Estimate the Endemic (SIR) Model of Monkey Pox Disease

Suhad Ali Shaheed Al-Temimi[1], Hamid Saad Nour AL-Shammrty[2]

Statistics Department, College of Administration and Economics, Mustansiriyah University, Baghdad, Iraq

College of Business Administration, AL-Bayan University, Baghdad, Iraq

E-mail:dr.suhadali@uomustansiriyah.edu.iq

https://www.researchgate.net/profile/Suhad-Shaheed-Al-Temimi

E-mail:Hamed.saad@albayan.edu.iq

Article Info

Page Number: 4921 - 4935

Publication Issue:

Vol 71 No. 4 (2022)

Abstract

Diseases are of great concern to the human race and we are still affected by the dramatic descriptions that reach us from the past, including the "Black Death", the plague that spread throughout Europe from 1347 to 1352 and caused 25 million victims, far from our lives, but Recent events, including the spread of the Corona pandemic, remind us that disease is a real problem for us.The definition of (endemic, epidemic, and pandemic) can be defined as endemic diseases that are always present throughout an area or group of people and remain more or less constant. Such as measles, smallpox, polio, etc.An epidemic can be defined as a disease that increases unexpectedly among a large number of people or an area. An example is Ebola, which spread rapidly throughout West Africa.A pandemic is a disease that is transmitted across multiple countries or continents, affecting large numbers of people. An example of this is COVID-19.Mathematical models represent a descriptionof infection increasing in a population over time. Epidemiological models divide the population intothree groups, each group contains individuals who are identical in terms of their condition with regard to the disease. The SIR model is a basic model from which many models are derived, and according to the nature of the epidemic, the three main parts are (Susceptible (S), Infected (I), Recovered or Resistant (R)). Diseases in which individuals acquire permanent immunity. And the endemic to which this model can be applied, include measles, smallpox, mumps, typhoid fever, and diphtheria.The research deals with Monkeypox (MPXV) a rare

viral die characterized by fever and a rash. This disease is a zoonotic viral disease transmitted to humans by animals. The transmission rate, recovery rate, and infected rate of Monkeypox were calculated using the (Runge-Kutta) method in the (MATLAB) program. The cumulative number (total cases) on a daily basis for the period from the beginning of the epidemic to (6/5/2022). The first infection occurred in the United Kingdom, within two weeks, the cumulative number of infections reached (350) infections around the world, the initial values were calculated and the parameter value of the average daily transmission of infection was (β = 0.2),Infection rate parameter (λ = 0.0625) days and the recovery rate ($\gamma = 0.0476$) then the calculated basic reproduction number is($\mathscr{R}_0 = 1.81$). The estimated parameter of the logisticmodel (β, λ and γ) was calculated using the (Runge-Kutta) method in the (MATLAB) program.The estimated parameters of (β = 0.16), (λ = 0.05), ($\gamma = 0.03808$) and, ($\mathscr{R}_0 = 1.82$).The result of the study finds that the spread of a Monkeypox virus is increasing and spreading.

Article History
Article Received*: 25 March 2022*
Revised*: 30 April 2022*
Accepted*: 15 June 2022*
Publication*: 19 August 2022*

Keywords-epidemiological model, the endemic SIR Model, MonkeypoxVirus, Analysis Data, Runge-Kutta method, the basic reproduction number.

I. INTRODUCTION:

Endemic usually leaves many communities untouched. These attacks often recur over periods of several years and may lessen in severity as the population develops some immunity. This is an important aspect of the relationship between epidemics and disease development. [5]

Infectious disease modeling is a tool that has been used to study the mechanisms by which diseases spread as well as to predict the future course of the outbreak of many epidemic diseases and also to evaluate and develop strategies to control epidemic outbreaks[15].The theory of pathogenic germs was first described by Jacob Henley (1809-1885) in 1840 and developed by Robert Koch (1843-1910), Joseph Lister (1827-1912), and Louis Pasteur (1822-1875) in the latter part of the nineteenth century and early Twentieth century / the tenth century. The history of Monkeypoxcentered on Africa, where many infections occurred in remote areas of the Congo Basin, and West Africa, where recent literature has considered the disease to be endemic. While the majority of infections occurred in this region between 1996 and 1997, it was noted that there are

gaps in the spread of the disease. This geographic gap is also due to the Monkeypoxspread in 2003 in the USA. While this was considered the first spread outside Africa, the literature has failed to link how the disease was first discovered in Denmark, the virus was transmitted to Africa.Historical studies indicate that Monkeypoxentered the United States when African rodents were imported as pets into the United States and then spread to domestic pets such as dogs, cats, and other domestic animals highly susceptible to infection.Because Monkeypoxis a virus, the primary method of transmission is generally through direct contact with an infected person through some form of body fluid such as blood or skin viruses.The incubation period for Monkeypox is usually 7 to 14 days but can range from 5 to 21 days [5]. The disease begins with Lymphadenopathy, fever, chills, aching headaches in the bones and muscles, fatigue, and sometimes backache. When a patient develops a fever and chills, within 3 days, the patient usually begins to develop the characteristic rash known as Monkeypox that begins on the face and spreads to the rest of the body.[6]

II. RESEARCH PROBLEM:

The problem of the study includes a sample of a community exposed to infection, including a limited number of people infected with Monkeypox, will the number of people infected with the infectious disease increase significantly, leading to an endemic? Or will the disease subside without spreading? And make a prediction of the number of injuries in the world.

III. RESEARCH OBJECTIVE:

Governments around the world dependon the estimate of mathematical models, to help guide mandatory decisions to address the spread of diseases and epidemics. The study aims to estimate (SIR)model (Susceptible, Infection, Recovered) model, as the (SIR) model is characterized by accurate results due to the large degrees of freedom and the calculation of ($\mathscr{R}_0$), which represents the number of basic reproduction to detect whether the epidemic has disappeared or not when the number of basic reproduction is less than (1) that is, the disease has receded and disappeared, or the transmission of infection from one individual to another is eliminated.

IV. LITERATURE REVIEW:

The first scientist who tried systematically to determine the causes of death as a result of viruses is (John Graunt) in his book (1662), and the scientist (Ross) (1910) contributed to the development of the field of epidemiological modeling of the malaria epidemic, and the model (Kermack-

Mckendrick) in In (1927) the first mathematical model that is most accurate in describing the spread of infectious diseases and can be used to provide a specific approach to fragmented epidemiological models. Population and these models succeeded in predicting the behavior of epidemics in many recorded epidemics, as well as the Red Frost model (1929), which is the simplest possible epidemiological model for the spread of an infectious disease such as colds in a small group of individuals, and the model was called (Reed-Frost) on The name of its founders is the so-called sequential binomial model [3], an epidemiological model (SIR), and the model is usually determined using discrete-time dynamics. In (1949) Bartlett studied the random behavior of Kermack models. - Mckendrick), and through him became More interested in analyzing random patterns of epidemics in continuous times [9]. As well as from the study (BECKER) (1989), which was mainly concerned with the statistical analysis of infectious diseases. The outbreaks of various epidemics have led to a re-attention to epidemiological models, including the SARS epidemic (2002-2003) as well as the possible pandemic of influenza (H5N1) (2005). Influenza (H1N1) in 2009. The outbreak of Ebola in 2014 and (covid-19) in (2019), with the reformulation of the fragmented models in line with the available data and data for the studied epidemic.In (2018), the researcher (Tonsing.C. et al.) discussed the application of Ordinary Differential Equation (ODE) models to describe the temporal evolution of epidemics and the application of parameter estimation and analysis based on (Profile likelihood) of two models of infectious diseases and comparison between them, and they used the model. The first represents the basic model (SIR) for data on influenza outbreaks in a boarding school in 1978, and the second model is more complex for vector-borne disease data for outbreaks of ZIKV virus (ZIKV) in Colombia between 2016/2015, and they used the optimization algorithm in estimating the parameters[8] [11].In the year 2020, the researcher (Sameni.R) presented a study of the patterns of the spread of epidemic diseases such as the Coronavirus from the perspective of mathematical modeling and based on fragmented models such as the (SIR) model and knowing the extent of the impact of social measures on the change in mortality rates and cases over time. To better understand the patterns of epidemic disease spread, a short introduction to modeling these systems was also provided and a source for simulations using the (MATLAB) program was provided.[4]

V. SIR MODEL:

The endemic SIR model is characterized by being easy, it was possible to estimate parameters from it and use these estimates to obtain an approximate comparison between the part of the herd's

immunogenicity and the immunity to different diseases. When individuals recover with permanent immunity, the model is the SIR. The model is a dynamic system that consists of a set of differential equations (ODE), which is associated with the description of the increase and temporal development and the different stages of the movement of individuals in groups over time as in Figure (1).[5][16]

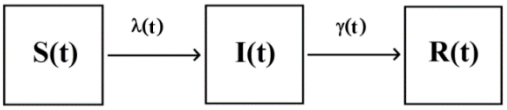


Figure (1) S-I-R model of diseases in which individuals acquire immunity

In figure (1) the parameters λ(t) and γ(t) respectively denote the rate at which susceptible become infected and the rate at which infective recover from the disease. The appropriate estimation procedure is based on the probability distribution accordingly.The model divides the population into three different groups: (susceptible, infected, and recovered).[6]

- Susceptible $S(t)$:: individuals who are healthy and can be infected at a time (t).
- Infected
  $I(t)$: individuals who are infected and are able to transmit the disease at a time (t).
- Recovered $R(t)$: individuals who are immune because have been infected and now have recovered at a time (t).

The general SIR model is one of the mathematical models used in epidemiology based on the number of studied variables. The recovering group gets immunity from the disease after being infected. It can be modeled as follows:

$Y_i = f\left(t, x_{(t)}, \theta\right) + u_i;\ i = 1, \dots, n\ ; \theta \in R^P, X \in R^r, f \in R^m \dots (1)$

Where $f\left(t, x_{(t)}, \theta\right)$represents a function of the variable Y_i in terms of the explanatory variables $(x_{(i)})$, (u_i)represents the term for random error, (P) the number of parameters in the model. (r) Anumber of state variables, (m) the number of differential equations.

The basic assumptions on which the SIR model are:

1- Recovered people are no longer susceptible to infection again.
2- The number of deaths from other causes (causes other than the infection or disease under study) is negligible. [7] [13]
3- The area under study is closed and isolated from other areas, meaning that:

$$S(t) + I(t) + R(t) = N$$

(N)Represents the sum total of the population which is closed. That is, the size of the community is fixed.

$$\mathrm{X} = \left[\beta_1, \dots, \beta_n, \lambda_1, \dots, \lambda_n, \gamma_1, \dots \gamma_n\right]^{\mathrm{T}} \quad ; i = 1,2, \dots, n \qquad \dots (2)$$

The observed data are arranged according to the value of (Y) and represent the daily total number (Infected, Recovered), where β rate of transmission.X Represents a vector containing the undefined values of the parameters., the parameters β,λ, and γ denote the rate of (transmission, infected and recover) respectively. The (SIR) model is described through three differential equations.[1]

$$\frac{dS}{dt} = -\beta SI \quad \dots(3)$$

$$\frac{dI}{dt} = \beta SI - \lambda I \quad \dots(4)$$

$$\frac{dR}{dt} = \lambda I \qquad \dots(5)$$

The initial conditions $S(0) > 0, I(0) \geq 0$ and$\mathscr{R}_0 \geq 0$, the response variable represents a vector of:[6] [10]

$$Y = [TI_1 \dots TI_n R_1 \dots R_n \ ]^T \qquad \dots (6)$$

Where TI_i Represents the total number of Infection, which is calculated as follows:

$$\mathrm{TI(t)} = \int_{t_0}^{t} \beta(t)\, S(t) I(t) \qquad \dots (7)$$

When writing the model in terms of differences, it becomes as follows: [2], [7]

$$\Delta S = -\frac{\beta}{N} SI \qquad \dots (8)$$

$$\Delta I = \frac{\beta}{N} SI - \lambda I - \gamma I \dots (9)$$

$$\Delta R = \lambda I \quad \dots (10)$$

Where ΔS, ΔI, and $\Delta\, Represent$ the change in suspects, Infection,andrecovery respectively and all depend on time (t).

$$\begin{bmatrix} S(t+1) - S(t) \\ I(t+1) - I(t) \\ R(t+1) - R(t) \end{bmatrix} = \begin{bmatrix} \Delta S(t) \\ \Delta I(t) \\ \Delta R(t) \end{bmatrix} \quad \dots (11)$$

The model equations can be expressed in the form of a regression equation as follows:

$$\begin{bmatrix} -\frac{SI}{N} & 0 & 0 \\ \frac{SI}{N} & -I & -I \\ 0 & I & 0 \end{bmatrix} \begin{bmatrix} \beta \\ \lambda \\ \gamma \end{bmatrix} \quad \dots (12)$$

By solving the equations (12) for the parameters, in other words, by recording the three variables in a specific field, they can be converted in terms of the parameters, we get:

$$\beta = \frac{N\Delta S}{SI} \dots (13)$$

$$\lambda = \frac{\Delta R}{I} \dots (14)$$

$$\gamma = \frac{\Delta D}{I} \quad \dots (15)$$

Then the fraction of the populationof the SIR Model are [4] [10]:

$s(t) = \frac{S(t)}{N}$the susceptible fraction of the population

$i(t) = \frac{I(t)}{N}$the infected fraction of the population

$r(t) = \frac{R(t)}{N}$the recovered fraction of the population

VI. BASIC REPRODUCTION NUMBER $\mathscr{R}_0$:

It is defined globally as the expected number of other cases that result from an infected person early in an epidemic. This indicator is one of the basic indicators for monitoring infection as a result of the endemic and is useful in determining whether the infectious disease can spread among a group of individuals or not, in other words, the speed of infection spread, i.e. describing the nature of the spread.When$\mathscr{R}_0 < 1$, the infection will end completely in the long term, meaning that the spread of the epidemic ends, and the epidemic will be controlled. If$\mathscr{R}_0 > 1$, the infected person is able to spread among all individuals, i.e. the community becomes epidemic, in other words, the transmission of infection between the population will increase [6].

The basic reproduction number ($\mathscr{R}_0$) is extracted as follows:[11]

$$\mathscr{R}_0 = \frac{\beta}{\lambda+\gamma} \quad \dots (16)$$

Including the demographic dynamics may allow the disease to end or persist in the population over time. For this reason, the model SIR has an equilibrium point if $E = (S^*, I^*, R^*)$satisfies the following system:[4] [15]

$$\frac{dS}{dt} = 0 \quad \dots(17)$$

$$\frac{dI}{dt} = 0 \quad \dots(18)$$

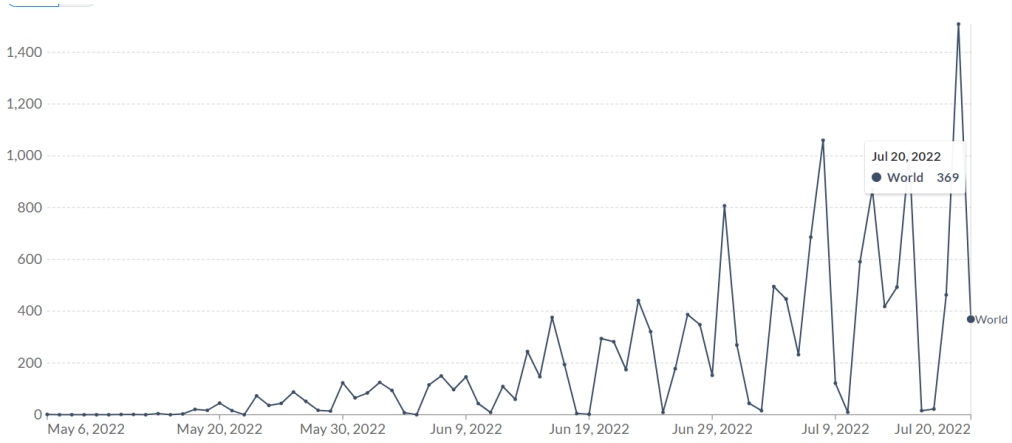
$$\frac{dR}{dt} = 0 \quad \dots(19)$$

If the equilibrium point for infection is zero (I* = 0), then the disease is extinct and E* is called disease-free equilibrium (DFE). If I*> 0, the disease persists in the population, and E is called endemic equilibrium (EE)

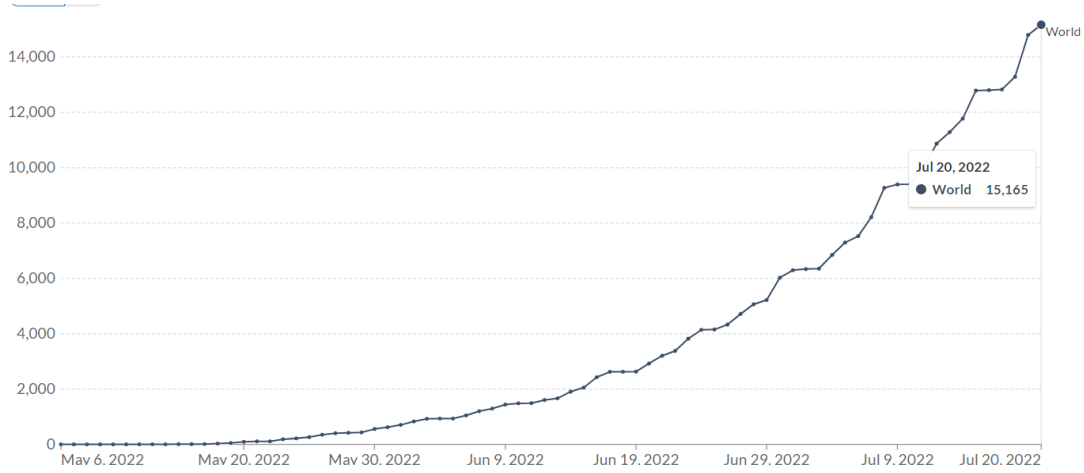
VII. APPLICATION :

The incubation period for Monkeypox is usually 7 to 14 days but can range from 5 to 21 days. The disease begins with Lymphadenopathy, fever, chills, aching headaches in the bones and muscles, fatigue, and sometimes backache[5]. Hugeness Lymphadenopathyis characteristic of monkeypox compared to other diseases that may at first appear similar to it (chickenpox, measles, and smallpox).The rash period usually begins within 1 to 3 days of the onset of the fever [5]. The rash is most often concentrated on the face and extremities, rather than the trunk. It affects the face (in 95 percent of cases), the palms of the hands, and the soles of the feet (in 75 percent of cases). The mucous membranes of the mouth (70% of cases), the genitals (30%), the conjunctiva (20%), and the cornea are also affected. Symptoms of monkeypox usually go away on their own after 2 to 4 weeks.Daily infections with the monkeypox virus in the world can be represented through the graph, since the first case appeared on May 6, 2022 , in the UK until July 22 of the same year, and the total number of confirmed cases in the world is (15165).[3]

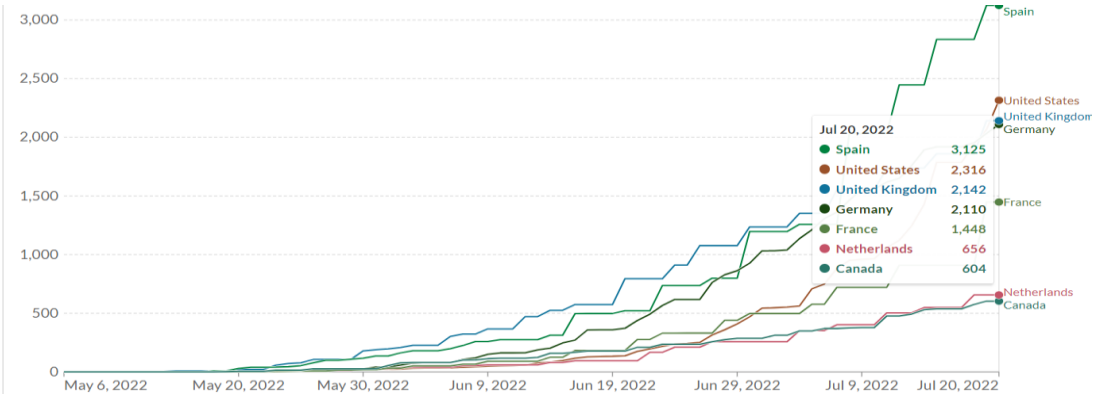
Finally, when designing a disease that is endemic, that is, persists indefinitely in a population, our SIR model should also include newly borne to replenish the level of those at risk for measles infection. In this case, the long-term behavior of the disease can again be related to the coefficient $\mathscr{R}_0$ [14] .The long-term proportion of susceptible individuals in a population, once the oscillations fade, is given by: $S^* = 1/\mathscr{R}_0$ and to compute the contact rate by:Contact rate= p(Infected) * number of contact.



Graph (1) shows the number of daily infections cases in the world of monkeypox virus



Graph (2) shows the cumulative infections cases in the world of monkeypox virus



Graph (3) shows Countries with the highest confirmed cases of monkeypox virus

VIII. ORDINARY DIFFERENTIAL EQUATIONS (RUNGE - KUTTA) (ODE(R.K)):

Solving differential equations is a very important mathematical tool of importance in many physical, engineering, social and economic issues as well as in environmental phenomena. There

are two types of mathematical equations (Ordinary Differential Equations (ODE) and Partial Differential Equations (OPE)).There are many ways to find the approximate numerical solution to the problem of prime values for coefficients of (SIR) model The most important of these methods are the (Runge - Kutta) (R.K) method. It is the most used method for calculating the approximate numerical solutions to the initial value problem and it will be relied upon in our current research.

In order to obtain approximate estimations of the initial value problem, there are several formulas for this method, including the third-degree Range Cotta (R.K) method, which is the most common and has higher ranks, but it is more difficult and takes a long time, as the initial value problem is studied as in Equation (1),

$X(t_{n+1}) = X(t) + T \sum_{i=1}^{z} b_i K_i$ …(20)

Where:

T: step size, time step size.

$X =$ represents vector of state (S, I, R).

The numerical equations used in the Runge-Kutta method for the SIR model are as follows: [9]

$$\left.\begin{aligned} S(t_{n+1}) &= S(t) + T \sum_{i=1}^{z} b_i{}^1 K^1{}_i \\ I(t_{n+1}) &= I(t) + T \sum_{i=1}^{z} b_i{}^2 K_i{}^2 \\ R(t_{n+1}) &= R(t) + T \sum_{i=1}^{z} b_i{}^3 K^3{}_i \end{aligned}\right\} \quad \ldots(21)$$

We can find $K^j{}_i$ as follow:

$$K_1{}^1 = f(t_n, S_n)$$

$$K_2{}^1 = f\left(t_n + c_2{}^1 T, S_n + a_{21}{}^1 T K_1{}^1\right)$$

$$\vdots$$

$$K_z{}^1 = f\left(t_n + c_z{}^1 T, S_n + a_{z1}{}^1 T K_1{}^1 + a_{z2}{}^1 T K_2{}^1 + \cdots + a_{z,z-1}{}^1 T K_{z-1}{}^1\right)$$

$$K_1{}^2 = f(t_n, I_n)$$

$$K_2{}^2 = f\left(t_n + c_2{}^2 T, I_n + a_{21}{}^2 T K_1{}^2\right)$$

$$\vdots$$

$$K_z{}^1 = f\left(t_n + c_z{}^2 T, I_n + a_{z1}{}^2 T K_1{}^2 + a_{z2}{}^2 T K_2{}^2 + \cdots + a_{z,z-1}{}^2 T K_{z-1}{}^2\right)$$

$$K_1{}^3 = f(t_n, R_n)$$

$$K_2{}^3 = f\left(t_n + c_2{}^3 T, R_n + a_{21}{}^3 T K_1{}^3\right);\ i = 1,2,3,\ldots,z\ ;\ j = 1,2,3$$

Where:

$a_{qs}{}^j$: represents the coefficient matrix for the R.K method.

$c_s{}^j, b_i{}^j$: represents the real coefficients, represents the weights and nodes of the expansion function of the Range Cotta matrix, $s = 2, \dots, i-1$

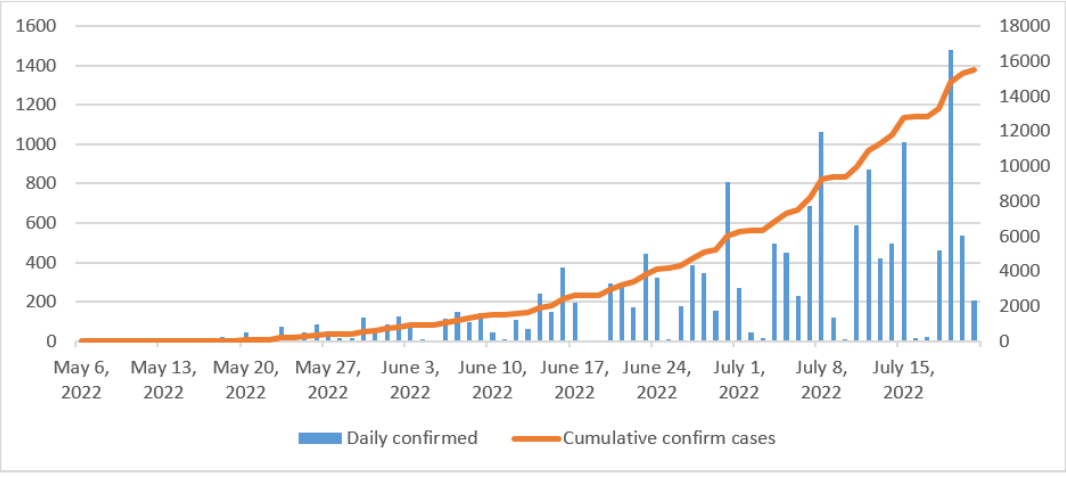
Normally (c_i) you must meet the following condition:

$$c_2 = a_{21}, c_3 = a_{31} + a_{32}, \dots, c_z = a_{z1} + a_{z2}, \dots + a_{z,z-1}$$

The equations of the R.K method with z-stages can be written in the so-called Butcher tableau, where the zero values on and above the diagonal are omitted, i.e., it is a lower trigonometric matrix.As the endemic SIR model is applied to simulate and predict the spread of the Coronavirus pandemic, we extract the transmission rate, recovery rate, and mortality rate. By fitting the collected data.

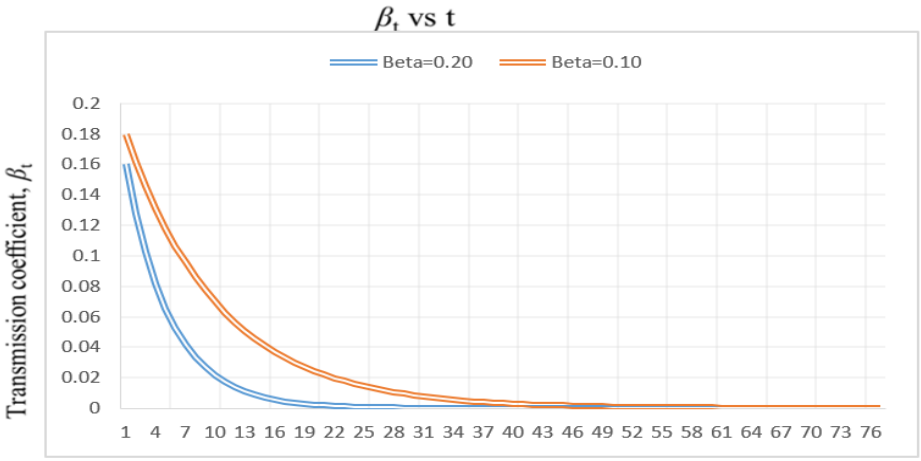
IX. THE INITIAL VALUES OF (β, λ and γ):

Based on the infection data that depend on the resource [3], the first infection occurred in the United Kingdom, within two weeks, the cumulative number of infections reached (350) infections around the world, the initial values were calculated and the parameter value of the average daily transmission of infection was (β = 0.2),Infection rate parameter (λ = 0.0625) days and the recovery rate ($\gamma = 0.0476$). Therefore, the estimated basic reproduction number($\mathscr{R}_0 = 1.816$). Graph(4)explain the dynamics of the two variables. [6] It can be seen that the susceptibility curve is decreasing all the time, because birth is not taken into account, andonce you become infected, you never return to the affected state.



Graph (4) represents the dynamics of daily and cumulative confirm cases

Based on the value of the basic reproduction($\mathscr{R}_0 = 1.816$),which indicates that the viruscontinues to spread with a noticeable increase. The long-term proportion of susceptible(S*=0.238).We use p=0.20 to represent the probability of being infected and the number of contact is (5) per week so the contact rate is 1 (0.20*5).



Graph (5) represents β_t vs time when $p = 0.10$, $p = 0.20$

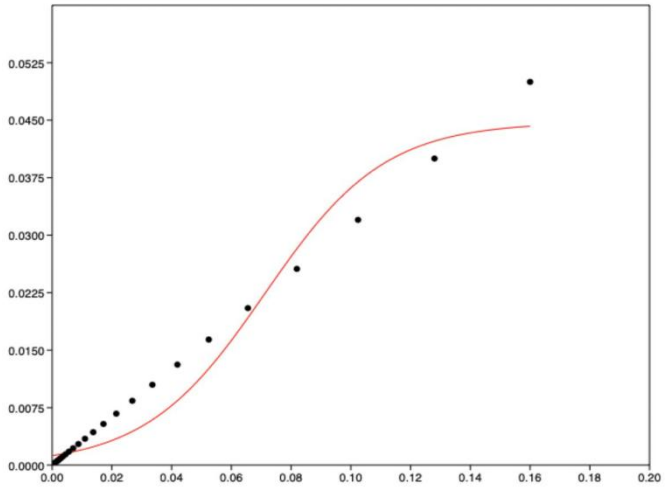
X. ESTIMATE THE PARAMETERS :

The transmission rate, recovery rate, and mortality rate of monkeypox were calculated using the (Runge-Kutta) method in the (MATLAB) program. The cumulative number (total cases) on a daily basis for the period from the beginning of the epidemic to (6/5/2022). And calculate the coefficient of determination for the explanatory variables of the (SIR) model, as shown in Table (1).

Table (1) results of Runge-Kutta method

0.16	**0.05**	**0.03808**	**1.82**	**0.805**

As the transmission rate was (0.16), the recovery rate, amounted to (0.05), while the death rate was (0.038), and through it, the basic reproduction number is calculated, whose value reached (1.82), which are values greater than one, and through it, we find that the spread of a smallpox virus Monkeys are increasing and spreading. It is noticeable that the results of the coefficient of determination ($R^2 = 0.805$) are good, which indicates the suitability of the estimators to a large extent to the real data.



Graph (6) represents logistic distribution for estimated parameters of the SIR Model

XI. CONCLUSIONS:

1. The SIR model was successfully measured to both observed cases of I and R since 6 May 2022 until 22 Jun 2022, with an estimated transmission rate was (β=0.16), the recovery rate, amounted to (0.05), while the recovery rate was (0.038),
2. Basic reproduction number whose value reached (1.82), which are values greater than one, and through it, we find that the spread of a smallpox virus Monkeys are increasing and spreading.
3. Mathematical models applied to the study of endemic diseases have a long tradition. The results that were reached showed the importance of predicting the development of the disease, and the impact of that development on society and the health system of developing and developed countries alike.

XII. ACKNOWLEDGEMENTS:

The authors acknowledge monkeypox data from OurWorldInData.org. We also to thank Mustansiriyah University (www.uomustansiriyah.edu.iq) Baghdad-Iraq for its support in the present work, we also thank all reviewers and the journal Editor-in-Chief for considering this paper and facilitating the review process.

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