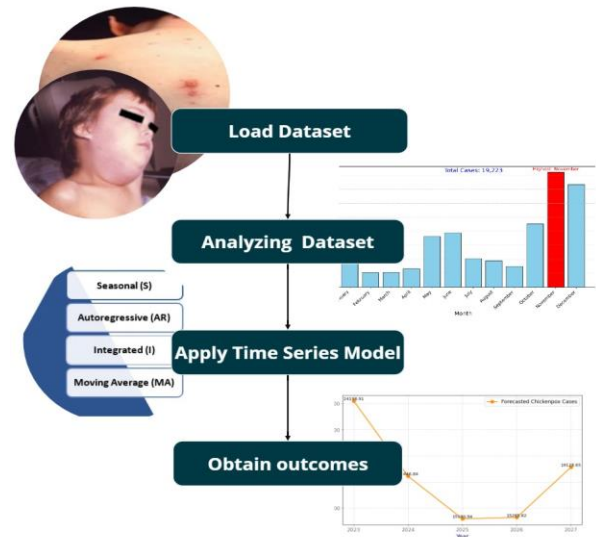


Figure 1. Research methodology.

3.2. Dataset

Datasets are collected from the Jordanian Department Of Statistics (DOS), namely diseases resulting from air pollution, which represent the number of cases of communicable diseases in the years (2000-2023) [24]. The Figure 2 shows the number of cases of infectious diseases in Jordan in 2023.

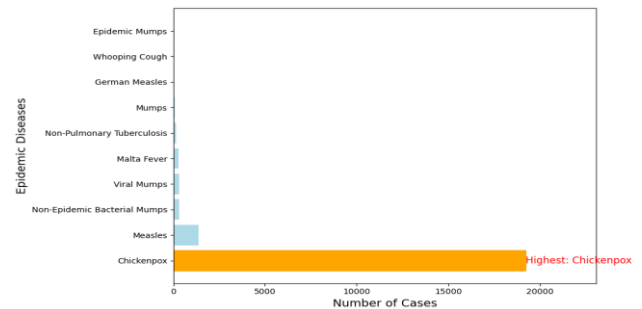


Figure 2. Number of communicable disease cases in Jordan (2023).

In Jordan in 2023, the disease with the most recorded cases of infection was Chickenpox, with the number of infections reaching 19, 223.

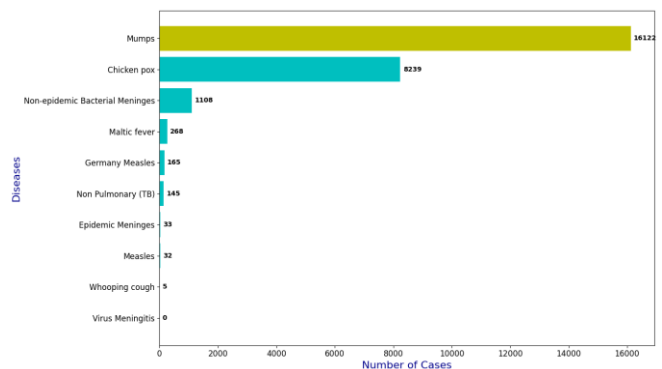


Figure 3. Number of epidemic diseases cases in Jordan (2000).

In Jordan in 2000, the largest number of epidemic cases was recorded by mumps, with the number of

infections reaching 16,122 , as shown in the Figure 3.

The symptoms of varicella, known as chickenpox, include little red pimples on the skin and a mild fever. It is normally at its mildest when first seen in childhood, but when it strikes an adult, it can be rather serious. Varicella zoster is the herpes virus that causes the illness [4]. The Figure 4 shows a case of chickenpox.



Figure 4. Chickenpox case [19].

I notice that chickenpox cases over the years have an upward curve from 2000 to 2023. This is a negative indicator , as shown in the Figure 5.

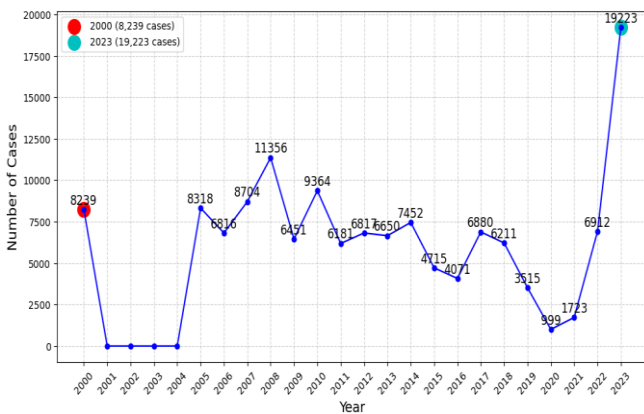


Figure 5. Number of chickenpox cases by Year (2000-2023) in Jordan.

According to Figure 6, Jordan had 19,228 occurrences of chickenpox in 2023. The month of November had the largest number of cases, totaling 4,114, making it the highest month of the year.

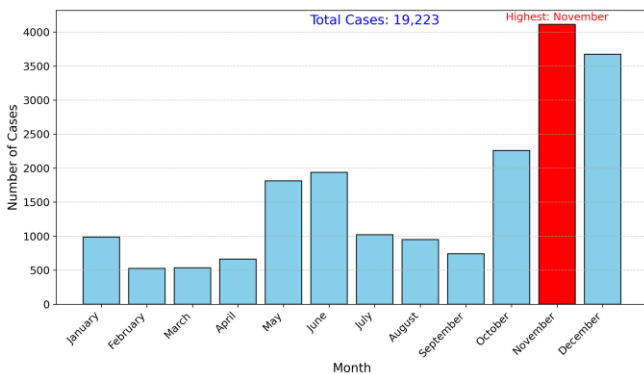


Figure 6. Jordan chickenpox cases by month in 2023.

The highly contagious virus known as mumps [14] is found worldwide in places where vaccination is not widely available. The hallmark of acute mumps infection is non-suppurative parotitis, which develops after symptoms of low-grade fever, muscle aches, malaise, and loss of appetite. Actual patients of mumps in people are displayed in Figure 7.



Figure 7. Actual cases of the mumps virus manifest in people [14].

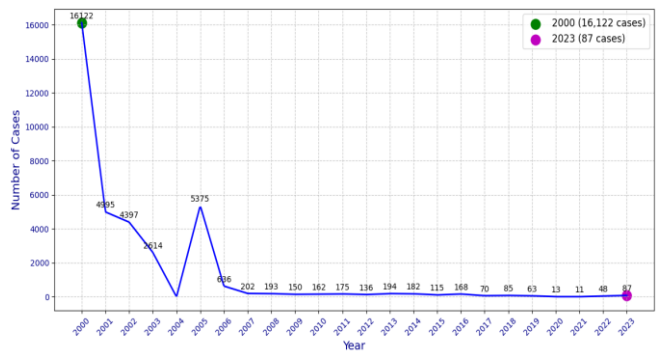


Figure 8. Number of mumps cases by Year (2000-2023) in Jordan.

Based on the Figure 8, it was noted that the number of mumps cases during the years (2000-2023) in Jordan is decreasing, and this is a positive indicator of the role of the health sector in Jordan in reducing the number of cases of infection.

3.4. Time Series Model

Seasonal Autoregressive Integrated Moving-Average with Exogenous Regressors (SARIMAX) is a variant of the ARIMA model that accounts for both seasonality and exogenous factors. SARIMAX models are among the most popular statistical models for forecasting, with outstanding predicting performance [8, 20].

The SARIMAX model nomenclature uses the parameters p, d, and q to indicate the autoregressive, differencing, and moving-average components, respectively. P, D, and Q are the identical components for the seasonal section of the model, with m denoting the number of periods in each season. p represents the order (number of time delays) of the model's autoregressive component. The degree of differencing (d) is the number of times past values were removed from the data. The order of the model's moving average is denoted by q. P is the order (number of time delays) of the seasonal component of the model. D is the seasonal model's degree of differencing (the number of times past

values are removed from the data). Q represents the order of the seasonal moving average in the model. m denotes the number of periods in each season.

4. Experiment Results

In this section of the research, all experiments were performed on the infectious disease statistics database using the predictive model, and the results were recorded. The experiments were performed manually using the Python programming language with the Google Colab environment.

4.1. SARIMAX Model in Forecasting Chickenpox Case in Jordan

4.1.1. Divide the Dataset into 80% Training and 20% Testing

The Total Chickenpox Cases (2000-2023) dataset was divided into training and testing rates of 80% and 20%, respectively, after the SARIMAX model was applied to it. The findings show that the Mean Absolute Error (MAE) is 6790 and the Mean Squared Error (MSE) is 64553157.

In 2023, the actual number of chickenpox cases was 19223 . The SARIMAX model predicted the number of cases to be 6920 when the training size was 80% and the testing was 20% using the SARIMAX mode seasonal order=(0, 1, 1, 12).

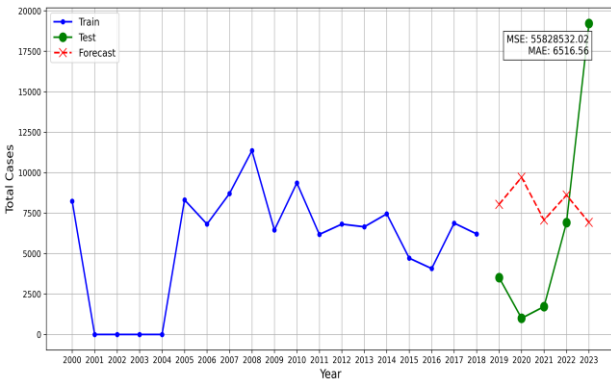


Figure 9. SARIMAX forecast of total chickenpox cases (2000-2023) training rate: 80%, Test rate: 20%.

The Figure 9 depicts the results of the SARIMAX predictive model on chickenpox cases in Jordan (2000-2023), with the data divided into 80% training and 20% testing.

4.1.2. Divided the Data into Training (78%), Validation (9%), and Test (13%)

In the second experiment to predict chickenpox cases in Jordan, the dataset was divided differently into three classes: training data (78%), validation data (9%), and test data (13%). After data division, the SARIMAX model was implemented to train, test, and predict the total chickenpox cases. The model gave an MSE of 70654870 and an MAE of 5646.

In 2023, 19223 chickenpox cases were reported; however, when using SARIMAX in seasonal order (1, 1, 1, 3) the prediction was 4780 cases. Figure 10 shows the results of the experiment.

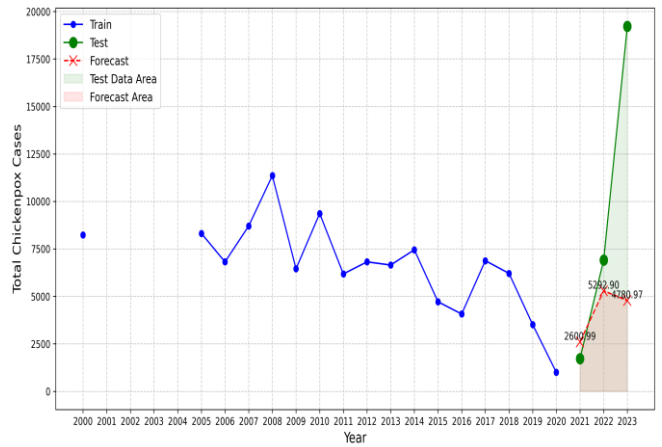


Figure 10. SARIMAX forecasting of total chickenpox cases (2000-2023) Training size: 78%, validation size: 9%, test size: 13%.

4.1.3. Forecasted Chickenpox Cases Next 5 years 2023-2027

The Jordanian DOS documented the number of chickenpox virus cases from 2000 to 2023. This data is employed in time series models to produce the best projections and results.

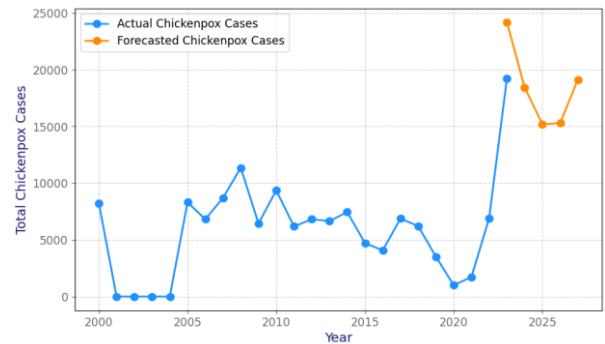


Figure 11. Actual and expected chickenpox cases in Jordan from 2000 to 2027.

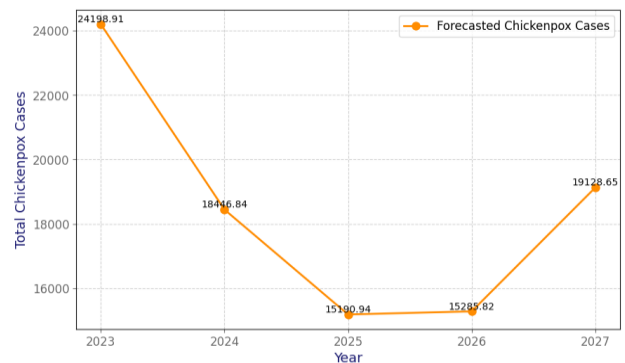


Figure 12. Projected chickenpox cases over the next five years (2023-2027).

In this experiment, the train was trained for 5 years (2000-2003), however, there was no test data. The

purpose was to forecast chickenpox cases for five years (2023-2027). Using the entire dataset, the model forecasts instances for 2023-2027. Given that the dataset was divided into the data train (100%). Figures 11, 12, and Table 2 show how to utilize the SARIMAX model to anticipate the total number of cases over the next five years using a seasonal order of (0, 1, 1, 12).

Table 2. Number of chickenpox cases expected over the next five years generated by the SARIMAX (0, 1, 1, 12) model.

Years	Forecasted chickenpox cases
2023	24198
2024	18446
2025	15190
2026	15285
2027	19128

4.2. SARIMAX Model in Forecasting Mumps Case in Jordan

4.2.1. Dividing the Dataset into 80% Training Size and 20% Testing Size with the SARIMAX (0, 1, 1, 12) Model

This experiment is based on Jordanian mumps case data from 2000 to 2023. The data was divided into two classes: training (80%) and testing (20%). The SARIMAX model with seasonal order=(0, 1, 1, 12) was used to train and test on the mumps dataset. The model produced results in which MSE reached 8375052 and MAE reached 2862. In this experiment, we observe an improvement in performance results as the amount of data increases. The Figure 13 show the result of the experiment. In this experiment, the expected model results were negative.

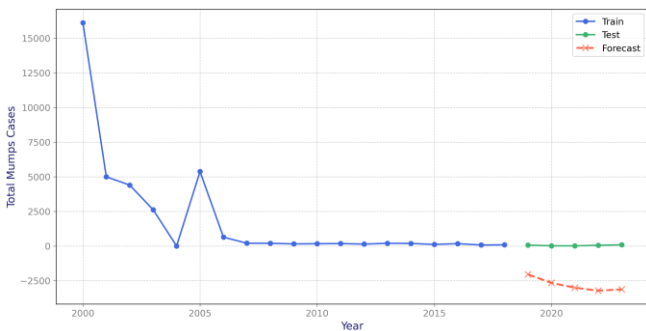


Figure 13. SARIMAX forecasting of total mumps cases (2000-2023) with training size 80% and testing size 20%.

4.2.2. Dividing the Mumps Data into Training (78%), Validation (9%), and Testing (13%)

In the second experiment to forecast total mumps cases using SARIMAX, the dataset was separated into three classes: a training set of 78%, a validation set of 9%, and a test set of 13%, with a seasonal order of (1, 1, 1, 3) for the SARIMAX model, yielding an MSE of 26629 and an expected MAE of 152. In this experiment, the results were improved when the dataset was divided into three sections: training, testing, and validation. The Figure 14

and Table 3 depict the experiment's performance outcomes.

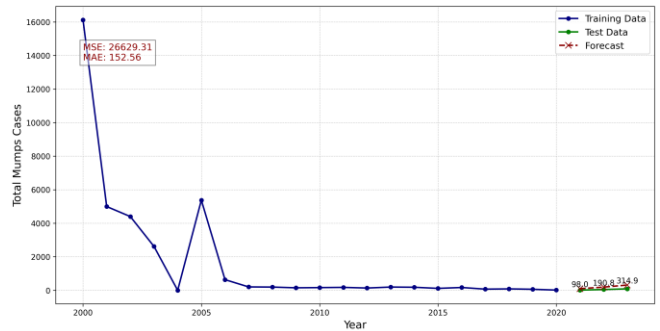


Figure 14. SARIMAX's predictions of total mumps cases when dividing the data into training (78%), validation (9%), and testing (13%).

Table 3. SARIMAX (1, 1, 1, 3) model forecasts for total mumps cases (2020-2023).

Year	Test data (true cases of mumps)	SARIMAX forecasting
2021	11	98
2022	48	190
2023	87	314

4.2.3. Forecast of Mumps Cases in Jordan for the Next Five Years 2024-2028

This experiment aimed to predict the incidence of mumps cases for five years for 2024-2028, with the SARIMAX model set to seasonality=(1, 1, 1, 12). The data were separated into three categories: training (78%),

Figure 15 and Figure 16 show the predicted mumps cases for the next five years: 48.26 in 2024, 15849.44 in 2025, 4722 in 2026, 4124 in 2027, and 2341 in 2028.

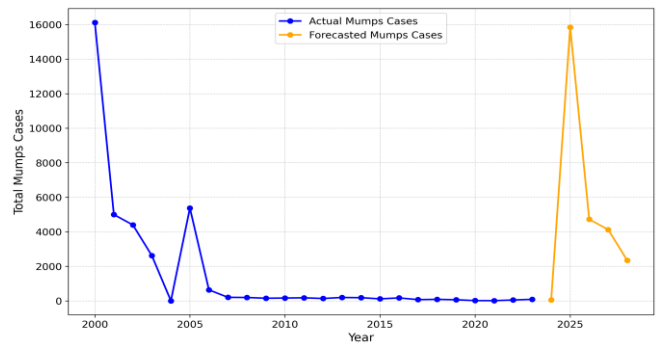


Figure 15. Five-year projection of mumps cases by SARIMAX model.

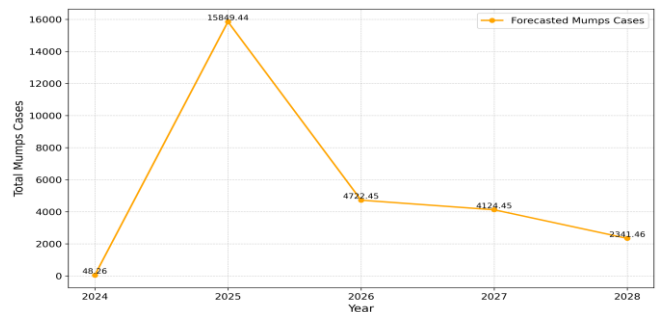


Figure 16. Number of predicted cases of mumps over the next five years (2024-2028).

5. Conclusions

A successful health system's major responsibility is to keep the people healthy, protect them from infectious and chronic diseases, and provide them with health care that is effective, safe, fair, high-quality, and as low-cost as feasible.

Viral illnesses spread rapidly by air, water, and direct touch. Infectious diseases threaten humans. To control the spread of infection, preventive measures must be implemented before any pest outbreak. The most common diseases in Jordan over the years were reviewed, and chickenpox and mumps were identified as the most common. Chickenpox disease has had the largest number of human infections in Jordan over the years, and in 2023, it exceeded the infection number by 19,000.

The study's goal is to forecast the spread of infectious illnesses in Jordan using real data obtained from an authoritative source. The time series SARIMAX model was applied to the dataset.

As a result of this research, multiple experiments were run on actual data indicating the number of chickenpox and mumps cases in Jordan from 2000 to 2023

The SARIMAX model was used on the chickenpox dataset (2000-2023), which was divided into 80% training and 20% testing rates, respectively. The data indicate an MAE of 6790 and an MSE of 64553157. In 2023, the actual number of chickenpox cases was 19223. The SARIMAX model predicted 6920 cases. The SARIMAX model predicts that the number of chickenpox cases in 2027 will be 19,128.

The Jordanian Ministry of Health can take precautionary measures in situations such as the deadly COVID-18 pandemic by anticipating the emergence of viral infections in Jordan's several governorates, therefore decreasing human deaths.

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