Math 4MB3 Project Notebook 2018

Sang Woo Park (The Infective Collective)

March 21, 2018 @ 11:35

Friday 9 March 2018

Group Meeting
Approximate Duration: 0.5 Hours

- Decided on a project topic. We will be studying spatial synchrony.

Wednesday 14 March 2018

Group Meeting
Approximate Duration: 1 Hour

- Discussed what papers we should read; spent most of the class time reading over papers.
- We want to come up with a reasonable model by 19 March.

Thursday 15 March 2018

Solo work *Approximate Duration: 30 minutes*

- Literature review and brainstorming.

There are number of models we can use for this study. One of the simplest model that we can use is the one used by (Grenfell et al., 1995). We can slightly generalize their model to make it more like the logistic map we studied in class. Assuming identical population size of N across patches, we can write

$$\begin{aligned}
\frac{dS_i}{dt} &= \mu(N - S_i) - \beta(t)\left(\sum_{j=1}^{n} m_{ij} I_j\right) S_i \\
\frac{dE_i}{dt} &= \beta(t)\left(\sum_{j=1}^{n} m_{ij} I_j\right) S_i - (\sigma + \mu) E_i \\
\frac{dI_i}{dt} &= \sigma E_i - (\gamma + \mu) I_i \\
\frac{dR_i}{dt} &= \gamma I_i - \mu R_i
\end{aligned}$$

On the other hand (slightly tangential but relevant to the project), we can write a discrete time model under the tSIR framework (Finkenstädt and Grenfell, 2000; Becker and Grenfell, 2017) and we might be able to apply the analytical result presented in class.

$$S_{i,t+1} = B_{i,t} + S_{i,t} - I_{i,t+1}$$
$$E[I_{i,t+1}] = \beta_{t+1} S_{i,t} \sum_{j=1}^{n} m_{ij} I_{j,t}$$

tSIR model is supposed to be a tool to estimate transmission rate over time using a GLM framework but parameter estimation becomes more difficult when we add spatial structures. Instead, we can try to use estimated transmission rates and compare how synchrony and coherence might vary. This is something I might do for my own interest when I have some extra time...

Friday 16 March 2018

Group work *Approximate Duration: 1 hour*

- Discussed different model structures
- We want to consider a discrete time model due to its simplicity
- Discussed various ways of discretizing the model

Saturday 17 March 2018

Solo work *Approximate Duration: 1.5 hours*

Consider an SIR model with spatial sturcture:

$$\frac{dS_i}{dt} = \mu(N - S_i) - \beta(t) \left(\sum_{j=1}^{n} m_{ij} I_j \right) S_i$$
$$\frac{dI_i}{dt} = \beta(t) \left(\sum_{j=1}^{n} m_{ij} I_j \right) S_i - (\gamma + \mu) I_i$$
$$\frac{dR_i}{dt} = \gamma I_i - \mu R_i$$

We want to discretize this model in a biologically sensible way. In the absence of natural birth, dynamics of the susceptible population can be described by

$$\frac{dS_i}{dt} = -\left(\beta(t) \left(\sum_{j=1}^{n} m_{ij} I_j \right) + \mu \right) S_i$$

Then, $\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)$ can be thought of as per capita "death rate". Then, it follows that

$$\begin{aligned}
\frac{dS_i}{dt} &= -\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)S_i \\
\implies \frac{1}{S_i}\frac{dS_i}{dt} &= -\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right) \\
\implies \int_t^{t+\Delta t}\frac{d\log S_i}{dt}dt &= -\int_t^{t+\Delta t}\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)dt \\
\implies \log\left(S_i(t+\Delta t)/S_i(t)\right) &= -\int_t^{t+\Delta t}\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)dt \\
\implies S_i(t+\Delta t) &= \exp\left(-\int_t^{t+\Delta t}\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)dt\right)S_i(t)
\end{aligned}$$

where

$$\exp\left(-\int_t^{t+\Delta t}\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)dt\right)$$

represents survival probability of a susceptible individual between time t and $t+\Delta t$. Assuming that Δt is sufficiently small, we have

$$-\int_t^{t+\Delta t}\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)dt \approx \left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t$$

By applying this approximation, we are essentially assuming that $I_j(t)$ does not vary much between t and $t+\Delta t$. We can do a second order approximation here to account for changes in $I_j(t)$ over Δ but we don't have to worry about that yet (He et al., 2009). Then, it follows that

$$S_i(t+\Delta t) = S_i(t) - \left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right)S_i(t)$$

It is convenient to express it this way because

$$\left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right)S_i(t)$$

represents the number of people that leave the susceptible compartment and incidence (number of people infected between time t and $t+\Delta t$) can approximated by

$$i_i(t) = \frac{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)}{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu}\left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right)S_i(t)$$

where $i_i(t)$ denotes incidence. i_i is a really terrible notation and I should come up with something better... Note that

$$\frac{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)}{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu}$$

is approximately equal to the probability that a infection occurs before a susceptible individual dies from natural mortality. Likewise, we can do similar analysis and derive survival probability of an infected individual between time t and $t+\Delta t$:

$$\exp\left(-(\gamma+\mu)\Delta t\right)$$

In this case, this is exact (not an approximation) because "death rate" does not vary over time. Hence, we have

$$I_i(t+\Delta t) = I(t) + i_i(t) - \left(1-e^{-(\gamma+\mu)\Delta t}\right) I(t)$$

we denote number of recovered individuals between t and $t+\Delta t$ by $r(t)$:

$$r_i(t) = \frac{\gamma}{\gamma+\mu}\left(1-e^{-(\gamma+\mu)\Delta t}\right) I(t)$$

Then, by similar argument

$$R_i(t+\Delta t) = R_i(t) + r_i(t) - \left(1-e^{-\mu\Delta t}\right) R_i$$

Then, the entire model is given by

$$\begin{aligned}
S_i(t+\Delta t) &= S_i(t) + b_i(t) - \left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right) S_i(t)\\
I_i(t+\Delta t) &= I(t) + i_i(t) - \left(1-e^{-(\gamma+\mu)\Delta t}\right) I(t)\\
R_i(t+\Delta t) &= R_i(t) + r_i(t) - \left(1-e^{-\mu\Delta t}\right) R_i
\end{aligned}$$

where

$$\begin{aligned}
b_i(t) &= \mu N \Delta t\\
i_i(t) &= \frac{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)}{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu}\left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right) S_i(t)\\
r_i(t) &= \frac{\gamma}{\gamma+\mu}\left(1-e^{-(\gamma+\mu)\Delta t}\right) I(t)
\end{aligned}$$

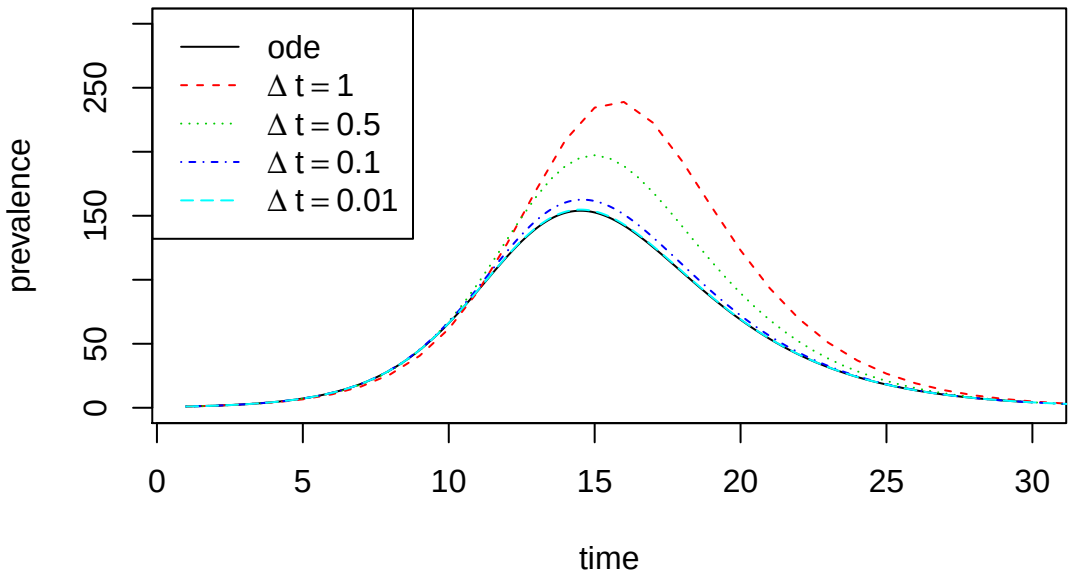
This doesn't exactly keep the population size constant and if we wanted to keep the population size constant, we would let

$$b_i(t) = \frac{\mu}{\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu}\left(1-e^{-\left(\beta(t)\left(\sum_{j=1}^{n} m_{ij}I_j\right)+\mu\right)\Delta t}\right) S_i(t) + \frac{\mu}{\gamma+\mu}\left(1-e^{-(\gamma+\mu)\Delta t}\right) I(t)$$

Since we have a nice probabilistic interpretation of the model, we can add stochasticity by adding appropriate binomial and multinomial random variables (beta binomial and dirichlet

multinomial for overdispersion in process error (Li et al., 2017) but we probably don't need to worry about this).

We can compare how different this model is from ODE through simulations. First, we can start with a simple SIR case without birth terms.



Note that our purpose is not necessarily to approximate the ode but to come up with a biologically reasonalbe discrete time model. It's worth keeping in mind that choices of Δt matters if it is too large with repsect to disease time scale but otherwise, we don't have to make it too small. We will still obtain qualitatively similar dynamics (but what happens when we include seasonal forcing?).

Monday 19 March 2018

Group Meeting
Approximate Duration: 1 Hour

- Discussed model further
- Discussed how we can implement stochastic model
- Divided up the work

Tuesday 20 March 2018

Solo work
Approximate Duration: 4 Hours

- Spent two hours trying to get an analytical handle on the model and got nowhere near.
- The following notes are my second attempt to get somewhere (hopefully).

Let's try to start with a simpler case. Hopefully, we can get more insight later on. Consider a coupled SI model. Assume that mixing matrix is give nby

$$M = \begin{bmatrix} 1-m_1 & m_2 \\ m_1 & 1-m_2 \end{bmatrix}$$

For sake of simplicity, assume $m_1 = m_2 = 1/2$. Then, it follows that

$$\begin{aligned} S_i(t+\Delta t) &= S_i(t) + \left(1 - e^{-\gamma \Delta t}\right) I_i(t) - \left(1 - e^{-\beta(t)(I_1+I_2)\Delta t/2}\right) S_i(t) \\ I_i(t+\Delta t) &= I_i(t) + \left(1 - e^{-\beta(t)(I_1+I_2)\Delta t/2}\right) S_i(t) - \left(1 - e^{-\gamma \Delta t}\right) I_i(t) \end{aligned}$$

Then, it follows that

$$\begin{aligned} S_2' - S_1' &= e^{-\beta(t)(I_1+I_2)\Delta t/2}(S_2 - S_1) + \left(1 - e^{-\gamma \Delta t}\right)(I_2 - I_1) \\ I_2' - I_1' &= e^{-\gamma \Delta t}(I_2 - I_1) + \left(1 - e^{-\beta(t)(I_1+I_2)\Delta t/2}\right)(S_2 - S_1) \end{aligned}$$

Note that

$$S_2 - S_1 = (N - I_2) - (N - I_1) = I_1 - I_2$$

Then,

$$\begin{aligned} I_2' - I_1' &= e^{-\gamma \Delta t}(I_2 - I_1) - \left(1 - e^{-\beta(t)(I_1+I_2)\Delta t/2}\right)(I_2 - I_1) \\ &= \left(e^{-\gamma \Delta t} + e^{-\beta(t)(I_1+I_2)\Delta t/2} - 1\right)(I_2 - I_1) \\ S_2' - S_1' &= e^{-\beta(t)(I_1+I_2)\Delta t/2}(S_2 - S_1) - \left(1 - e^{-\gamma \Delta t}\right)(S_2 - S_1) \\ &= \left(e^{-\gamma \Delta t} + e^{-\beta(t)(I_1+I_2)\Delta t/2} - 1\right)(S_2 - S_1) \end{aligned}$$

So it seems that

$$e^{-\gamma \Delta t} + e^{-\beta(t)(I_1+I_2)\Delta t/2} - 1$$

could be the quantity that determines synchrony and coherence. Suppose that Δt is sufficiently small. Then, it follows that

$$\begin{aligned} e^{-\gamma \Delta t} + e^{-\beta(t)(I_1+I_2)\Delta t/2} - 1 &\approx 1 - \gamma \Delta t + 1 - \beta(t)(I_1 + I_2)\Delta t/2 - 1 \\ &= 1 - \gamma \Delta t - \beta(t)(I_1 + I_2)\Delta t/2 \end{aligned}$$

It seems to me that this quantity would be less than 1 but greater than 0 if Δt is small? Then, I think we obtain coherence.

It might be easier to work with a continuous time model for analytical results. Consider the following coupled SIS model:

$$\begin{aligned} \frac{dS_1}{dt} &= \gamma I_1 - \beta(t)\left((1-m_1)I_1 + m_2 I_2\right) S_1 \\ \frac{dS_2}{dt} &= \gamma I_2 - \beta(t)\left(m_1 I_1 + (1-m_2) I_2\right) S_2 \\ \frac{dI_1}{dt} &= \beta(t)\left((1-m_1)I_1 + m_2 I_2\right) S_1 - \gamma I_1 \\ \frac{dI_2}{dt} &= \beta(t)\left(m_1 I_1 + (1-m_2) I_2\right) S_2 - \gamma I_2 \end{aligned}$$

Then, necessary condition is that

$$\frac{dI_1}{dt} - \frac{dI_2}{dt} \to 0.$$

Note that

$$\begin{aligned}
\frac{dI_1}{dt} - \frac{dI_2}{dt} &= \beta(t)\left((1-m_1)I_1 + m_2 I_2\right) S_1 - \beta(t)\left(m_1 I_1 + (1-m_2)I_2\right) S_2 - \gamma(I_1 - I_2) \\
&= \beta(t)\left(\left((1-m_1)I_1 + m_2 I_2\right)(1-I_1) - \left(m_1 I_1 + (1-m_2)I_2\right)(1-I_2)\right) - \gamma(I_1 - I_2) \\
&= \beta(t)((I_1 - m_1 I_1 + m_2 I_2)(1-I_1) - (m_1 I_1 + I_2 - m_2 I_2)(1-I_2)) - \gamma(I_1 - I_2) \\
&= \beta(t)((1-2m_1)I_1 + (m_1 - 1)I_1^2 - (1-2m_2)I_2 - (m_2 - 1)I_2^2) - \gamma(I_1 - I_2)
\end{aligned}$$

Again, when $m_1 = m_2 = 1/2$, we have

$$\begin{aligned}
&\beta(t)((1-2m_1)I_1 + (m_1 - 1)I_1^2 - (1-2m_2)I_2 - (m_2 - 1)I_2^2) - \gamma(I_1 - I_2) \\
&= -\beta(t)(I_1^2 - I_2^2)/2 - \gamma(I_1 - I_2) \\
&= \left(-\beta(t)(I_1 + I_2)/2 - \gamma\right)(I_1 - I_2)
\end{aligned}$$

Hence,

$$-\max\beta(t) - \gamma < \frac{d\log(I_1 - I_2)}{dt} = -\beta(t)(I_1 + I_2)/2 - \gamma < -\gamma$$

Therefore, it must become coherent as $\log(I_1 - I_2) \to -\infty$. When $m_1 = m_2 = m$,

$$\begin{aligned}
&\beta(t)((1-2m_1)I_1 + (m_1 - 1)I_1^2 - (1-2m_2)I_2 - (m_2 - 1)I_2^2) - \gamma(I_1 - I_2) \\
&= \beta(t)((1-2m)(I_1 - I_2) + (m-1)(I_1^2 - I_2^2)) - \gamma(I_1 - I_2) \\
&= \left(\beta(t)(1 - 2m + (m-1)(I_1 + I_2)) - \gamma\right)(I_1 - I_2)
\end{aligned}$$

Hence,

$$\frac{d\log(I_1 - I_2)}{dt} = (\beta(t)(1 - 2m + (m-1)(I_1 + I_2)) - \gamma)$$

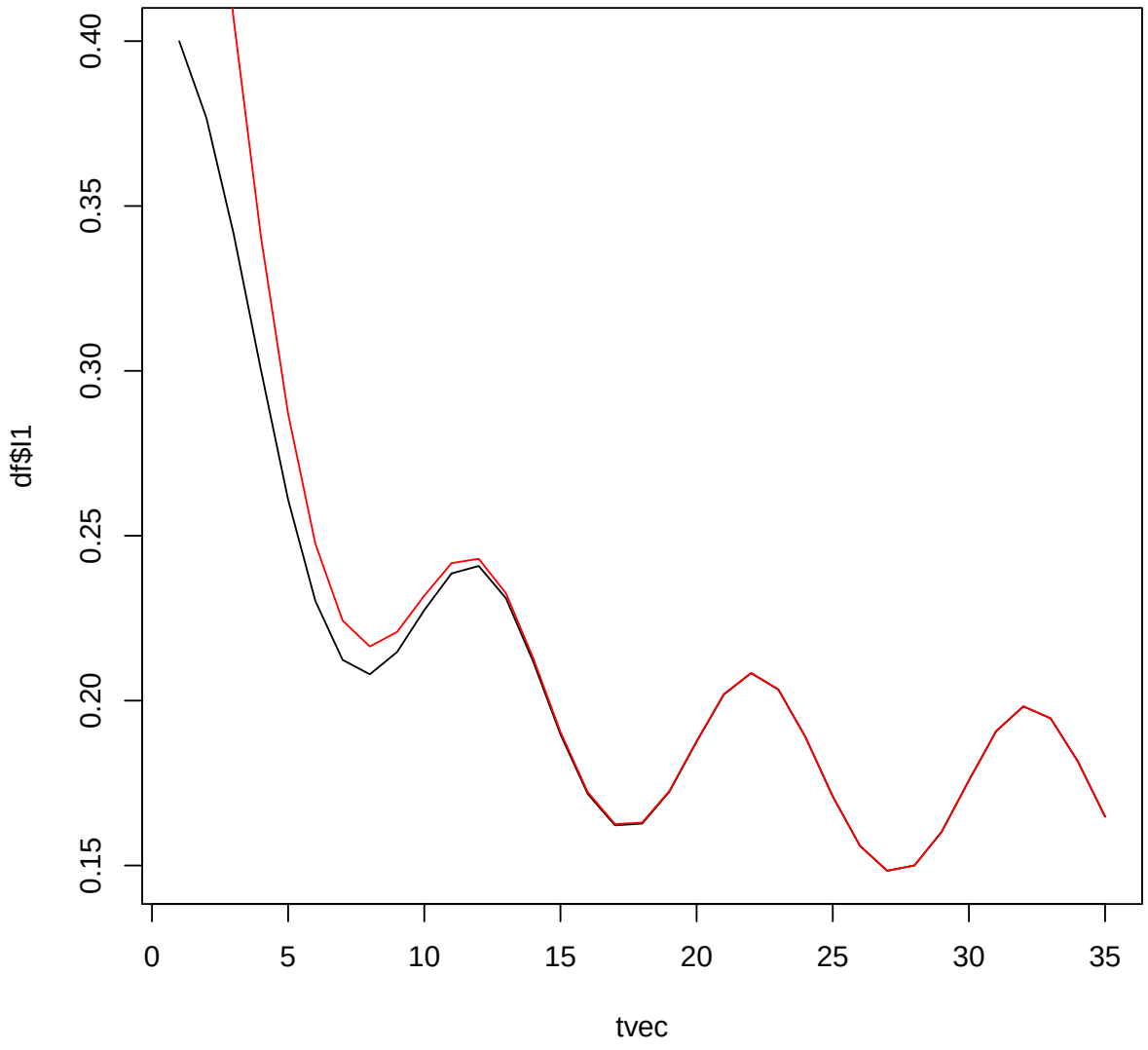
Note that

$$\beta(t)(1-2m+(m-1)(I_1+I_2))-\gamma = \beta(t)(1-2m)-\beta(t)(1-m)(I_1+I_2)-\gamma < \beta(t)(1-2m)-\gamma$$

Then, when $\beta(t)(1-2m) - \gamma < 0$, this system *can* be coherent.

```
SI.grad <- function(t, y, par) {
    with(as.list(c(y, par)), {
        beta <- b0 * (1 + b1 * cos (2 * pi * t/period))

        dI1 <- beta * ((1 - m) * I1 + m * I2) * (1 - I1) - gamma * I1
        dI2 <- beta * (m * I1 + (1-m) * I2) * (1 - I2) - gamma * I2
        list(c(dI1, dI2))
    })
}
```

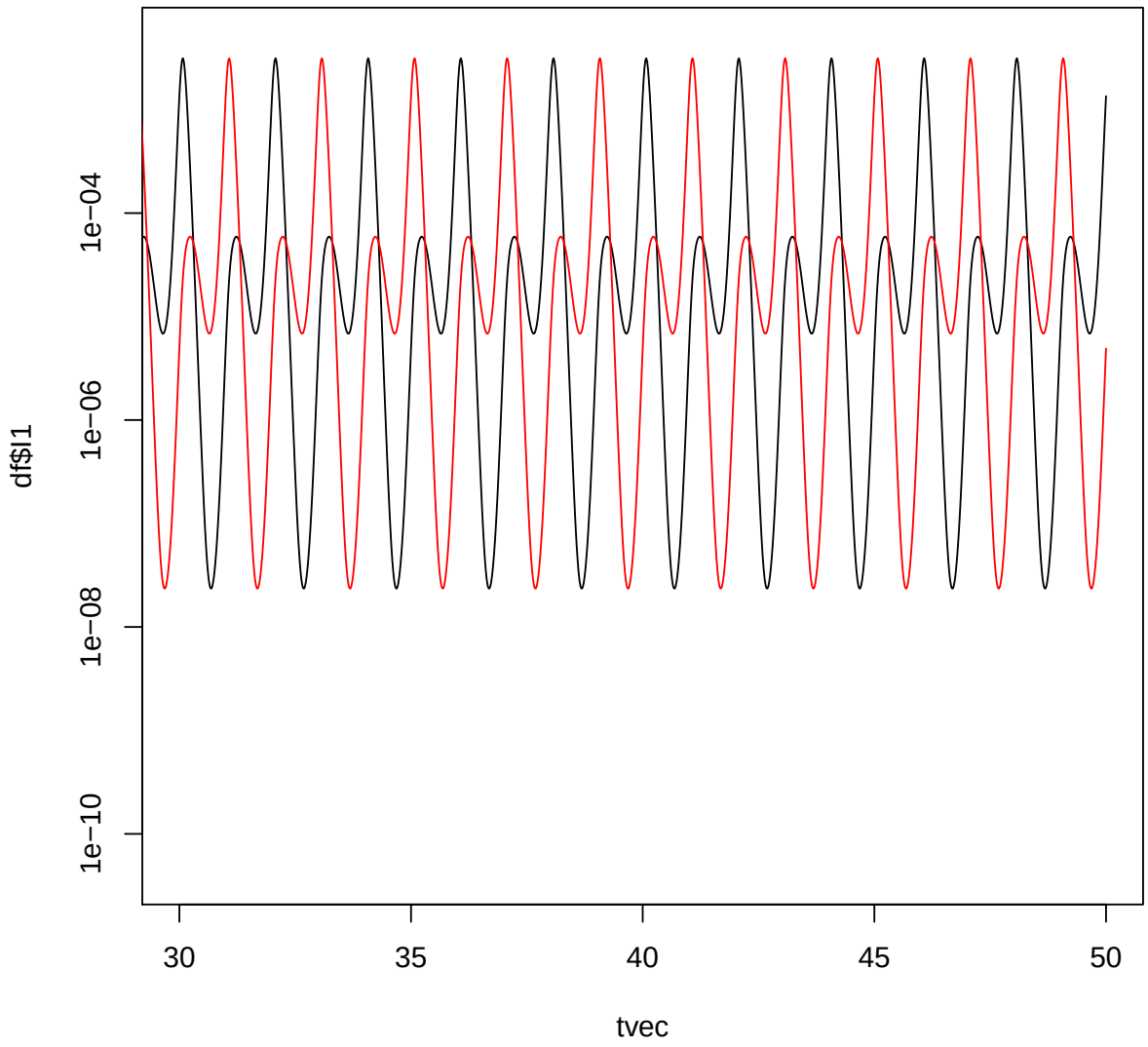
```
par <- c(b0=0.6, b1=0.2, gamma=0.5, m = 0.2, period=10)
y <- c(I1=0.4, I2=0.6)
tvec <- seq(from=1, to=35, by=1)

df <- as.data.frame(ode(y, tvec, SI.grad, par))

plot(tvec, df$I1, type="l")
lines(tvec, df$I2, col=2)
```



I think seasonal forcing is too strong in this case...??? We get dynamics that are not interesting at all. However, I think we can use this method as a stepping stone to try to tackle more sophisticated models.

Now, let's think about the big model instead of SIS

```
SI.grad <- function(t, y, par) {
    with(as.list(c(y, par)), {
        beta <- b0 * (1 + b1 * cos (2 * pi * t/period))

        inf1 <- beta * ((1 - m) * I1 + m * I2) * S1

        dS1 <- mu * (1 - S1) - inf1
        dI1 <- inf1 - (gamma + mu) * I1
        dR1 <- gamma * I1 - mu * R1

        inf2 <- beta * (m * I1 + (1-m) * I2) * S2

        dS2 <- mu * (1 - S2) - inf2
        dI2 <- inf2 - (gamma + mu) * I2
        dR2 <- gamma * I2 - mu * R2

        list(c(dS1, dI1, dR1, dS2, dI2, dR2))
    })
}

## parameters taken from Earn et al

par <- c(b0=1250, b1=0.15, gamma=365/5, m = 0.001, mu = 0.02, period=1)
y <- c(S1=0.05, I1=0.001, R1=1-0.05-0.001, S2=0.07, I2=0.001, R2=1-0.07-0.001)
tvec <- seq(from=1, to=50, by=1/52)

df <- as.data.frame(rk(y, tvec, SI.grad, par))

plot(tvec, df$I1, type="l", xlim=c(30, 50), log='y')
lines(tvec, df$I2, col=2)
```



Total time spent on this project

Group work: n hours

Solo work: m hours

References

Becker, A. D. and B. T. Grenfell (2017). tsir: An r package for time-series susceptible-infected-recovered models of epidemics. *PloS one 12*(9), e0185528.

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He, D., E. L. Ionides, and A. A. King (2009). Plug-and-play inference for disease dynamics: measles in large and small populations as a case study. *Journal of the Royal Society Interface*.

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