Simulating Competing Hazards

Modifying our Simple Model

Previously, we modeled a simple infected cohort. Now, we will add disease-induced mortality to the model in order to explore the notion of competing hazards. With this model, we will be able to calculate the case fatality rate (CFR). The model to specify has 3 "compartments": I (infected), R (recovered) and M (dead).
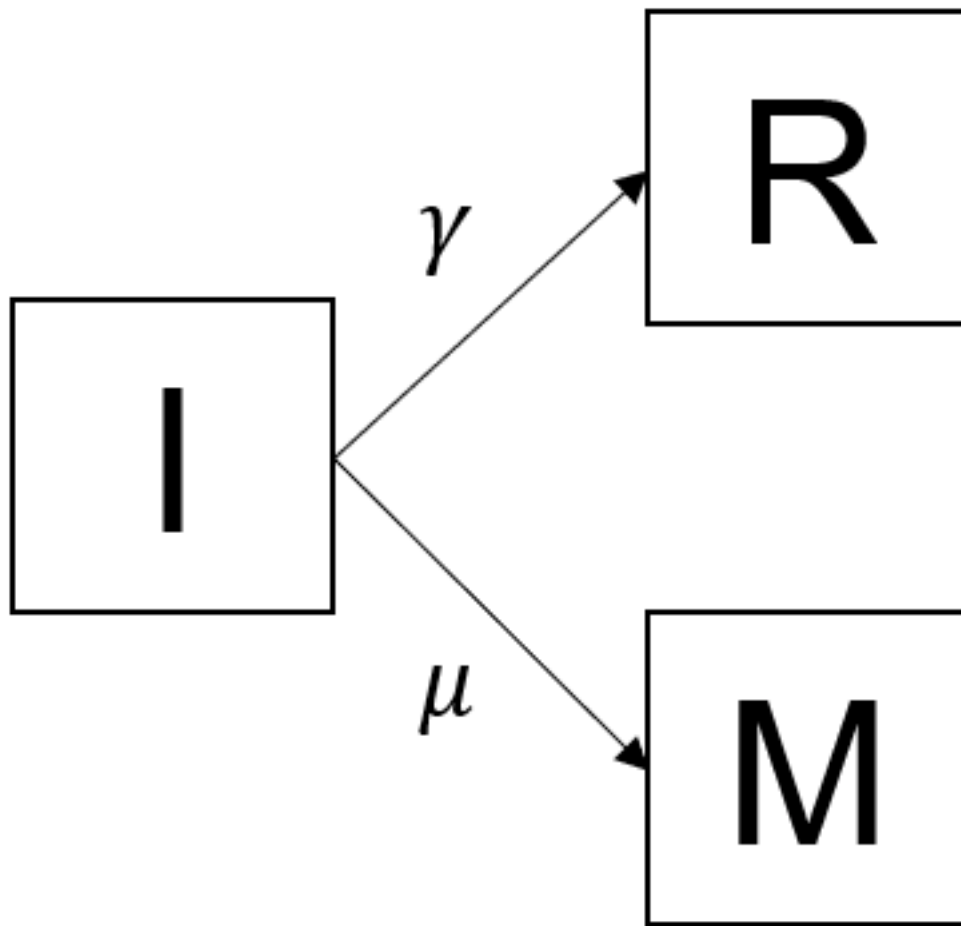
The differential equations for the model are as follows:

$$\frac{dI}{dt} = -\gamma I - \mu I \tag{1}$$

$$\frac{dR}{dt} = \gamma I \tag{2}$$

$$\frac{dM}{dt} = \mu I \tag{3}$$

γ (*gamma*) represents the recovery rate while μ (*mu*) represents the morality rate. According to our setup, all members of the infected cohort either transition into the recovery compartment or mortality compartment.

To describe our model, we can use the model function we initially made to model an infected cohort with some changes.

Building the Model

We will begin first by loading in the required libraries.

```
library(deSolve)
library(reshape2)
library(ggplot2)
```

Now, we will use our model from before, but add a new compartment for the morality rate.

```
cohort_model <- function(time, state, parameters) {

    with(as.list(c(state, parameters)), {

        dI <- (-1)*(gamma)*(I) - (mu)*(I)
        dR <- (gamma)*(I)
        dM <- (mu)*(I)

```

```
        return(list(c(dI, dR, dM)))
    })
}
```

We now must initialize our initial state values, parameters, and times. At the start, we know there are 10^6 infected people, and that no one has recovered or died yet. The recovery rate γ is 0.1 days^{-1} and the mortality rate μ is 0.2 days^{-1}. Similar to before, we want to model the course of the infection over 4 weeks or 28 days.

```
initial_number_infected <- 1000000
initial_number_recovered <- 0
initial_number_dead <- 0 # new compartment

recovery_rate <- 0.1
morality_rate <- 0.2 # new rate to consider

follow_up_duration <- 28
times <- seq(from = 0, to = follow_up_duration, by = 1)

initial_state_values <- c(I = initial_number_infected,
                          R = initial_number_recovered,
                          M = initial_number_dead)

parameters <- c(gamma = recovery_rate, mu = morality_rate) # two parameters are now used
```

We can now use the deSolve package to solve the differential equations.

```
output <- as.data.frame(ode(y = initial_state_values,
                            times = times,
                            func = cohort_model,
                            parms = parameters))
```
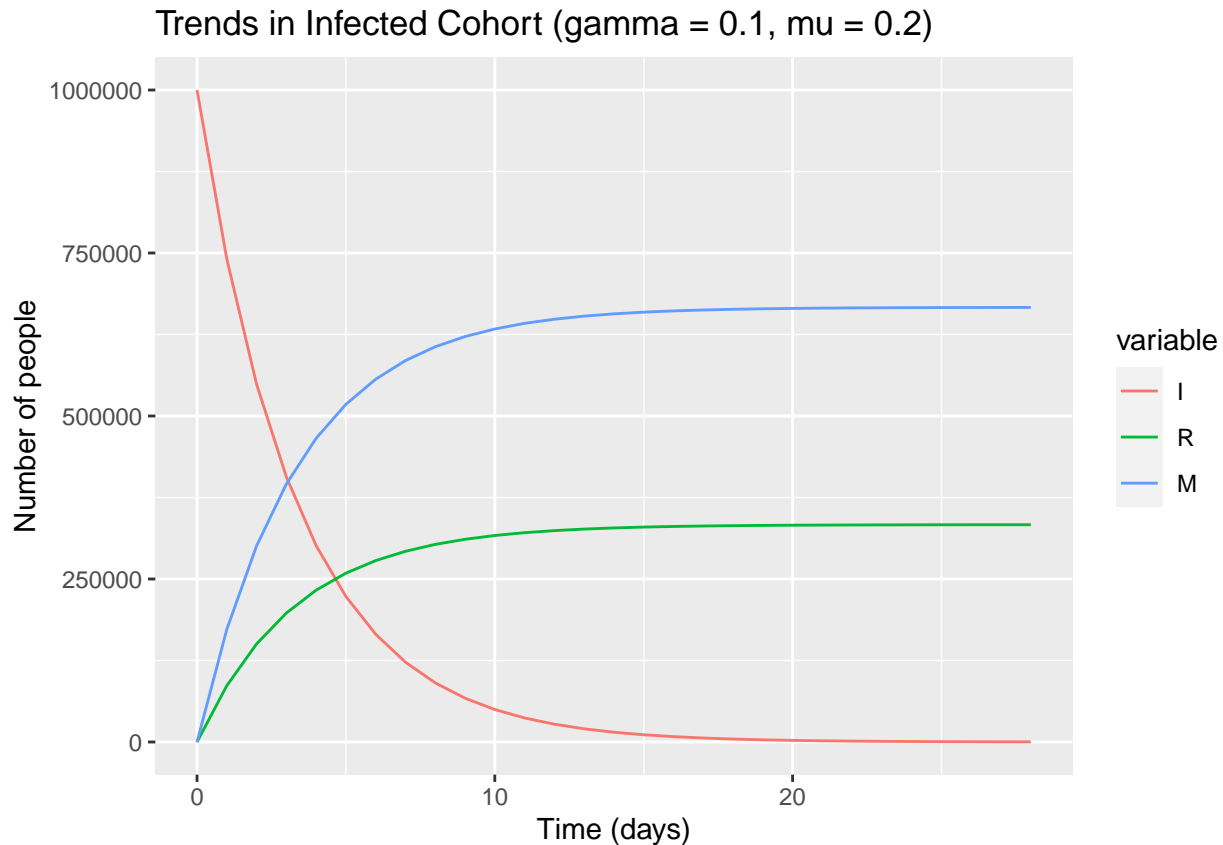
```
output_long <- melt(as.data.frame(output), id = "time")# we turn this dataset into a long format,
                                                        # so that the number in each compartment at each time

ggplot(data = output_long,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("Trends in Infected Cohort (gamma = 0.1, mu = 0.2)")
```

Trends in Infected Cohort (gamma = 0.1, mu = 0.2)

We see that at the end of 28 days, more people have died than recovered. This is because of the mortality and recovery rates. The mortality rate μ (*mu*) was 0.2, and was greater than recovery rate γ (*gamma*) at 0.1.

Questions

Based on the model output, what proportion of the initially infected cohort died before recovering over the 4 week period?

To answer this question, we can use our output to see how many infected persons died.

```
as.numeric(output[output["time"] == 28][4])
```

```
## [1] 666516.8
```

We see that 666517 persons, approximately, died before they recovered. This computes a proportion of $\frac{666516.8}{1000000} \approx 0.6665168$.

Calculate the case fatality rate

We'll use the following formula to compute the case fatality rate:

$$CFR = \frac{\mu}{\mu + \gamma}$$

```
cfr <- (0.2)/(0.2 + 0.1)
cfr
```

```
## [1] 0.6666667
```

We see that the case fatality rate is 0.6666, which is nearly exactly how many infected persons died from the model.

Which value of μ do you need to get a case fatality rate of 50% assuming γ stays fixed?

We can use the following math:

$$CFR = \frac{\mu}{\mu + \gamma} \tag{4}$$

$$\mu = CFR(\mu + \gamma) \tag{5}$$

$$\mu = \mu CFR + \gamma CFR \tag{6}$$

$$\mu - \mu CFR = \gamma CFR \tag{7}$$

$$\mu(1 - CFR) = \gamma CFR \tag{8}$$

$$\mu = \frac{\gamma CFR}{1 - CFR} \tag{9}$$

Then, using conditions μ with CFR = 0.50 and $\gamma = 0.1$:

$$\mu = \frac{0.1 * 0.50}{1 - 0.50} \tag{10}$$

$$\mu = 0.1 \tag{11}$$

If γ stays fixed at 0.1, then the only value of μ that could provide a CFR of 0.5 is 0.1 as well, because then they would be equal competing hazards. We will now simulate the model again using this new μ value to verify.

```
recovery_rate5 <- 0.1
recovery_rate5 <- 0.1

parameters5 <- c(gamma = recovery_rate5, mu = recovery_rate5)

output5 <- as.data.frame(ode(y = initial_state_values,
                             times = times,
                             func = cohort_model,
                             parms = parameters5))

output_long5 <- melt(as.data.frame(output5), id = "time")# we turn this dataset into a long format,
                                              # so that the number in each compartment at each time

ggplot(data = output_long5,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("Trends in Infected Cohort (gamma = 0.1, mu = 0.1)")
```

Trends in Infected Cohort (gamma = 0.1, mu = 0.1)
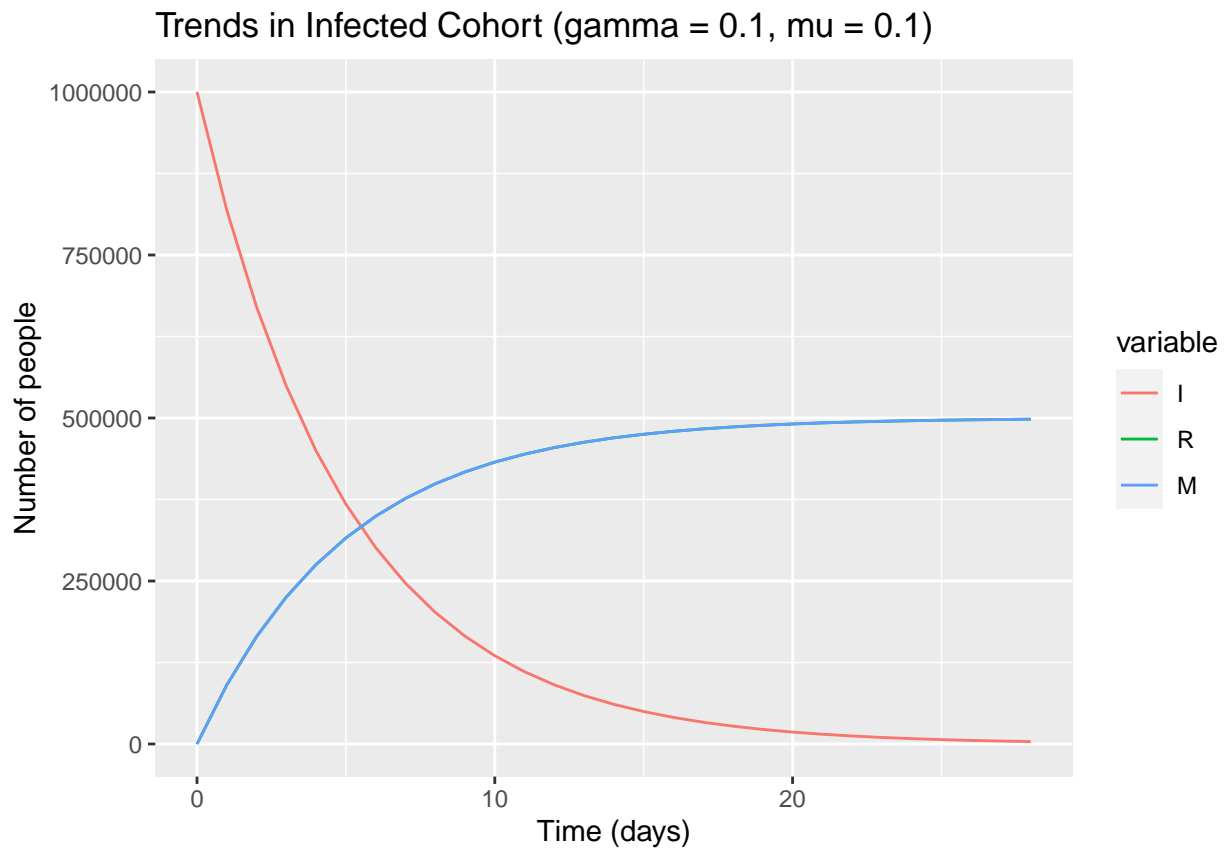
Here, the recovery and mortality lines are on top of each other because they share the same values. We see and verify that our case mortality rate is 0.5.

```
fatalities <- output5[output5["time"] == 28][3]
fatalities/1000000
```

```
## [1] 0.4981511
```

$0.4981511 \approx 0.5$, so we can verify our CFR is 0.5.