Ordinary Differential Equations

Modern Techniques in Modelling

Outline for session 1

- What are ordinary differential equations (ODEs)?
- How do we use ODEs to model an epidemic?
- Using the R package `deSolve`
  - Practical: SI, SIR, SEIR models in R

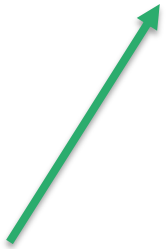
Ordinary differential equations

Reminder: Difference equations

In the previous session, we explored difference equations:

$$
\begin{aligned}
S(t+1) &= S(t) &&- \beta\, S(t)\, I(t) \\
I(t+1) &= I(t) &&+ \beta\, S(t)\, I(t) - \gamma\, I(t) \\
R(t+1) &= R(t) &&+ \gamma\, I(t)
\end{aligned}
$$

next value = current value + change in value



These changes are the interesting part –
they are what define the behaviour of the system.

Ordinary differential equations

Difference equations

$$
\begin{aligned}
S(t+1) &= S(t) - \beta\, S(t)\, I(t) \\
I(t+1) &= I(t) + \beta\, S(t)\, I(t) - \gamma\, I(t) \\
R(t+1) &= R(t) + \gamma\, I(t)
\end{aligned}
$$

Ordinary differential equations have a similar structure, but only the rate of change is given:

$$
\begin{aligned}
dS(t)/dt &= -\beta\, S(t)\, I(t) \\
dI(t)/dt &= \beta\, S(t)\, I(t) - \gamma\, I(t) \\
dR(t)/dt &= \gamma\, I(t)
\end{aligned}
$$

The explicit dependence on time is often omitted (e.g. S is written instead of $S(t)$)

Ordinary differential equations

Difference equations

$$
\begin{aligned}
S(t+1) &= S(t) - \beta\, S(t)\, I(t) \\
I(t+1) &= I(t) + \beta\, S(t)\, I(t) - \gamma\, I(t) \\
R(t+1) &= R(t) + \gamma\, I(t)
\end{aligned}
$$

Ordinary differential equations have a similar structure, but only the rate of change is given:

$$
\begin{aligned}
dS/dt &= -\beta\, S\, I \\
dI/dt &= \beta\, S\, I - \gamma\, I \\
dR/dt &= \gamma\, I
\end{aligned}
$$

The explicit dependence on time is often omitted
(e.g. S is written instead of $S(t)$)

Ordinary differential equations

Mathematically, dX/dt represents the derivative of *X* with respect to time (i.e. the rate at which *X* is changing over time).

For example, is *S* is the number of susceptibles, *t* is measured in days, and we have

$$dS/dt = -\beta\, S\, I = -2$$

then this means the number of susceptibles is currently shrinking at a rate of 2 people per day, and in one day's time will have around* 2 people fewer.

* not exactly 2, because over the course of that day, the value of $-\beta\, S\, I$ will change!

We will look at examples in the next section.

How do we model an infectious disease outbreak using ODEs?

Turning a model diagram into ODEs

With variables:

S the number of susceptible people

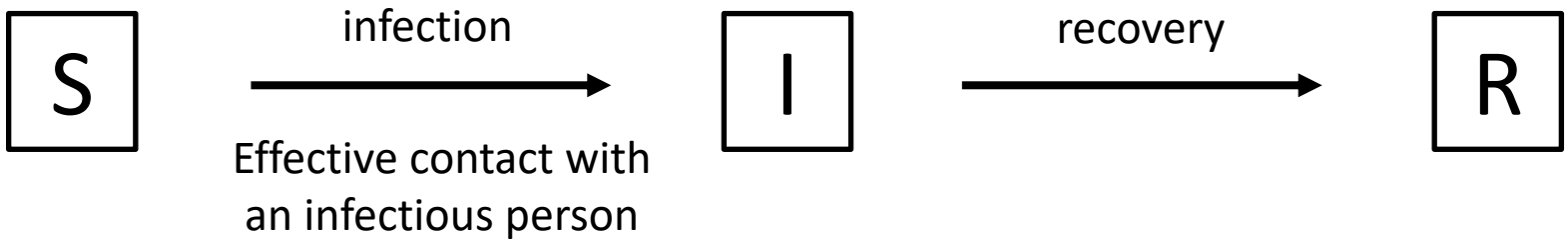
I the number of infectious people

R the number of recovered people

$N = S + I + R$ the total number of people

Let's look at the "infection" and "recovery" transitions in more detail.

Turning a model diagram into ODEs



Rate of effective contact with an infectious person:

A person contacts c people per day…

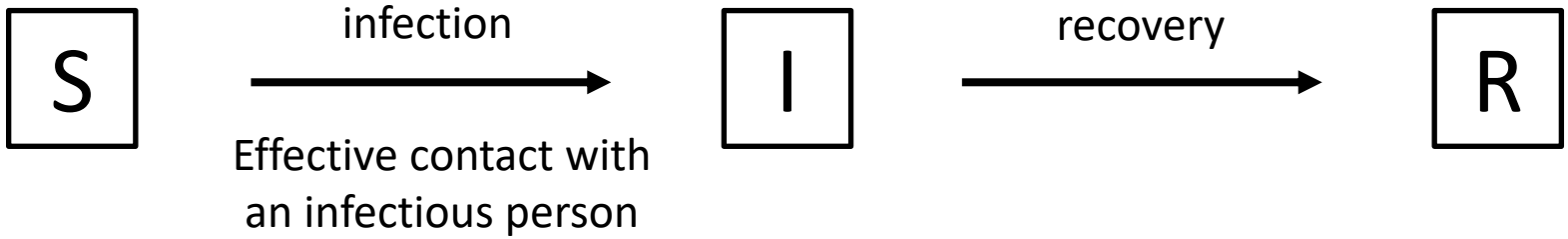
A fraction $I/(S+I+R) = I/N$ of these contacts are infectious…

A fraction p of these contacts with infectious people are effective…

And there are S susceptible people in total at risk of infection.

$$\text{rate}(S \rightarrow I) =$$

Turning a model diagram into ODEs



Rate of effective contact with an infectious person:

A person contacts c people per day…

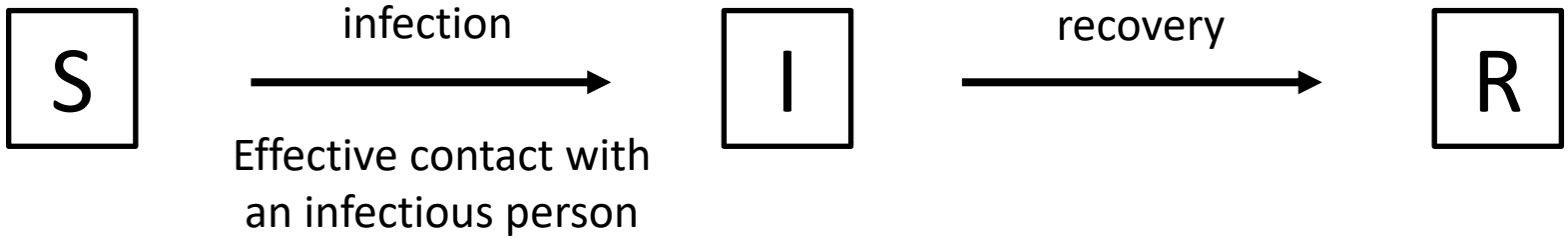
A fraction $I/(S+I+R) = I/N$ of these contacts are infectious…

A fraction p of these contacts with infectious people are effective…

And there are S susceptible people in total at risk of infection.

$$\text{rate}(\text{S} \rightarrow \text{I}) = c \times I/N \times p \times S$$

Turning a model diagram into ODEs



Rate of effective contact with an infectious person:

A person contacts c people per day…

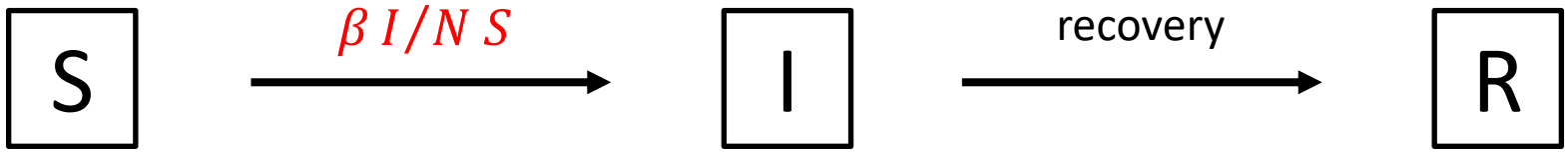
A fraction $I/(S+I+R) = I/N$ of these contacts are infectious…

A fraction p of these contacts with infectious people are effective…

And there are S susceptible people in total at risk of infection.

$$\text{rate}(\text{S} \rightarrow \text{I}) = \beta \times I/N \times S \qquad (\beta = cp)$$

Turning a model diagram into ODEs



Rate of effective contact with an infectious person:

A person contacts c people per day…

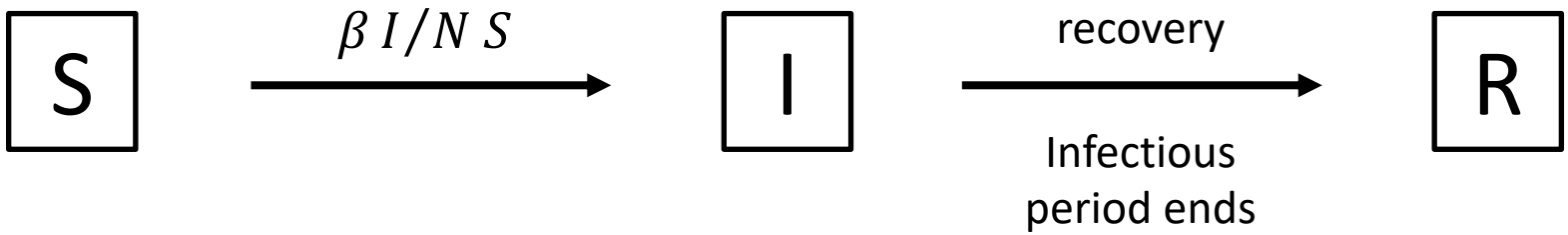
A fraction $I/(S+I+R) = I/N$ of these contacts are infectious…

A fraction p of these contacts with infectious people are effective…

And there are S susceptible people in total at risk of infection.

$$\text{rate}(\text{S} \rightarrow \text{I}) = \beta \times I/N \times S \qquad (\beta = cp)$$

Turning a model diagram into ODEs



Rate of recovery:

Suppose we know the infectious period lasts for d days…

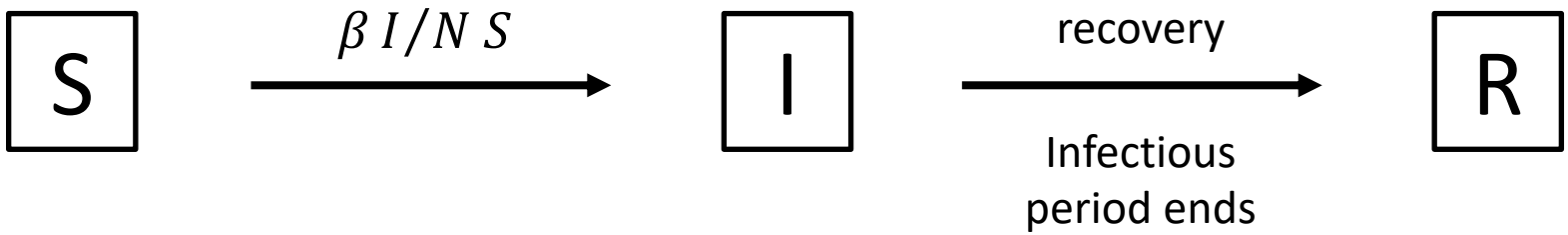
Then the rate of recovery is $1/d$ per day…

(e.g. if something happens 2x per day, on average it happens every 0.5 days)

And there are I infectious people in total at "risk" of recovery.

$$\text{rate}(\mathrm{I} \rightarrow \mathrm{R}) =$$

Turning a model diagram into ODEs



Rate of recovery:

Suppose we know the infectious period lasts for d days…

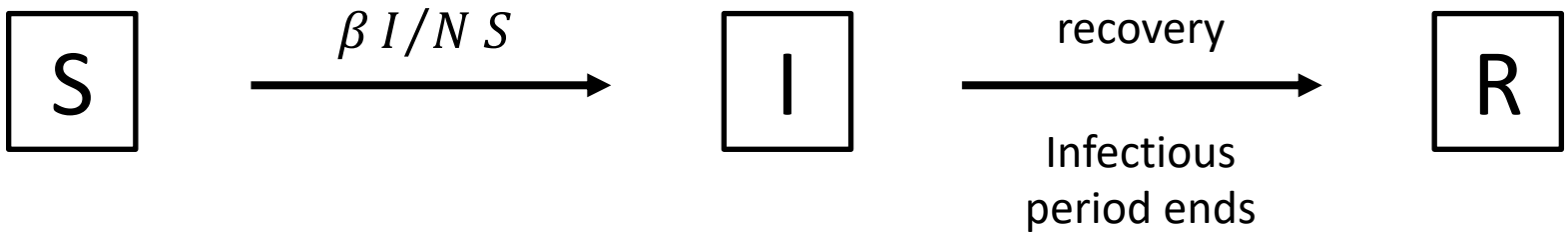
Then the rate of recovery is $1/d$ per day…

(e.g. if something happens 2x per day, on average it happens every 0.5 days)

And there are I infectious people in total at "risk" of recovery.

$$\text{rate}(\text{I} \rightarrow \text{R}) = \boxed{1/d} \times I$$

Turning a model diagram into ODEs



Rate of recovery:

Suppose we know the infectious period lasts for d days…

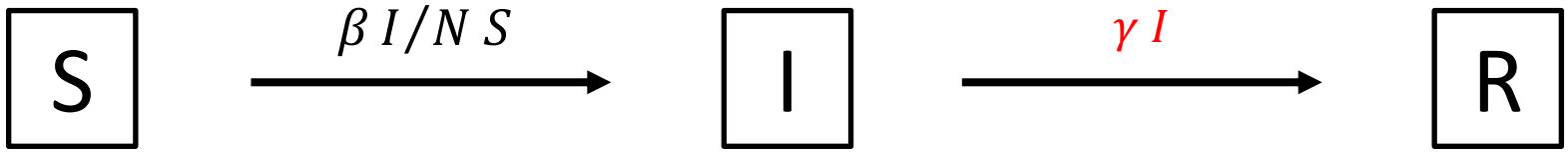
Then the rate of recovery is $1/d$ per day…

(e.g. if something happens 2x per day, on average it happens every 0.5 days)

And there are I infectious people in total at "risk" of recovery.

$$\text{rate}(\text{I} \rightarrow \text{R}) = \gamma \times I \qquad (\gamma = 1/d)$$

Turning a model diagram into ODEs



Rate of recovery:

Suppose we know the infectious period lasts for d days…

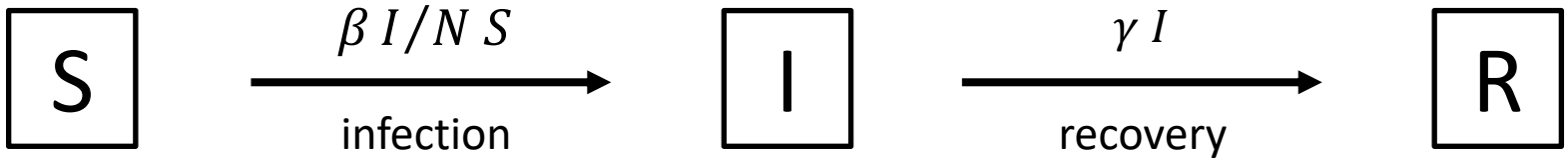
Then the rate of recovery is $1/d$ per day…

(e.g. if something happens 2x per day, on average it happens every 0.5 days)

And there are I infectious people in total at "risk" of recovery.

$$\text{rate}(\text{I} \rightarrow \text{R}) = \gamma \times I \qquad (\gamma = 1/d)$$

Turning a model diagram into ODEs



Note that above, both transitions are specified as:

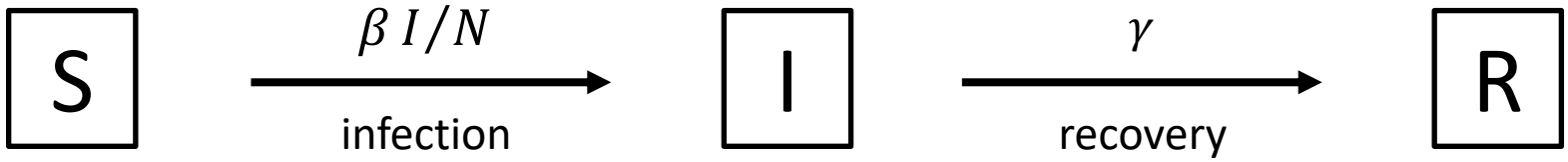
"rate per person per day" times "number of people at risk"

infection: $\beta\, I/N$ times S

recovery: γ times I

Often in model diagrams, the "number of people at risk" term is omitted, and implied by where the arrow is coming from.

Turning a model diagram into ODEs



Note that above, both transitions are specified as:

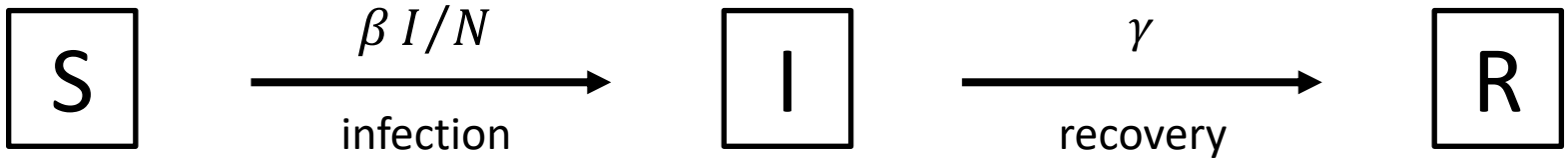
"rate per person per day" times "number of people at risk"

infection: $\beta\, I/N$ times S

recovery: γ times I

Often in model diagrams, the "number of people at risk" term is omitted, and implied by where the arrow is coming from.

Turning a model diagram into ODEs

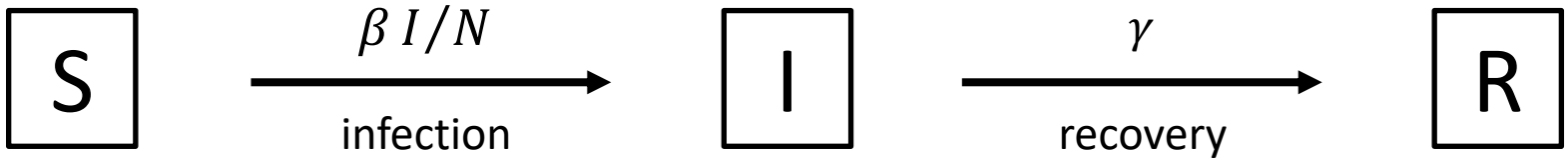


To turn this into ODEs, we include each rate twice:

once negative for the "leaving" (subtracting from) compartment,
and once positive for the "entering" (adding to) compartment.

$$
\begin{aligned}
dS/dt &= -(\beta I/N)S \\
dI/dt &= (\beta I/N)S - \gamma I \\
dR/dt &= \gamma I
\end{aligned}
$$

Turning a model diagram into ODEs



A full ODE model specification has the following elements:

System of ordinary differential equations

$$dS/dt = -(\beta I/N)S$$
$$dI/dt = (\beta I/N)S - \gamma I$$
$$dR/dt = \gamma I$$
$$N = S + I + R$$

Initial conditions

$$S(0) = 9{,}999$$
$$I(0) = 1$$
$$R(0) = 0$$

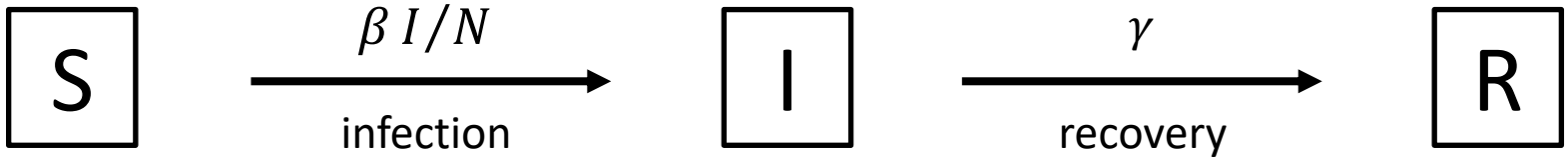
Parameters

$$\beta = 0.8$$
$$\gamma = 0.4$$

Times to solve system for

$$t \in \{0, 1, 2, \ldots, 60\}$$

Turning a model diagram into ODEs



A full ODE

System of ord

dS/dt =

dI/dt =

dR/dt =

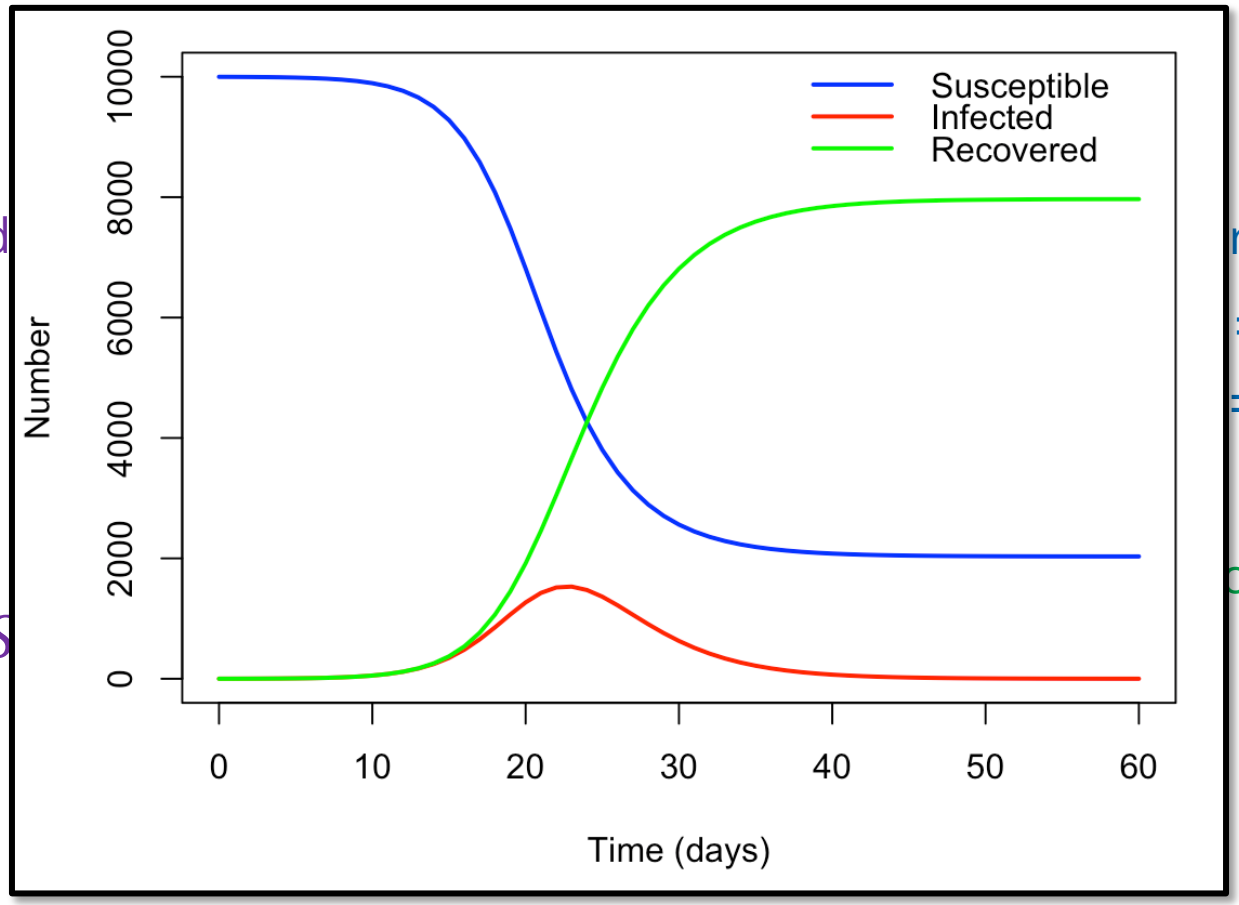
$N = S$

rameters

$= 0.8$

$= 0.4$

or



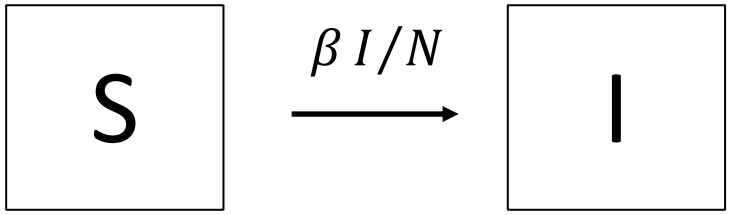
Solving ODE models in R with the deSolve package

Using the R package deSolve

- R package which can numerically solve ODEs
- Provides the function `ode()` to solve your model
- You provide to `ode()`:
  - `y`, initial conditions
  - `times`, time points to solve the system for
  - `parms`, parameters
  - `func`, the system of ODEs as an R function
  - (optionally, others we will discuss later…)
- `ode()` returns a matrix with numerical solutions to the ODEs and the times

Susceptible Infected (SI) model

Individuals are either susceptible or infected:



Susceptible individuals become infected via transmission rate β.

$$dS/dt = -(\beta I/N)S$$
$$dI/dt = (\beta I/N)S$$

Solving SI model using deSolve

- Provide to `ode()`:
  - `y`, initial conditions

Assume we have population of $N = 100$, with 1 infected individual:

```
N <- 100
I_0 <- 1
S_0 <- N - I_0

y <- c(S = S_0, I = I_0)
```

Solving SI model using deSolve

- Provide to `ode()`:
  - `times`, time points to solve the system for

Let's solve the equation over a period of 50 days, which we will write inside a vector as follows:

```
times <- seq(from = 0, to = 50, by = 1)
# or times <- 0:50
```

Solving SI model using deSolve

- Provide to `ode()`:
  - `parms`, parameters

We have just one parameter, the transmission rate:

```
parms <- c(beta = 0.4)
```

Solving SI model using deSolve

- Provide to `ode()`:
  - `func`, the system of ODEs as an R function

```
SI_model <- function(times, state, parms)
{
  # Get variables
  S <- state["S"]
  I <- state["I"]
  N <- S + I
  # Get parameters
  beta <- parms["beta"]
  # Define differential equations
  dS <- -(beta * I / N) * S
  dI <- (beta * I / N) * S
  res <- list(c(dS, dI))
  return (res)
}
```

Solving SI model using deSolve

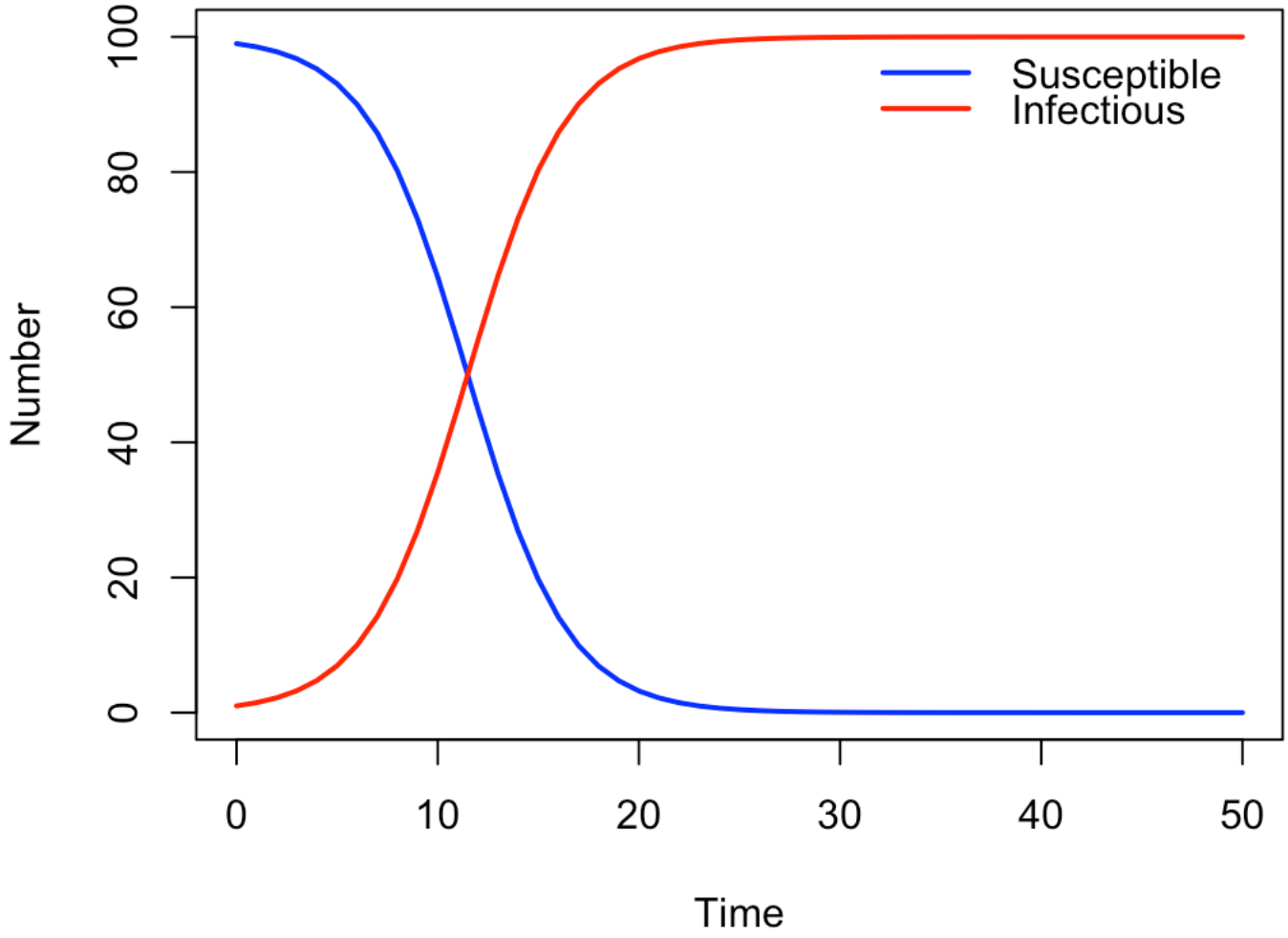
```
# Solve equations
output_raw <- ode(y = y, times = times,
                  func = SI_model, parms = parms)

# Convert matrix to data frame for easier manipulation
output <- as.data.frame(output_raw)

head(output)
```

```
##   time        S        I
## 1    0 99.00000 1.000000
## 2    1 98.60400 1.396000
## 3    2 98.05340 1.946605
## 4    3 97.28991 2.710090
## 5    4 96.23525 3.764747
## 6    5 94.78605 5.213953
```

Solving SI model using deSolve



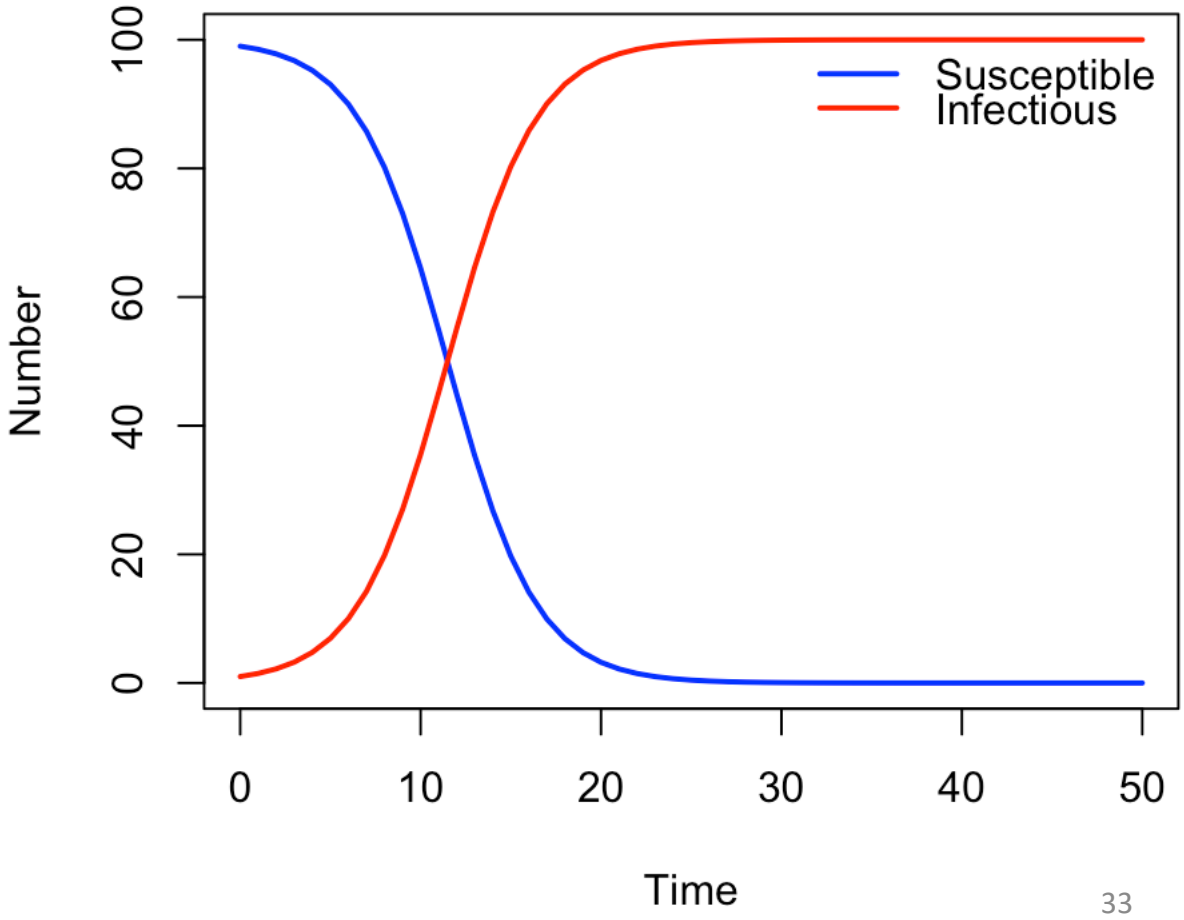
Practical 1
Solving ODEs using `deSolve`

Practical 1

- Objective: Solve SI, SIR, SEIR models using `deSolve`
- Answer questions 1, 2 and 3
- Question 4, adding vaccination, is optional.

Practical 1: SI model

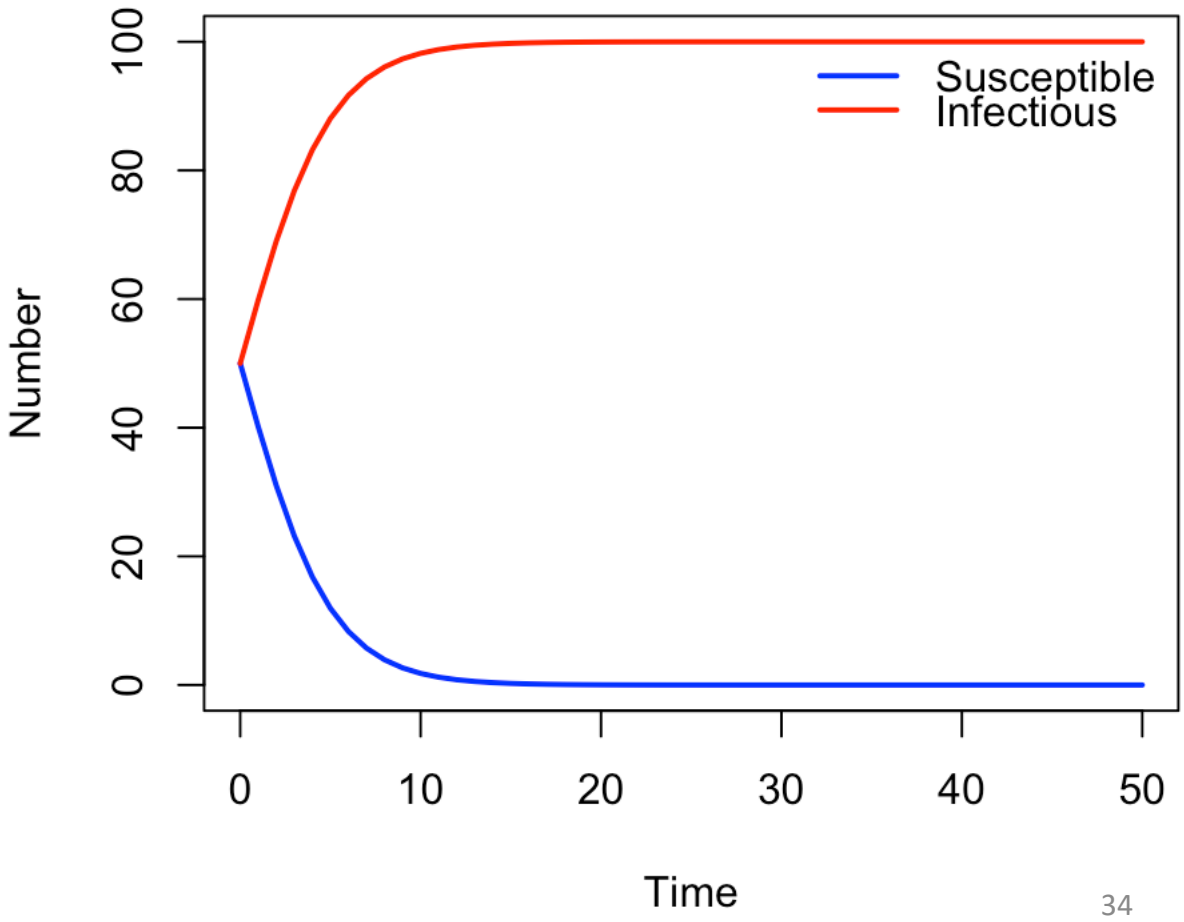
1a. Increase the initial number of infectious individuals. What happens to the output?



Practical 1: SI model

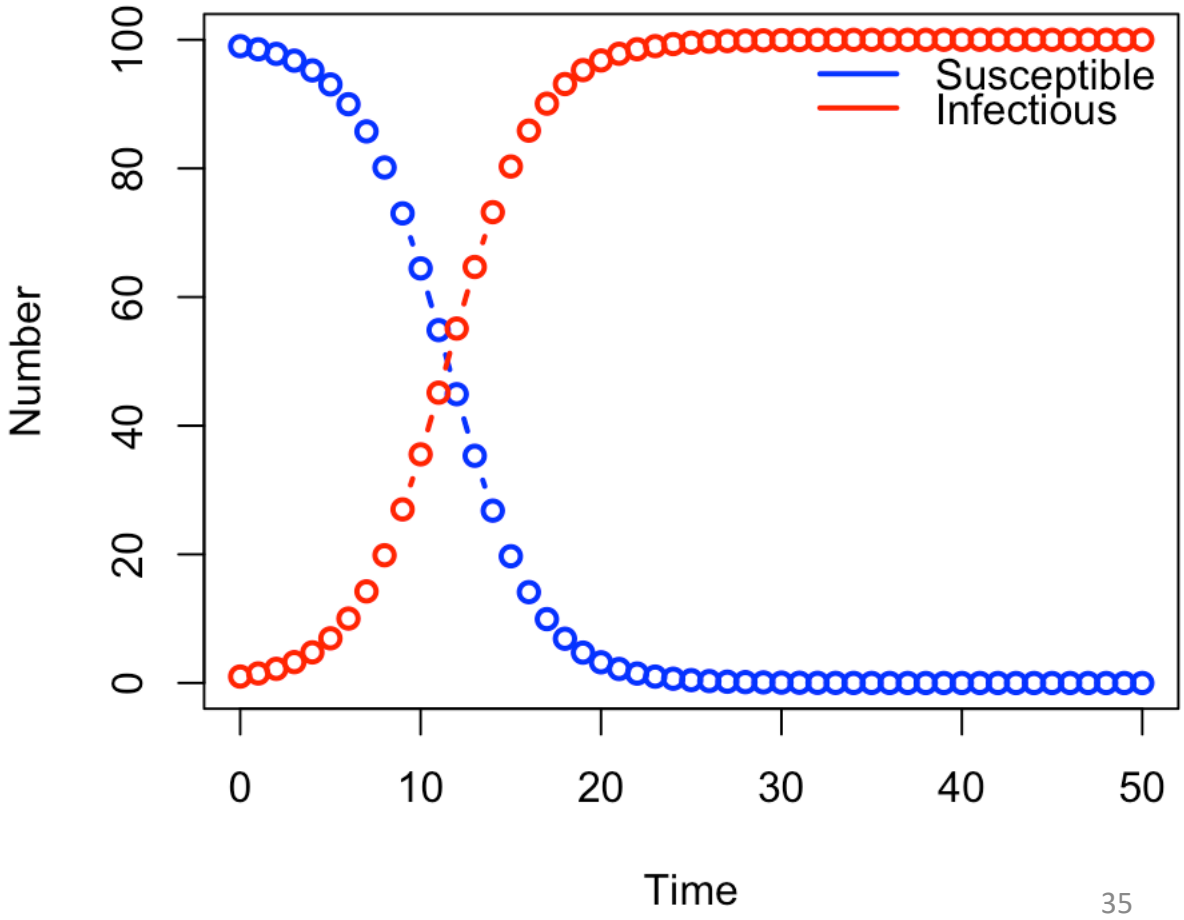
1a. Increase the initial number of infectious individuals. What happens to the output?

The number of infectious has a higher starting point, but the same growth rate from that level, and the same endpoint.



Practical 1: SI model

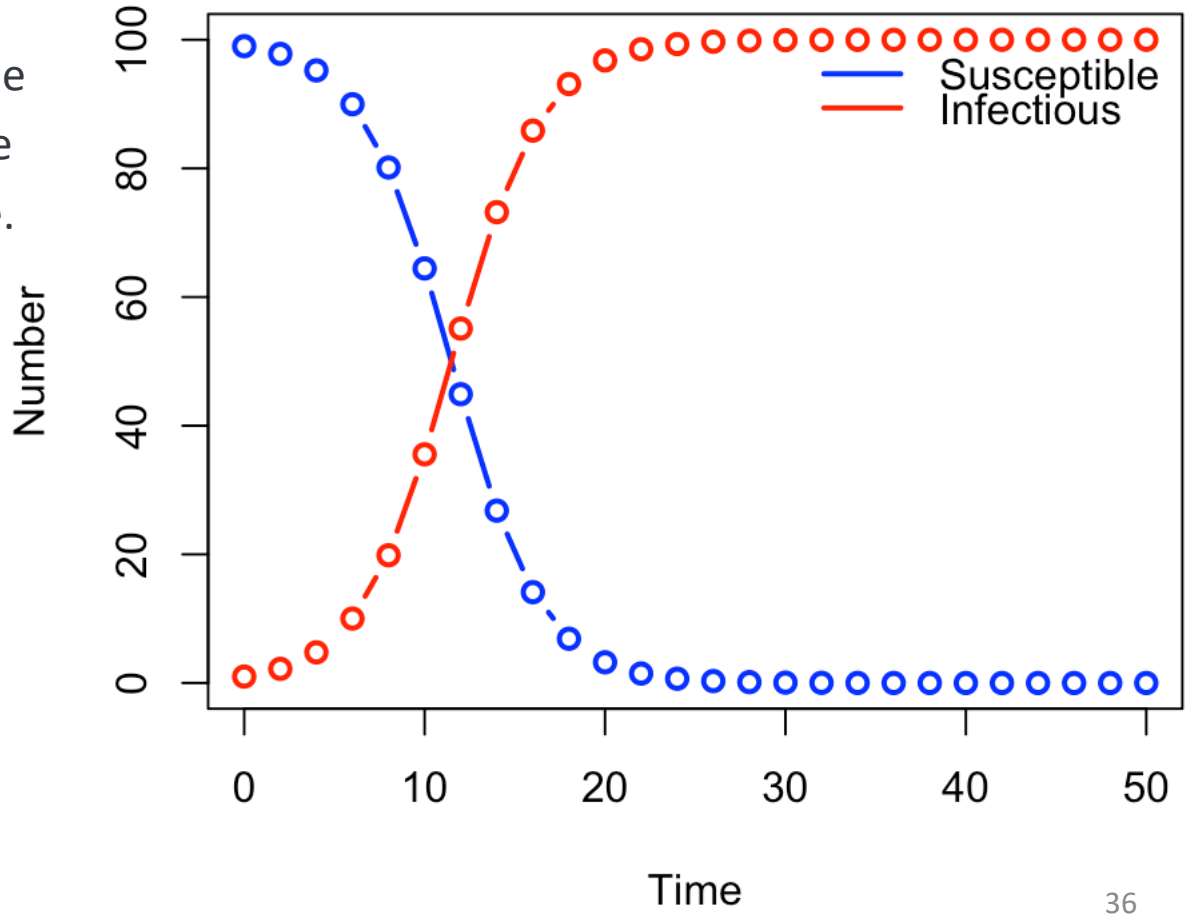
1c. Increase the value of the `by` argument (in the `times` vector).
What happens to the output?



Practical 1: SI model

1c. Increase the value of the `by` argument (in the `times` vector).
What happens to the output?

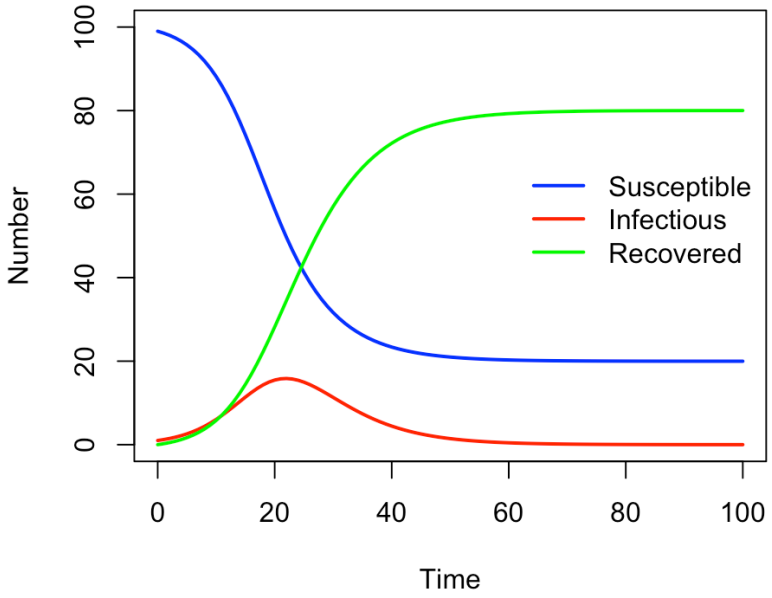
The solution points become more spaced out, but trace the same underlying curve.



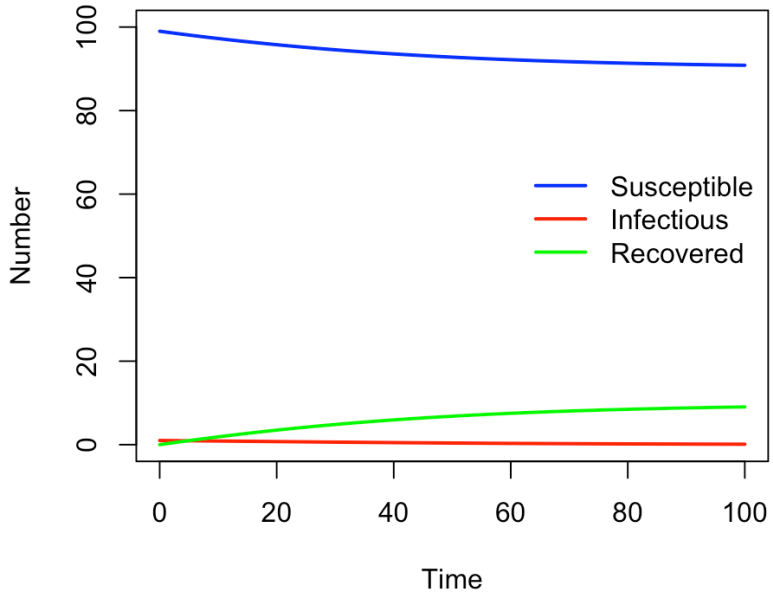
Practical 1: SIR model

2b. Change the value of the transmission rate so that the basic reproduction number is less than one, i.e. $R_0 < 1$. What happens to the output?

$\beta = 0.4, \gamma = 0.2$



$\beta = 0.19, \gamma = 0.2$

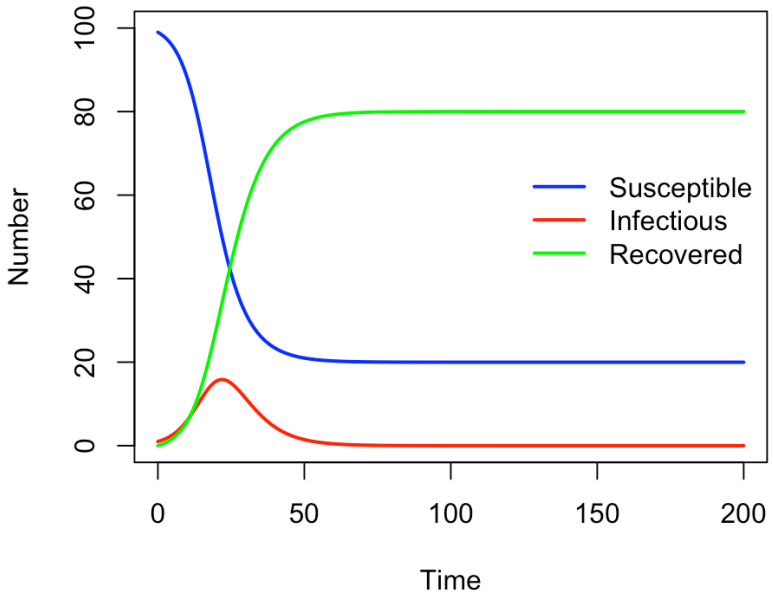


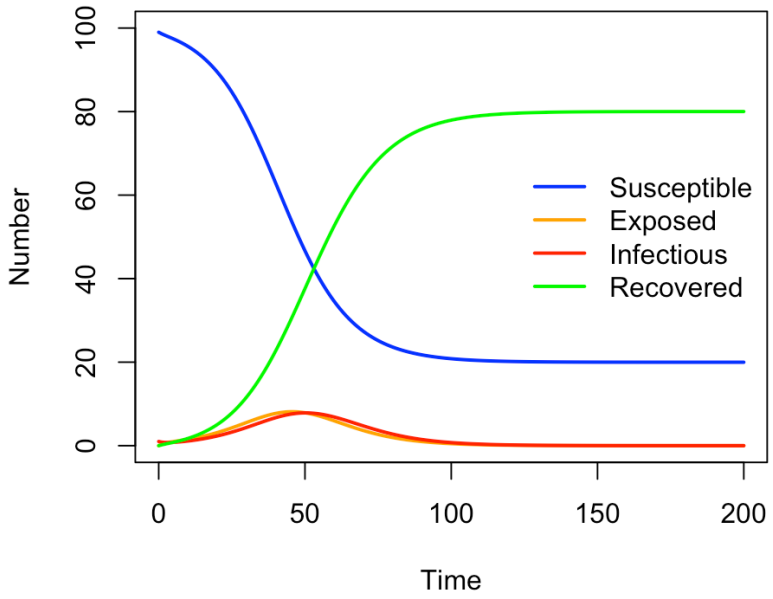
Recall that for an SIR model, the basic reproduction number $R_0 = \beta/\gamma$.

When $R_0 < 1$, the epidemic does not take off.

Practical 1: SEIR model

3b. How does the model output differ from the SIR model you coded previously?





Approximately the same number of people get infected, but the epidemic takes approximately twice as long; generation interval is twice as long.

See Wallinga and Lipsitch 2007, especially section 3a, for discussion of the generation interval, the growth rate and the reproduction number in epidemic models.

ODEs session 1 summary

- ODE models are specified in terms of state variables and their rates of change
- We have seen how to construct ODE systems starting from a flowchart-style model diagram
- To solve an ODE model, we need to provide initial conditions for the state variables, parameter values, and times over which to solve the model
- We have learned how to use `deSolve` to solve ODEs in R
- Next session: Advanced use of `deSolve`.