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SEIRV MODEL OF MEASLES

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Abstract

This paper presents a comprehensive mathematical model for transmission dynamics of measles, incorporating the SEIRV model. Measles, a highly contagious disease, remains a significant public health challenge despite the availability of effective vaccines. The SEIRV model extends the classical SEIR model by including vaccination subgroup, allowing for more accurate representation of immunization strategies and their impact on disease spread. Simulations using real data for North Macedonia have been performed. Also, the basic reproduction number is derived to determine the threshold for disease eradication.

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Key Words and Phrases: measles, mathematical model, SEIRV, simulation

1. Introduction

Measles is a highly contagious viral disease caused by the genus Morbillivirus, a member of Paramyxovirdae family (see [1]). Characterized by symptoms such as fever, cough and distinctive red rush, measles can lead to severe health complications including pneumonia, encephalitis and even death particularly in young unvaccinated children and individuals with compromised immune system. The virus is transmitted through respiratory droplets when an infected individual coughs or sneezes, making it one of the most easily spread infectious diseases (see [2], [3]).

Despite the availability of an effective vaccine, measles remains a significant public health challenge in many parts of the world. Vaccination programs have drastically reduced the incidence of measles in numerous countries, but outbreaks still occur, often linked to areas with low vaccination coverage. The persistence of measles in influenced by factor such as vaccination hesitancy, lack of access to health care and population movement (see [4]).

Mathematical models of infectious diseases serve as simplified representation of complex processes. By incorporating various factors such as transmission rate, contact rate, recovery rate and population dynamics,

these models allow researchers to simulate disease outbreaks and evaluate potential strategies. The main aim is to predict the course of an epidemic and identify critical points for intervention and optimize public health response. The recent COVID-19 pandemic has highlighted the critical role of mathematical models in guiding global response efforts (see [5], [6]). Among the various models developed, the Susceptible-Infectious-Recovered (SIR), (see [7]) and Susceptible-Exposed-Infectious-Recovered (SEIR) (see [8]) models are foundational frameworks in epidemiology. Both SIR and SEIR models have been extensively applied to study various infectious diseases, offering insights into disease transmission dynamics, potential outbreak sizes, and the impact of public health interventions. Understanding the dynamics of measles infection (see [9]), including transmission rates and the impact of vaccination is crucial for public health effort aimed at controlling and eventually eliminating this disease. Research and modeling of measles transmission can provide valuable insights for developing strategies to enhance vaccination coverage and prevent outbreaks, ultimately aiming to achieve and maintain herd immunity.

In this paper, the classical SEIR model is enhanced by vaccination subgroup which represents the individuals who have been immunized and are assumed to be protected against measles, thereby significantly reducing the number of individuals that are suspected to get measles infection. This paper aims to apply the SEIRV model to measles data from North Macedonia including vaccination coverage and reported cases of measles with focus on understanding the impact of vaccination on disease transmission. By providing a detailed analysis of measles dynamics in North Macedonia, this study seeks to raise awareness of the need to increase the vaccination rate.

2. **SEIRV Model**

In this paper measles infectious spread is described with SEIRV model. This model is based on traditional epidemiology SIR model developed by Kermack and McKendrick (see [7]). At all times, the total population is decided into 5 subgroups: susceptible, infected, exposed, recovered and vaccinated representing different stages of disease in the population:

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

where t is in time units (days, years).

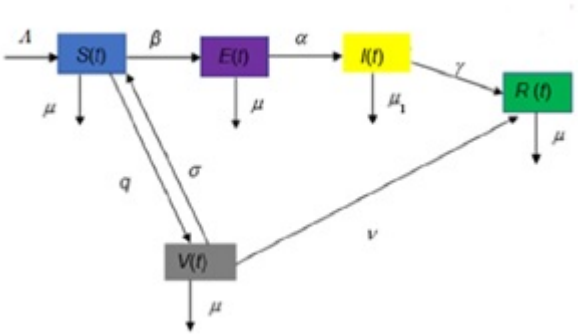

FIGURE 1. SEIRV model of measles

The susceptible individuals are those who are susceptible to the infection and have not been vaccinated or infected. Exposed individuals are those who have been in contact with infected individual but are not yet infectious. Individuals who are infected and can transmit the measles to other individuals are part of infected compartment. Recovered individuals are those that have recovered from the measles infection and have gained immunity. Vaccinated individuals are those that have been vaccinated and are immune to measles infection. The model used in this research is represented in Figure 1.

The recruitment rate of susceptible individuals in the population is Λ . The susceptible subgroup is increased by recruitment rate Λ and rate of ineffective vaccination σ and decreased by transmission rate β and vaccination rate q. The exposed subgroup is formed by interaction of susceptible individual with infectious individual. This subgroup is increased by transmission rate β and decreased by incubation rate α. Exposed individuals who develop the disease move to infected subgroup and can spread the disease. The exposed subgroup is increased by incubation rate α and is decreased by recovery rate γ and mortality rate due measles μ_1. The recovery subgroup includes the recovered individuals and is increased by successful vaccination rate ν and recovery rate γ. The vaccination subgroup includes fully vaccinated individuals who after gaining immunity transfer to recovered subgroup. This group increases with vaccination rate q and decreases by unsuccessful vaccination rate σ and successful vaccination rate ν. All the subgroups except infected are decreased by natural mortality rate μ. In this model it is assumed

that gained immunity to the measles is permanent which means that individual can be infected only once with measles. The SEIRV model is represented with system of first order differential equations as:

$$\begin{aligned}
\frac{dS(t)}{dt} &= \Lambda - \frac{\beta S(t) I(t)}{N} - qS(t) + \sigma V(t) - \mu S(t) \\
\frac{dE(t)}{dt} &= \frac{\beta S(t) I(t)}{N} - \alpha E(t) - \mu E(t) \\
\frac{dI(t)}{dt} &= \alpha E(t) - \gamma I(t) - \mu_1 I(t) \\
\frac{dR(t)}{dt} &= \gamma I(t) + \nu V(t) - \mu R(t) \\
\frac{dV(t)}{dt} &= qS(t) - \sigma V(t) - \nu V(t) - \mu V(t)
\end{aligned} \tag{2}$$

with initial conditions

$$\begin{aligned}
S(0) = S_0 \geq 0, E(0) = E_0 \geq 0, I(0) = I_0 \geq 0, \\
R(0) = R_0 \geq 0, V(0) = V_0 \geq 0.
\end{aligned} \tag{3}$$

THEOREM 2.1. *The feasible solution set for the initial conditions given with Equation (3)*

$$\Omega = \left\{ x = (S, E, I, R, V) \in \mathbf{R}^5 : 0 \leq N \leq \frac{\Lambda}{\mu} \right\}$$

is bounded region.

P r o o f. The total population in any given time is:

$$N(t) = S(t) + E(t) + I(t) + R(t) + V(t),$$

and thus:

$$\begin{aligned}
\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} &= \Lambda - \mu (S + E + I + R + V) \\
&= \Lambda - \mu (N - I) - \mu_1 I, \qquad (4) \\
\frac{dN}{dt} &= \Lambda - (N - I) - \mu_1 I \leq \Lambda - \mu N. \qquad (5)
\end{aligned}$$

Then it can be deducted that:

$$\frac{dN}{dt} \leq \Lambda - \mu N. \tag{6}$$

Solving the following ordinary differential equation:

$$\frac{dN}{dt} + \mu N = \Lambda,$$

it is obtained the general solution:

$$N = \frac{\Lambda}{\mu} + C_0 e^{-\mu t}.$$

For initial condition $t = 0$ it is following:

$$N_0 = \frac{\Lambda}{\mu} + C_0 \Rightarrow C_0 = N_0 - \frac{\Lambda}{\mu},$$

So, for the particular solution it is obtained:

$$N = \frac{\Lambda}{\mu} + \left(N_0 - \frac{\Lambda}{\mu}\right) e^{-\mu t} = N_0 e^{-\mu t} + \frac{\Lambda}{\mu}\left(1 - e^{-\mu t}\right).$$

Because of (6), it follows that:

$$N \leq N_0 e^{-\mu t} + \frac{\Lambda}{\mu}\left(1 - e^{-\mu t}\right).$$

Taking that

$$t \to \infty,$$

it is obtained that:

$$N \leq \frac{\Lambda}{\mu}. \tag{7}$$

Since, it is proven that

$$\Omega = \left\{ x = (S, E, I, R, V) \in \mathbf{R}^5 : 0 \leq N \leq \frac{\Lambda}{\mu} \right\}$$

is a bounded region. □

Corollary 2.1. *The total population at any given time is nonnegative where the initial condition of the model (2) is nonnegative since the total population is*

$$N(t) = S(t) + E(t) + I(t) + R(t) + V(t),$$

and from Theorem 1, $S(t) \geq 0$, $E(t) \geq 0$, $I(t) \geq 0$, $R(t) \geq 0$, $V(t) \geq 0$.

The basic reproduction number (see [10]), denoted as $\Re_0$, is defined as expected number of secondary cases produced by one infected individual over the infectious period. The reproduction number is crucial in understanding the potential for spreading measles infection. In this

paper, the reproduction number $\Re_0$ for disease-free equilibrium will be found.

One solution for model (2), where E=0, I=0 is a disease-free equilibrium point:

$$X^* = (S^*, E^*, I^*, R^*, V^*) =$$

$$\frac{\Lambda(\sigma+\nu+\mu)}{(\sigma\mu+(q+\mu)(\mu+v))}, 0, 0, \frac{vq\Lambda}{\mu(\sigma\mu+(q+\mu)(\mu+v))}, \frac{q\Lambda}{(\sigma\mu+(q+\mu)(\mu+v))}, \tag{8}$$

The basic reproduction number for model (2) in disease-free equilibrium point is:

$$\Re_0 = \frac{\beta\mu(\sigma+\nu+\mu)}{(q+\mu)(\nu+\mu)+\sigma\mu} \cdot \frac{\alpha}{(\alpha+\mu)(\gamma+\mu_1)}.$$

The next generation matrix is derived from two matrices $\Im$ and Υ, The matrix $\Im$ (x) represents the rate of appearance of new infection, while the matrix Υ represents the rate of transfer of individuals into and out of compartments.

Let $X = (S, E, I, R, V)^T$ then model (2) can be written as:

$$\frac{dX}{dt} = \Im(x) - \Upsilon(x),$$

where:

$$\Im(X) = \begin{bmatrix} 0 \\ \frac{\beta SI}{N} \\ 0 \\ 0 \\ 0 \end{bmatrix},$$

and

$$\Upsilon(X) = \begin{bmatrix} \frac{\beta SI}{N} + qS + +\mu S - \sigma V - \Lambda \\ (\alpha+\mu)E \\ (\gamma+\mu_1)I - \alpha E \\ \mu R - \gamma I - \nu V \\ (\sigma+\nu+\mu)V - qS \end{bmatrix}.$$

The infected subgroups are exposed E and infected I. The matrix F represents infection transmission in exposed, while the matrix presents

the infected compartments. The matrices are 2×2 Jacobian matrices at the disease-free equilibrium point (8):

$$F\left(X^*\right) = \begin{pmatrix} 0 & \frac{\beta S^*}{N^*} \\ 0 & 0 \end{pmatrix},$$

and

$$V\left(X^*\right) = \begin{pmatrix} (\alpha+\mu) & 0 \\ -\alpha & (\gamma+\mu_1) \end{pmatrix}.$$

In the equilibrium point, the total population is $N^* = S^* + E^* + I^* + R^* + V^* = \frac{\Lambda}{\mu}$ therefore it follows:

$$F\left(X^*\right) = \begin{pmatrix} 0 & \frac{\mu\beta S}{\Lambda} \\ 0 & 0 \end{pmatrix}.$$

The next generation matrix is:

$$FV^{-1} = \begin{pmatrix} 0 & \frac{\beta\mu(\sigma+\nu+\mu)}{(q+\mu)(\nu+\mu)+\sigma\mu} \\ 0 & 0 \end{pmatrix} \cdot \begin{pmatrix} \frac{1}{\alpha+\mu} & 0 \\ \frac{\alpha}{(\alpha+\mu)(\gamma+\mu_1)} & \frac{1}{\gamma+\mu_1} \end{pmatrix}. \tag{9}$$

Hence, the reproduction number is:

$$\Re_0 = \frac{\beta\mu(\sigma+\nu+\mu)}{(q+\mu)(\nu+\mu)+\sigma\mu} \cdot \frac{\alpha}{(\alpha+\mu)(\gamma+\mu_1)}. \tag{10}$$

3. **Simulation and results**

In 2023, only one case of measles has been reported in North Macedonia. In the period from 2014 to 2023 a total of 2020 infected individuals have been registered, as shown in Table 1. Epidemics were registered in 2014, 2017, 2018 and 2019 (see [11]). The last epidemic in North Macedonia began in late 2018 and ended in 2019 with total of 1901 infected individuals in 24 cities.

WHO recommends vaccination coverage of rate of 95% to achieve herd immunity (see [12]). The total coverage of MRP vaccine in North Macedonia in 2022 is 70.7% (see [13]) which led to epidemic in the period 2018-2019. The recovery time from measles is 2 to 3 weeks, so that if the recovery time is 2 weeks, the recovery rate is 0.071.

The incubation period for measles can vary from 7-21 days, (see [14]), so that if the incubation period is set to 8 days, the incubation rate is 0.125. Mortality rate of measles is 1 to 2 per 1000 infected individuals

Year	Number of infected
2014	116
2015	1
2016	0
2017	19
2018	64
2019	1819
2020	0
2020	0
2021	0
2022	0
2023	1

TABLE 1. Number of measles infection cases in North Macedonia.

Parameter	Value
Λ	21960
β	0.9
α	0.125
γ	0.1428
σ	0.007
ν	0.993
q	0.744
μ	0.00214
μ_1	0.001

TABLE 2. Parameter values for North Macedonia.

(see [14]). The rate of unsuccessful vaccination is approximately 5% among all vaccinated individuals (see [15]).

In order to illustrate the impact of vaccination, the represented model was developed in AnyLogic (visit [16]). For simplicity it was estimated that the infants and the newborns are fully immunized for measles. Parameter's values are given in Table 2. The first simulations were performed for vaccination rate of 0.95. The results in Figure 2 show that as the transmission rate decreases, the number of infected

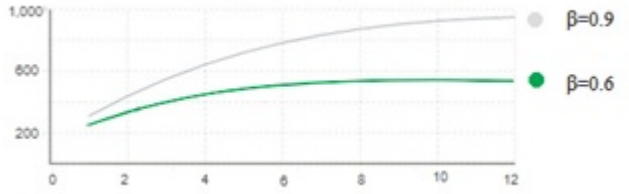

FIGURE 2. Number of infected individuals for transmission rate 0.9 and 0.6 for vaccination rate 0.95

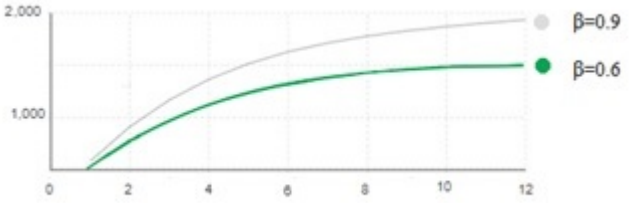

FIGURE 3. Number of infected individuals for transmission rate 0.9 and 0.6 for vaccination rate 0.744

individuals decreases. When the transmission rate is set to 0.9 the number of infected individuals is under 1000. When the transmission rate decreased to a value of 0.6 the number of infected individuals decreased to around 600.

In 2018, the vaccination coverage against measles in N. Macedonia is only 74.4%, therefore, the next set of simulations are performed for vaccination rate 0.744 and transmission rate 0.6 and 0.9. The results are shown in Figure 3.

From Figure 3 can be concluded that the number of infected individuals is higher for higher transmission rate, i.e. the number of infected individuals increases as the transmission rate increases. When the transmission rate is 0.6 the number of infected individuals is around 1600, and when the transmission rate increases to 0.9, the number of infected individuals is increased at almost 2000 infected individuals.

4. Conclusion

In this paper SEIRV model of measles is represented. The SEIRV model serves as a valuable tool for public health authorities in designing and evaluating vaccination policies ultimately contributing to the global effort to control and eliminate measles. The SEIRV model successfully predicts the transmission dynamic of measles disease. This model indicates that the spread of disease depends on the transmission rate and the contact between susceptible individuals with infected individuals in the population. Simulation results show that the number of infected individuals increases as the transmission rate increases.

Also, in this paper the need of higher vaccination coverage is emphasized. The results of the simulation show that by increasing the vaccination rate to 0.95, as per WHO recommendation for immunization, the number of infected individuals decreases significantly.

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