Measles Worksheet

From 1/30 lecture – But Slower

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1/31/2017

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Goals for today

1. Go over the measles handout

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1. Go over the measles handout
    - Sort of. Not going to answer the questions for you. Just going to help you go through the code to answer them on your own.

Question 1

Make an SIR model for measles

Question 1

- Measles epidemic:
  - Population: 1 million
  - Probability of infection is $.75$ if in contact with an infectious person
  - 12 respiratory contacts **per week**
  - Disease duration of 1 week
  - For now, use SIR framework

```r
library(deSolve)

parms <- c(beta = 0.333, k = 3 , r = 0.333)
inits <- c(S = 499, I = 1, R = 0)
dt <- seq(0, 300, 1)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Start with the boilerplate code we gave you last week.

```r
library(deSolve)

parms <- c(beta = 0.333, k = 3 , r = 0.333)
inits <- c(S = 499, I = 1, R = 0)
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    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Modify the parameters we were given.

```r
library(deSolve)

parms <- c(beta = 0.75, k = 12 , r = 1)
inits <- c(S = 999999, I = 1, R = 0)
dt <- seq(0, 300, 1)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Modify the parameters we were given.

- 12 contacts per week
- disease duration is 1 week
- .75 probability of infectiousness
- 1 million people in the population

```r
library(deSolve)

parms <- c(beta = 0.75, k = 12 , r = 1)
inits <- c(S = 999999, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Make sure your time scale makes sense given your parameters.

- 300 weeks seems too long, so we change it to 10 weeks.
- 1 week at a time is too coarse, so we change it to days ($\frac{1}{7}$)

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parms <- c(beta = 0.75, k = 12 , r = 1)
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        dR <- r * I

        der <- c(dS, dI, dR)

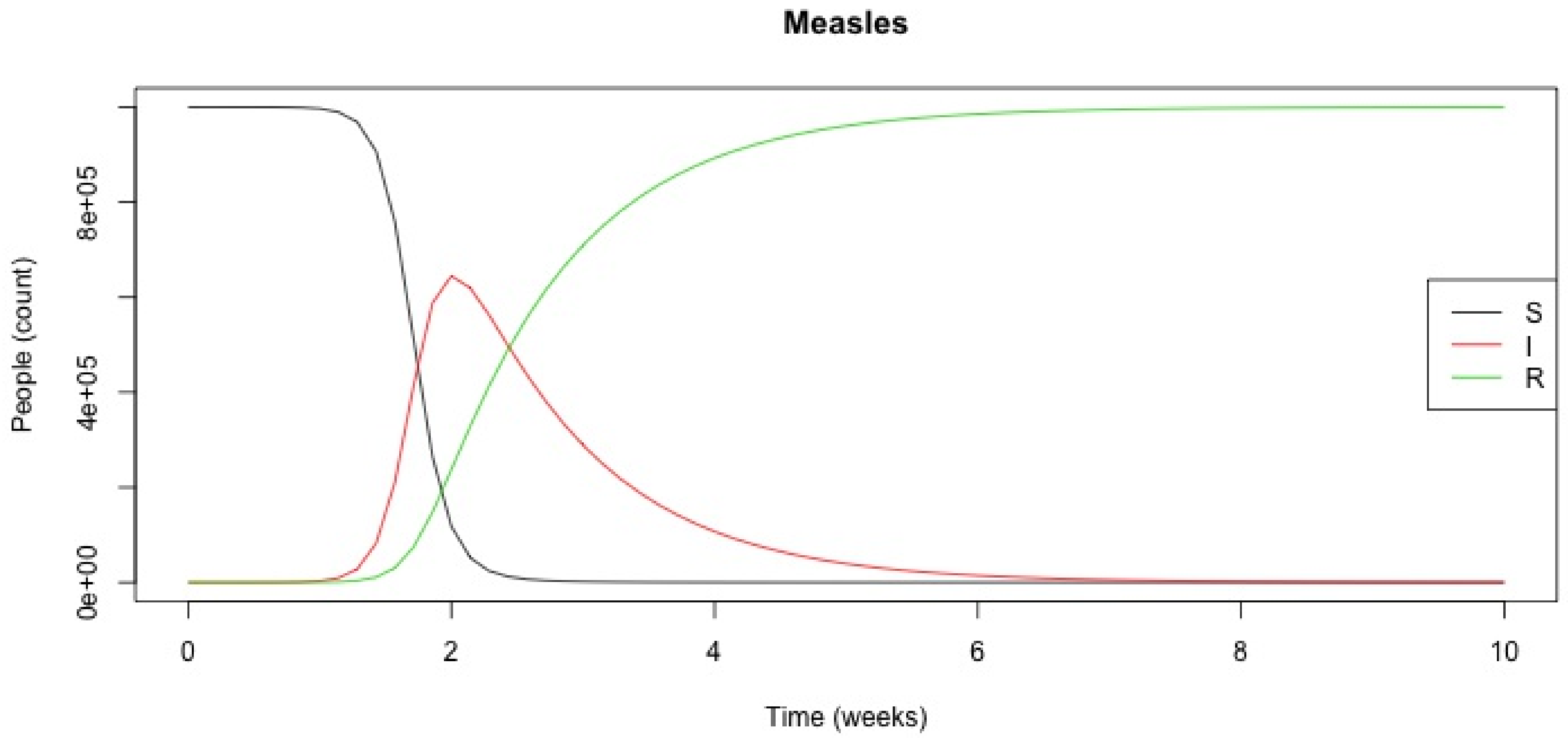
        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Make sure your time scale makes sense given your parameters.

- 300 weeks seems too long, so we change it to 10 weeks.
- 1 week at a time is too coarse, so we change it to days ($\frac{1}{7}$)
    - But **any** small number would work

```r
matplot(x = simulation[, 1], y = simulation[, 2:4], type = "l",
        lty = 1, xlab = "Time (weeks)", ylab = "People (count)",
        main = "Measles")
legend(x = "right", legend = c('S', 'I', 'R'),
       col = 1:3, lty = 1)
```



Time-steps are arbitrary

For example, let's do days

```r
parms <- c(beta = 0.75, k = 12/7 , r = 1/7)
inits <- c(S = 999999, I = 1, R = 0)
dt <- seq(0, 10 * 7, 1)

simulation_days <- as.data.frame(ode(y = inits, times = dt,
                                      func = SIR, parms = parms))
```

- Since our `parms` are in units of weeks, we divide by 7 to make them days
- We change our time-steps to be 70 units of 1 day to match our previous simulation

```r
parms <- c(beta = 0.75, k = 12/7 , r = 1/7)
inits <- c(S = 999999, I = 1, R = 0)
dt <- seq(0, 10 * 7, 1)

simulation_days <- as.data.frame(ode(y = inits, times = dt,
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```

- Since our `parms` are in units of weeks, we divide by 7 to make them days
- We change our time-steps to be 70 units of 1 day to match our previous simulation
- **NOTE:** We save the simulations in different variable

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parms <- c(beta = 0.75, k = 12/7 , r = 1/7)
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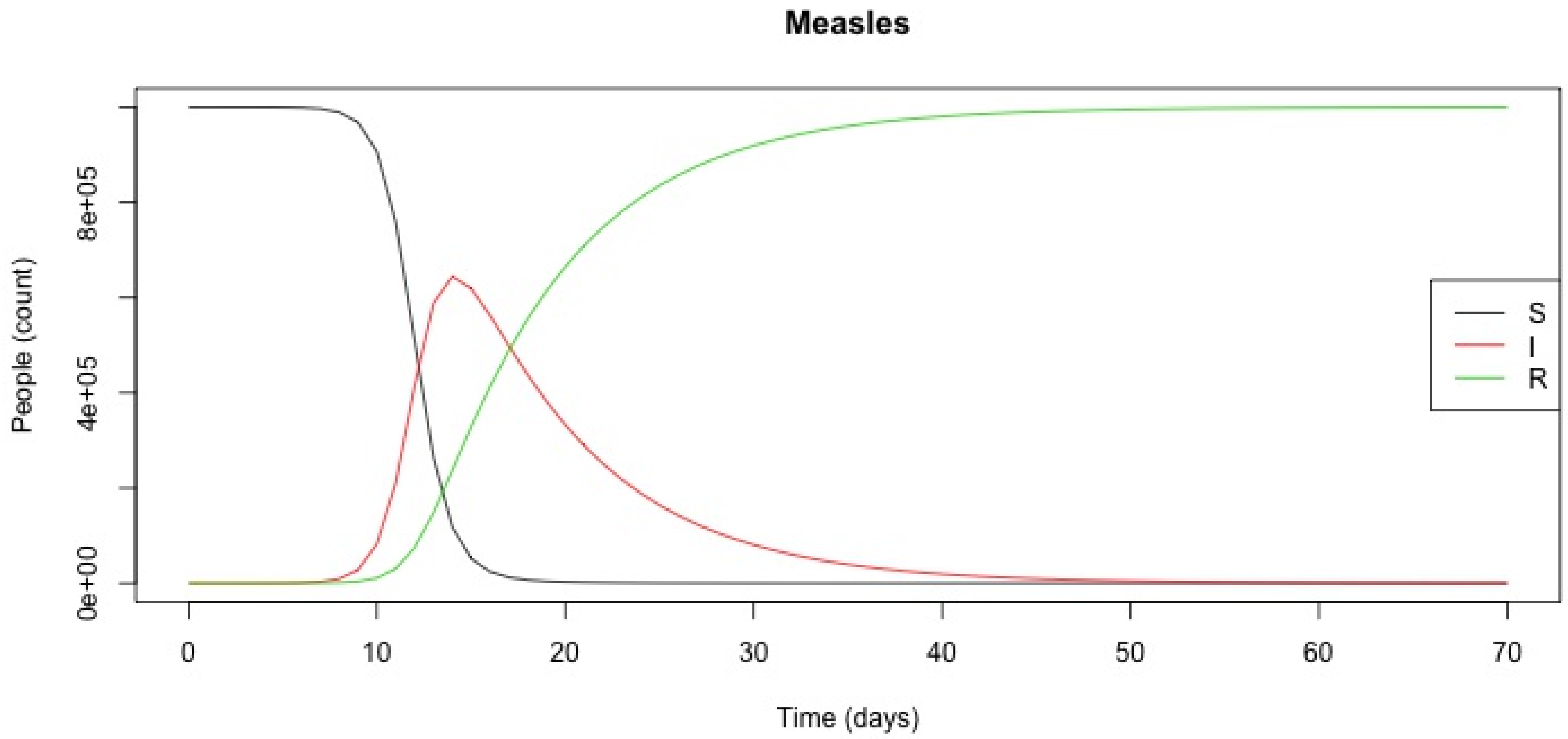
dt <- seq(0, 10 * 7, 1)

simulation_days <- as.data.frame(ode(y = inits, times = dt,
                                     func = SIR, parms = parms))
```

- Since our `parms` are in units of weeks, we divide by 7 to make them days
- We change our time-steps to be 70 units of 1 day to match our previous simulation
- **NOTE:** We save the simulations in different variable
- How will the plot change?

```r
matplot(x = simulation_days[, 1], y = simulation_days[, 2:4], type = "l",
        lty = 1, xlab = "Time (days)", ylab = "People (count)",
        main = "Measles")
legend(x = "right", legend = c('S', 'I', 'R'),
       col = 1:3, lty = 1)
```



The plot does not change.

We can verify this by looking directly at the data.

```
head(simulation)
```

```
##     time      S       I      R
## 1 0.0000 999999   1.000  0.000
## 2 0.1429 999997   3.136  0.267
## 3 0.2857 999989   9.833  1.104
## 4 0.4286 999965  30.832  3.729
## 5 0.5714 999891  96.671 11.960
## 6 0.7143 999659 303.054 37.764
```

```
head(simulation_days)
```

```
##   time      S       I      R
## 1    0 999999   1.000  0.000
## 2    1 999997   3.136  0.267
## 3    2 999989   9.833  1.104
## 4    3 999965  30.832  3.729
## 5    4 999891  96.671 11.960
## 6    5 999659 303.054 37.764
```

The top is in weeks, the bottom is in days.

Do this for chickenpox (b=.51)

and then mumps (b=.38)*

(You can do this on your own — I believe in you.)

* Don't forget to save the results in different variables.

Hopefully, your code looks like this:

```
parms_mumps <- c(beta = 0.38, k = 12 , r = 1)
parms_cpox <- c(beta = .51, k = 12, r = 1)
sim_mumps <- as.data.frame(ode(y = inits, times = dt,
                               func = SIR, parms = parms_mumps))
sim_cpox <- as.data.frame(ode(y = inits, times = dt,
                               func = SIR, parms = parms_cpox))
```

- Just make a new set of `parms` for each disease

Hopefully, your code looks like this:

```
parms_mumps <- c(beta = 0.38, k = 12 , r = 1)
parms_cpox <- c(beta = .51, k = 12, r = 1)
sim_mumps <- as.data.frame(ode(y = inits, times = dt,
                               func = SIR, parms = parms_mumps))
sim_cpox <- as.data.frame(ode(y = inits, times = dt,
                              func = SIR, parms = parms_cpox))
```

- Just make a new set of `parms` for each disease
- Change the parameter as appropriate

Hopefully, your code looks like this:

```
parms_mumps <- c(beta = 0.38, k = 12 , r = 1)
parms_cpox <- c(beta = .51, k = 12, r = 1)
sim_mumps <- as.data.frame(ode(y = inits, times = dt,
                               func = SIR, parms = parms_mumps))
sim_cpox <- as.data.frame(ode(y = inits, times = dt,
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- Just make a new set of `parms` for each disease
- Change the parameter as appropriate
- Run the new simulations and save the results in new variables

Hopefully, your code looks like this:

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parms_mumps <- c(beta = 0.38, k = 12 , r = 1)
parms_cpox <- c(beta = .51, k = 12, r = 1)
sim_mumps <- as.data.frame(ode(y = inits, times = dt,
                               func = SIR, parms = parms_mumps))
sim_cpox <- as.data.frame(ode(y = inits, times = dt,
                              func = SIR, parms = parms_cpox))
```

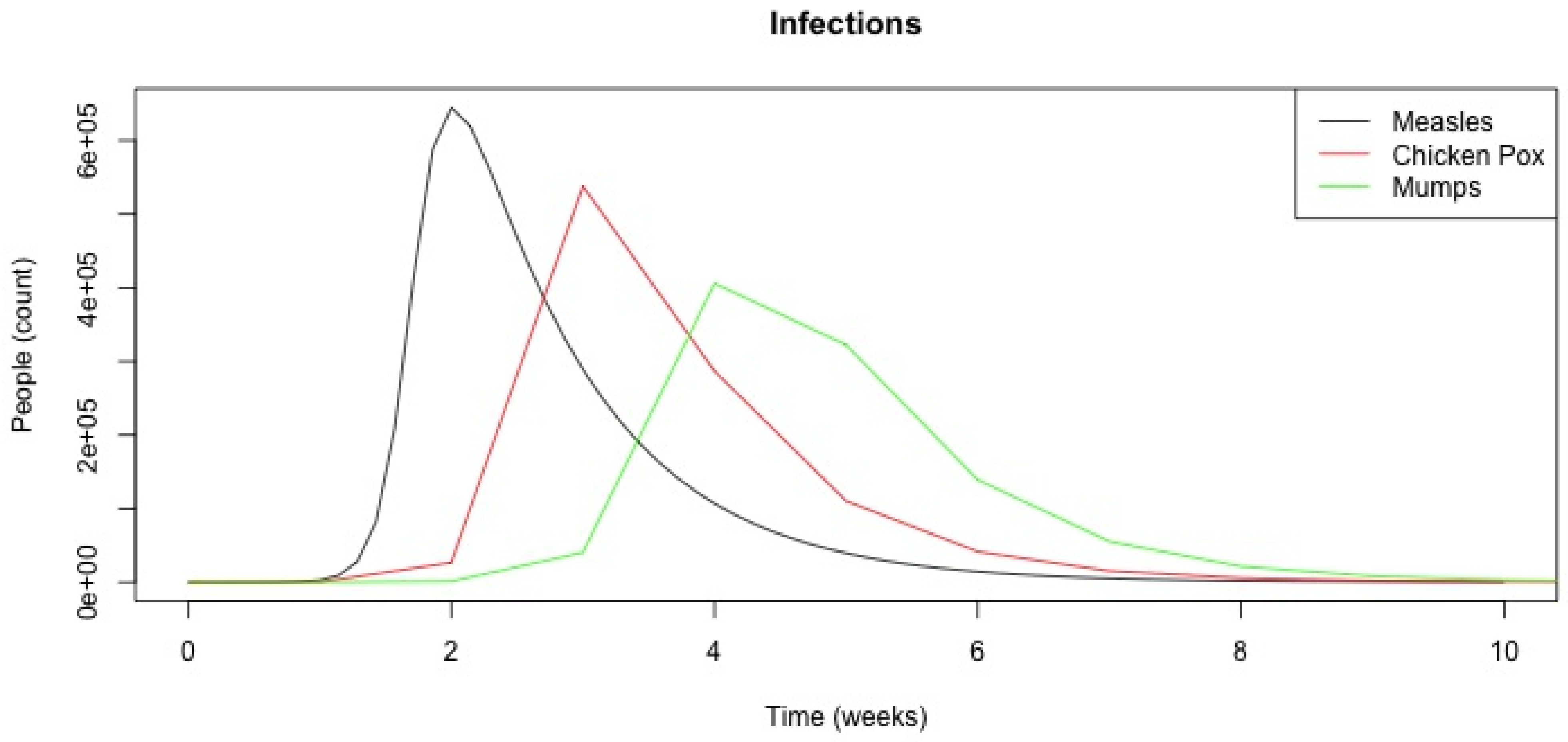
- Just make a new set of `parms` for each disease
- Change the parameter as appropriate
- Run the new simulations and save the results in new variables
- `dt` didn't change, our model (`SIR()`) didn't change, and `inits` didn't change.

How to plot multiple things

For example, to compare infectious curves

Compare multiple infectious curves

```
plot(x = simulation$time, y = simulation$I, type = "l",
     xlab = "Time (weeks)", ylab = "People (count)", main = "Infections")
lines(x = sim_cpox$time, y = sim_cpox$I, col = "red")
lines(x = sim_mumps$time, y = sim_mumps$I, col = "green")
legend(x = "topright", legend = c('Measles', 'Chicken Pox', 'Mumps'),
       col = c("black", "red", "green"), lty = 1)
```



Wait, what?

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```

- Plot one of the curves (see last week's slides or `help(plot)`) for more.
  - `type = 'l'` means you want a `l`ine.
  - `xlab`, `ylab`, and `main` are the x-axis, y-axis, and main labels, respectively.

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legend(x = "topright", legend = c('Measles', 'Chicken Pox', 'Mumps'),
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  - `type = 'l'` means you want a `l`ine.
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- Now plot a second curve, using `lines()` — make sure to give it a different color.
  - Recall you use `lines()` to **add** to an existing `plot()` object.

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- Now plot a second curve, using `lines()` — make sure to give it a different color.
  - Recall you use `lines()` to **add** to an existing `plot()` object.
- Add the third curve — again, make sure to give it a different color.

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- Now plot a second curve, using `lines()` — make sure to give it a different color.
  - Recall you use `lines()` to **add** to an existing `plot()` object.
- Add the third curve — again, make sure to give it a different color.
- Add a legend, specifying each line in order under `legend` and each color in order under `col`.

How to find the time of max infections

Also, how to use max()

When was the peak of infections?

We could just eyeball it, but instead, let's find the value of our `time` column when the peak of the **measles** epidemic occurred.

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```
simulation$time[which.max(simulation$I)]
```

```
## [1] 2
```

When was the peak of infections?

We could just eyeball it, but instead, let's find the value of our `time` column when the peak of the **measles** epidemic occurred.

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simulation$time[which.max(simulation$I)]
```

```
## [1] 2
```

So the epidemic occurred at exactly two weeks — aggreeing with our plot.

Ok, what's happening?

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- `which.max()` is a function that returns the index (location) of the maximum value in a vector

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- So we are saying "find the row index that corresponds to the highest value of `simulation$I`"

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- `which.max()` is a function that returns the index (location) of the maximum value in a vector
- `$` is shorthand for specifying a single column
- `[ ]` is shorthand for selecting a specific subset
- So we are saying "find the row index that corresponds to the highest value of `simulation$I`"
- Now take that row index and return the corresponding value of `simulation$time`

Let's verify

Find the maximum value of `simulation$I`:

Let's verify

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```
max(simulation$I)
```

```
## [1] 644530
```

Let's verify

Find the maximum value of `simulation$I`:

```
max(simulation$I)
```

```
## [1] 644530
```

Which index is this max value? (`TRUE` means we hit the max, `FALSE` otherwise)

```
max(simulation$I) == simulation$I
```

```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [12] FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [23] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [34] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [45] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [56] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [67] FALSE FALSE FALSE FALSE FALSE
```

Note here that the only `TRUE` is in the 15th position.

Let's verify

So we could just ask for the 15th row of `simulation$time`:

Let's verify

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```
simulation$time[15]      ## equiv: simulation[15, 'time']
```

```
## [1] 2
```

Let's verify

So we could just ask for the 15th row of `simulation$time`:

```
simulation$time[15]     ## equiv: simulation[15, 'time']
```

```
## [1] 2
```

Or we could just pass the entire boolean vector:

```
simulation$time[max(simulation$I) == simulation$I]
```

```
## [1] 2
```

Let's verify

So we could just ask for the 15th row of `simulation$time`:

```
simulation$time[15]     ## equiv: simulation[15, 'time']
```

```
## [1] 2
```

Or we could just pass the entire boolean vector:

```
simulation$time[max(simulation$I) == simulation$I]
```

```
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```

Or better yet, just stick to `which.max()`

Aside: Boolean vectors

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What does this return? (Recall what `seq()` does from our last lab)

```
seq(-5, 5, 1) >= 0
```

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- How long will the return vector be?
- How many `FALSE`?
- How many `TRUE`?

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What does this return? (Recall what `seq()` does from our last lab)

```
seq(-5, 5, 1) >= 0
```

- How long will the return vector be?
- How many `FALSE`?
- How many `TRUE`?

  ```
  print(seq(-5, 5, 1) >= 0)
  ```

```
##  [1] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Use one of these methods to find the time of maximum infection for mumps and chickenpox*

* Just use `which.max()`.

Answers

```
simulation$time[which.max(simulation$I)]
```

```
## [1] 2
```

```
sim_mumps$time[which.max(sim_mumps$I)]
```

```
## [1] 4
```

```
sim_cpox$time[which.max(sim_cpox$I)]
```

```
## [1] 3
```

NOTE: My answers will be rounded. Yours should not be.

Find the peak number of infected for each of the three epidemics

Answers

```
max(simulation$I)
```

```
## [1] 644530
```

```
max(sim_mumps$I)
```

```
## [1] 405947
```

```
max(sim_cpox$I)
```

```
## [1] 537860
```

Question 4

SEIR Models

Write out an SEIR model

With parameter a for the rate from latent to infectious

Seriously, write it out

Always write/draw models before coding them

```r
parms <- c(beta = .75, k = 12 , r = 1)
inits <- c(S = 999999, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Start with the boilerplate code again

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
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        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

- Introduce a new parameter `a` be the rate from latent to infectious.

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
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        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

- Introduce a new parameter `a` be the rate from latent to infectious.
- If the duration of the latent period is 12 days, what is the rate per day?

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
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        der <- c(dS, dI, dR)

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simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

- Introduce a new parameter `a` be the rate from latent to infectious.
- If the duration of the latent period is 12 days, what is the rate per day? **1/12**

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 10, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

- Introduce a new parameter `a` be the rate from latent to infectious.
- If the duration of the latent period is 12 days, what is the rate per day? **1/12**
    - Note, we want the rate to be per week (since our time-steps are in weeks) so `* 7`

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 25, 1/7)

SIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

- Need to add an initial value for our new compartment `E`
- Also, intuitively, delaying infectiousness will delay the epidemic so we should expand our time

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 25, 1/7)

SEIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + I + R
        dS <- - (beta * k * S * I) / N
        dI <- + (beta * k * S * I) / N - r * I
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Change the function name to reflect our new model

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 25, 1/7)

SEIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + E + I + R
        dS <- - (beta * k * S * I) / N
        dE <- + (beta * k * S * I) / N - (a * E)
        dI <- + (a * E) - (r * I)
        dR <- r * I

        der <- c(dS, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Add `E` into our total population count `N` and then put in the compartment

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 25, 1/7)

SEIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + E + I + R
        dS <- - (beta * k * S * I) / N
        dE <- + (beta * k * S * I) / N - (a * E)
        dI <- + (a * E) - (r * I)
        dR <- r * I

        der <- c(dS, dE, dI, dR)

        return(list(der))
    })
}

simulation <- as.data.frame(ode(y = inits, times = dt,
                                func = SIR, parms = parms))
```

Adjust the `I` compartment since things can only come from `E` now.

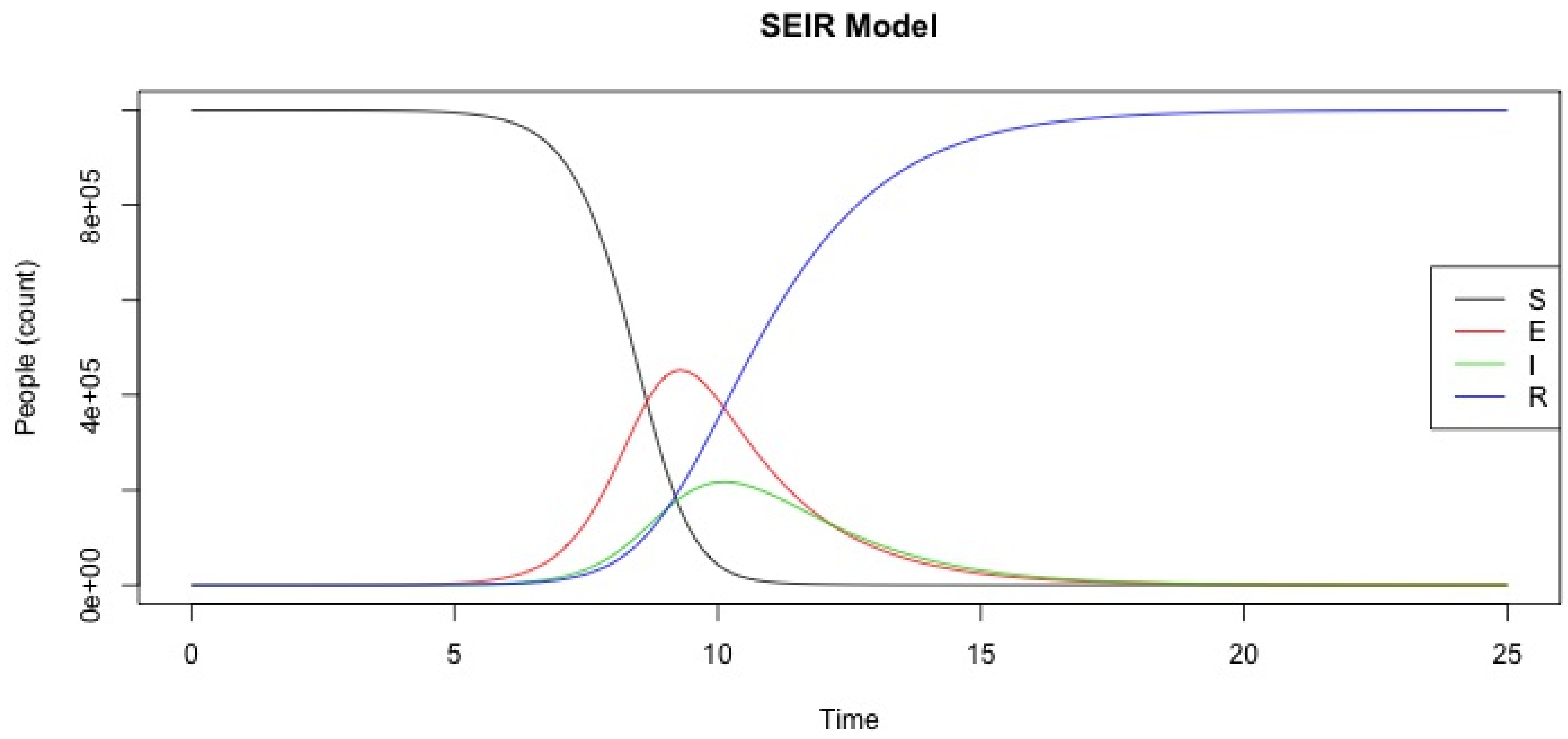
Don't forget to return the `dE` compartment.

```r
parms <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1)
inits <- c(S = 999999, E =0, I = 1, R = 0)
dt <- seq(0, 25, 1/7)

SEIR <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + E + I + R
        dS <- - (beta * k * S * I) / N
        dE <- + (beta * k * S * I) / N - (a * E)
        dI <- + (a * E) - (r * I)
        dR <- r * I

        der <- c(dS, dE, dI, dR)

        return(list(der))
    })
}

sim_seir <- as.data.frame(ode(y = inits, times = dt,
                              func = SEIR, parms = parms))
```

Save it into a new variable and make sure to use the correct model.

Plot should look like this

```
sim_seir <- as.data.frame(ode(y = inits, times = dt,
                              func = SEIR, parms = parms))
matplot(x = sim_seir[, 1], y = sim_seir[, 2:5], type = "l",
        lty = 1, xlab = "Time", ylab = "People (count)", main = "SEIR Model")
legend(x = "right", legend = c('S', 'E', 'I', 'R'), col = 1:4, lty = 1)
```



With a neighbor, add births/deaths to your SEIR model

You can only be born S but you can die in any compartment*

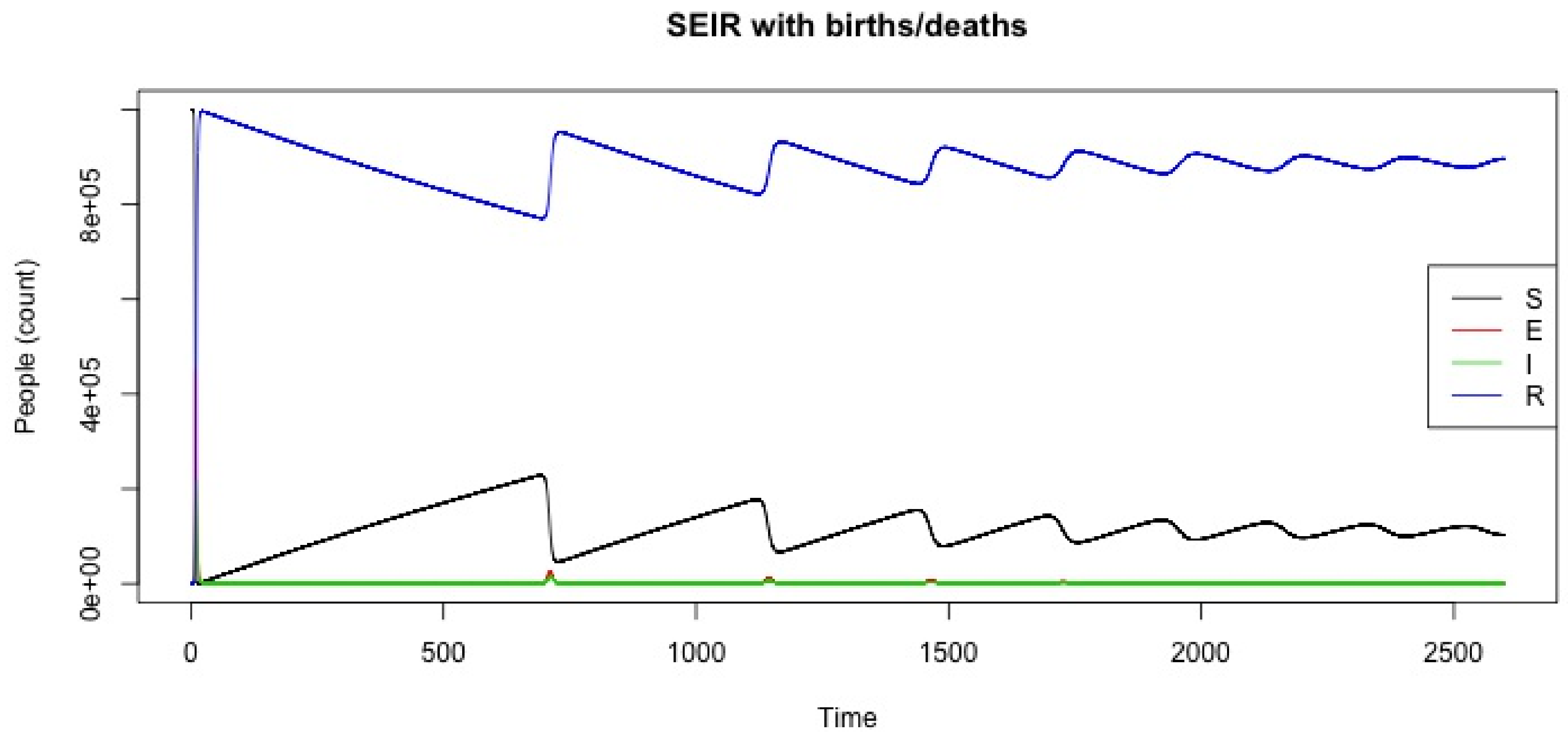
*Keep births and deaths equal assuming an annual fertility and mortality rate of .02

Your code should look similar

```r
# added births and deaths as weekly rates (divide by 52 weeks)
parms_bd <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
              b = .02/52, d = .02/52)
# Look at 50 years
dt_bd <- seq(0, 52 * 50, 1/7)

SEIR_bd <- function(t, x, parms){
    with(as.list(c(parms, x)), {

        N <- S + E + I + R
        dS <- - (beta * k * S * I) / N + (b * N) - (d * S)
        dE <- + (beta * k * S * I) / N - (a * E) - (d * E)
        dI <- + (a * E) - (r * I) - (d * I)
        dR <- r * I  - (d * R)

        der <- c(dS, dE, dI, dR)

        return(list(der))
    })
}
simulation_bd <- as.data.frame(ode(y = inits, times = dt_bd,
                                   func = SEIR_bd, parms = parms_bd))
```

Your plot should look like this

```r
matplot(x = simulation_bd[, 1], y = simulation_bd[, 2:5], type = "l",
        lty = 1, xlab = "Time", ylab = "People (count)",
        main = "SEIR with births/deaths")
legend(x = "right", legend = c('S', 'E', 'I', 'R'), col = 1:4, lty = 1)
```



Challenge questions

See if you can reparaterize the same model, but in time steps of years.

Question 5

With a neighbor, plot only infected individuals

(and only for t > 5 years)

Hints

Hints

We went over all the code you need to do this

Hints

We went over all the code you need to do this

Boolean vectors are your friend

Hints

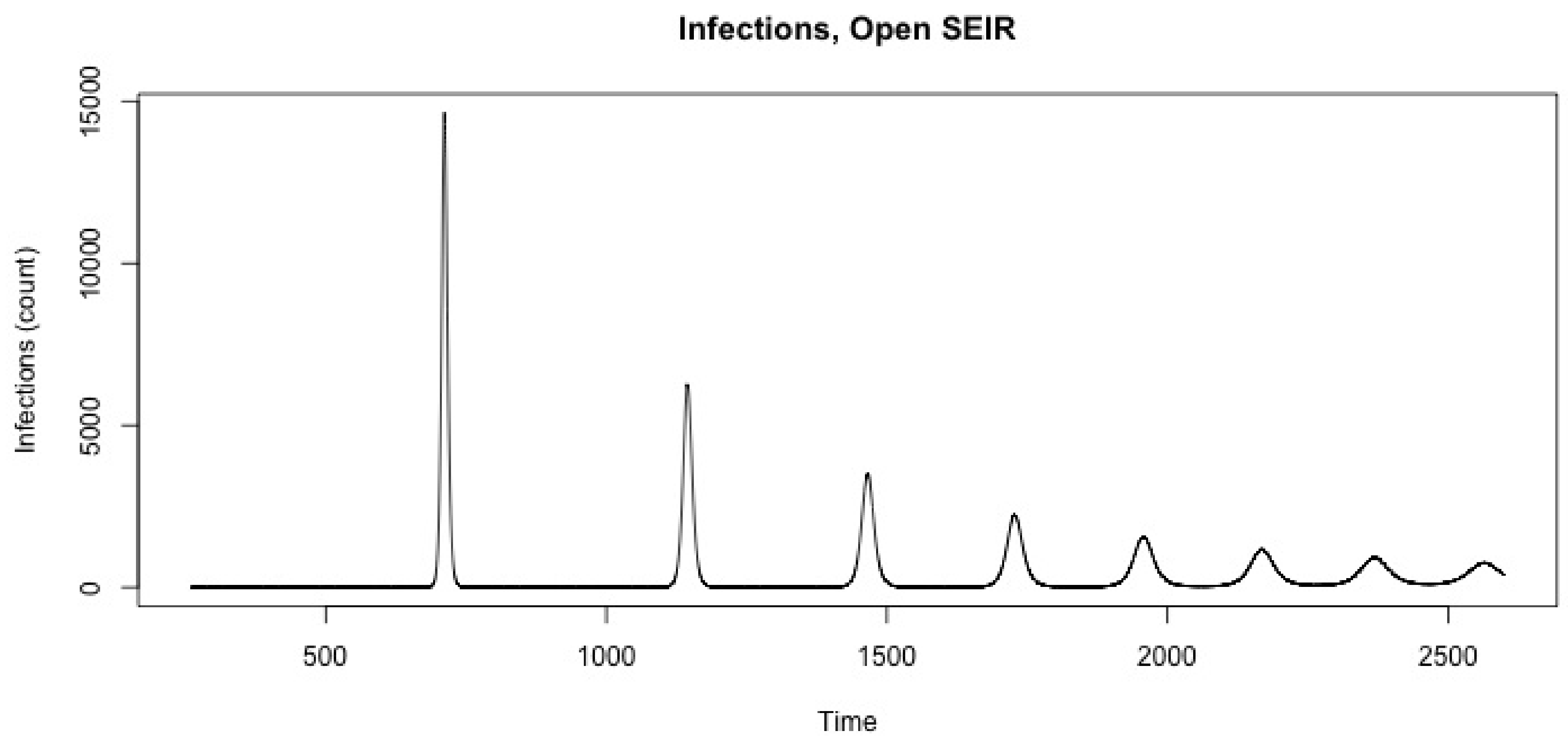
We went over all the code you need to do this

Boolean vectors are your friend

How you parameterized time matters

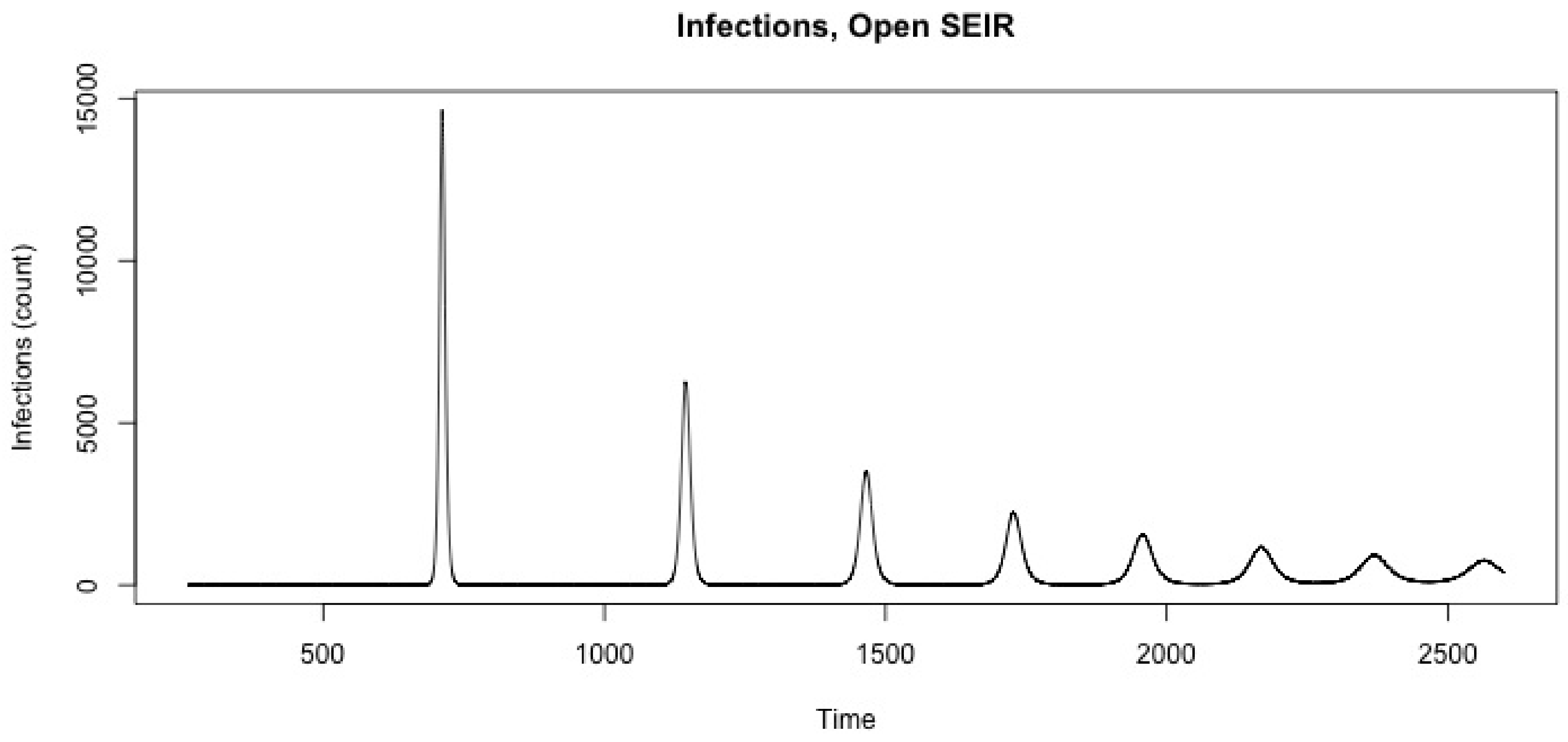
Your plot should look like this

```
plot(x = simulation_bd$time[simulation_bd$time >= 5 * 52],
     y = simulation_bd$I[simulation_bd$time >= 5 * 52],
     type = "l", lty = 1, xlab = "Time", ylab = "Infections (count)",
     main = "Infections, Open SEIR")
```



Or save the vector

```
y5_higher <- simulation_bd$time >= 5 * 52
plot(x = simulation_bd$time[y5_higher],
     y = simulation_bd$I[y5_higher],
     type = "l", lty = 1, xlab = "Time", ylab = "Infections (count)",
     main = "Infections, Open SEIR")
```



Question 6

What the for-loop?

(The magic of not copying and pasting)

For-loop basics

Suppose you want to sweep through many values of a parameter.

For-loop basics

Suppose you want to sweep through many values of a parameter.

You could just do this:

```
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .020/52, d = .020/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .025/52, d = .025/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .030/52, d = .030/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .035/52, d = .035/52)
```

For-loop basics

Suppose you want to sweep through many values of a parameter.

You could just do this:

```
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .020/52, d = .020/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .025/52, d = .025/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .030/52, d = .030/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .035/52, d = .035/52)
```

But that's error-prone, tedious, and ugly.

For-loop basics

Suppose you want to sweep through many values of a parameter.

You could just do this:

```
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .020/52, d = .020/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .025/52, d = .025/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .030/52, d = .030/52)
parms_bd1 <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
               b = .035/52, d = .035/52)
```

But that's error-prone, tedious, and ugly.

So we're going to use a loop.

For-loop basics

The anatomy of a for loop

```
for (placeholder_variable in list_of_values) {
    ## Do something -- hopefully more useful than printing
    print(placeholder_variable)
}
```

For-loop basics

The anatomy of a for loop

```
for (placeholder_variable in list_of_values) {
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    print(placeholder_variable)
}
```

- `for()` declares you are going to make a loop in the `{`brackets`}`

For-loop basics

The anatomy of a for loop

```r
for (placeholder_variable in list_of_values) {
    ## Do something -- hopefully more useful than printing
    print(placeholder_variable)
}
```

- `for()` declares you are going to make a loop in the {brackets}
- To use `for()` we need to give it something to loop through — `list_of_values`

For-loop basics

The anatomy of a for loop

```
for (placeholder_variable in list_of_values) {
    ## Do something -- hopefully more useful than printing
    print(placeholder_variable)
}
```

- `for()` declares you are going to make a loop in the {brackets}
- To use `for()` we need to give it something to loop through — `list_of_values`
- We also need to give it a `placeholder_variable` we will use to refer to the current value from `list_of_values` inside of the {brackets}.

For-loop basics

The anatomy of a for loop

```
for (placeholder_variable in list_of_values) {
    ## Do something -- hopefully more useful than printing
    print(placeholder_variable)
}
```

- `for()` declares you are going to make a loop in the `{`brackets`}`
- To use `for()` we need to give it something to loop through — `list_of_values`
- We also need to give it a `placeholder_variable` we will use to refer to the current value from `list_of_values` inside of the `{`brackets`}`.
- Finally, we do something to that `placeholder_variable` and then move on to the next value

For-loop basics

The anatomy of a for loop

```r
sentence <- c("The", "magic", "of", "for", "loops")
for (word in sentence) {
    ## Do something -- hopefully more useful than printing
    print(word)
}
```

```
## [1] "The"
## [1] "magic"
## [1] "of"
## [1] "for"
## [1] "loops"
```

For-loop basics

The anatomy of a for loop

```r
sentence <- c("The", "magic", "of", "for", "loops")
for (word in sentence) {
    ## Do something -- hopefully more useful than printing
    print(word)
}
```

```
## [1] "The"
## [1] "magic"
## [1] "of"
## [1] "for"
## [1] "loops"
```

So the first time this loop ran, `word` had the value of "The"

For-loop basics

The anatomy of a for loop

```r
sentence <- c("The", "magic", "of", "for", "loops")
for (word in sentence) {
    ## Do something -- hopefully more useful than printing
    print(word)
}
```

```
## [1] "The"
## [1] "magic"
## [1] "of"
## [1] "for"
## [1] "loops"
```

So the first time this loop ran, `word` had the value of "The"

The second time, `word` had the value of "magic" and so on.

For-loop basics

Sidenote, you can also loop by index

```r
sentence <- c("The", "magic", "of", "for", "loops")
for (idx in 1:5) {
    ## Do something -- hopefully more useful than printing
    print(sentence[idx])
}
```

```
## [1] "The"
## [1] "magic"
## [1] "of"
## [1] "for"
## [1] "loops"
```

Very common because it is more general

Useful when you only care about the position of an element (and not the element itself).

For-loop basics

Appending data with loops

```r
multiplier <- 1:5
holder <- NULL
for (x in multiplier) {
    results <- 1:10 * x
    holder <- cbind(holder, results)
}
```

What is this code doing?

For-loop basics

Appending data with loops

```r
multiplier <- 1:5
holder <- NULL
for (x in multiplier) {
    results <- 1:10 * x
    holder <- cbind(holder, results)
}
```

What is this code doing?

- `multiplier` is just a sequence `1, 2, 3, 4, 5`

For-loop basics

Appending data with loops

```r
multiplier <- 1:5
holder <- NULL
for (x in multiplier) {
    results <- 1:10 * x
    holder <- cbind(holder, results)
}
```

What is this code doing?

- `multiplier` is just a sequence `1, 2, 3, 4, 5`
- Variables inside the `{`brackets`}` of the `for` loop get overwritten with every loop, so we create an empty (`NULL`) variable **outside** of the `for` loop to store results.

For-loop basics

Appending data with loops

```r
multiplier <- 1:5
holder <- NULL
for (x in multiplier) {
    results <- 1:10 * x
     holder <- cbind(holder, results)
}
```

What is this code doing?

- `multiplier` is just a sequence `1, 2, 3, 4, 5`
- Variables inside the `{`brackets`}` of the `for` loop get overwritten with every loop, so we create an empty (`NULL`) variable **outside** of the `for` loop to store results.
- Then we column `bind` our inside-the-loop results to the outside-the-loop variable we made

For-loop basics

Appending data with loops

```
print(holder)
```

```
##       results results results results results
##  [1,]       1       2       3       4       5
##  [2,]       2       4       6       8      10
##  [3,]       3       6       9      12      15
##  [4,]       4       8      12      16      20
##  [5,]       5      10      15      20      25
##  [6,]       6      12      18      24      30
##  [7,]       7      14      21      28      35
##  [8,]       8      16      24      32      40
##  [9,]       9      18      27      36      45
## [10,]      10      20      30      40      50
```

Back to Question 6

With a neighbor, make a vector containing 5 equally spaced values of the birth/death parameter between .013 and .025.*

*See `help(seq)` for options

Back to Question 6

Now make a for loop that runs ode on each value of this vector and use the "appending trick" to save only the infectious column from each run into a new variable*

*Change your time scale to 25 years instead of 50

Back to Question 6

Now plot your five infectious columns

for time >= 5 years

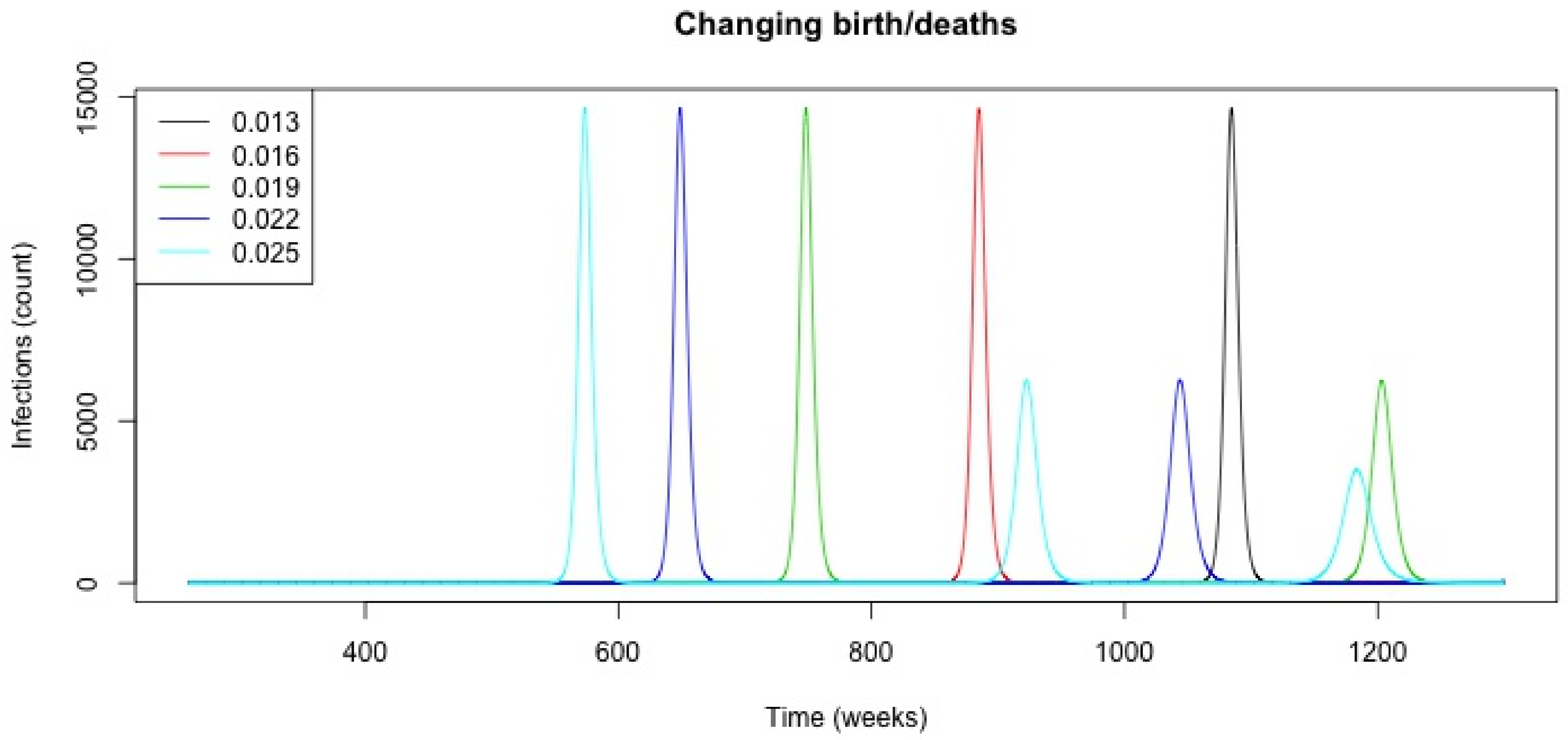
Changing birth/death rates

```r
bd_rates <- seq(from = .013, to = .025, length.out = 5)
dt_bd <- seq(0, 25 * 52, 1/7)
holder <- NULL
for (bd in bd_rates) {
    parms_bd <- c(beta = .75, a = 1/12 * 7, k = 12 , r = 1,
                  b = bd/52, d = bd/52)
    simulation_bd <- as.data.frame(ode(y = inits, times = dt_bd,
                                       func = SEIR_bd, parms = parms_bd))
    holder <- cbind(holder, simulation_bd$I)
}
```

Nothing on this slide is new. We're just piecing together different things we've done before. Review it slowly if it doesn't make sense to you yet.

Changing birth/death rates

```
t5_more <- simulation_bd$time >= 52 * 5
matplot(simulation_bd$time[t5_more], holder[t5_more, ], type = 'l',
        lty = 1, xlab = "Time (weeks)", ylab = "Infections (count)",
        main = "Changing birth/deaths")
legend(x = "topleft", legend = bd_rates, col = 1:5, lty = 1)
```



That's it.

Thanks