BIOS 26210: Lab Exercise 5

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Exercise 1

1a.

At the fixed points, $\dot{I} = \beta(N-I)I - \gamma I = 0$, we then have two fixed points $I_1^* = 0$ and $I_2^* = N - \frac{\gamma}{\beta}$.

The first fixed point $I_1^* = 0$ means that if nobody is infected by an epidemic, then it is predictable that nobody will be infected as time goes on. And the second fixed point $I_2^* = N - \frac{\gamma}{\beta}$ is equivalent to $S = \frac{\gamma}{\beta}$ and $\gamma = \beta S$, because we have $N = I + S$. It means that if the recovery rate of infected individuals (γ) is equal to the rate of infection (βS), then the number of infected individuals (I) will stay constant (at the fixed point), which makes sense apparently.

1b.

Let $f(I) = \dot{I} = \beta(N-I)I - \gamma I$, then $\frac{df(I)}{dI} = \beta(N-I) - \beta I - \gamma = \beta(N-2I) - \gamma$

At fixed point $I^* = 0$, $\frac{df(I)}{dI} = \beta N - \gamma$. Since N is a constant, if $\gamma < \beta N$, then $\frac{df(I)}{dI} > 0$, the fixed point $I^* = 0$ is **unstable**, which means that if the recovery rate is less than the infection rate, even a small number of infected individuals could lead to a wide spread of the epidemic, and if $\gamma > \beta N$, then then $\frac{df(I)}{dI} < 0$, the fixed point $I^* = 0$ is **stable**, which means that if the epidemic is quite easy to recover (the recovery rate is greater than the infection rate), just a few infected individuals would not cause a widely-spreaded epidemic and the epidemic will soon disappear.

At fixed point $I^* = N - \frac{\gamma}{\beta}$, we have:

$$\frac{df(I)}{dI} = \beta(N-2I) - \gamma = \beta(\gamma/\beta - I) - \gamma = \gamma - \beta I - \gamma = -\beta I < 0$$

So the fixed point $I^* = N - \frac{\gamma}{\beta}$ is **stable**, it means that if currently the number of infected individual is around $(N - \frac{\gamma}{\beta})$, then in the predictable future the number of infected individual will approach $N - \frac{\gamma}{\beta}$ gradually and stay at that point.

1c.

On plotting the numerical solution as in Fig 5-1c below, we could see that when the step size Δt is large, the numerical solution oscillate and when the step size Δt is small the oscillation of the numerical solution is not observable.

The behavior of the numerical solution is consistent with the theoretically predicted behavior when the time step is small ($\Delta t = 0.1$day and $\Delta t = 1$ days). And the oscillation for the numerical solution of large time step suggests the imprecision introduced by the large time step in the numerical solution.

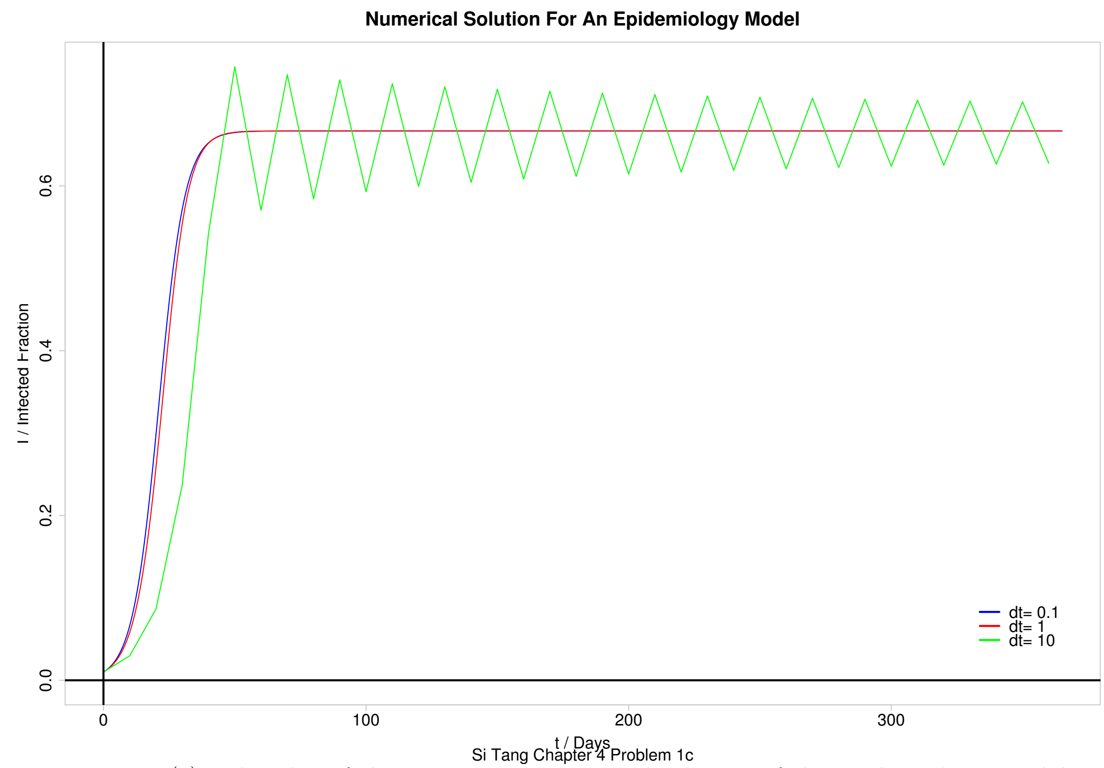

Fig. 5-1(c). The plot of the year-round numerical solution of the epidemiology model with $\beta = 0.3/\text{day}$ and $\gamma = 0.1/\text{day}$, starting at $(t_0 = 0, I_0 = 0.01)$, with three different time steps: $\Delta t = 0.1$ day, blue; $\Delta t = 1$ day, red and $\Delta t = 10$ days, green.

1d.

On plotting the numerical solution as in Fig 5-1d below, we could see that when the step size equals to 20 days, the numerical method is not stable. The numerical solution oscillate around zero, which is qualitatively different from the theoretical prediction.

When the step size is 0.1 day or 10 days, the numerical solution is stable, and when the step size is 20 days, the numerical solution is not stable.

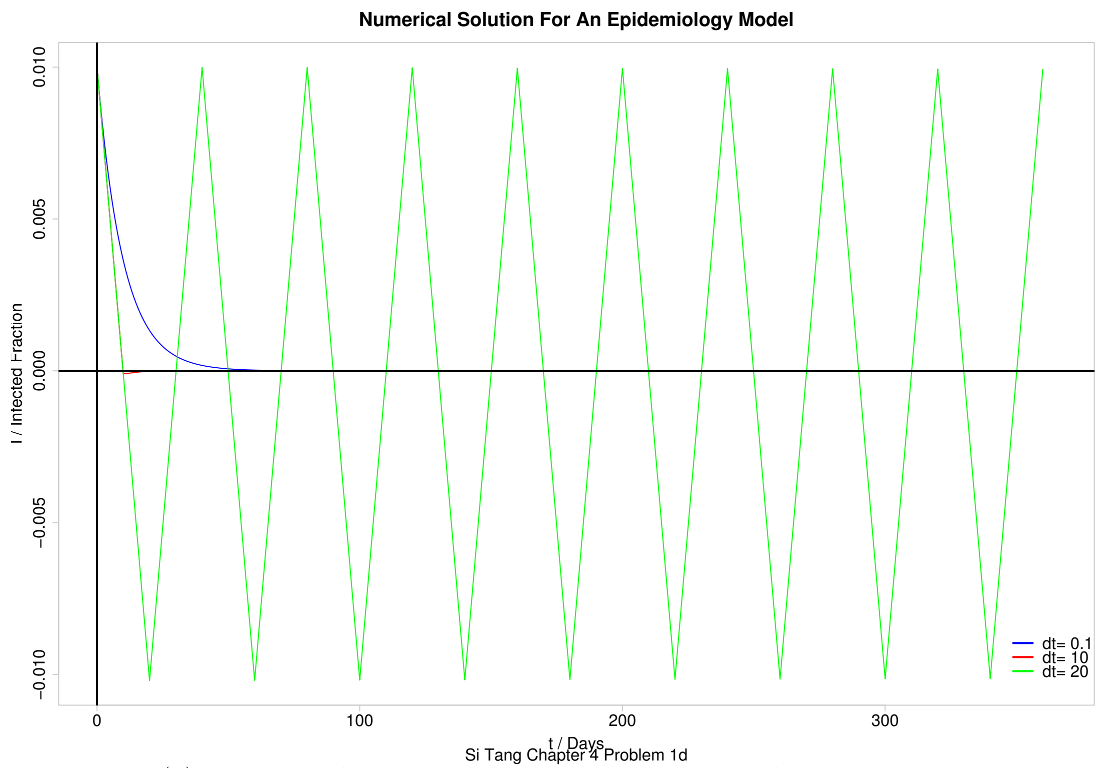

Fig. 5-1(d). The plot of the year-round numerical solution of the epidemiology model with $\beta = 0.1$/day and $\gamma = 0.2$/day, starting at $(t_0 = 0, I_0 = 0.01)$, with three different time steps: $\Delta t = 0.1$ day, blue; $\Delta t = 1$ day, red and $\Delta t = 10$ days, green.

Exercise 2

In order to generate a visually pleasant figure for the solution, I use the following values for k_+, k_- , R_0 and S in this problem.

$k_+ = 10^{-2}M^{-1}s{-}1$, $k_- = 10^{-5}s^{-1}$
$S = 10^{-2}$M, $R_0 = 0.01$M

You can change these parameters in my code if you like.

2a.

The ODE model for the concentration of the receptor molecule is :

$$\frac{dR}{dt} = \dot{R} = k_-C - k_+S \cdot R = k_-(R_0 - R) - k_+S \cdot R$$

2b.

At the fixed point, $\frac{dR}{dt} = \dot{R} = 0$, then $k_+S \cdot R = k_-(R - R_0)$ and $R = \frac{k_-R_0}{k_+S+k_-}$

Let $f(R) = \frac{dR}{dt} = \dot{R} = k_-(R_0 - R) - k_+S \cdot R$, then $\frac{df(R)}{dR} = -k_+S - k_- < 0$.
So the fixed point is stable.

2c.

$$\begin{aligned}
\frac{dR}{dt} &= k_-(R_0 - R) - k_+S \cdot R \\
\frac{dR}{dt} + (k_+S + k_-) \cdot R &= k_-R_0 \\
\frac{dR}{dt}e^{(k_+S+k_-)t} + R \cdot k_+S \cdot e^{(k_+S+k_-)t} &= k_-R_0 \cdot e^{(k_+S+k_-)t} \\
\frac{d(e^{(k_+S+k_-)\cdot t} \cdot R)}{dt} &= k_-R_0e^{(k_+S+k_-)t} \\
Re^{(k_+S+k_-)t} &= \frac{k_-R_0}{k_+S + k_-}e^{(k_+S+k_-)t} + C_0 \\
R &= \frac{k_-R_0}{k_+S + k_-} + C_0e^{-(k_+S+k_-)t}
\end{aligned}$$

Using the initial condition t=0 R=R0, then $C_0 = R_0(1 - \frac{k_-}{k_+S+k_-})$.
So the analytical solution is:

$$R = \frac{k_-R_0}{k_+S + k_-} + R_0(1 - \frac{k_-}{k_+S + k_-})e^{-(k_+S+k_-)t}$$

2d.

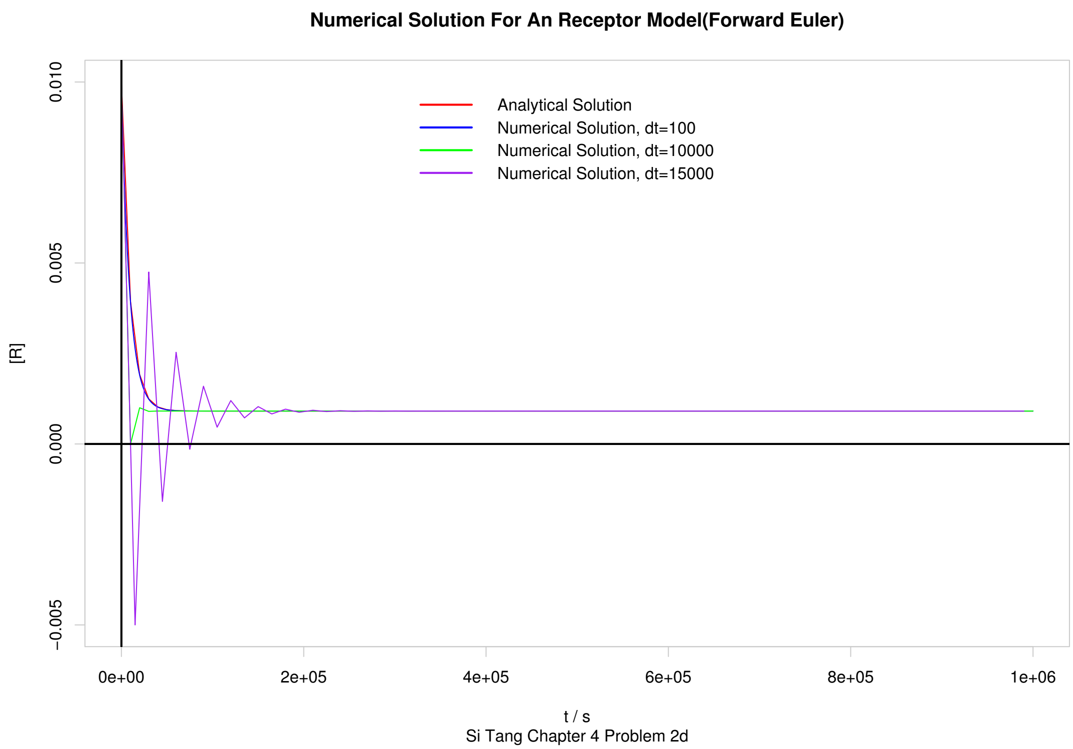

Fig. 5-2(d). The plot of the numerical solution of the receptor model with $k_+ = 10^{-2}M^{-1}s^{-1}$ and $k_- = 10^{-5}s^{-1}$ and $S = 10^{-2}$ M, starting at $(t_0 = 0, R_0 = 0.01M)$, to $t_{\max} = 10^6$s with time steps: $\Delta t = 100, 10000, 15000s$; also plot the analytical solution in red.

2e.

Plot the total error against time steps as in Fig. 5-2(e).

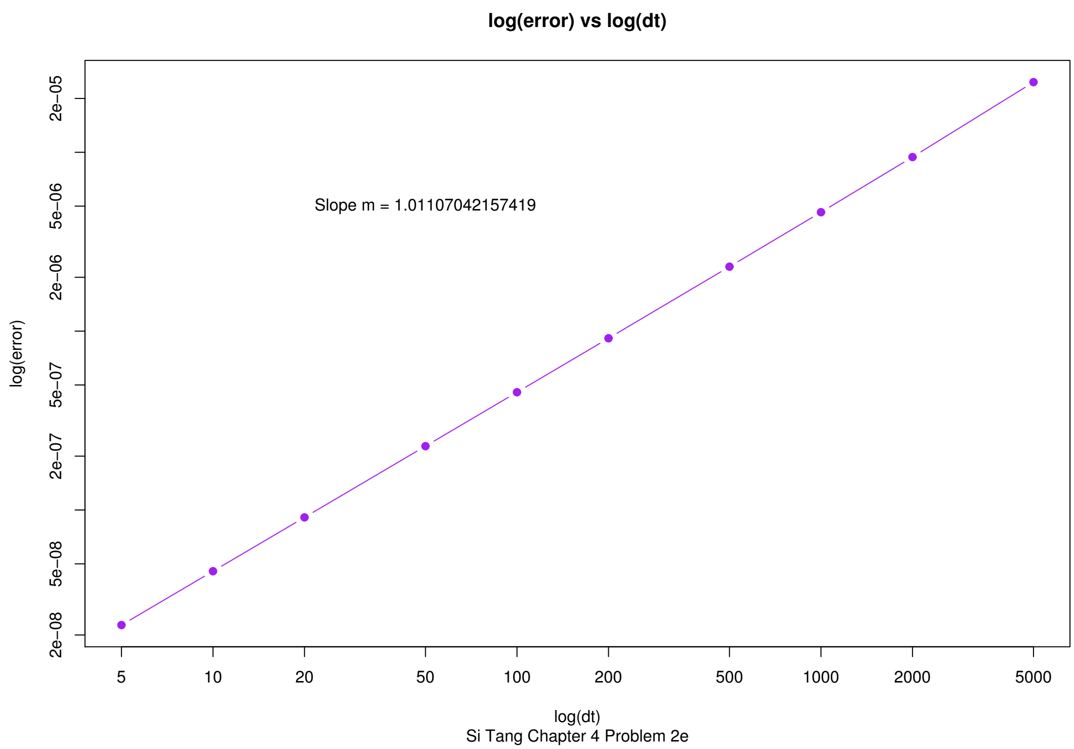

Fig. 5-2(e). The plot of the total error of the numerical solution with $k_+ = 10^{-2}M^{-1}s^{-1}$ and $k_- = 10^{-5}s^{-1}$ and $S = 10^{-2}$M, starting at $(t_0 = 0, R_0 = 0.01M)$, to $t_{\max} = 10^6$s with time steps: $\Delta t = 2, 5, 10, 20, 50, 100, 200, 500, 1000, 2000, 5000$ s

2f.

Plot the backward Euler numerical solution with different time steps as in Fig. 5-2(f).

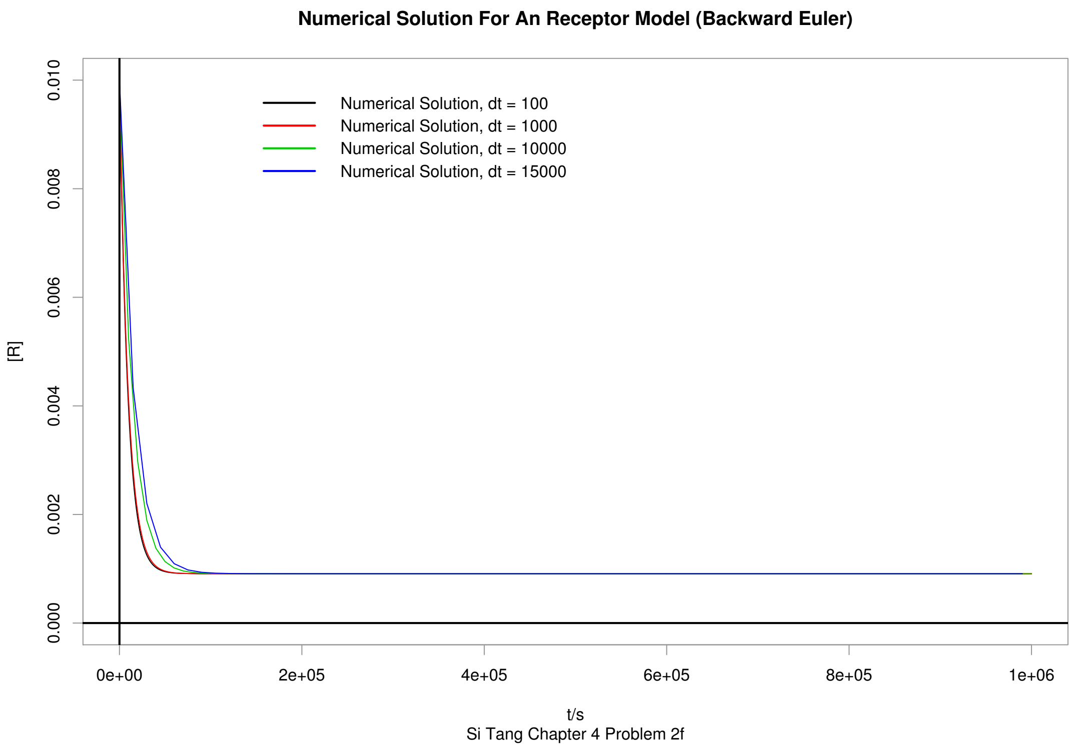

Fig. 5-2(f). The plot of the numerical solution of the receptor model with $k_+ = 10^{-2}M^{-1}s^{-1}$ and $k_- = 10^{-5}s^{-1}$ and $S = 10^{-2}$M, starting at $(t_0 = 0, R_0 = 0.01M)$, to $t_{max} = 10^6$s with time steps: $\Delta t = 100, 1000, 10000, 15000s$.