

Mathematical Modelling on Chickenpox Using the Basic Reproduction Number

Harpreet Kaur¹ and Atendra Singh Yadav²

^{1,2}Department of Mathematics, Guru Kashi University, Talwandi Sabo, Punjab, India

Emails: toorharpreet1286@gmail.com, drasyadavmathematics@gmail.com

Abstract

Chickenpox (varicella) is still a major public health issue especially among young children. This study develops an enhanced SIR-based compartmental model to investigate the transmission dynamics of chickenpox, incorporating vaccination as a critical control mechanism. The model includes a vaccination rate parameter that directly reduces the susceptible population, thereby lowering the force of infection and altering the disease progression. Numerical simulations are performed under various vaccination scenarios, with results showing a marked decline in infection levels as vaccination coverage increases. The disease-free equilibrium becomes globally asymptotically stable when the fundamental reproduction number R_0 is smaller than one, the disease free equilibrium is globally asymptotically stable indicating effective containment of outbreaks. The model emphasizes the need of ongoing immunization campaigns in stopping major spread and lowering the healthcare load. Furthermore underlined is the part mathematical modeling plays in public health policies since it offers a quantitative framework to assess and maximize vaccination campaigns. Future directions of research call for including age structure, spatial heterogeneity, seasonal effects, declining immunity, and behavioral dynamics in addition to real-time surveillance data. These improvements would increase the prediction capacity of the model and enable more responsive, data-driven decision-making in the control of epidemic. The overall results highlight the critical importance of vaccination and show mathematical modeling as a necessary instrument in public health planning and epidemic readiness.

Key Terms: Chickenpox Virus, Mathematical modelling, Jacobian Matrix and Routh Hurwitz Criteria.

1. Introduction

Sometimes referred to as varicella medically, the highly contagious varicella-zoster virus (VZV) causes chickenpox. Usually mild in young people in good health, it can be quite problematic for adults, pregnant women, and immunocompromised people. The global disease load highlights the need of effective control strategies particularly in countries with limited access to immunization. Long-standing dependence on mathematical models in epidemiological research has helped to better understand disease transmission dynamics and assesses the probable influence of public health initiatives. Among these methods, compartmental models such as SIR (Susceptible-Infectious-Recovered) model and its variants provide a disciplined framework to investigate the evolution of infectious diseases inside a population but often lack the complexity required to reflect the nuances of chickenpox epidemiology [Hussien, H. H., et al., 2025].

In the framework of chickenpox, estimating and interpreting reproduction number (R_0) is crucial to understand the degree of the epidemic and design appropriate containment methods including thresholds for vaccination coverage [Ibrahim et al., 2025]. While indicates that the disease will sweep throughout the population, suggests eventual disease elimination [Huang, S. Z., 2008]. Mathematical modeling allows researchers to recreate multiple epidemic scenarios, assess the sensitivity of transmission dynamics to several parameters, and predict outbreak pathways under different conditions [Siettos, 2013]. This work authentically shows the spread of chickenpox and tries to construct a mathematical model utilizing the fundamental reproduction number to evaluate disease persistence and control strategies. By incorporating real data and theoretical analysis, the study intends to give the better

Furthermore, compared to empirical research, mathematical modelling provides a reasonably affordable and moral method of investigating infectious diseases. These models can now include greater complexity, including age structure, spatial distribution, and vaccine effects, given the ongoing growth of computer tools and the growing availability of epidemiological data. In the framework of chickenpox, this study will investigate how these elements affect R_0 and pinpoint important intervention locations to stop spread. In the end, the results of this study can be applied not only for control of chickenpox but also as a template for modelling related infectious illnesses, therefore supporting the larger area of epidemiological research and public health planning.

2. Model Formulation:

2.1 The parameters mentioned in both Table 1 and Table 2 are helpful in formation of improved mathematical model.

Table 1: Illustration of Various Parameters for chickenpox

S. No.	Notations	Parameter Interpretation	Initial Values [17]
1	Λ	Rate of Birth	2.01
2	β	Rate of Transmission	1
3	α	Cure Rate of Infected Patient	3
4	γ	Rate of Recovery	99.8%
5	μ	Rate of Death	0.112
6	ξ_1	Rate of Vaccination	99%
7	ξ_2	Vaccine Efficacy	$0 \leq \xi_2 \leq 1$

Table 2: Illustration of all Variables

S. No.	Notations	Parameter Interpretation	In India [17]
1	$S(t)$	Suspected Class	27288
2	$I(t)$	Infected Class	27288
3	$V(t)$	Vaccinated Class	27288
4	$R(t)$	Recovered Class	27257
5	$T(t)$	Incubation Time	100 days

2.2 Basic SIR Model

The basic SIR model categories the population into three different compartments Susceptible (S), Infectious (I), and Recovered (R).The basic SIR model is one of the easiest foundational model in the field of epidemiology and it is appropriate for all transmissible diseases where revived individuals do not experience any reinfection after recovery from the disease. According to Originally developed by Kermack and McKendrick in 1927, the SIR model explains individual flow throughout time between the compartments using an ordinary differential equation system., the governing equations of SIR model are given below:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

Here, β is the disease's transmission rate, which combines the contact rate with the probability of disease spread per contact While γ shows the recovery rate—that is, the fraction of infectious people who recover within given time interval.

The reproduction number R_0 is given by

$$R_0 = \frac{\beta}{\gamma} = 0.01 < 1 \tag{4}$$

The characteristics equation of the given system is given by $|J_1 - \lambda I| = 0$;

$$|J_1 - \lambda I| = \begin{vmatrix} -\beta I - \lambda & -\beta S & 0 \\ \beta I & \beta S - \gamma - \lambda & 0 \\ 0 & \gamma & -\lambda \end{vmatrix}$$

That is $\lambda[\lambda^2 + \lambda(\beta I - \beta S + \gamma) + \beta I\gamma] = 0 \tag{5}$

Which implies, $\lambda = 0, \frac{-(\beta I - \beta S + \gamma) \pm \sqrt{(\beta I - \beta S + \gamma)^2 - 4\beta I\gamma}}{2}$

That is $\lambda_1 = 0, \lambda_{2,3} = 49.9 \pm 1649.5i$.

Since all eigenvalues are either positive and zero. This indicates that the system will therefore be stable.

2.3 Assumptions of the mathematical Model:

- a. The total population changes due to births and natural deaths.
- b. A fraction of susceptible individuals is vaccinated.
- c. Recovered individuals acquire lifelong immunity.
- d. No exposed compartment keeping it a true SIR variant.
- e. Vaccination reduces susceptibility, possibly not fully effective.

2.4 Improved Vaccinated SIR model:

The SIR model with vaccination class is represented by the governing equations like:

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{N} - \xi_1 S - \mu S \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} + \frac{\beta VI}{N} - \frac{\beta \xi_2 VI}{N} - \gamma I - \mu I \tag{2}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{3}$$

$$\frac{dV}{dt} = \xi_1 S + \frac{\beta \xi_2 VI}{N} - \frac{\beta VI}{N} - \mu V \tag{4}$$

Where *Total population* (N) = $S + I + R + V$

2.5. Disease-Free Equilibrium (DFE):

At DFE, $I = 0$. Let the system settle with:

$$S^* = \frac{\Lambda}{\mu + \xi_1}, I^* = 0, R^* = 0 \text{ and } V^* = \frac{\Lambda \xi_1}{(\mu + \xi_1)\mu}$$

2.6 Analysis of the Basic Reproduction Number (R_0):

The value of R_0 for the extended model is computed using a next-generation matrix approach. The fundamental reproduction number corresponds to the greatest eigenvalue found by assessing the Jacobian matrix in the disease-free equilibrium. Evaluating the risk of an epidemic and determining the vaccination threshold required to reach herd immunity depend on this value.

Mathematically, we have $R_0 = \frac{\beta}{\mu + \gamma} \left(\frac{S^* + (1 - \xi_2)V^*}{N^*} \right)$

Substituting DFE, we get

$$R_0 = \frac{\beta}{\mu + \gamma} \left(\frac{\Lambda \left[1 + \frac{\xi_1(1 - \xi_2)}{\mu} \right]}{(\mu + \xi_1)N^*} \right)$$

$$R_0 = 0.0899 < 1$$

If vaccination is perfect ($\xi_2 = 0.5$), the term reduces and R_0 decreases.

Since both models provided the same interpretation of result so, we can conclude that for $R_0 < 1$, infection will die out.

3. Graphically Analysis:

The following figure shows graphical representation of SIRV Model simulation of chickenpox disease over the period of 100 days. Each curve in graph shows how the number of susceptible, infected, recovered and vaccinated class vary over time.

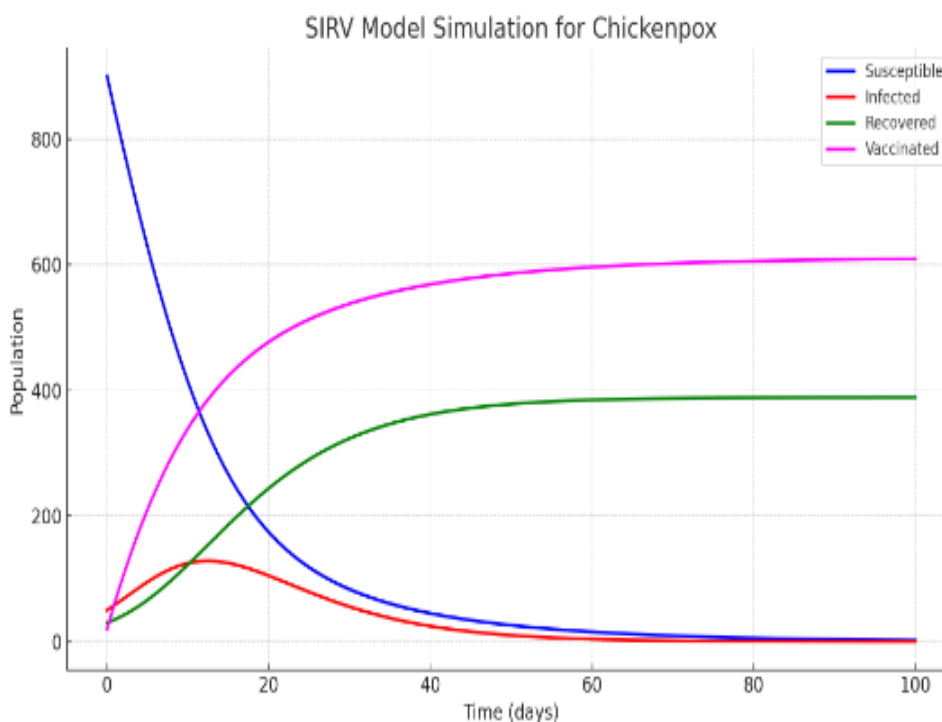


Figure 1: SIRV Model Simulation over 100 days

4. Numerical Simulations:

Numerical simulations are conducted using biologically reasonable parameter values to demonstrate the dynamics of the extended model for chickenpox transmission. The model incorporates key epidemiological factors, including vaccination, to assess its impact on disease prevalence. Special attention is given to scenarios where value of the basic reproduction number R_0 is less than one, indicating that the illness is not expected to spread in the population under these conditions. The simulations explore various vaccination rates to analyze their influence on the overall incidence of chickenpox. Results reveal a significant decline in the number of infections as vaccination coverage increases. This aligns with theoretical expectations: when $R_0 < 1$, the disease cannot sustain itself, and outbreaks are effectively suppressed. The model outcomes clearly highlight the role of immunization in controlling and potentially eradicating chickenpox. Even modest increases in vaccination rates lead to pronounced reductions in disease burden. These

findings reinforce the importance of maintaining high vaccination coverage as a critical public health strategy. Overall, the simulations validate that targeted vaccination programs are effective tools in limiting the transmission of chickenpox and preventing future outbreaks, particularly in communities where R_o has been successfully reduced below the epidemic threshold.

5. Discussion:

Comparatively to the standard SIR model the extended SIR model including a vaccinated compartment, offers a more realistic and detailed picture of chickenpox transmission dynamics. Unlike the fundamental SIR model, it allows public health initiatives such immunization campaigns, which are vital in modern efforts at disease control. By means of this model, we find that raising the vaccination rate directly lowers the vulnerable population, hence lowering the new infection count. The model also provides another important realization in its adaptability in assessing several vaccination approaches. For high-risk groups, for example, models including mass vaccination against focused campaigns can be run and compared. Furthermore, sensitivity analysis helps identify the factors most influencing disease dynamics, hence leading more sensible use of resources and policy-making. The results of the model confirm the validity of current data on the effectiveness of varicella vaccination and underline the need of keeping high immunization coverage to stop epidemic.

6. Conclusion:

This study presents an advanced SIR-type compartmental model that integrates vaccination as a control parameter, enhancing the quantitative understanding of chickenpox dynamics. The model equations incorporate a vaccination rate term that effectively transitions susceptible individuals into the recovered class, thereby reducing the force of infection. Simulation outcomes across varying vaccination coverage levels demonstrate a pronounced sensitivity of the infection trajectory to this control parameter, confirming the threshold behavior governed by R_o . The model serves not only as a theoretical framework but also as a predictive tool, enabling optimization of vaccination strategies under resource constraints. Beyond highlighting vaccination's impact, the mathematical formulation underscores the utility of dynamic modeling in informing health interventions. Future extensions could include age-structured compartments,

spatial diffusion terms for regional heterogeneity, periodic forcing functions to capture seasonality, and waning immunity rates to reflect reinfection potential. Incorporating time-dependent parameters, data assimilation techniques, and feedback control based on behavioral response and policy adherence would further enhance the model's real-time applicability. Such refinements aim to improve forecasting precision and guide adaptive public health responses.

References:

1. Almualllem, N. A., Ali, H. M., Elsaid, E. M., Eid, M. R., & Hassanin, W. S. (2025). Mathematical Simulation of Optimal Control Measures to Avoid Chickenpox Infection. *International Journal of Mathematics and Mathematical Sciences*, 2025(1), 3238188.
2. Bais, V. K., & Kumar, D. (2016, March). Mathematical analysis on bronchitis infection. In *2016 3rd International Conference on Computing for Sustainable Global Development (INDIACom)* (pp. 1861-1864). IEEE.
3. Briat, C. and Verriest, E.I., 2009. A new delay-SIR model for pulse vaccination. *Biomedical signal processing and control*, 4(4), pp.272-277.
4. Deguen, S., Thomas, G., & Phong Chau, N. (2000). Estimation of the contact rate in a seasonal SEIR model: application to chickenpox incidence in France. *Statistics in Medicine*, 19(9), 1207–1216.
5. Ferguson, Neil & Anderson, Roy & Garnett, G. (1996). Mass vaccination to control chickenpox: The influence of zoster. *Proceedings of the National Academy of Sciences of the United States of America*. 93. 7231-5. 10.1073/pnas.93.14.7231.
6. Gupta, V., Kumar, S., & Mahajan, S. (2021). Seasonal variation and role of meteorological conditions in reported chicken pox cases in a residential hostel of Ramgarh. *International Journal of Community Medicine Public Health*, 8(3), 1191.
7. Hussien, H. H., Genawi, K. R., Hagabdulla, N. H., & Ahmed, K. M. (2025). Understanding the Basic Reproduction Number (R_0): Calculation, Applications, and Limitations in Epidemiology. *Open Journal of Epidemiology*, 15(2), 272-295.
8. Huang, S. Z. (2008). A new SEIR epidemic model with applications to the theory of eradication and control of diseases, and to the calculation of R_0 . *Mathematical Biosciences*, 215(1), 84-104.
9. <https://health.py.gov.in/chicken-pox>

10. Ibrahim, K. G., Andrawus, J., Abubakar, A., Yusuf, A., Maiwa, S. I., Bitrus, K., ... & **Jonathan, J.** (2025). Mathematical analysis of chickenpox population dynamics unveiling the impact of booster in enhancing recovery of infected individuals. *Modeling Earth Systems and Environment*, 11(1), 1-14.
11. Jose, S. A., Raja, R., Dianadvinnarasi, J., Baleanu, D., & Jirawattanapanit, A. (2023). Mathematical modeling of chickenpox in Phuket: Efficacy of precautionary measures and bifurcation analysis. *Biomedical Signal Processing and Control*, 84, 104714.
12. Kaur, H. ., & Yadav, A. S. (2025). Compartmental Analysis of Influenza A (H1N1) Virus using Induced SEIR Model. *Journal of Neonatal Surgery*, 14(14S), 794–800.
13. Kaur , H., & Yadav, A. S. (2025). Mathematical Modelling to Analysis the Behaviour of Monkey Pox using Basic Reproduction Number. *South Eastern European Journal of Public Health*, 4368–4374.
14. Khan, V., Sanghai, A. A., Zala, D. B., Babariya, M. J., & Das, V. K. (2024). A deep dive into chickenpox epidemiology and outbreaks: A retrospective study in a tribal-dominated district of Western India. *Indian Journal of Medical Sciences*, 76(1), 36-42.
15. Kumar, V., Kumar, D., & Pooja. (2016). SIR model of Swine Flu in Shimla. In *Advanced Computing and Communication Technologies: Proceedings of the 9th ICACCT, 2015* (pp. 297-303). Springer Singapore.
16. Kumar, V., & Kumar, D. (2018, April). Analysis of epidemic model using basic reproduction number. In *Proceedings of 3rd International Conference on Internet of Things and Connected Technologies (ICIoTCT)* (pp. 26-27).
17. Minhas, A., Singh, M., Prasad, N. S. N., & Bhardwaj, A. (2022). Geospatial Epidemiology of chicken-pox disease in India between 2015-2021: A GIS based analysis. *Indian Journal of Community Health*, 34(1), 78-81.
18. Ospina Giraldo, J., & Hincapié Palacio, D. (2007). Deterministic SIR (Susceptible–Infected–Removed) models applied to varicella outbreaks. *Epidemiology & Infection*, 136(5), 679–687.
19. Rafferty, E., McDonald, W., Qian, W., Osgood, N. D., & Doroshenko, A. (2018). Evaluation of the effect of chickenpox vaccination on shingles epidemiology using agent-based modeling. *PeerJ*, 6, e5012.

20. Singh, K. P., Jain, P., Prakash, O., Khan, D. N., Gupta, S., Prakash, S., ... & Jain, A. (2014). Outbreaks of measles and chickenpox in eastern Uttar Pradesh, India. *Clinical Epidemiology and Global Health*, 2(1), 3-9.
21. Singh, M. P., Chandran, C., Sarwa, A., Kumar, A., Gupta, M., Raj, A., & Ratho, R. K. (2015). Outbreak of chickenpox in a Union Territory of North India. *Indian Journal of Medical Microbiology*, 33(4), 524-527.
22. Steiner, K., Wallrafen, N., & Weiss, D. (2018). Development of a Mathematical Model of the Spread of Chicken Pox in a Contained Population.
23. Siettos, C. I., & Russo, L. (2013). Mathematical modeling of infectious disease dynamics. *Virulence*, 4(4), 295-306.
24. Zhang, Y., et al. (2022). A Dynamic Compartmental Model to Explore the Optimal Strategy of Varicella Vaccination: An Epidemiological Study in Jiangsu Province, China. *Vaccines*, 8(1), 17.
25. Zhang, Y., et al. (2022). Modelling the transmission and control strategies of varicella among school children in Shenzhen, China. PubMed Central.