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Modeling the spread of rubella disease using a stochastic delay dynamic system

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1. Introduction

- Rubella is a serious and highly contagious human disease caused by the rubella virus
- **Symptom:** Most adults who get rubella usually have a mild illness, with low-grade fever, sore throat, and a rash that starts on the face and spreads to the rest of the body.

In children, rubella is usually mild, with few noticeable symptoms:

- a red rash is typically the first sign, a low-grade fever, headache, mild pink eye (redness or swelling of the white of the eye), general discomfort , swollen and enlarged lymph nodes, cough and runny nose

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- Transmission: Rubella spreads through direct contact with discharge from the nose and throat. The virus that causes rubella can also be spread from a pregnant mother to her fetus through the bloodstream.

Modeling of Rubella

- Mathematical model is useful for describing and analyzing dynamic behavior, spread, and control strategies to create visualizations of infection over time.
- Lahrouz, et al 2011. Developed a Rubella model that shows the contact that occurs during the incubation and infection period has a significant impact on the extent of transmission of all types of infectious diseases.
- Prawoto, et al 2020. Developed a mathematical model of Rubella dynamics of and showed re-infection with vaccine-induced transmission have great impact.
- Grant, et al 2019 developed with the assumption that the first vaccine develops active immunity throughout life is inconsistent and MMR vaccination was recommended twice for the development of active immunity (protection against the rubella virus).

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- Al Qurashi, M.M. 2020, developed a mathematical SEIR model of rubella epidemics with an optimized order using fractional differential equations
- Atangana, A. and Alkahtani, B.S.T. 2016, developed SEIRV mathematical model of rubella disease dynamics with the aim of extending the model to support studies of viral spread in the target population.
- Metcalf, et al, 2012 Developed a mathematical model and showed that the non-linear epidemic dynamics of rubella interact in complex ways with both fertility and spatial heterogeneity, leading to increased vaccination rates across a global spectrum of demographic and epidemiological contexts.
- Yang, et al, 2019. developed a deterministic mathematical SEIVR model to describe the direct or indirect transmission of rubella.

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- Metcalf, et al2012. modeled to study the unpredictability of interpersonal contact and environmental factors of rubella Dynamics.
- To the best of our knowledge, no studies have considered randomness and time delay simultaneously.
- Therefore, in this study, we developed a model of the dynamics of rubella disease using **a stochastic-delay deferential equation,** second vaccination, and vertical transmissions.

Model Description

- The model divides the total population into six compartments, namely: susceptible S(t), vaccinated V(t), protected P(t), exposed E(t), infected I(t), and recovered R(t).
- Individuals in the susceptible class have increased by recruitment rates π, a first vaccination influx ω, and rates of immune loss among convalescent individuals with the rate of ρ as well as increased contact rates β and first-time vaccination rates α decrease this class.
- Individuals in the infected class will increase at a rate of β through contact and vertical transmission of disease from mother to infant a rate of ϑ, decrease at a rate of γ, and die from rubella disease at a rate of ε.

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- The recovery class increases with the rate of recovery of γ from an infected person and decreases with the rate of loss of immunity ρ.
- The class of vaccinated individuals increases as the first dose of vaccine is administered to susceptible individuals at a rate of α.
- This class is reduced by administering a second dose of vaccine at a rate of δ and tapering the first dose of vaccine at a rate of ω.
- The protected class will be expanded by administering the first and second doses of vaccine at a rate of δ.
- All classes are have natural death rate μ.

Model Assumptions

- Individuals will become infected by direct contact with the respiratory droplets of an infected individual or by vertical transmission from mother to fetus.
- Individuals infected with rubella will recover or die due to rubella disease.
- The recovered and first-vaccinated individual is vulnerable to rubella disease.
- A person who receives two doses of the MMR vaccine will get active immunity (protected against the rubella virus).

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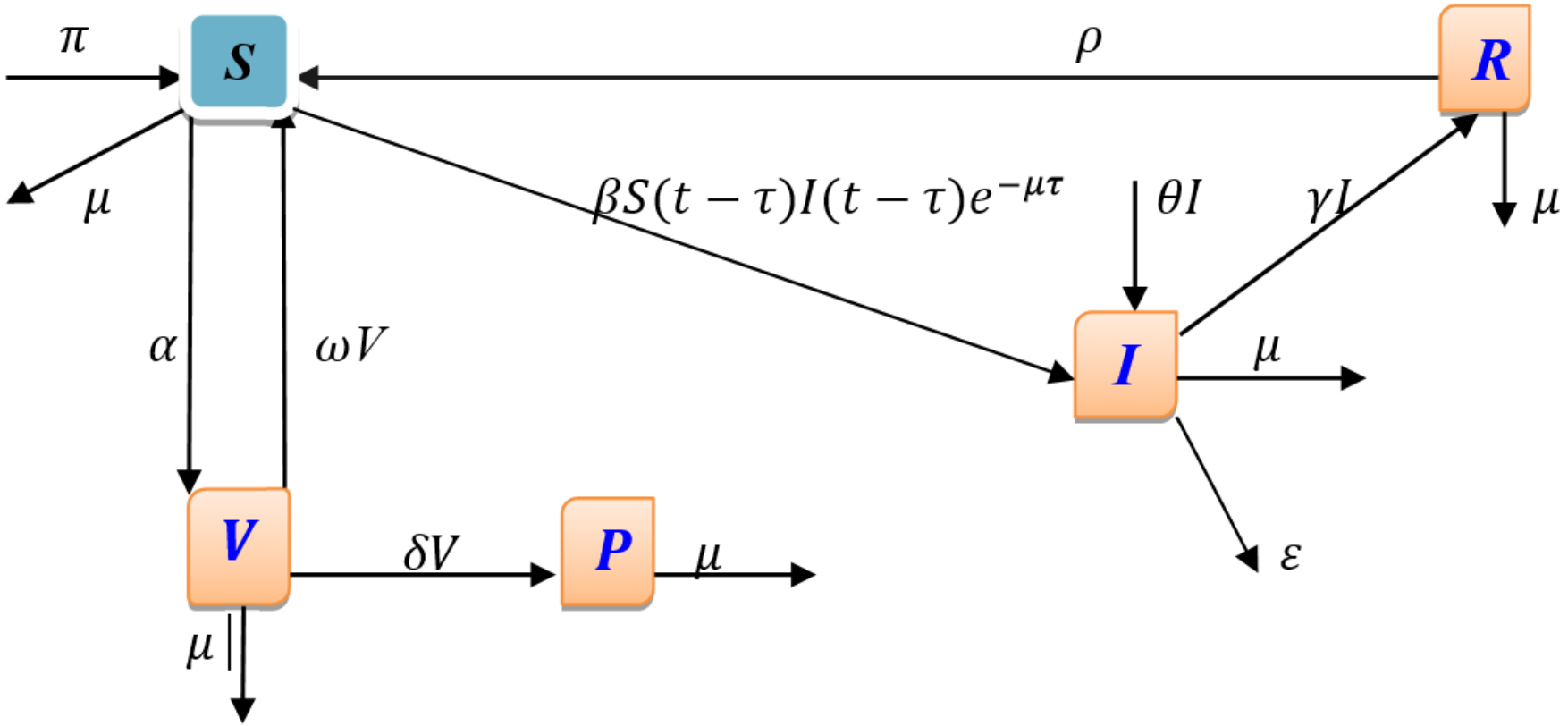
- Based on the behavior of rubella, we assumed that an individual infected for a time $t-\tau$, but not yet infectious (exposed) person would become infected after a period of time τ. The probability of an individual surviving the incubation period $[t-\tau, t]$ defined by the bi-linear incidence $\beta S(t-\tau)I(t-\tau)e^{-\mu\tau}$, where, $t-\tau$ is the incubation period.

Flow Diagram of the model



Model Equation

- $$\begin{cases} dS = [\pi + \rho R + \omega V - \beta S(t-\tau)I(t-\tau)e^{-\mu\tau} - (\alpha+\mu)S]dt + \sigma_1 S dB_1(t) \\ dV = [\alpha S - (\omega+\mu+\delta)V]dt + \sigma_2 V dB_2(t) \\ dP = [\delta V - \mu P]dt + \sigma_3 P dB_3(t) \\ dI = [\beta S(t-\tau)I(t-\tau)e^{-\mu\tau} + \theta I - (\mu+\gamma+\varepsilon)I]dt + \sigma_4 I dB_4(t) \\ dR = [\gamma I - (\mu+\rho)R]dt + \sigma_5 R dB_5(t). \end{cases}$$

Qualitative Analysis of the model

- Basic Reproduction numbers

$R_0{}^S = \frac{\theta}{\mu+\gamma+\varepsilon} + \frac{\beta\pi(\delta+\mu+\omega)}{((\alpha+\mu)(\delta+\mu)+\omega\mu)(\mu+\gamma+\varepsilon)}$ considering only Stochastic model

$R_0{}^D = \frac{\theta}{\mu+\gamma+\varepsilon} + \frac{\beta\pi(\delta+\mu+\omega)e^{-\mu\tau}}{((\alpha+\mu)(\delta+\mu)+\omega\mu)(\mu+\gamma+\varepsilon)}$ Considering only Delay model

$R_0{}^{SD} = \frac{\theta}{\mu+\gamma+\varepsilon} + \frac{\beta\pi(\delta+\mu+\omega)e^{-\mu\tau}}{((\alpha+\mu)(\delta+\mu)+\omega\mu)(\mu+\gamma+\varepsilon)} - \frac{{\sigma_4}^2}{2(\mu+\gamma+\varepsilon)}$. Stochastic-delay model

This implies $R_0{}^D < R_0{}^S$ and $R_0{}^{SD} = R_0{}^D - \frac{{\sigma_4}^2}{2(\mu+\gamma+\varepsilon)}$.

This tells that the basic reproductive number of the stochastic delay model is the difference between the basic reproductive number of the delay model and some value. Which means that that always $R_0{}^{SD} < R_0{}^D$.

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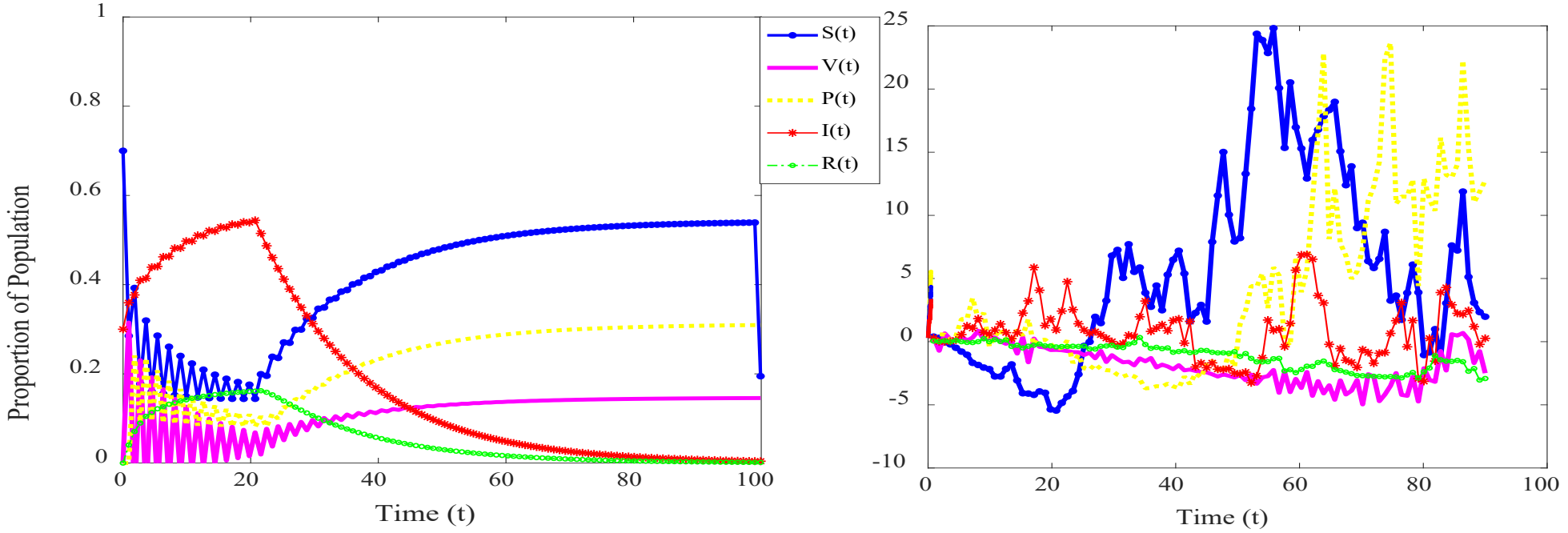
- **Sensitivity Analysis**

Parameter	Description	Sensitivity indices
θ	vertical transmission rate	1.4223
π	Recruitment rate	0.0891
β	Contact rate	0.0891
ω	Rate of waning out of the first vaccination dose	0.00046518
δ	Rate of the second vaccination dose	−0.0453
γ	Recovery rate	−0.3061
α	First vaccination dose	−0.0011
σ_4	Intensity rate	−2.5285

Numerical Simulation

- **Trends of delay and stochastic-delay models**



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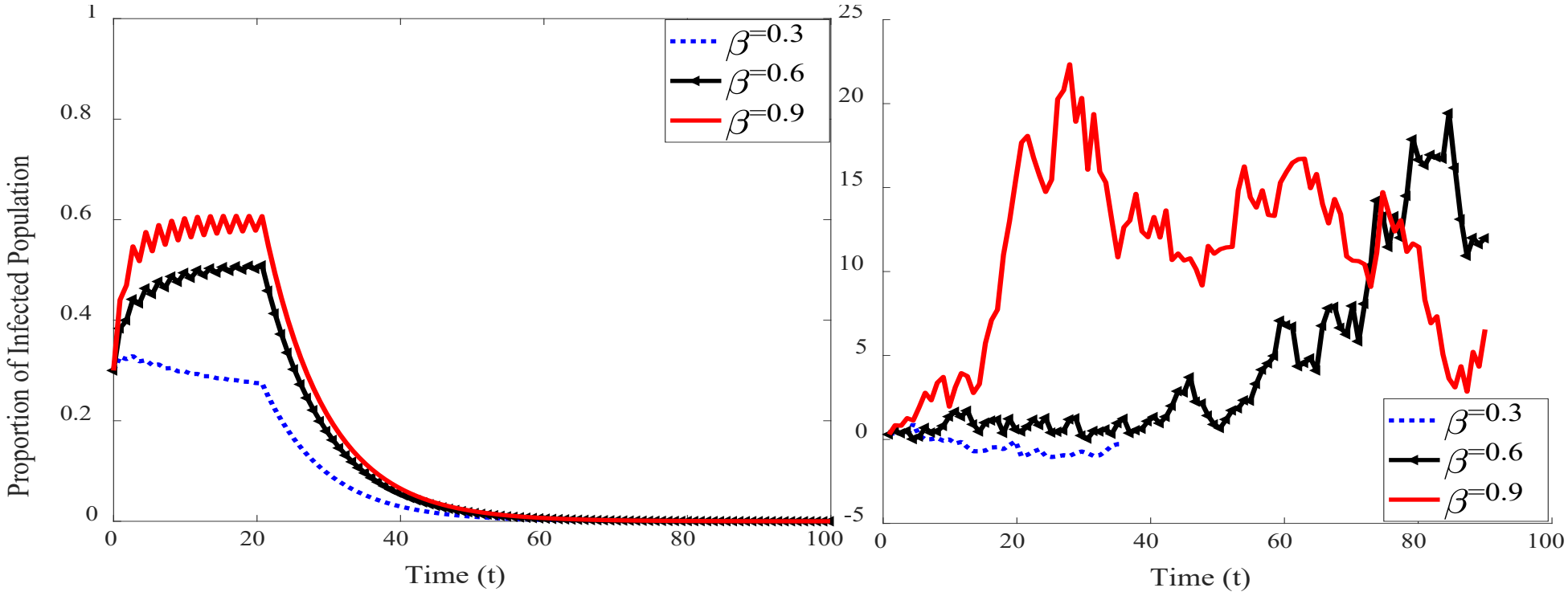
- **Effect of contact rates on rubella-infected individuals for delay and Stochastic delay models**



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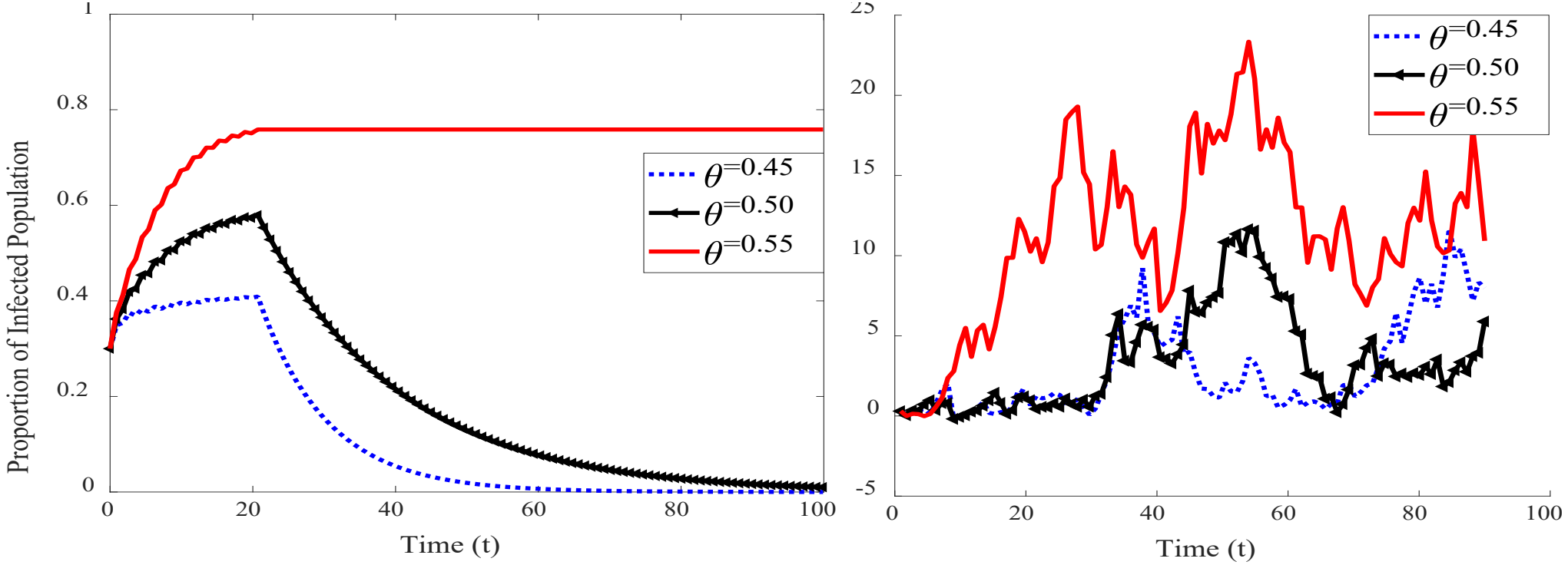
- **Effect of vertical transmission rates on rubella dynamics for Delay and Stochastic-delay models**



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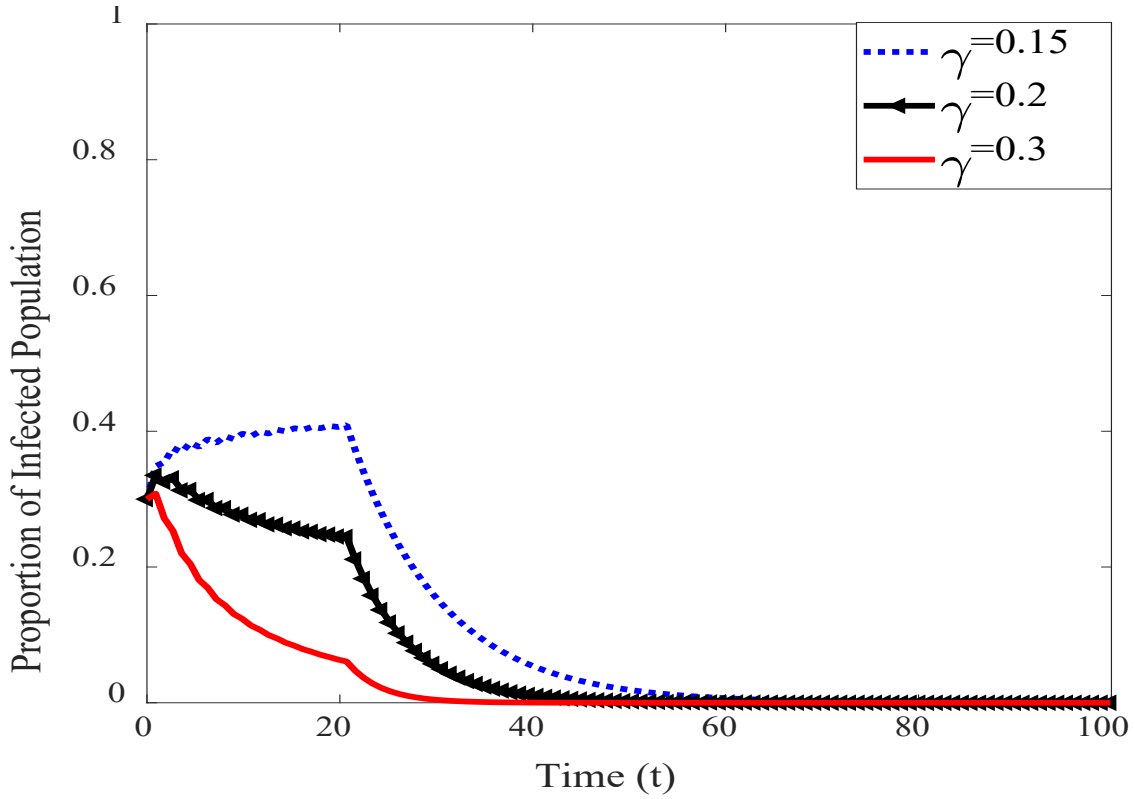
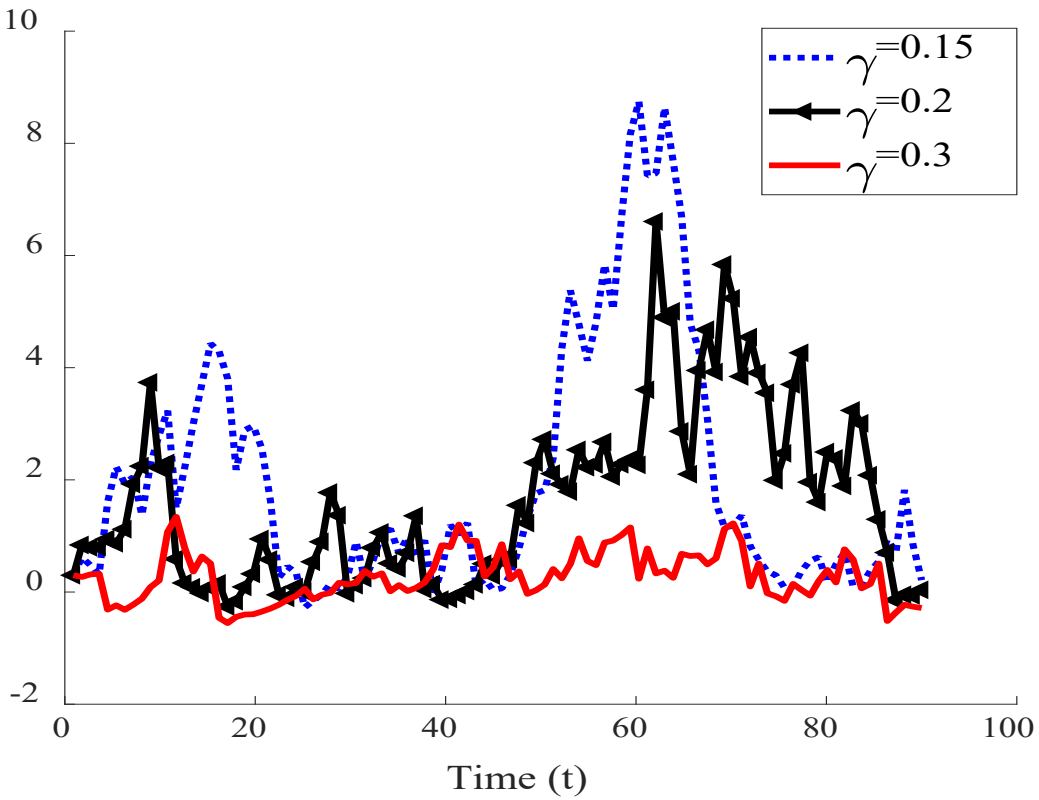
- **Effect of recovery rates on Delay and Stochastic- delay models**





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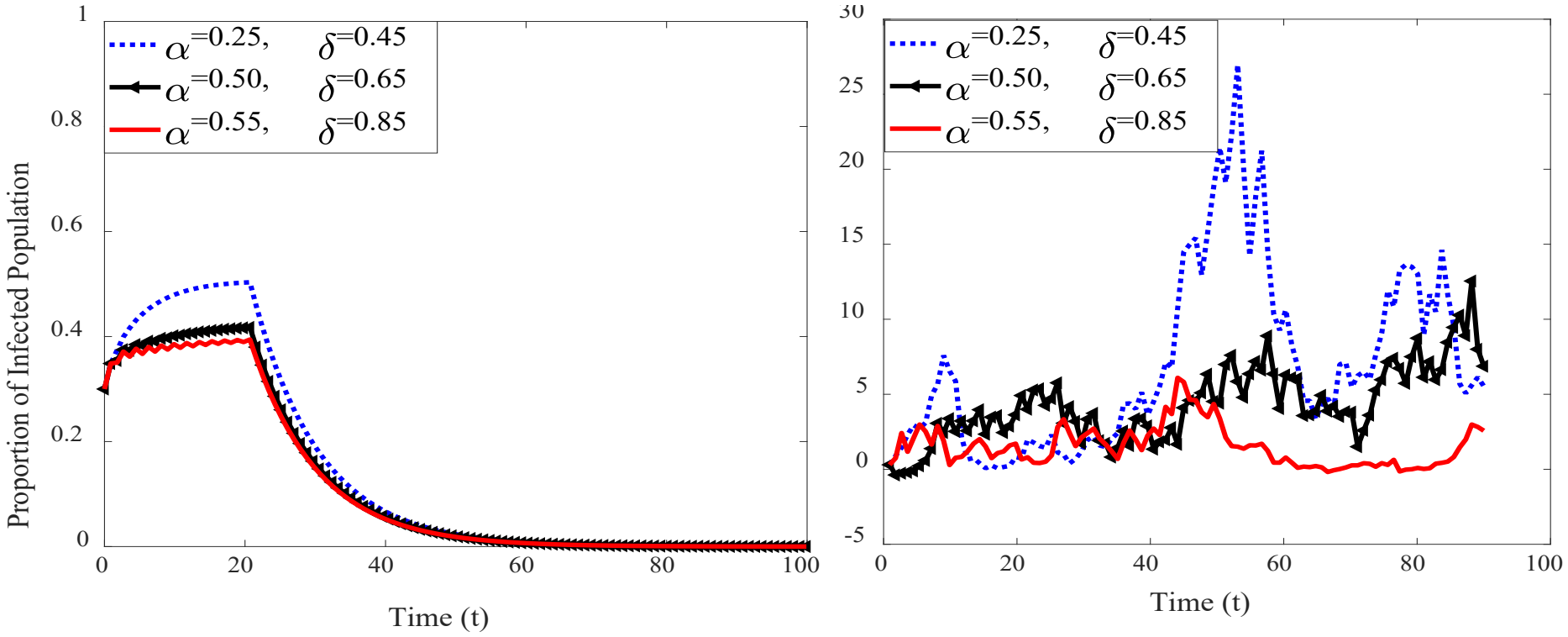
- **Effect of vaccination rates on Delay and Stochastic- delay models**



Summary and Conclusion

- This study was conducted to investigate the dynamics of rubella disease using a stochastic-delay mathematical modeling approach.
- Based on the biological behavior of rubella disease dynamics, a stochastic delay model of SVPIRS was developed that considered vertical transmission and two vaccination doses.
- A basic qualitative analysis of the model was performed. The local stability of the disease-free equilibrium point of the model is determined using the Jacobi method.
- To determine the presence of rubella disease in the community, basic reproductive number was calculated using a next-generation matrix.

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- To perform numerical simulations, the values of some fundamental parameters are taken from published studies, while others are assumed.
- Finally, we discuss the results of numerical simulations using computer software, demonstrate the effect of the parameters, and present the results graphically.
- Results show reduced rates of infected newborns, and increase in recovery rates, incubation periods, and first and second-dose vaccination rates all play a role in control.

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- From the qualitative analysis of the model, we find that the basic reproductive number of the stochastic model appears to be smaller than that of the delay model of due to environmental variation-induced dynamics of rubella disease.
- This means that consideration of environmental factors plays a role in minimizing the average number of secondary infections.
- Because stochastic-delay model includes dynamic behavior, stochastic factors, and latencies, the basic reproductive number obtained from stochastic-delay model is smaller than those for delay and stochastic models.
- This shows that the mathematical model of stochastic delay is closer to reality.

Next stage of the work

- We are collecting real current data, we will try to calibrate
- We will try to see using neural network method
- We will try analyze using spatial modeling technique

Thank you for your Attention!!