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Enhancing Tuberculosis Modeling: The True Positive Vaccinated Approach Utilizing a Specialized Runge-Kutta Method

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Abstract

The paper presents the True Susceptible-Vaccinated-Infected-Recovered (SVIR) model for TB control, utilizing a novel methodology that incorporates the 6th Order Runge-Kutta method for precise and effective simulation. The approach focuses on four primary areas: true positive susceptible, true positive vaccination, true positive infected, and true positive recovered. The model's true positive susceptible component identifies individuals at risk who have not yet contracted an infection, enabling targeted preventative treatments. Herd immunity is bolstered by the genuine positive vaccination element, ensuring that effectively immunized individuals are accurately represented in the model. The component that is truly positive for TB accurately tracks the disease's spread, providing crucial information for containment strategies. The truly positive recovered component monitors individuals who have overcome the illness, offering valuable insights into recovery patterns.

Keywords: True positive susceptible (TPS), True positive vaccinated (TPV), True positive infected (TPI), True positive Recovered (TPR), Runge Kutta 6th order, SVIR model.

1. Introduction

According to the World Health Organization (WHO), 95% of TB infections and 98% of TB fatalities occur in underdeveloped countries. In 2009, there were 9 million new cases of tuberculosis (TB) and 3 million TB-related deaths globally. Without proper treatment and management, TB is projected to claim the lives of 35 million individuals over a 20-year period [3].

Recognizing the problem, the WHO declared TB a global emergency in 1993 [12]. Over the past decade, tuberculosis (TB) has caused more deaths than any other microbe, averaging over 1.65 million fatalities annually between 2010 and 2019. South Sulawesi Health Ministry's data revealed 8,939 major cases of TB in 2011, an increase from 7,783 cases the previous year. Notably, Takalar Regency saw the highest growth in cases (almost 109%), followed by Pare-Pare (79%), Pinrang (75%), Makassar (70%), with Luwu (33%) and Jeneponto (36%) at the lower end. Multiple factors contribute to the high number of patients, including poor home environments. The disease also spreads easily due to the lack of lighting in homes, with ten people at risk of contracting TB from a single patient. Risky behaviors contribute significantly, especially for those with HIV/AIDS, with an annual harmful behavior contribution of 5–10%, and the prevalence of food malls exacerbating the situation.

Various researchers have constructed models of infectious diseases. For instance, a TB-transmission model was conducted, albeit without seeking the model's numerical solution. Instead, the perturbed ascetic method was employed to find a numerical solution, omitting the use of Runge-Kutta. Therefore, this research aims to establish the numerical solution [3, 12, 14, 19-20, 23-26]. Mathematical modeling provides valuable insights into epidemic dynamics and aids in their control. Interest in studying such models has increased since the 20th century. The mathematical modeling of infectious diseases has evolved significantly.

The initial analysis of mathematical modeling for epidemic spread dates back to 1766 when Bernoulli proposed the idea of illness. Kermack and McKendrick suggested a deterministic model in 1927 known as the Susceptible-Infected-Recovered (SIR) model, although it lacks additional

compartments and control techniques such as age and sex effects, vaccination, therapy, isolation, and quarantine. Consequently, numerous researchers have focused on developing more accurate models [11–28].

2. Mathematical Model

The transmission of infectious diseases is quantitatively modeled using the compartmental SVIR model in epidemiology. This model creates four compartments within the population: Susceptible (S), Vaccinated (V), Infectious (I), and Recovered (R).

The equations presented depict a variation of the SIR (Susceptible, Infected, and Recovered) model in epidemiology that accounts for vaccination. Here is the breakdown of what each parameter represents:

TP S: Represents susceptible individuals susceptible to contracting the disease.

TP I: Represents infected individuals who have contracted the disease and have the potential to spread it.

TPR: Signifies recovered individuals who have recuperated from the disease and gained immunity, or have deceased.

TPV: Signifies vaccinated individuals who have developed immunity against the disease.

N: Total population, where N = S + I + R + V.

β: The transmission rate of the disease, indicating how easily the disease spreads from infected individuals to susceptible ones.

γ: The recovery rate, determining how swiftly infected individuals recuperate and transition to the recovered class.

μ: The natural death/birth rate, signifying the rate at which individuals perish (and are replenished by births) in the population.

ρ: The vaccination rate, indicating the speed at which susceptible individuals are vaccinated and move into the vaccinated class.

The equations themselves illustrate the movement of individuals between these compartments (Susceptible, Vaccinated, Infected, and Recovered) over time.

$$\frac{\mathrm{dTPS}}{\mathrm{dt}} = \frac{(\mathrm{TPS})(\mathrm{TPI})}{N} - \mathrm{P}(\mathrm{TPS}) + \mu(\mathrm{TPV} + \mathrm{TPR}) \quad (1)$$

$$\frac{\mathrm{dTPV}}{\mathrm{dt}} = \rho * \mathrm{TPS} - \mu * \mathrm{TPV} \quad (2)$$

$$\frac{\mathrm{dTPI}}{\mathrm{dt}} = \frac{\beta(\mathrm{TPS})(\mathrm{TPI})}{N} - \gamma * \mathrm{TPI} \quad (3)$$

$$\frac{\mathrm{dTPR}}{\mathrm{dt}} = \gamma * \mathrm{TPR} - \mu * \mathrm{TPR} \quad (4)$$

The initial conditions involved

(0)≥TPS_0≥0, T(0)≥TPV_0≥0, TPI(0)≥TPI_0≥0, (0)≥TPR_0≥0

2.1 Stability Analysis

The Jacobian matrix are used to find the stability analysis

$$\begin{bmatrix} -\frac{\beta TPI}{N} - \mu - \rho & 0 & -\frac{TPS\beta}{N} & 0 \\ \rho & -\mu & 0 & 0 \\ \frac{TPI\beta}{N} & 0 & -\gamma - \mu + \frac{TPS\beta}{N} & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix}$$

The characteristic equation coefficients are

[1, $\mu+\gamma+\beta$, $\beta*\gamma+\beta*\mu+\rho-N*\mu$, $N*\mu*\gamma-\gamma-\beta*\rho$, −1]

The values are λ_1=−2, λ_2=−2, λ_3=−1

Therefore, the system is stable.

2.2 The Parameters and initial conditions of the model

The values are obtained from the reference [10, 23]

N = 8034776 (Total number of population),

ρ=3.267e^{-3}(infection Rate)

γ =3.5e^{-4}(Recovery rate)

σ=3.1e^{-3}(natural mortality rate) t max = 200 dt = 0.1

N represents the total population, which is 8,034,776.

ρ is the infection rate, set at3.267e^{-3}

γ denotes the recovery rate and is given as3.5e^{-4}.

σ* is the natural mortality rate, set at3.1e^{-3}.

t_max is the maximum time for the model, set at100,200,300,400.

dt is the time step, set at

0.1,0.2,0.3,0.4,0.5,0.6,0.7.

TPS_0 represents the initial susceptible population, set at 15,073.

TPV_0 denotes the initial vaccinated population, established as 6,000.

TPI_0 indicates the initial infected population, stated as 7,087.

TPR_0 represents the initial recovered population, totaling 3,771.

These parameters and initial conditions serve as the basis for calculating the true positive values for each category: susceptible (TPS), vaccinated (TPV), infected (TPI), and recovered (TPR).

These true positive values offer an accurate representation of each category's status concerning the total population (N) at any given time step (dt) [10].

3. Methodology

Here, we are employing the 6th-order Runge-Kutta method with 7 stages. This method is utilized for computing the aforementioned model, utilizing the Runge-Kutta technique for calculations.

K_1 □□*f*(*yn*) □□□*yn*

K_2 □□*f*(*yn*□*h*/3*K*1) □□□*yn*(1□*h*□/ 3)

K_3 □□*f*(*yn*□ 2*h*/3K_2) □□□*yn* (1□ 2*h*□ / 3(1□*h*□/ 3))

K_4 □□*f*(y_n□*h*/12K_1□*h*/3K_2□*h*/12K_3)

□□□□□□□y_n(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3)))

K_5

□□*f*(y_n□25*h*/48K_1□55*h*/24K_2□35*h*/48K_3□15*h*/8K_4)

□□□□□□□□y_n(1□25*h*□/48□55*h*□/24(1□*h*□/3)□35*h*□/48(1□2*h*□/3(1□*h*□/3))□15*h*□/8(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3))))

K_6

□□*f*(y_n□3*h*/20K_1□11*h*/20K_2□*h*/8K_3□*h*/2K_4□*h*/10K_5)

□□□□□□□□□y_n(1□3*h*□/20□11*h*□/20(1□*h*□/3)□*h*□/8(1□2*h*□/3(1□*h*□/3))□*h*□/2(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3)))□□*h*/10(1□25*h*□/48□55*h*□/24(1□*h*□/3)□35*h*□/48(1□2*h*□/3(1□*h*□/3))□15*h*□/8(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3)))))

K_7

□□*f*(y_n□261*h*/260K_1□33*h*/13K_2□43*h*/156K_3□118*h*/39K_4□32*h*/195K_5□80*h*/39K_6)

□□□□*y*$_n$(1□261*h*□/260□33*h*□/13(1□*h*□/3)□43*h*□/15(1□2*h*□/3(1□*h*□/3))-
118*h*□/39(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3)))□32□*h*/195(1□25*h*□/48□55*h*□/24(1□*h*□/3)□□□□□35*h*□/48(1□2*h*□/3(1□*h*□/3))□15*h*□/8(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3))))□80*h*□/391□3*h*□/20□11*h*□/20(1□*h*□/3)□*h*□/8(1□2*h*□/3(1□*h*□/3))□*h*□/2(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3)))□□*h*/10(1□25*h*□/48□55*h*□/24(1□*h*□/3)□35*h*□/48(1□□2*h*□/3(1□*h*□/3))□15*h*□/8(1□*h*□/12□*h*□/3(1□*h*□/3)□*h*□/12(1□2*h*□/3(1□*h*□/3))))))

Computing using Python 3.8.16 version,weget

T	dt	TPS	TPV	TPI	TPR
100	0.1	892.0622	23091.88	4457.969	402.0853
100	0.2	892.1251	23093.54	4456.398	401.9404
100	0.3	892.2131	23095.85	4454.201	401.7376
100	0.4	892.4504	23102.08	4448.276	401.1927
100	0.5	893.2079	23121.97	4429.364	399.4542
100	0.6	-479786	449457.6	59116.13	56.4787
100	0.7	22373986	-3295858	-1.9E+07	17517.43
200	0.1	884.3652	22889.57	4650.295	419.7694
200	0.2	884.4156	22890.9	4649.034	419.6533
200	0.3	884.4934	22892.94	4647.089	419.4742

200	0.5	885.2947	22914.02	4627.054	417.6299
200	0.4	884.6787	22897.82	4642.455	419.0477
200	0.6	1.16E+08	7405887	-1.2E+08	-38815.5
300	0.1	878.1672	22726.41	4805.363	434.0553
300	0.2	878.2069	22727.46	4804.371	433.9638
300	0.3	878.2573	22728.79	4803.109	433.8475
300	0.4	878.4157	22732.96	4799.144	433.482
300	0.5	878.9073	22745.91	4786.838	432.3477
300	0.6	1.16E+08	7405887	-1.2E+08	-38815.5
400	0.1	873.2577	22597.02	4928.323	445.3967
400	0.2	880.6935	22792.94	4742.136	428.2281
400	0.3	885.7029	22924.76	4616.848	416.6905
400	0.4	873.4516	22602.14	4923.465	444.9484
400	0.5	873.8381	22612.33	4913.782	444.0548
400	0.6	1.16E+08	7405887	-1.2E+08	-38815.5

Table1: TPS,TPV,TPI,TPR values for tuberculosis using Runge Kutta sixth order method

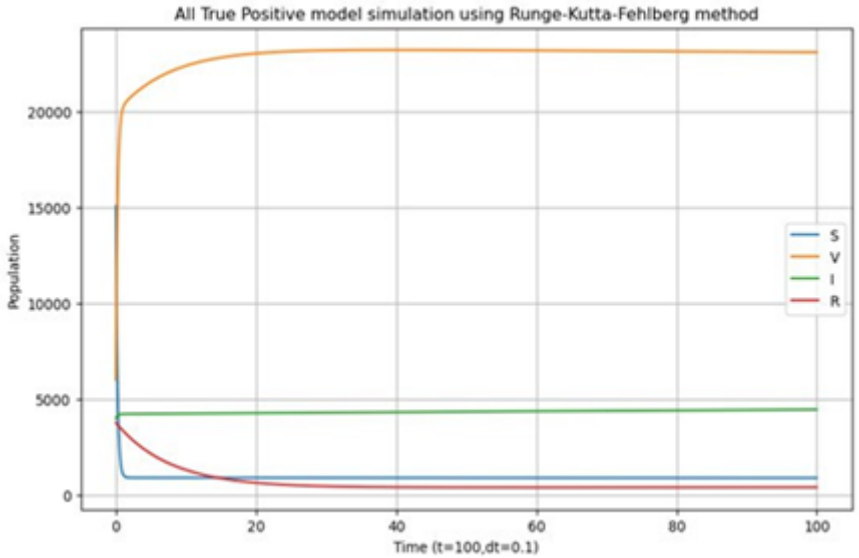

Figure 1: All True Positive Value t = 100, dt = 0.1

The immunization starts at a high point and gradually declines. In an epidemiological model, this trend could symbolize a susceptible population that diminishes as individuals either become immune or get infected. As time progresses, the numbers of the Recovered and the Infected elevate from their initial low points. In the same scenario, these could represent an immune or recovered population (R) and an infected population (I). The count of affected individuals increases as more people acquire the disease, and then diminishes as more individuals recover or succumb. As individuals recover from the virus, the population of those who have recovered gradually grows.

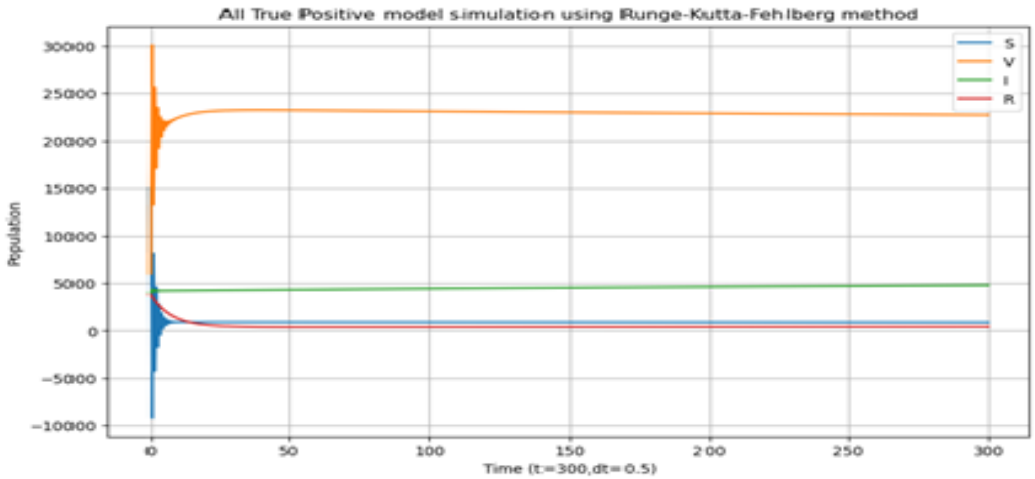

Figure 2: All True Positive Value t = 300, dt = 0.5

The vaccination rate begins at a high level and gradually decreases. In an epidemiological model, this trend might represent a susceptible population that diminishes as individuals either become immune or get infected.

Starting with low figures, the count of infected and susceptible individuals gradually rises. In the same scenario, these could be interpreted as an immune or recovered population (R) and an infected population (I). The number of affected individuals increases as more people contract the disease, then decreases as more individuals recover or pass away. As individuals recover from the virus, the count of the recovered population grows.

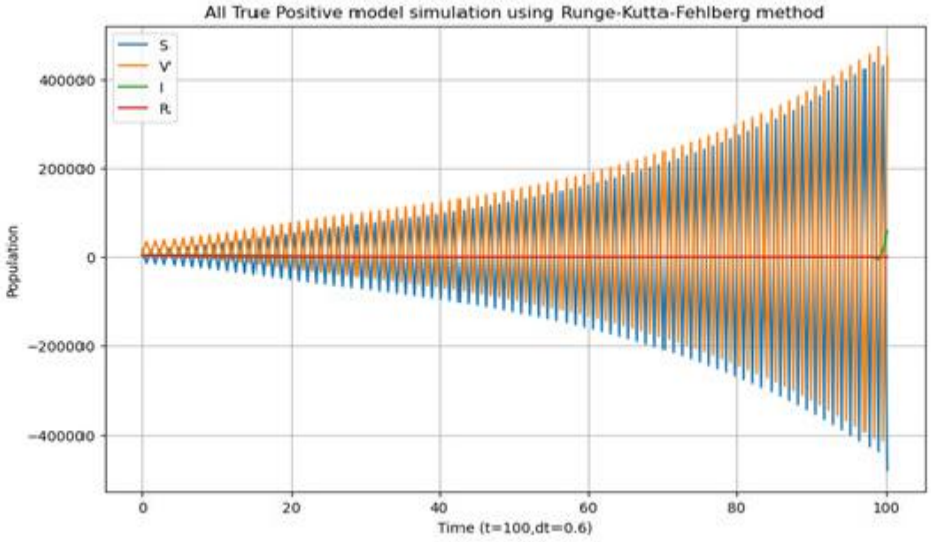

Figure3: All True Positive Value t = 100, dt = 0.6

Over time, the value of the susceptible group gradually decreases from its initial high level. In an epidemiological model, this decline could represent a susceptible population that diminishes as more people become infected.

As time progresses, the number of Vaccinated and Infected individuals gradually increases from their initial low levels. In the same context, these numbers might signify an immune population and an infected population (I). The count of affected individuals rises as more people contract the disease, then diminishes as more people recover or pass away. As individuals recover from the virus, the population of those who have recovered grows.

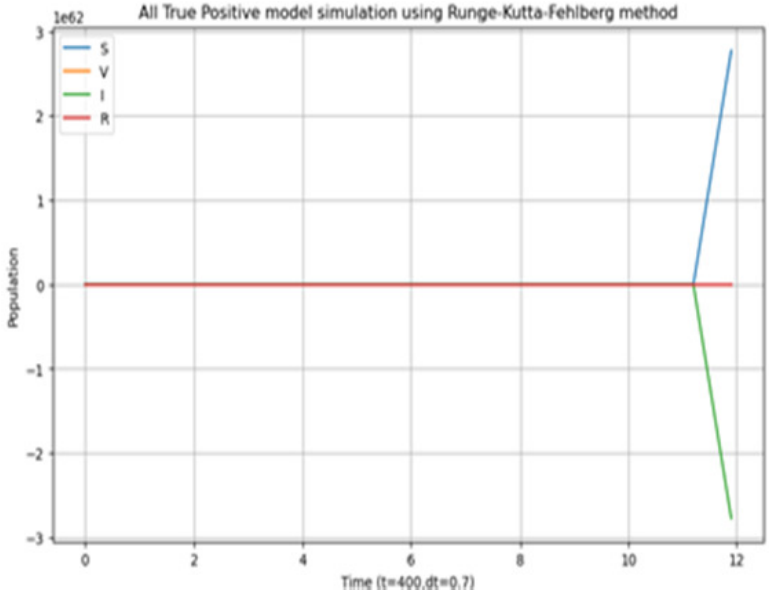

Figure 4: All True Positive Value t = 400, dt = 0.6

Starting around 1.5 e^{62}, the susceptible population swiftly climbs to approximately 3 e^{62} at roughly 12 on the x-axis. This may indicate a rapid expansion of the population.

On the x-axis, the infection rate initiates at about -2 $e^{62}$and quickly plummets to roughly -3e^{62} around 12. This could indicate a sharp decline in the population.

The Recovered count begins at approximately 0 and remains stable until around 10 on the x-axis. Subsequently, it rapidly accelerates to approximately 2 e^{62} at about 12 on the x-axis. This pattern might be an example of a population that stabilizes for a while before experiencing rapid growth.

4. Numerical Results and Discussion

The results presented in Tables 1 display a treatment administered over a four-week period, accounting for 100 hours per week. In this context, 't' represents specific time points, namely t = 100, 200, 300, and 400, corresponding to the consecutive weeks from the first to the fourth week of treatment, respectively. The time step (dt) used in this study ranges from 0.1 to 0.7 days, each value representing a day within the seven-day period of a week. The model employed for this analysis is the All Positive Vaccinated Model, utilizing the 6th order Runge-Kutta method for computations.

Our findings indicate that when t = 100, the treatment concludes after 7 days (dt = 0.7), revealing the number of recovered individuals. Similarly, when t = 200 (end of the second week), the treatment also concludes after 7 days (dt = 0.7). Finally, for t = 300 and 400, the treatment concludes in 6 days (dt = 0.6). Notably, we observed an increase in the number of recoveries by the sixth day itself during these weeks.

5. Conclusion

The 'All True Positive Vaccinated Model' for tuberculosis, using the 6th order Runge-Kutta method, has consistently demonstrated accurate predictions for post-vaccination recovery times. Our results consistently indicate a recovery period of 7 days across multiple time intervals (t = 100, 200, 300, and 400). This reliability in predictions emphasizes the potential of our model as a robust tool for understanding the dynamics of tuberculosis recovery after vaccination. Furthermore, these findings could be pivotal in shaping future strategies for disease control and prevention.

References

[1] Allen.L.J, Jones.M.A, and Martin.C.F, "A discrete-time model with vaccination for a measles epidemic," Math. Biosci 105 (1) (1991), pp. 111–131.

[2] Althomsons SP, Winglee K, Heilig CM, Talarico S, Silk B, Wortham J, Hill AN, Navin

TR. "Using Machine Learning Techniques and National Tuberculosis Surveillance Data to Predict Excess Growth in Genotyped Tuberculosis Clusters." Am J Epidemiol. 2022.

[3] Bernoulli. D Essay on a New Analysis of the Mortality Caused by Smallpox and the Advantages of Inoculation to Prevent It." Mem. Math. Phys. Acad. Roy. Sci. Paris 1760.

[4] Bolker and Grenfell.B, "Space, Persistence and Dynamics of measles epidemic," Philos. Trans. R. Soc. Lond., B, Biol. Sci. 348 (1995), pp. 309–320.

[5] Burzynski J, Mangan JM, Lam CK, Macaraig M, Salerno MM, deCastro BR, Goswami ND, Lin CY, Schluger NW, Vernon A; eDOT Study Team. "In-Person vs Electronic Directly Observed Therapy for Tuberculosis Treatment Adherence: A Randomized Noninferiority Trial." JAMA Netw Open. 2022 Jan 4;5(1):e2144210.

[6] Capasso.V and Serio.G, "A generalization of the Kermack-McKendrick deterministic epidemic model," Math. Biosci 42 (1–2) (1978), pp. 43–61.

[7] d'Onofrio, "Pulse vaccination strategy in the SIR epidemic model: Global asymptotic stable eradication in the presence of vaccine failures," Math. Comput. Model. 36 (4–5) (2002), pp. 473–489.

[8] Deakin.M.A.B, "A standard form for the Kermack-McKendrick epidemic equation," Bull. Math. Biol. 37 (1975), pp. 91–95.

[9] El-Doma . M, "Stability analysis of a general age-dependent vaccination model of a vertically transmitted disease," International Centre for Theoretical Physics, Trieste (Italy), 1995.

[10] Esteva.L and Vargas.C, "Analysis of dengue disease transmission," Math. Biosci 150 (2) (1998), pp. 131–151.

[11] Greenhalgh, "Some results for an SEIR epidemic model with density dependence in the death rate," IMA J Math Appl Med Biol 9 (2) (1992), pp. 67–106.

[12] Hamer.W.H, "Epidemic disease in England," Lancet 1 (1906), pp. 733–739.

[13] Hethcote.H.W, "Qualitative analyses of communicable disease models," Math. Biosci 28 (3–4) (1976), pp. 335–356.

[14] Kermack.W.O and McKendrick.A.G, "A contribution to the mathematical theory of epidemics," Proc, R. Soc. Lond. A 115 (1927), pp. 700–721.

[15] Kryrchko.Y.N and Blyuss. K.B, "Global properties of a delayed SIR model with temporary immunity and nonlinear incidence rate," Nonlinear Anal Real World Appl 6 (3) (2005), pp. 495–507.

[16] Kuznetsov.Y.A and Piccardi.C, "Bifurcation analysis of periodic SEIR and SIR epidemic models," J. Math. Biol 32 (2) (1994), pp. 109–121.

[17] Li.M.Y and Muldowney.J.S, "Global stability for the SEIR model in epidemiology," Math. Biosci 125 (2) (1995), pp. 155–164.

[18] Liddo .A.D, "A S-I-R vector disease model with delay," Mathematical Modelling 7 (5–8) (1986), pp. 793–802.

[19] Lotka.A.J, "Elements of physical biology," Williams & Wilkens, Baltimore (1925). Reprinted as "Elements of Mathematical Biology," Dower, New York, 1956.

[20] Lotka.A.J, "Martini's equation for the epidemiology of immunizing diseases," Nature 111 (2793) (1923), pp. 633–634.

[21] Peter J. Dodd, Debebe Shaweno, Chu-Chang Ku, Philippe Glaziou, Carel Pretorius, Richard J. Hayes, Peter MacPherson, Ted Cohen & Helen Ayles, "Transmission modeling to infer tuberculosis incidence prevalence and mortality in settings with generalized HIV epidemics," Nature Communications, vol. 14, article number: 1639.

[22] Ramadhan, N. R., Minggi.I, and S. Side. "The accuracy comparison of the RK-4 and RK-5 methods of the SEIR model for tuberculosis cases in South Sulawesi." Journal of Physics: Conference Series, vol. 1918, no. 4, IOP Publishing, 2021.

[23] Ross.R and Hudson.H.P, "An application of the theory of probabilities to the study of a priori pathometry: II," Proc. R. Soc. London A 93 (1917), pp. 212–224.

[24] Ross.R and Hudson.H.P, "An application of the theory of probabilities to the study of a priori pathometry: III," Proc. R. Soc. London A 93 (1917), pp. 225–240.

[25] Ross.R, "An application of the theory of probabilities to the study of a priori pathometry: I," Proc. R. Soc. London A 92 (1916), pp. 204–230.

[26] Ross.R, "The Prevention of Malaria," 2nd ed., Murray, London, 1911.

[27] Satsuma.J, Willox.R, Ramani.A, Grammaticos.B, and Carstea. A.S, "Extending the SIR epidemic model," Phys. A 336 (3–4) (2004), pp. 369–375.

[28] Shulgin.B, Stone.L, and Agur.Z, "Pulse vaccination strategy in the SIR epidemic model," Bull. Math. Biol. 60 (6) (1998), pp. 1123–1148.

[29] Side.S, "A susceptible-infected-recovered model and simulation for transmission of tuberculosis," Adv Sci Lett 21 (2) (2015), pp. 137–139.

[30] Stone.L, Shulgin .B, and Agur.Z, "Theoretical examination of the pulse vaccination policy in the SIR epidemic model," Math. Comput. Model. 31 (4–5) (2000), pp. 207–215.

[31] Takahashi, Spreadbury.J, and Scotti.J, "Modeling the spread of tuberculosis in a closed population," Laporan Hasil Penelitian, 2010.