Switch: Jurnal Sains dan Teknologi Informasi
Volume. 3 Nomor. 1 Tahun 2025
e-ISSN : 3032-3320, dan p-ISSN : 3032-3339, Hal. 114-125
DOI: https://doi.org/10.62951/switch.v3i1.333
Available online at: https://journal.aptii.or.id/index.php/Switch

Stochastic SEIR Model for Simulating Epidemic Dynamics in Limited Populations

Agung Pratama[1*], **Danu Ariandi**[2]
[1-2]Universitas Islam Negeri Sumatera Utara, Indonesia
Email: agungpratama26051@gmail.com [1], danuariandi123@gmail.com [2]

Jl. Lap. Golf No.120, Kp. Tengah, Kec. Pancur Batu, Kabupaten Deli Serdang, Sumatera Utara 20353
Author correspondence: agungpratama26051@gmail.com*

***Abstract**. The stochastic SEIR model offers an innovative approach to understanding the spread of infectious diseases, particularly tuberculosis, in limited populations. This study adopts a stochastic model to capture random variability in individual interactions, often overlooked in deterministic models. The population is divided into four main categories: Susceptible (S), Exposed (E), Infected (I), and Recovered (R), with transitions between categories determined by probabilities based on epidemiological parameters. Through simulations, the model demonstrates its capability to depict more realistic patterns of disease spread, including fluctuations in case numbers and epidemic duration. The findings indicate that stochastic variability plays a crucial role in understanding the dynamics of tuberculosis transmission, especially in small populations or when the number of individual contacts is limited. The stochastic SEIR model can serve as an effective tool for policymakers to evaluate various intervention strategies, such as vaccination, transmission control, and treatment, as well as to design public health policies that are data-driven and adaptive to epidemiological uncertainties.*

***Keywords**: Epidemic, SEIR. Simulation, Epidemiology, Population*

1. INTRODUCTION

Infectious diseases are significant health issues in human life, and their transmission can lead to epidemics. An epidemic, or disease outbreak, occurs when the number of affected individuals increases noticeably in a specific region and time (Aziezah, Sumarno, and Jaharuddin 2024). To understand this phenomenon, mathematical models are used to describe the spread of diseases, which are known as epidemiological models. One of the commonly used models to describe the disease spread process is the Susceptible-Infected-Recovered (SIR) model (Aidid Muhammad Arif 2020). According to (Rohimasanti, Respatiwulan, and Pratiwi 2021), this model divides the population into three main groups:

a. Susceptible (S): Individuals who are not yet infected but are at risk of contracting the disease after coming into contact with infected individuals,
b. b.Infected (I): Individuals who are infected and can transmit the disease to others,
c. Recovered (R): Individuals who have recovered from the infection and are assumed to have immunity and cannot be infected again.

(Brauer, Driessche, and Wu 2008) Explain that the SIR model represents the disease transmission pattern, where individuals who recover acquire immunity against the disease. Epidemiological models can also be analyzed probabilistically (Siettos and Russo 2013), describing the disease spread process as random with a certain probability. Changes in the

Received: Oktober 19, 2024; Revised: November 17, 2024; Accepted: Desember 19, 2024;Online Available:Desember 23, 2024

number of infected individuals depend on the probability of specific events. The disease transmission process, being stochastic, is time-dependent and related to probability, referred to as a stochastic process. (Halloran et al. 2010) State that infection spreads from one individual to another in a population in discrete time units, forming a transmission chain influenced by a binomial probability distribution. An epidemic is considered to end when there are no more infected individuals.

In this study, we use a stochastic SEIR model to simulate the dynamics of disease spread within a limited population. The stochastic approach allows us to consider the natural variability in the processes of transmission and recovery, which are often overlooked in deterministic models. By conducting this simulation, we hope to provide better insights into how diseases spread in small populations and how interventions can influence this spread (Khaerunnisa, Nasution, and Huda 2022).

This study aims to develop a stochastic SIR epidemiological model with the number of infected individuals following a binomial distribution and variability in the recovery period. The model will be simulated, and the results will be interpreted. This research is expected to contribute to the understanding of stochastic models with binomial distribution in the context of disease transmission, specifically the SIR model (Wicaksono, Respatiwulan, and Susanti 2019).

2. LITERATURE REVIEW

The SEIR (Susceptible-Exposed-Infectious-Recovered) model is a compartmental-based mathematical model commonly used to study the spread of infectious diseases with an incubation period. This model divides the population into four main compartments: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). The deterministic approach in the SEIR model is generally used for large populations, where changes in the number of individuals in each compartment are assumed to be continuous and predictable using average parameters. However, for small populations, this approach often proves inaccurate as it neglects individual variability and random fluctuations. Therefore, a stochastic approach is needed to capture more realistic dynamics of disease transmission (Cocomello and Ramanan 2023).

In the stochastic approach, probability is introduced into the transitions between compartments. The probability of contact between susceptible and infected individuals significantly affects the transmission rate, while variation in the incubation period reflects the different times individuals take before becoming infectious. Additionally, the dynamics of recovery or death, which vary across individuals depending on factors such as age, health condition, and access to medical services, also influence disease spread in this model.

(Hernández et al. 2020) developed a new stochastic formulation that uses more flexible incubation and recovery time distributions, differing from traditional approaches that assume exponential distributions. This approach provides more realistic results, particularly in the context of epidemics in small populations. Modeling disease dynamics in small populations presents specific challenges, including:

a. High Variability

In small populations, individual interactions have a significant impact on disease transmission dynamics. Stochastic fluctuations, such as slight changes in contact rates or infection opportunities, can lead to substantial differences in simulation outcomes. This highlights the importance of using a stochastic approach to obtain more accurate results than deterministic models that rely on average values.

b. Epidemic Extinction

In small populations, epidemics often end more quickly due to the limited number of susceptible individuals or the breakdown of the transmission chain. For example, in a small community that successfully controls disease spread through isolation or quarantine, the disease cannot spread further. This phenomenon is rarely observed in deterministic models (Cocomello and Ramanan 2023).

c. Intervention Analysis

Interventions such as vaccination or quarantine have a significant impact on epidemic dynamics in small populations. Stochastic simulations allow for evaluating these policies by accounting for stochastic fluctuations, providing a more realistic view than deterministic models (Hernández et al. 2020).

Although the stochastic SEIR model has been widely applied, several research gaps still need attention:

a. Spatial Dynamics Integration: Integrating spatial dynamics into the model can help understand disease spread in small communities with limited mobility, such as villages or remote areas.
b. Individual Heterogeneity: The impact of differences in social contact levels between individuals on epidemic outcomes needs further investigation. Factors such as age, occupation, and social interaction patterns can influence disease transmission.
c. Parameter Validation: It is essential to validate model parameters using empirical data from small populations to ensure the accuracy of simulation results.

3. METHODS

The stochastic SEIR model is developed by dividing the population into four compartments Susceptible (S), Exposed (E), Infected (I), and Recovered (R) and utilizing the Monte Carlo method to simulate the dynamics of disease spread in a limited population, considering epidemiological parameters such as the infection rate (β), the transition rate from Exposed to Infected (σ), and the recovery rate (γ), thereby enabling a more realistic analysis of disease spread patterns and the evaluation of public health intervention effectiveness.

4. RESULTS AND DISCUSSION

The SEIR (Susceptible-Exposed-Infected-Recovered) model is one of the most commonly used mathematical models in epidemiology to model the spread of infectious diseases (Taghizadeh and Mohammad-Djafari 2022). This model describes the progression of the disease from one individual to another within a population by dividing the population into four categories: susceptible individuals, individuals who are exposed but not yet infected, infected individuals, and recovered individuals (Zhao, Wang, and Wang 2024).

The stochastic approach in epidemiological modeling is crucial, particularly in small populations, as it accounts for natural variability and uncertainty in the transmission and recovery processes (Afriansyah, Sumarno, and Mangku 2023). This stochastic approach allows the model to capture the random fluctuations that occur in disease spread, which are often overlooked in deterministic models. This makes the stochastic model more realistic and relevant for smaller, dynamic populations (Engbert et al. 2021).

Here are some common assumptions used in the stochastic SEIR model for simulating epidemiological dynamics in a limited population:

1. Closed Population

   Assuming that the modeled population is closed, meaning there is no immigration or emigration during the simulation period and the population size remains constant (except for deaths due to the disease), this model becomes simpler and easier to analyze. However, in reality, this scenario may not be realistic as migration can significantly affect disease transmission. Therefore, while this assumption helps to simplify the model, it is important to consider that, in real-world situations, population changes due to migration could have a substantial impact on the dynamics of the epidemic.

2. Homogeneous Mixing

   Assuming that individuals in the population mix homogeneously, meaning each individual has an equal probability of interacting with others, this model overlooks the reality that human interactions often occur within specific groups, such as families, schools, or workplaces. These complex social network structures can influence disease transmission, and therefore, the assumption of homogeneous mixing is often unrealistic (Nisa, Rahman, and Kusumastuti 2022).

3. Fixed Latent (Incubation) and Infection Periods

The assumption that the model has a fixed and constant latent period (the time between infection and becoming infectious) and an infection period for all individuals simplifies the model but does not reflect reality. In practice, the latent and infectious periods can vary among individuals, and this variability can be modeled by using probability distributions for the durations of the latent and infectious periods.

4. Probability Transmision Konstant

The assumption that the probability of disease transmission from an infected individual to a susceptible individual is constant throughout the simulation period simplifies the model. However, in reality, the transmission probability can be influenced by various factors such as population density, individual behavior, and public health interventions like mask usage or social distancing measures.

5. Lifetime Immunity

The assumption that individuals who recover from the disease will gain lifelong immunity may not always be accurate, as some diseases only provide temporary immunity. Therefore, this assumption can overly simplify the model and may not be accurate for all types of diseases.

6. Death Only Due to the Disease

The assumption that death occurs only due to the modeled disease and not from other causes overlooks the reality that death can result from various factors, which may be correlated with the occurrence of the disease. This can reduce the accuracy of the model in predicting the overall impact of the disease (Lee et al. 2020).

7. Distribution of Recovery Time

The assumption that the recovery time for infected individuals follows a specific probability distribution, such as exponential, gamma, or Weibull, implies that the choice of distribution will affect the dynamics of the simulation. A more realistic distribution will yield a more accurate simulation.

8. Stochastic Process

The assumption that the model uses a stochastic approach, where changes in population compartments are modeled as probabilistic processes, allows the model to account for random fluctuations that may occur in disease transmission, providing a more realistic depiction of epidemic dynamics (Greenhalgh 2021).

It is important to remember that the stochastic SEIR model is a simplification of reality. Using more realistic assumptions will result in a more complex model, but also a more accurate one. The choice of assumptions will depend on the goals of the simulation and the available data. For instance, if data on social networks is available, the assumption of homogeneous mixing can be disregarded and replaced with a model that accounts for network structure (Anderson 1991).

The stochastic SEIR model for simulating epidemic dynamics in a limited population considers the probabilities of transitions between compartments (Susceptible-Exposed-Infectious-Recovered). Due to its stochastic nature, the recovery time is not deterministic, but instead follows a probability distribution. Below are some approaches to modeling recovery time:

1. Exponential Distribution

Approach: Recovery time is often modeled using an exponential distribution due to its simplicity and its "memoryless" property (the probability of recovery within a given time interval is independent of how long the individual has been infected). The recovery rate parameter (γ) determines the average recovery time (1/γ).

Implementation: In simulations, recovery times for each infected individual can be generated using a random number generator that follows an exponential distribution. Many programming libraries (such as NumPy in Python) provide functions for this purpose (Hassan et al. 2024).

2. Gamma Distribution

Approach: The Gamma distribution offers greater flexibility compared to the exponential distribution. It has two parameters: the shape parameter (k) and the scale parameter (θ). The shape parameter affects the curve's form, while the scale parameter influences its scale. By selecting appropriate parameters, the Gamma distribution can approximate various recovery time

Implementation: Similar to the exponential distribution, random recovery times can be generated using a random number generator that follows the Gamma distribution (Zhang et al. 2020).

3. Distribusi Weibull

Approach: The Weibull distribution also provides high flexibility and is frequently used to model time-to-event data, including recovery time. It has two parameters: the shape parameter (k) and the scale parameter (λ).

Implementation: Similar to the previous distributions, random recovery times can be generated using a random number generator that follows the Weibull distribution (Ríos-Gutiérrez, Torres, and Arunachalam 2023).

4. Choice of Distribution

The choice of the appropriate distribution depends on empirical data regarding recovery time. If data is available, a goodness-of-fit test can be performed to determine the most suitable distribution. If no data is available, the exponential distribution is often the initial choice due to its simplicity. The Gamma and Weibull distributions offer greater flexibility to adapt to more complex recovery time patterns (Guan et al. 2020).

5. Integration into the SEIR Model

After selecting a recovery time distribution, you need to integrate it into your SEIR model. When individuals in the "I" (Infectious) compartment recover, their recovery time will be determined based on the chosen distribution. Once this time has elapsed, they will transition to the "R" (Recovered) compartment.

Remember to adjust the distribution parameters (γ, k, θ, λ) based on relevant epidemiological data or reasonable assumptions. Monte Carlo simulations can be employed to run the simulation multiple times, providing a statistical overview of the epidemic dynamics (Bellomo, Burini, and Outada 2022).

Case Study

In the year 202X, a new infectious disease emerged in Alpha City, a small town with a population of approximately 10,000 people. The disease exhibits a transmission pattern similar to influenza, with an incubation period before an individual becomes contagious. To design an effective mitigation strategy, the city government needs to understand the disease's transmission dynamics. However, due to the small population size, random variations in disease spread become a significant factor that must be considered. To address this, the Stochastic SEIR Model is utilized to simulate the epidemic dynamics. This model considers four population compartments:

1. S (Susceptible): Individuals who are vulnerable and have not yet been exposed to the disease.
2. E (Exposed): Individuals who have been exposed to the disease but are not yet infectious.
3. I (Infectious): Individuals who are infectious and capable of transmitting the disease.
4. R (Recovered): Individuals who have recovered or died and are no longer susceptible to infection.

Table 1. Simulation Parameters

Parameter	Description	Value
Population (N)	Initial Population Conditions	10,000
Beta (β)	Transmission Rate	0.3
Sigma (σ)	Rate of Transition from E (Exposed) to I (Infectious)	0.2
Gamma (γ)	Recovery Rate from I (Infected) to R (Recovered)	0.1
Timesteps	Number of Simulation Days (Timesteps)	100

Table 2. Initial Population Conditions

Category	Description	Value
S (Susceptible)	Susceptible Individuals	9,995
E (Exposed)	Exposed Individuals	0
I (Infected)	Infected Individuals	5
R (Recovered)	Recovered Individuals	0

Simulation Results:

Table 3. Simulation Results

Day	Susceptible	Exposed	Infected	Recovered
0	9995	0	5	0
1	9992	3	4	1
2	9991	2	5	2
3	9991	2	3	4
4	9991	2	3	4

This table shows the number of individuals in each compartment (Susceptible, Exposed, Infected, and Recovered) for each day of the simulation. Over time, the number of individuals in each compartment changes according to the dynamics of disease transmission, with individuals moving from one compartment to another. These changes are influenced by factors such as the disease transmission rate, the rate of transition from exposed to infected, and the recovery rate of infected individuals. Thus, this table illustrates how the disease spreads through the population and how the number of susceptible, exposed, infected, and recovered individuals fluctuates over the course of the simulation.

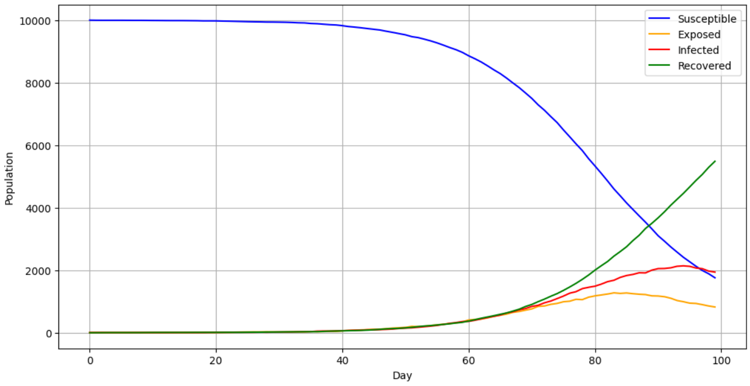

Figure 1. SEIR Stochastic Model Simulation

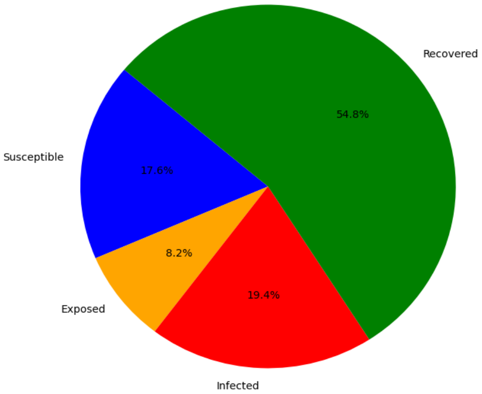

Figure 2. Population Distribution on Day 99

The image shows the simulation of the SEIR model, which stands for Susceptible, Exposed, Infected, Recovered, which is used to model the spread of infectious diseases.

Explanation:

1) Susceptible (Blue). This line represents the number of individuals who are susceptible to the disease. It starts at the highest point and gradually decreases as individuals get exposed and infected.
2) Exposed (Orange).This line represents the number of individuals who have been exposed to the disease but are not yet infectious. This number increases as susceptible individuals get infected and then plateaus and decreases as they become infected.
3) Infected (Red). This line represents the number of individuals who are actively infected with the disease. It starts low, peaks, and then decreases as individuals recover.
4) Recovered (Green). This line represents the number of individuals who have recovered from the disease. This number starts low, increases gradually, and eventually plateaus as most individuals recover.

5. CONCLUSION

The stochastic SEIR model provides a comprehensive framework for simulating the dynamics of infectious disease spread, particularly in limited populations. By accounting for the inherent randomness in disease transmission and recovery processes, the model addresses the limitations of deterministic approaches and offers a more realistic representation of epidemic dynamics. From the case study of a new disease outbreak in Alpha City, the simulation results demonstrate the importance of considering variability in small populations. Key insights include:

1. The significant role of stochastic variability in shaping disease spread, particularly in small or isolated populations.
2. The dynamic transitions between population compartments (Susceptible, Exposed, Infected, and Recovered) as influenced by epidemiological parameters such as transmission rate (\(\beta \)), transition rate (\(\sigma \)), and recovery rate (\(\gamma \)).
3. The ability of the model to predict epidemic peaks, duration, and the impact of interventions, providing a statistical basis for evaluating public health strategies.

The simulation highlights the value of integrating probabilistic processes into epidemiological modeling, as it allows for more accurate predictions and better-informed decision-making. This research underlines the applicability of the stochastic SEIR model as a powerful tool for policymakers in designing data-driven and adaptive public health policies, such as vaccination campaigns, social distancing measures, and treatment strategies. Future studies can build on this work by incorporating more complex factors such as migration, heterogeneous mixing patterns, and temporary immunity, thereby enhancing the model's relevance to real-world scenarios.

REFERENCES

Afriansyah, D., Dilla, H., Sumarno, H., & Mangku, I. W. (2023). Model stokastik epidemik SIRS insiden tak linear dengan vaksinasi. *MILANG Journal of Mathematics and Its Applications*, *19*(1), 11–22. https://doi.org/10.29244/milang.19.1.11-22

Aidid, M. A., Kasim, M., & Tiro, M. (2020). Analisis model epidemi stokastik SEIR pada penyakit tuberculosis di Kota Makassar dengan ABSEIR. *Prosiding Seminar Nasional Venue Artikulasi-Riset, Inovasi, Resonansi-Teori, dan Aplikasi Statistika (VARIANSI)*, *2*(2), 160–170.

Anderson, R. M. (1991). *Infectious diseases of humans: Dynamics and control*. Oxford University Press.

Aziezah, N., Sumarno, H., & Jaharuddin, J. (2024). Model stokastik pada penyebaran penyakit tuberkulosis. *Jurnal Derivat: Jurnal Matematika dan Pendidikan Matematika, 11*(2), 72–80. https://doi.org/10.31316/jderivat.v10i2.5573

Bellomo, N., Burini, D., & Outada, N. (2022). Multiscale models of COVID-19 with mutations and variants. *Networks and Heterogeneous Media, 17*(3), 293–310. https://doi.org/10.3934/nhm.2022008

Brauer, F., Van den Driessche, P., & Wu, J. (2008). *Mathematical epidemiology* (Vol. 1).

Cocomello, J., & Ramanan, K. (2023). Exact description of limiting SIR and SEIR dynamics on locally tree-like graphs. *Unpublished manuscript*, 1–45.

Engbert, R., Rabe, M. M., Kliegl, R., & Reich, S. (2021). Sequential data assimilation of the stochastic SEIR epidemic model for regional COVID-19 dynamics. *Bulletin of Mathematical Biology, 83*(1), 1–16. https://doi.org/10.1007/s11538-020-00834-8

Greenhalgh, T. (2021). Miasmas, mental models and preventive public health: Some philosophical reflections on science in the COVID-19 pandemic. *Interface Focus, 11*(6). https://doi.org/10.1098/rsfs.2021.0017

Guan, J., Wei, Y., Zhao, Y., & Chen, F. (2020). Modeling the transmission dynamics of COVID-19 epidemic: A systematic review. *Journal of Biomedical Research, 34*(6), 422–430. https://doi.org/10.7555/JBR.34.20200119

Halloran, M. E., Longini, I. M., & Struchiner, C. J. (2010). Binomial and stochastic transmission models. In *Design and analysis of vaccine studies* (pp. 63–84).

Hassan, M. H., El-Azab, T., Alnemer, G., & Sohaly, M. A. (2024). Analysis time-delayed SEIR model with survival rate for COVID-19 stability and disease control. *Unpublished manuscript*, 1–16.

Hernández, P., Pena, C., Ramos, A., & Gómez-Cadenas, J. J. (2020). A simple formulation of non-Markovian SEIR. *Unpublished manuscript*, 1–21.

Khaerunnisa, N. A., Nasution, Y. N., & Huda, M. N. (2022). Analisis kestabilan model epidemik SEI pada penyebaran penyakit tuberkulosis. *BASIS Jurnal Ilmiah Matematika, 1*(1), 16–29.

Lee, G., Choi, W., Jo, H., Park, W., & Kim, J. (2020). Analysis of motor control strategy for frontal and sagittal planes of circular tracking movements using visual feedback noise from velocity change and depth information. *PLoS ONE, 15*(11), 1–22. https://doi.org/10.1371/journal.pone.0241138

Nisa, K., Rahman, H., & Kusumastuti, A. (2022). Model epidemi suspected exposed infected recovered (SEIR) pada penyebaran COVID-19 orde-fraksional. *Jurnal Riset Mahasiswa Matematika, 1*(3), 156–164. https://doi.org/10.18860/jrmm.v1i3.14440

Ríos-Gutiérrez, A., Torres, S., & Arunachalam, V. (2023). An updated estimation approach for SEIR models with stochastic perturbations: Application to COVID-19 data in Bogotá. *PLoS ONE, 18*(8), 1–30. https://doi.org/10.1371/journal.pone.0285624

Rohimasanti, W., Respatiwulan, & Pratiwi, H. (2021). Model epidemi stokastik SIR rantai binomial. *Seminar Nasional Official Statistics, 2020*(1), 1239–1246. https://doi.org/10.34123/semnasoffstat.v2020i1.674

Siettos, C. I., & Russo, L. (2013). Mathematical modeling of infectious disease dynamics. *Virulence, 4*(4), 295–306.

Taghizadeh, E., & Mohammad-Djafari, A. (2022). SEIR modeling, simulation, parameter estimation, and their application for COVID-19 epidemic prediction. *Physical Sciences Forum, 18*. https://doi.org/10.3390/psf2022005018

Wicaksono, D., Respatiwulan, & Susanti, Y. (2019). Model discrete time Markov chain (DTMC) susceptible infected recovered (SIR) pada pola penyebaran penyakit cacar air. *Prosiding Seminar Nasional Sains & Entrepreneurship VI, 1*(1), 1–8.

Zhang, Z., Zeb, A., Hussain, S., & Alzahrani, E. (2020). Dynamics of COVID-19 mathematical model with stochastic perturbation. *Advances in Difference Equations, 2020*(1), 1–12. https://doi.org/10.1186/s13662-020-02909-1

Zhao, Y., Wang, H., & Wang, D. (2024). The dynamic behavior of a stochastic SEIRM model of COVID-19 with standard incidence rate. *Mathematics, 12*(19). https://doi.org/10.3390/math12192966