Journal of Applied Mathematics and Physics, 2023, 11, 3625-3640
https://www.scirp.org/journal/jamp
ISSN Online: 2327-4379
ISSN Print: 2327-4352

A Method for Constructing Mathematical Modeling of the Spread of a New Crown Pneumonia Epidemic Based on the Effect of Temperature

Zhening Bao

Sino-Canada School, Suzhou, China
Email: baozhening@126.com

How to cite this paper: Bao, Z.N. (2023) A Method for Constructing Mathematical Modeling of the Spread of a New Crown Pneumonia Epidemic Based on the Effect of Temperature. *Journal of Applied Mathematics and Physics*, **11**, 3625-3640.
https://doi.org/10.4236/jamp.2023.1111228

Received: October 10, 2023
Accepted: November 21, 2023
Published: November 24, 2023

Abstract

To better predict the spread of the COVID-19 outbreak, mathematical modeling and analysis of the spread of the COVID-19 outbreak is proposed based on data analysis and infectious disease theory. Firstly, the mathematical model indicators of the spread of the new coronavirus pneumonia epidemic are determined by combining the theory of infectious diseases, the basic assumptions of the spread model of the new coronavirus pneumonia epidemic are given based on the theory of data analysis model, the spread rate of the new coronavirus pneumonia epidemic is calculated by combining the results of the assumptions, and the spread rate of the epidemic is inverted to push back into the assumptions to complete the construction of the mathematical modeling of the diffusion. Relevant data at different times were collected and imported into the model to obtain the spread data of the new coronavirus pneumonia epidemic, and the results were analyzed and reflected. The model considers the disease spread rate as the dependent variable of temperature, and analyzes and verifies the spread of outbreaks over time under real temperature changes. Comparison with real results shows that the model developed in this paper is more in line with the real disease spreading situation under specific circumstances. It is hoped that the accurate prediction of the epidemic spread can provide relevant help for the effective containment of the epidemic spread.

Keywords

Pneumococcal Pneumonia, Outbreak, Dispersion Model, Mathematical

Modeling, Prediction

1. Introduction

Novel Coronavirus Pneumonia is an infectious disease caused by the Severe Acute Respiratory Syndrome Coronavirus, which after more than two years of spread has become one of the worst pandemics of all time [1]. The new coronavirus wild-type strain detected in 2019 evolved from three consecutive alpha mutations on an influenza virus. New Crown pneumonia is much more contagious than regular influenza, infecting approximately 2 to 2.5 people in 1 patient, with a severe disease rate of 20% and a mortality rate of 4%. The Pfizer vaccine was the first to be put into use in December 2020, and the availability of the vaccine led to a brief containment of the epidemic, as the New Crown virus at this time could not resist the immune system. Some vaccines are 95.6% effective. The implementation of patient isolation, vaccination, and other preventive measures controlled the spread of the epidemic to a certain extent, and the number of daily infections of *C. neoformans* began to stabilize globally, and people are looking forward to the end of the global epidemic. At present, the epidemic of *C. neoformans* is still spreading worldwide, posing a great threat to the safety of people's lives and the social development of the country [2]. The limitations of the technology lead to the current treatment being still based on adjuvant and conservative treatment, and whether it can be cured mainly depends on the patient's immune function. Due to the constant change of temperature in the four seasons, the spreading mode of the epidemic is also constantly changing, and the traditional prediction methods may deviate from the real situation. Modeling analysis of epidemic data can enrich and improve the expression of prediction results and predict the development of the epidemic more accurately. Analyzing data on the spread of epidemics in different countries or regions helps to understand the characteristics of epidemics at different stages, and points out the direction for the next prevention and control priorities as well as the main prevention and control measures. By analyzing the transmission process and evaluating the effectiveness of various anti-epidemic measures through modeling methods, the problem can be transformed from qualitative to quantitative analysis, and the development of the disease in different situations can be explored by changing some parameters in the model within a reasonable range. This can help various units in different countries and regions to allocate resources in a timely and effective manner during emergencies, reduce the rate of infection and death, increase the cure rate, effectively maintain social stability, and safeguard people's lives and property. In this paper, we assemble the spreading process of the new coronary pneumonia epidemic involves multiple factors and variables, which are analyzed and predicted through mathematical modeling. The designed predictive analysis based on the SEIR model can predict the number of infections,

deaths, and the end of the epidemic in the future period.

2. Constructing a Mathematical Model of the Spread of the New Coronary Pneumonia Epidemic

2.1. Indicators of Mathematical Modeling of the Spread of the New Crown Pneumonia Epidemic

The main indicators of the mathematical modeling of the spread of the pericoronitis epidemic include the rate of self-healing of the latent population of pericoronitis, the mortality rate of the infected population, the recovery rate of the infected population, and the rate of recovery. In the early stages of an epidemic, the number of infections usually grows exponentially. That is the number of new infections per day increases by a fixed percentage. This ratio is known as the growth rate. According to the mathematical model, the number of infections should satisfy the following differential equation: the rate of change in the number of infections is equal to the product of the rate of transmission the proportion of susceptible people, and the recovery factor. The calculation of the growth rate can be done at different stages of the epidemic. The value of growth rate is usually high at the beginning of the epidemic when almost everyone is susceptible and the recovery of the infected has not yet begun. Over time, as part of the population begins to recover, the value of the growth rate decreases. This process can be accurately described by the mathematical model [3]. It is important to note that the growth rate is not a fixed value, it varies with region and time. This variation is usually related to factors such as people's precautions, treatments, and social behavior. Therefore, the calculation of the growth rate can provide an important basis for the prediction of the spread of the new Crown pneumonia epidemic and its prevention and control.

2.2. Underlying Assumptions

The spread model of the CKP outbreak consists of four compartments: the susceptible population (S), the latent population (E), the infected population (I), and the emigrating population (R). The susceptible population is the group of people who are not yet sick, but lack immunity and are susceptible to infection after contact with an infected person, the number of which is recorded at t as $(S)t$. The latent population is the asymptomatic population that is in the latent period of the disease and is not contagious, and its number is recorded as $(E)t$ at the time. Infected people are those who have been infected with the disease and are contagious, and their number is recorded as at $(I)t$. The outgoing population is the population that has recovered from the disease or died and is no longer transmissible and is denoted as $R(t)$ [4] at t. The following assumptions were made when studying the relationship between the populations.

1) The total number of people N remains the same, then a permanent formula can be obtained as:

$$N = S(t) + E(t) + I(t) + R(t) \tag{1}$$

2) A susceptible person has a certain probability of being in contact with an infected person, the contact rate is recorded as *a*, and after contact with an infected person, the susceptible person has a certain probability of contracting the disease, the rate of contracting the disease is recorded as *b*, and the rate of contagion β is the probability of transmitting the disease to the susceptible person, the $\beta = ab$.

3) At the moment, the average incubation period of a disease is 1/*a*, and a certain percentage of incubators turn into infected individuals, the percentage is recorded as *a*; a certain percentage of infected individuals turn into emigrants, the percentage is recorded as γ.

The corresponding set of equations for modeling the spread of the new Crown pneumonia outbreak is:

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI \\ \dfrac{\mathrm{d}E}{\mathrm{d}t} = \beta SI - aE \\ \dfrac{\mathrm{d}I}{\mathrm{d}t} = aE - \gamma I \\ \dfrac{\mathrm{d}R}{\mathrm{d}t} = \gamma I \end{cases} \tag{2}$$

The modeling of the spread of the new Crown pneumonia outbreak has the following properties:

1) As time tends to infinity, the number of infected people drops to 0, *i.e.*, the number of eventually infected people in the system is 0.

2) If $S(t) \le \gamma / R$, the infected population gradually decreases to zero as time increases; conversely, if $S(t) > \gamma / R$, the infected population gradually increases, reaches a maximum $S(t) = \gamma / R$, and then decreases.

3) As time increases, the numbers of susceptible, latent, infected, and emigrating populations change regularly based on variables such as exposure, transmission, disease incidence, recovery, and latent transformation.

4) The basic number of infections for modeling the spread of a new coronary pneumonia outbreak: the basic number of infections is the average number of secondary infections from individual infections in a susceptible population in the early stages of an outbreak, in the absence of external intervention, and is denoted as R_0.

From the above assumptions, we can get the basic infectious number of the spread model of the new Crown pneumonia epidemic $R_0 = S(0)\beta/\gamma$, which is mainly used in the early stage of the epidemic to estimate whether the epidemic will break out in the future or not. If $R_0 < 1$, the infection will gradually disappear; $R_0 > 1$ the infection will continue to spread and an outbreak will occur if it is not controlled; if, the outbreak does not occur but will become endemic.

2.3. Calculation of the Propagation Rate

The basic number of infections in each country or region in the past time is first

derived from the available data using the information on the successive intervals of the disease R_0. Based on the results, the transmission rate of the latent population $\varepsilon(T)$ and the transmission rate of the infected population $a(T)$ are derived as a function of temperature, using the underlying assumptions, where t is the time interval.

$$R_0 = \frac{I(r+t)}{I(r)} \tag{3}$$

For this purpose, define $X = \{S, E, I, R\}$. Assume that there is a disease-free equilibrium (DFE) in the system, *i.e.*, $E_0 = (S, 0, 0, 0)$... First, derive the next-generation matrix for the created system. Define the matrix F to denote the rate at which new individuals enter the infectious E zones, and define the matrix V to denote the rate at which individuals move from the E and I zones to the non-infectious R D zones. The matrices F V can be written respectively as

$$F = \begin{bmatrix} k\varepsilon(T) \\ 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \beta + \delta_E \\ -\beta \end{bmatrix} \tag{4}$$

Assuming that the transmission rate of exposed persons is linearly correlated with infected persons, $a(T) = c\varepsilon(T)$ then R_0 corresponding to the spread model of the new Crown pneumonia outbreak is the maximum eigenvalue of FV^{-1}:

$$R_0(T) = \rho\left(FV^{-1}\right) = \frac{k\varepsilon(T)}{\beta + \delta_E} + \frac{k\alpha(T)\beta}{(\beta + \delta_E)(\delta_D + \delta_E)} \tag{5}$$

δ_E and δ_D represent the self-healing rate of the latent population and the mortality rate of the infected population, respectively. Finally, the rate of spread of the epidemic as a function of temperature is obtained:

$$\varepsilon(T) = \frac{R(0)(T)(\beta + \delta_E)(\delta_D + \delta_E)}{k(\delta_D + \beta + \delta_E)} \tag{6}$$

2.4. Realization Model Construction

In this paper, we modeled the spread of the pneumococcal pneumonia outbreak based on the basic assumptions, using temperature as a variable, and considered the effects caused by the infectious capacity of the latent population and changes in temperature on the rate of spread of the pneumococcal pneumonia outbreak.

1) Based on the basic assumptions, the New Crown Pneumonia Outbreak Dissemination Model divides the population into five categories: the susceptible population at (S), the latent population at (E), the infected population at (I), the recovered population at (R), and the dead population at (D). The susceptible population is the group of people who have not yet been infected with the disease but lack immunity and are susceptible to infection after contact with an infected person, whose number is recorded as at $tS(t)$. The latent population is the

asymptomatic people who are in the latent period of the disease and are infectious, and their number is recorded as at $E(t)t$. Infected people are those who are infected with the disease and are contagious, and their number is recorded as at $I(t)t$. Recovered people are those who have recovered from the disease, and their number is recorded as at $R(t)t$. Dead people are those who died during the spread of the disease, and their number is recorded as at $D(t)t$. Both the recovered people and the dead people are no longer capable of spreading the disease.

2) In the real world, during the initial spread of the new coronavirus, the rate of infant illness is very low therefore the model does not take into account the impact of dynamics such as the birth of infants on the spread of the epidemic [5]. The infected population is cured and is no longer capable of transmission, so the own population is considered a closed system, *i.e.*

$N = S(t) + E(t) + I(t) + R(t) + D(t)$ always holds.

3) The exposure rate is a linear function of the probability that latent and infected individuals have different probabilities of becoming recovered, and recovered individuals develop antibodies against the disease [6]. With the assumptions held, the structure of the model for the spread of the new Crown pneumonia outbreak is shown in **Figure 1**.

In the modeling of the spread of the new Crown pneumonia outbreak, the latent population spreads the disease to the susceptible population, a portion of the latent population cures itself, and temperature also influences the spread of the outbreak. **Table 1** describes what each parameter in the model represents.

The process of spreading an epidemic can be broken down into the following processes.

A susceptible person has a certain probability of converting to a latent person due to exposure to a latent or infected population. At a temperature of T, the transmission rate of the latent population is $\varepsilon(T)$ and the transmission rate of the infected population is $a(T)$, so the equation for the change in the susceptible population is:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \left(-ka(T)\frac{I}{N(t)} - k\varepsilon(T)\right)S(t) \tag{7}$$

When a portion of the susceptible population becomes latent, there is a probability that a latent person will knife become infected and a probability that δ_E will recover, so the equation for the change in the latent population is:

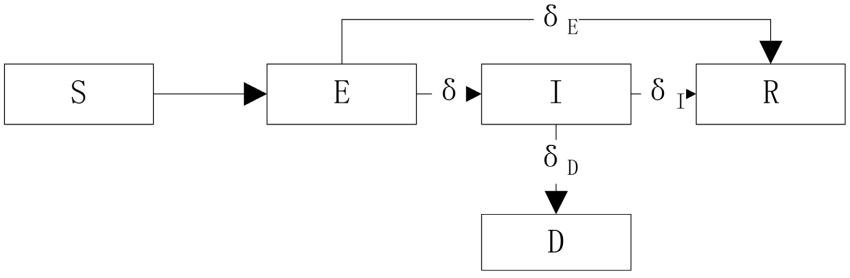

Figure 1. Structure of the model for the spread of the new Crown pneumonia epidemic.

Table 1. Meaning of each parameter represented in the spread model of the new crown pneumonia epidemic.

symbol	significance
$\varepsilon(T)$	Latent population transmission rate
$a(T)$	Transmission rate of infected population
β	morbidity
δ_E	Self-healing rate of latent population
δ_D	Mortality rate of the infected population
δ_I	Recovery rate of the infected population
k	Per capita daily contact number

$$\frac{\mathrm{d}E}{\mathrm{d}t}=\left(-ka(T)\frac{I(t)}{N(t)}+k\varepsilon(T)\frac{E(t)}{N(t)}\right)S(t)-(\beta+\delta_E)E(t) \tag{8}$$

When a portion of the latent population becomes infected, an infected person has a probability δ_D of dying and a probability δ_I of recovering, so the equation for the change in the infected population is: δ

$$\frac{\mathrm{d}I}{\mathrm{d}t}=\beta E(t)-\delta_I(t)-\delta_D(t) \tag{9}$$

The recovered population changes from the infected and latent populations, the dead population changes from the infected population, the latent population has a self-recovery rate of δ_E, the infected population has a recovery rate of δ_I, and the infected population has a mortality rate of δ_D, so the equations for the changes in the recovered and dead populations are:

$$\frac{\mathrm{d}R}{\mathrm{d}t}=\delta_I I(t)+\delta_E E(t) \tag{10}$$

$$\frac{\mathrm{d}D}{\mathrm{d}t}=\delta_D I(t) \tag{11}$$

Generalizing and summarizing the above, the improved differential equation system for the spread model of the new Crown pneumonia epidemic is obtained and the overall differential equation system is as follows.

$$\begin{cases}\dfrac{\mathrm{d}S}{\mathrm{d}t}=\left(-ka(T)\dfrac{I}{N(t)}-k\varepsilon(T)\right)S(t)\\ \dfrac{\mathrm{d}E}{\mathrm{d}t}=\left(-ka(T)\dfrac{I(t)}{N(t)}+k\varepsilon(T)\dfrac{E(t)}{N(t)}\right)S(t)-(\beta+\delta_E)E(t)\\ \dfrac{\mathrm{d}I}{\mathrm{d}t}=\beta E(t)-\delta_I(t)-\delta_D(t)\\ \dfrac{\mathrm{d}R}{\mathrm{d}t}=\delta_I I(t)+\delta_E E(t)\\ \dfrac{\mathrm{d}D}{\mathrm{d}t}=\delta_D I(t)\end{cases} \tag{12}$$

3. Prediction and Analysis of the Spread of the New Crown Pneumonia Epidemic

In this section, several countries that were invaded by the Alpha Neoguana strain at the beginning of the outbreak of the *C. neoformans* pneumonia epidemic are selected as the study subjects, and the designed *C. neoformans* pneumonia outbreak spreading model is used to analyze, validate, and predict the changes in the outbreak, and to compare with the actual results.

3.1. Data Collection and Analysis

After the outbreak of *C. neoformans* pneumonia, countries have been updating their data daily. The *C. neoformans* pneumonia data used in this paper are from the Johns Hopkins University *C. neoformans* data repository, which contains five attributes: name of the country, date, number of people diagnosed, number of people cured, and number of people who died. The average of the last two days is used to replace missing parts of the data, and the seven-day moving average of the number of people of interest is used as the average daily number to avoid large fluctuations in the data [7]. There are differences in the populations of different countries and regions, so the outbreak data were processed to obtain the number of people infected with NCP per million person days for each country and region. In this paper, outbreak data from several countries and regions were used, and **Figure 2** depicts the relationship between the spread of the epidemic over time, where the horizontal coordinate indicates the date and the vertical coordinate indicates the number of people infected per million person-days. Analysis of the data reveals that from July to September 2020, the rate of outbreak spread was flat, with fewer than 100 infections per million person-days in several places. From September 2020 onwards, the new Crown pneumonia outbreak spread rapidly in all country regions, with a rapid increase in the number of daily infections. Over time, the growth rate of the outbreak slowed in each

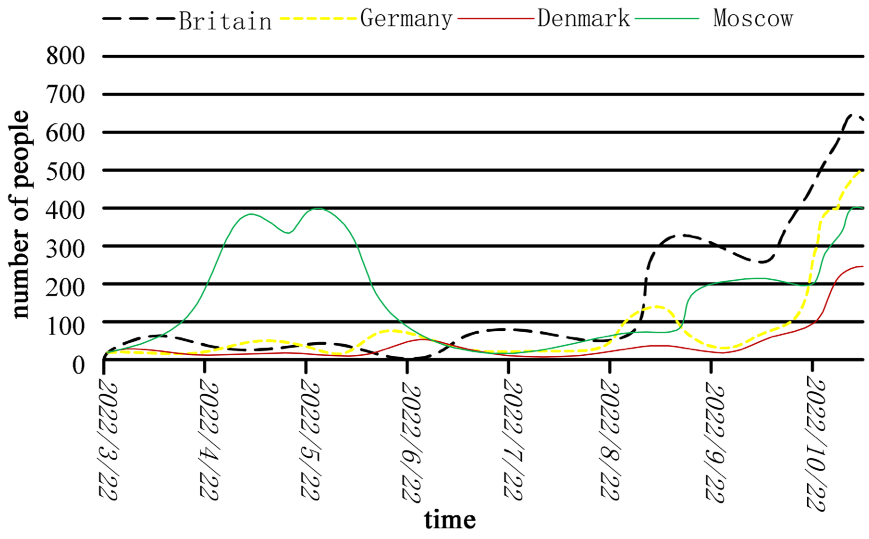

Figure 2. Spread of the epidemic in selected areas over time.

country-region, with the rate of spread in St. Petersburg approaching a plateau after mid-November 2020, with the number of daily infections per million people varying in the range of 700 - 800 per million people.

According to the results of our research, the incubation period of neocoronavirus alpha strains is mostly 5 to 7 days, with a maximum of 14 days, and the incubation period of neocoronavirus was set at 7 days in this paper.

Due to the differences in latitude and terrain patterns, there are differences in the climate of different countries or regions, of which temperature is one of the variables that best reflect climate change and the influence of temperature on the spread of the epidemic is considered in the constructed model. By collecting data on temperature changes in each country or region, it can be found that from July to September 2020, the temperature in each country or region fluctuates slightly and maintains a relatively stable high temperature. With the arrival of fall, after September 2020, the average temperature in each country region was decreasing, which was compared with the changes in the new crown pneumonia epidemic to obtain the relationship between the temperature and the number of infections per million person-days in each country region, as shown in **Figure 3**. Where the horizontal coordinate represents temperature and the vertical coordinate represents the number of infections per million person days [8]. Analyzing the data, it can be found that in the pre-spreading process of the new Crown pneumonia epidemic, the relationship between temperature and the number of daily infected people in each country region has the same general trend: when the temperature is high, the disease spreads less because of the increase in the human immunity and the shorter survival time of the virus. When the average daily temperature is above 20 degrees Celsius, the number of daily infections per million people is generally lower than 50 in all regions of the country. During small decreases in temperature, human resistance decreases, virus survival time increases, and the population contact rate remains essentially the same, resulting

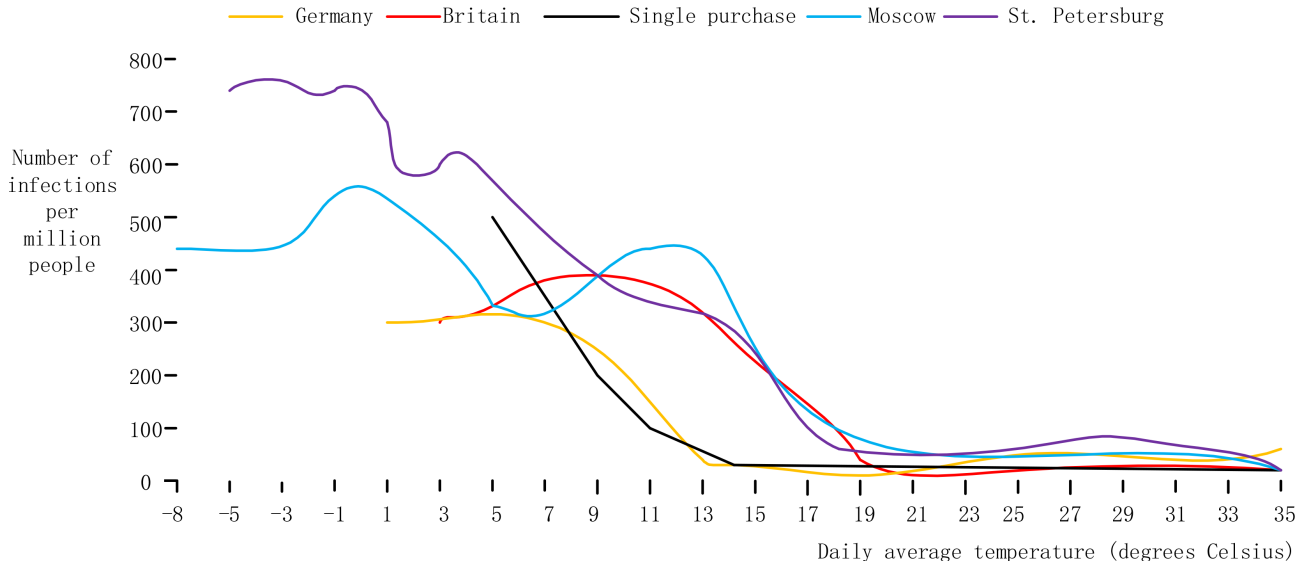

Figure 3. Rough statistical plot of the number of infections per million person days versus temperature change.

in higher rates of disease transmission. At temperatures between 9 degrees Celsius and 13 degrees Celsius, the number of infected persons per million person-days can increase by up to 70 for every 1-degree decrease in temperature. As the temperature continues to drop, the virus activity decreases, although the body's resistance decreases, and people go out less frequently due to the low temperature, resulting in a decrease in the rate of contact with the population and a decrease in the rate of spread of the disease. At temperatures below 9 degrees Celsius, except for St. Petersburg, which has extreme weather, the number of infections per million person-days increases by up to 20 per 1-degree drop in temperature in different countries and regions. By looking at **Figure 4**, it can be seen that the number of daily infections per million people in the different country regions decreases as the temperature increases. Equation (13) describes the relationship between the number of daily infections and temperature.

$$f(t)=\frac{c}{1+a*\mathrm{e}^{bt}} \tag{13}$$

In the formula, $f(t)$ is the number of infections per million person-days at the average temperature of t degrees Celsius in the second half of each year, c is the limiting value of the number of infections per million person-days, and b is the rate of change. The values of the parameters can be obtained by polynomial fitting. The results of the run are:

$$f(t)=\frac{1000}{1+0.2\mathrm{e}^{0.124t+1.71}} \tag{14}$$

The adjusted goodness of fit R^2 reaches 86%, so it can be used to characterize the relationship between temperature and the number of infections per million person days.

3.2. Forecast Results and Analysis

The basic number of infections R_0 is a key parameter in describing the transmissibility of a disease. It is the average number of secondary infections that arise from individual infections in a susceptible population in the absence of external intervention and is an important indicator of the prevalence of an infectious disease. Based on previous data on daily infections and information on disease sequence intervals, we can infer the basic number of infections per country or region in the past R_0. However, differences in latitude and terrain patterns lead to different ranges of annual temperature variation intervals in different countries or regions, and the relationship between temperature and the basic number of infections R_0 in different countries has a large deviation [9]. Therefore, using the data normalization method to deal with the temperature data of each place, the relationship between temperature and the basic infectious number R_0 can be figured out more accurately. **Figure 4** depicts the relationship between normalized temperature and the basic infectious number.

Basic contagion number R_0 versus air temperature obtained by quadratic curve fitting.

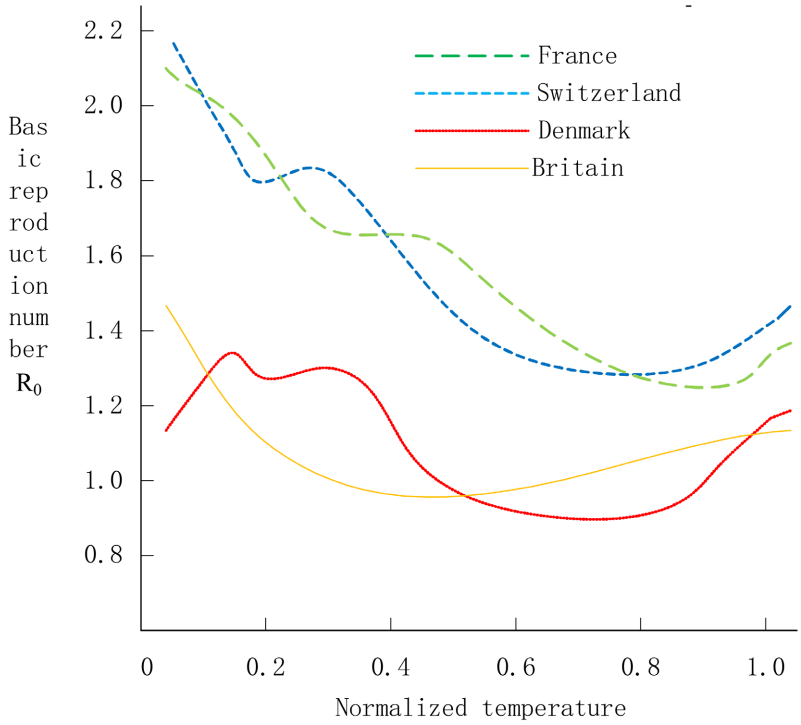

Figure 4. Plot of normalized temperature versus the basic infectious number R_0.

$$R_0(T) = 2.27T^2 - 2.5T + 1.6 \tag{15}$$

Equation (15) describes the course of the population in each compartment in the model of the spread of the new Crown pneumonia outbreak and β denotes the incidence of infection at the mean daily incubation period. This number is roughly equal to the reciprocal of the mean incubation period. For this paper, the incubation period for neocoronavirus was set to 7 days, so that $\beta = 1/7$.

Studies have shown that there is asymptomatic infection during transmission of the NeoCuan alpha strain, and that recovered NeoCuan alpha infected individuals have a very low rate of reinfection [10]. Studies have shown that the average recovery time for patients is 14 days, so the incubator self-healing rate is public $\delta_E = 1/14$; the average time to cure is 30 days. The mortality rate of patients is about 4%, and its average time is 20 days, and the mortality rate of infected people is good $\delta_D = 0.2\%$. The epidemic transmission capacity of the latent and infected populations of the new crown alpha strain epidemic is similar, assuming that the spread model of the new crown pneumonia epidemic $\alpha(T) = \varepsilon(T)$. Based on Equations (6) and (15), it is derived that

$$\varepsilon(T) = \frac{R(0)(T)(\beta + \delta_E)(\delta_D + \delta_E)}{k(\delta_D + \beta + \delta_E)} \tag{16}$$

The formula T describes the normalized air temperature for different country regions. As shown in **Figure 5**, this section collects the temperature data of Hungary and Austria from 2015 to 2019 and predicts the change of temperature data by calculating the average value [11].

According to Equation (16) and the change of average daily temperature in different countries to calculate the epidemic transmission rate in different countries in different periods $\alpha(T)$, at this time t represents the time, the use of Equation (2) to predict the change of the epidemic in different countries, **Figure 6** depicts Hungary, Austria in the period from May 30, 2020, to December 30, 2020 epidemic data prediction results and the real value of the comparison.

Figure 6 depicts the results of using the *C. neoformans* outbreak spread model to predict the spread of the outbreak in the countries of Austria and Hungary. In 2020, the spread of the outbreak in both countries was relatively stable during the warmer months of June through September, but the total number of existing infections in Austria far exceeded those in Hungary, resulting in a faster rate of outbreak spread. With the arrival of autumn, the number of NCP infections increased rapidly and at an accelerating rate in early September 2020, and as of

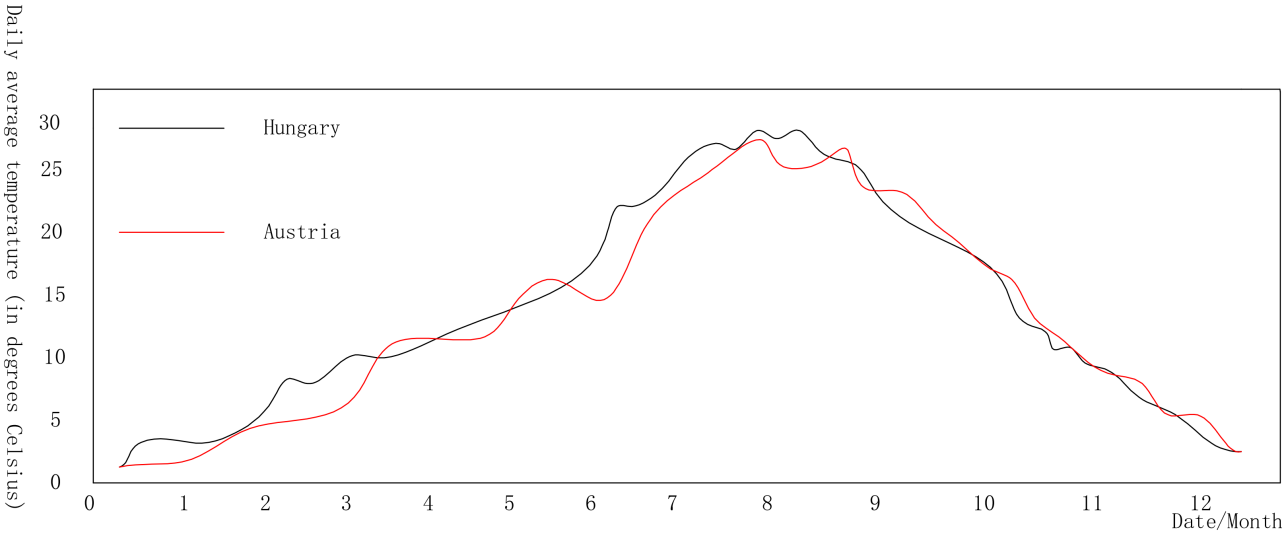

Figure 5. Map of temperature data for Hungary and Austria from 2015 to 2019.

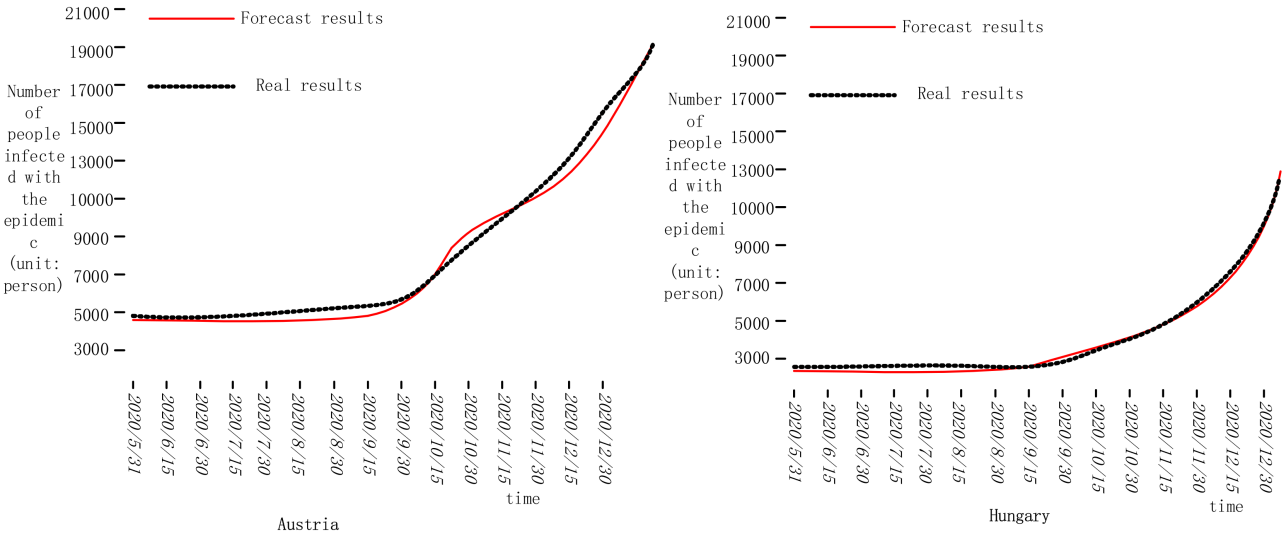

Figure 6. Comparison of the predicted results of the epidemic data with the real values.

October 10, 2020, the cumulative number of NCP infections in Hungary exceeded 40,000, and the cumulative number of NCP infections in Austria exceeded 80,000. The results show that the average absolute percentage error of the model's prediction results for the epidemic change in Hungary is 8.2%, and the average absolute percentage error of the prediction results for the change in Austria is 4.$%. Since the traditional SEIR model predicts results by theoretically analyzing the spread of the epidemic, some factors affecting the spread of the epidemic are not taken into account. In the early stage of the epidemic spread, the spread of the epidemic relies entirely on the effective contact between the virus-carrying population and the susceptible population, at which time the contact range is smaller, the spread of the epidemic is shorter, and there is less interference from other factors, so the designed model for the spread of the epidemic of New Crown Pneumonia is more suitable for predicting the initial changes of the epidemic. In the real situation, the epidemic spread environment changes from time to time, such as changes in temperature caused by changes in viral activity, human resistance, and the frequency of going out, which will affect the spread of the epidemic, through the conversion of these factors into variables, analyze the relationship between the rate of transmission and the temperature, based on the hypothesis theory, the use of the temperature data in previous years to predict the rate of transmission of the new coronavirus in real-time, to build the new coronavirus spread model. The spread model was constructed. Through the comparison of theoretical analysis and real data, it can be found that the *C. neoformans* epidemic spread model can predict the development of the epidemic very well.

3.3. Model Comparison and Analysis

After the outbreak of COVID-19, people infected with COVID-19 were found in various countries and regions. On January 15th, 2020, the first case of COVID-19's disease appeared in Japan. In order to analyze and verify the spread of Japanese epidemic, the temperature data in Japan are collected and analyzed first. The daily average temperature changes in Japan from 2015 to 2019 were collected. On January 5, the daily average temperature in Japan was about 6 degrees Celsius, and then gradually increased, with a slight fluctuation in the middle. At the end of June, the average temperature today reached 25 degrees Celsius. The relationship between daily average temperature and time is obtained by fitting, as shown in the following formula, where t stands for temperature, t stands for time, and January 28, 2020 is the starting date, at which time $t = 1$.

$$T = 0.115t + 5.658 \tag{17}$$

Related research shows that there is asymptomatic infection in this model, and the rehabilitation population has a very low reinfection rate. Related research shows that the average recovery time of patients is 14 days, so the self-healing rate of the Infiltrator is 1/14; the average cure time was 30 days, and the recovery rate of infected people was 1/30. Related research shows that the mortality rate

of patients is about 4%, the average hospitalization time is 20 days, and the mortality rate of infected people is 0.2%. The comparison between the predicted results of the model and the true results is shown in Table 2.

Since the emergence of infected people in Japan in February 2020, the outbreak began to spread. With the arrival of spring and rising temperatures, the ability of virus transmission has decreased and the spread of the epidemic has been controlled. The model takes into account the effect of temperature change on the spreading ability of the epidemic, and its timely correction can predict the spread of the epidemic more accurately.

3.4. Reflections and Perspectives on the Model Results

In the analysis process, a model for the spread of the new coronary pneumonia epidemic was established by combining the data of the new coronary pneumonia epidemic and considering the influence of temperature changes on the disease's ability to spread. The model adds the death population to the basic assumptions, considers the disease transmission rate as the dependent variable of temperature, and analyzes and verifies the spread of the epidemic over time under actual temperature changes. In contrast to the traditional hamartia model, the virus transmission rate in the spread model of the new Crown pneumonia outbreak was a mean absolute percentage error of 9.8% for the parameter results that varied with temperature. The epidemic prevention and control model is flawed. On the one hand, the model considers fewer factors and fails to take into account factors such as person-day movement, overseas transfusion, vaccination, and individual variability, which can lead to bias in the prediction of the number of infected people; on the other hand, the model is only applicable to the initial stage of the spread of the neo coronavirus pneumonia epidemic because with the mutation of the virus, there will be problems such as the number of people rescued is unstable, and the specific conditions in different regions are different, etc., and with the recurrence of neocoronavirus pneumonia epidemics, the above mathematical model may no longer be applicable. According to relevant studies, the number of vaccinated people is close to saturation, and the resistance of vaccinated people is decreasing. Without the support of vaccine efficiency-related data, the prediction results still have some deviation compared with the real data. Since there are too many uncertainties in the spread of the epidemic, and the complexity and variability of the virus itself and the external environment will have an impact on the spread of the epidemic, there are still many problems that

Table 2. Forecast results and real results of epidemic spread in COVID-19, Japan (unit: person).

date	2020/4/20	2020/4/26	2020/5/2	2020/5/8	2020/5/14	2020/5/20	2020/5/26	2020/5/31
real value	498.68	355.86	289.29	154.57	77.54	42.62	29.97	41.43
Conventional prediction	555.60	377.62	299.26	186.29	112.62	99.83	99.85	70.60
Model Prediction	498.03	363.08	288.15	155.50	76.89	43.60	27.99	41.40

deserve to be investigated. Future research can further divide the population according to gender, age group, occupation and other classification criteria, analyze the new crown infection rate, mortality rate and recovery rate of different populations in specific environments, more accurately analyze and predict the spread of the epidemic, and provide references for the prevention and control of the epidemic.

4. Concluding Remarks

The outbreak and spread of the new coronary pneumonia epidemic is one of the more serious and widespread public health events in recent pediatric years. We used a mathematical modeling approach to conduct an in-depth analysis and study of the spread of the new crown pneumonia epidemic. The future development trend of the epidemic was predicted and analyzed by modeling and taking into account various factors affecting the spread of the epidemic, such as population movement, community transmission, and medical resources. According to the study, it was found that the spread of the new coronary pneumonia epidemic is complex and uncertain, and is affected by a variety of factors, which were analyzed and compared to identify the key factors affecting the spread of the epidemic and to provide a scientific basis for the development of effective preventive and control measures. The modeling simulation of the spread of the *C. neoformans* epidemic can not only give the corresponding epidemic prevention and control measures to effectively control the spread and development of the epidemic but also can prove that the national policy on epidemic prevention and control is scientific and effective.

Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

References

[1] Li, B.S., Deng, A.P., Li, K.B., *et al*. (2022) Viral Infection and Transmission in a Large Well-Traced Outbreak Caused by the Delta SARS-CoV-2 Variant. *Nature Communications*, **13**, Article No. 460. https://doi.org/10.1038/s41467-022-28089-y

[2] Kumar, S., Tao, Q.Q., Weaver, S., *et al*. (2021) An Evolutionary Portrait of the Progenitor SARS-CoV-2 and Its Dominant Offshoots in COVID-19 Pandemic. *Molecular Biology and Evolution*, **38**, 3046-3059. https://doi.org/10.1093/molbev/msab118

[3] Bolze, A., Luo, S.S., White, S., *et al*. (2022) SARS-CoV-2 Variant Delta Rapidly Displaced Variant Alpha in the United States and Led to Higher Viral Load. *Cell Reports Medicine*, **3**, Article 100564. https://doi.org/10.1016/j.xcrm.2022.100564

[4] Adhikary, A. and Pal, A. (2022) A Six Compartments with Time-Delay Model SHIQRD for the COVID-19 Pandemic in India: During Lockdown and Beyond. *Alexandria Engineering Journal*, **61**, 1403-1412. https://doi.org/10.1016/j.aej.2021.06.027

[5] Baleanu, D., Abadi, M.H., Jajarmi, A., *et al*. (2022) A New Comparative Study on

the General Fractional Model of COVID-19 with Isolation and Quarantine Effects. *Alexandria Engineering Journal*, **61**, 4779-4791. https://doi.org/10.1016/j.aej.2021.10.030

[6] Muroya, Y., Nakata, Y., Izzo, G., *et al.* (2011) Permanence and Global Stability of a Class of Discrete Epidemic Models. *Nonlinear Analysis*: *Real Applications*, **12**, 2105-2117. https://doi.org/10.1016/j.nonrwa.2010.12.025

[7] Chaurasia, V. and Pal, S. (2020) COVID-19 Pandemic: ARIMA and Regression Model-Based Worldwide Death Cases Predictions. *SN Computer Science*, **1**, Article No. 288. https://doi.org/10.1007/s42979-020-00298-6

[8] Zhang, J., Lou, J., Ma, Z.E., *et al.* (2005) A Compartmental Model for the Analysis of SARS Transmission Patterns and Outbreak Control Measures in China. *Applied Mathematics and Computation*, **162**, 909-924. https://doi.org/10.1016/j.amc.2003.12.131

[9] Pitchaimani, M. and Devi, A.S. (2022) Fractional Dynamical Probes in COV1D-19 Model with Control Interventions: A Comparative Assessment of Eight Most Affected Countries. *The European Physical Journal Plus*, **137**, Article No. 370. https://doi.org/10.1140/epjp/s13360-022-02556-3

[10] Nian, F.Z., Shi, Y.Y. and Cao, J. (2022) COVID-19 Propagation Model Based on Economic Development and Interventions. *Wireless Personal Communications*, **122**, 2355-2365. https://doi.org/10.1007/s11277-021-08998-9

[11] Wang, J.B., Chan, Y.-C., Niu, R.W., *et al.* (2022) Modeling the Impact of Vaccination on COVID-19 and Its Delta and Omicron Variants. *Viruses*, **14**, 1482. https://doi.org/10.3390/v14071482