Spreading of diseases

Simple models, Common Questions and Assumptions

We will be discussing here models for directly transmitted infectious diseases: simple deterministic, compartmentalized models

● How is the disease spread among the population?

The disease is spread by human contact

● How do we go about modeling the spreading?

The population can be divided into a set of distinct compartments, or the individuals into distinct conditions, with respect to disease status

   ● Susceptible (S) - individuals who are not infected, or are in a uninfected state, and they can catch the disease

   ● Infected (I) - infected individuals can spread the disease to susceptible individuals

   ● Recovered (R) - individuals in the recovered compartment are assumed to be immune for life. They also do not infect others

- What about those deadly epidemics where all infected never recover and eventually die?

  We can allow deaths and reduce the different populations correspondingly - even the uninfected can have a natural death rate. In such cases, the total population is no longer constant

- What about those diseases where the recovered are again subject to infection?

  For these, there will be no Recovered category. Those who recover fall back into the Susceptible category

- Can we also model those diseases (chicken pox, dengue) where individuals experience a long incubation duration (the "Exposed" category), such that the individual is infected but not yet infectious?

  This can also be studied in the SEIR(S) model [Susceptible-Exposed-Infectious-Recovered(-Susceptible)]

Assumptions of "classical" SIR, SIS, SEIR models

The classical models of epidemics have been constructed as sets of ordinary differential equations (ODEs), which implies several simplifying assumptions:

- time and population sizes change on continuous scales, with all processes occurring continuously and simultaneously

- there is complete mixing within the classes or compartments of the model

- a given set of initial conditions always lead to exactly the same outcome

https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology

SIR Model

The SIR model of epidemics

In this type of models, we assume

- encounters between infected and susceptible individuals occurs at a rate proportional to their respective numbers (denoted by I and S) in the population

  - the rate of infection is then defined as $\beta S I$, where β is a parameter for infectivity

- infected individuals recover with a constant rate at any time

  - constant per capita recovery rate r, giving an overall rate of recovery rI.

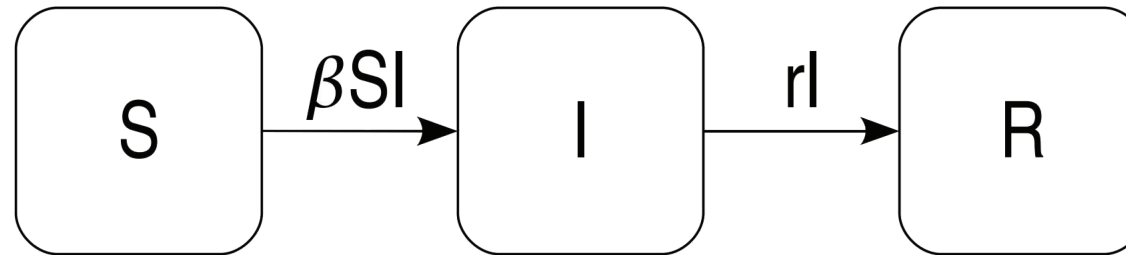# Scheme of the SIR model

A simple schematic representation of the SIR model is then

- The rate of change (reduction) in the Susceptible population is by infection

- The Infected population has an addition (Susceptibles that got infected) and a reduction (the Infected who recovered)

- The rate of change of the Recovered population is directly proportional to the existing Infected population

The SIR model can then be expressed as a set of differential equations:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI,$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - rI,$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = rI$$

S $\xrightarrow{\beta\text{SI}}$ I $\xrightarrow{\text{rI}}$ R
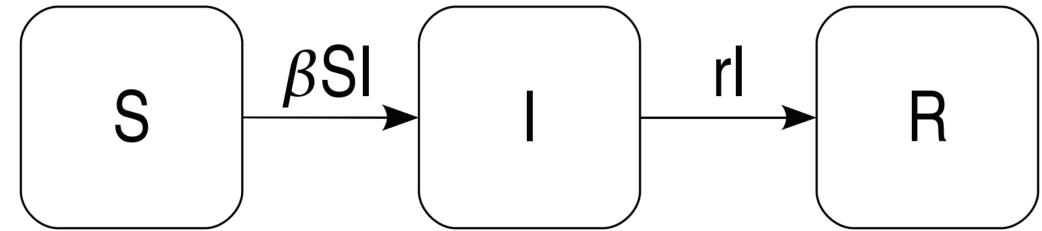
- This model is applicable to mild, short-lived epidemic in a closed population, in which the total population $N = (S + I + R)$ is constant, i.e. $\dfrac{\mathrm{d}N}{\mathrm{d}t} = 0$

- The first 2 equations do not involve the recovered population R at all, and can be considered as a closed set.

- Once we solve the first 2 equations for S and I, R can be deduced as $R = N - S - I$.

Some initial observations

The SIR model equations allow us to draw a few immediate statements:

- The epidemic will start/continue if and only if $\mathrm{d}I/\mathrm{d}t > 0$. From the second of the SIR equations (ie $\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - rI$), this implies $\beta S/r > 1$

- If initially (i.e. $t = 0$), the population is large (i.e. $N \gg 1$) and disease-free (i.e. $S(t = 0) \approx N$), then an epidemic will start to develop only if

$$R_0 \equiv \frac{\beta N}{r} > 1$$

R_0 is referred to as the basic reproductive ratio in epidemiology.

Herd Immunity

How Do You Achieve Herd Immunity?

There are two ways this can happen:

- Developing resistance naturally. When your body is exposed to a virus or bacteria, it makes antibodies to fight off the infection. When you recover, your body keeps these antibodies and will defend against another infection

- Vaccines can also build resistance. They make your body think a virus or bacteria has infected it. You don't get sick, but your immune system still makes protective antibodies

Herd Immunity cont'd

When does a community reach herd immunity?

- It depends on the basic reproductive ratio, R_0. The R_0 tells you the average number of people that a single person with the virus can infect if those people aren't already immune. The higher the R_0, the more people need to be resistant to reach herd immunity

- Suppose R_0 for COVID-19 is between 2 and 3. This means that one person can infect two to three other people. It also means 50% to 67% of the population would need to be resistant before herd immunity kicks in and the infection rates start to go down

How quickly does it spread?

R_0 is a measure of how quickly the epidemic will spread

How quickly does it spread?
Basic reproduction value

Mers	Ebola	Small pox	Measles
0.7	1.7	7	17

Source: ECDC, UMICH, Lancet

"Normalized" SIR formulation

We can "normalize" the populations so that the solutions are applicable for any total population size N

- Define $S' \equiv S/N$, $I' \equiv I/N$ and $R' \equiv R/N$

In terms of these normalized populations, the SIR equations

$$\left\{ \frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI, \quad \frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - rI, \quad \frac{\mathrm{d}R}{\mathrm{d}t} = rI \right\} \quad \text{become}$$

$$\frac{\mathrm{d}S'}{\mathrm{d}t} = -rR_0 S'I',$$

$$\frac{\mathrm{d}I'}{\mathrm{d}t} = rI'(R_0 S' - 1),$$

$$\frac{\mathrm{d}R'}{\mathrm{d}t} = rI'$$

We now have

$0 \leq S' \leq 1,$
$0 \leq I' \leq 1,$
$0 \leq R' \leq 1$

and two parameters, namely R_0 and r

Computational simulations

We can solve the (first two) SIR equations using the Python ODE integrator

We will be interested in the development of the epidemic when only a very small number ($I' \ll 1$) infected individuals are introduced into the population

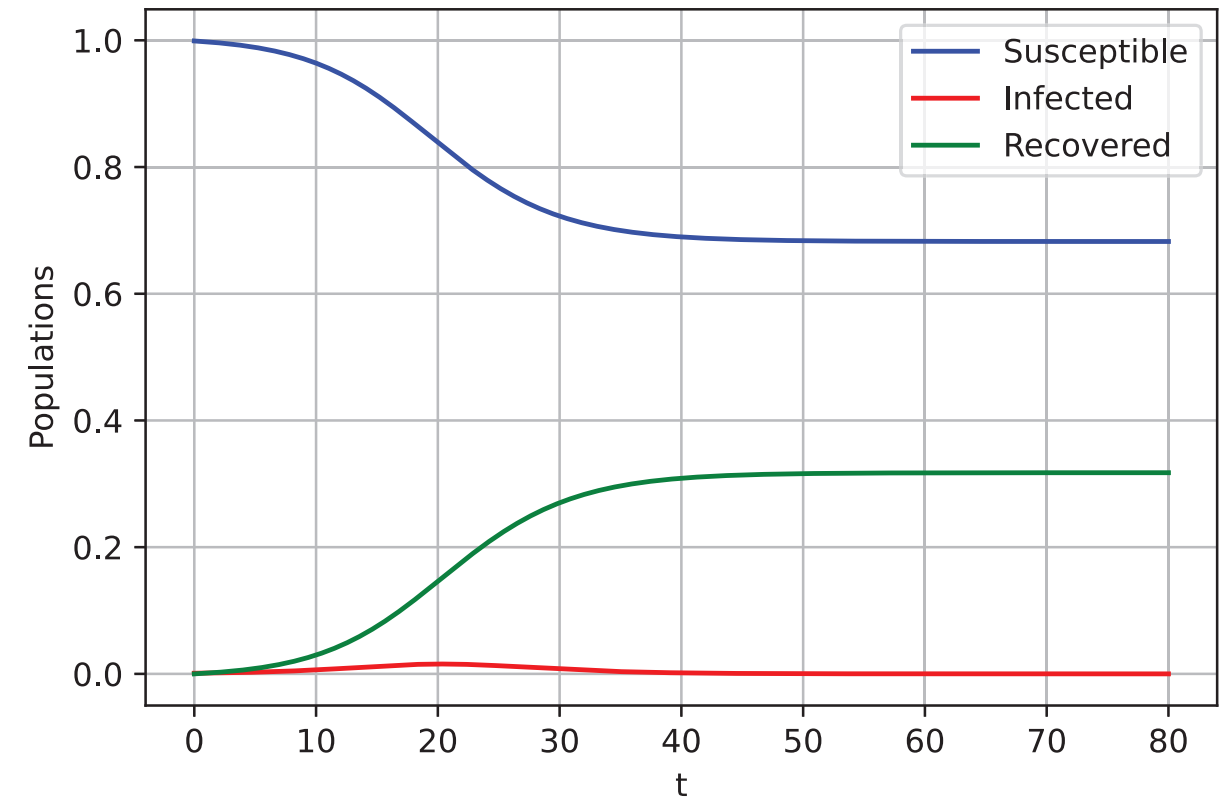In such cases, we will use the initial conditions

$$S'(t = 0) \approx 1, \quad I'(t = 0) \ll 1, \quad R'(t = 0) = 0$$

Set $r = 1.0$ and vary the parameter R_0 to see what the possible scenarios are
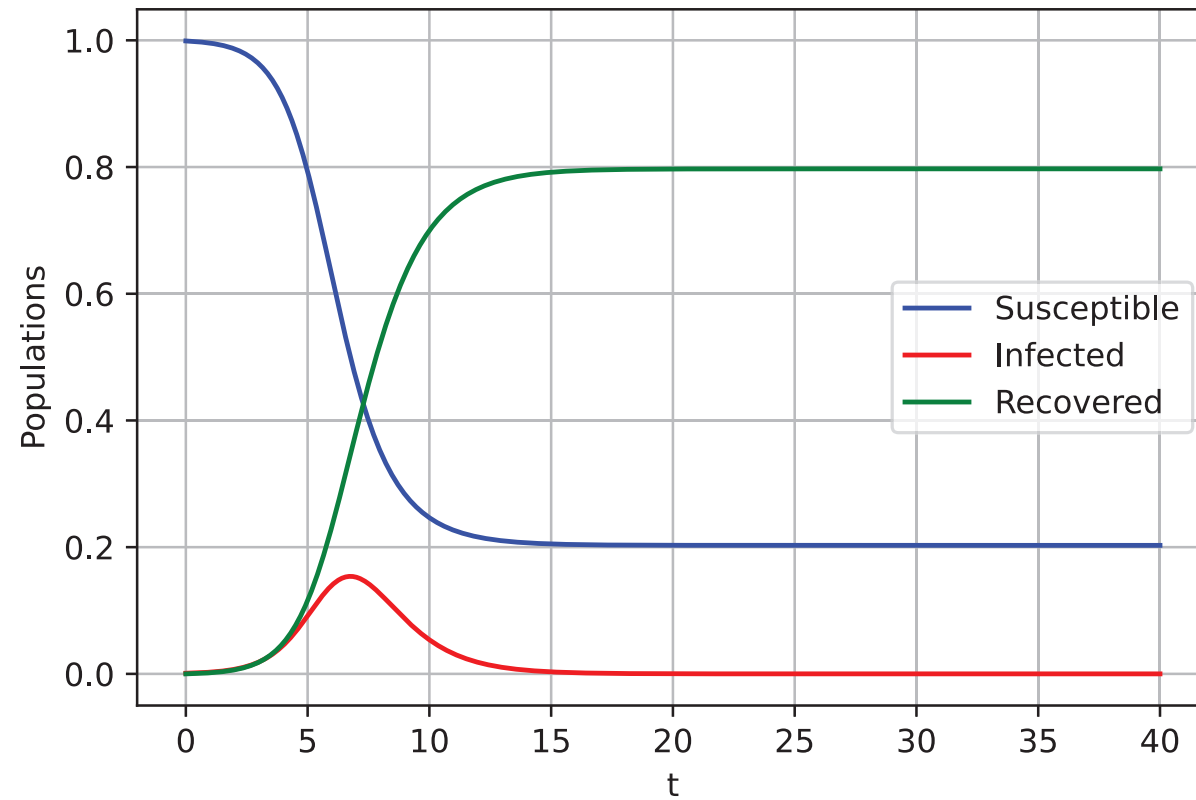
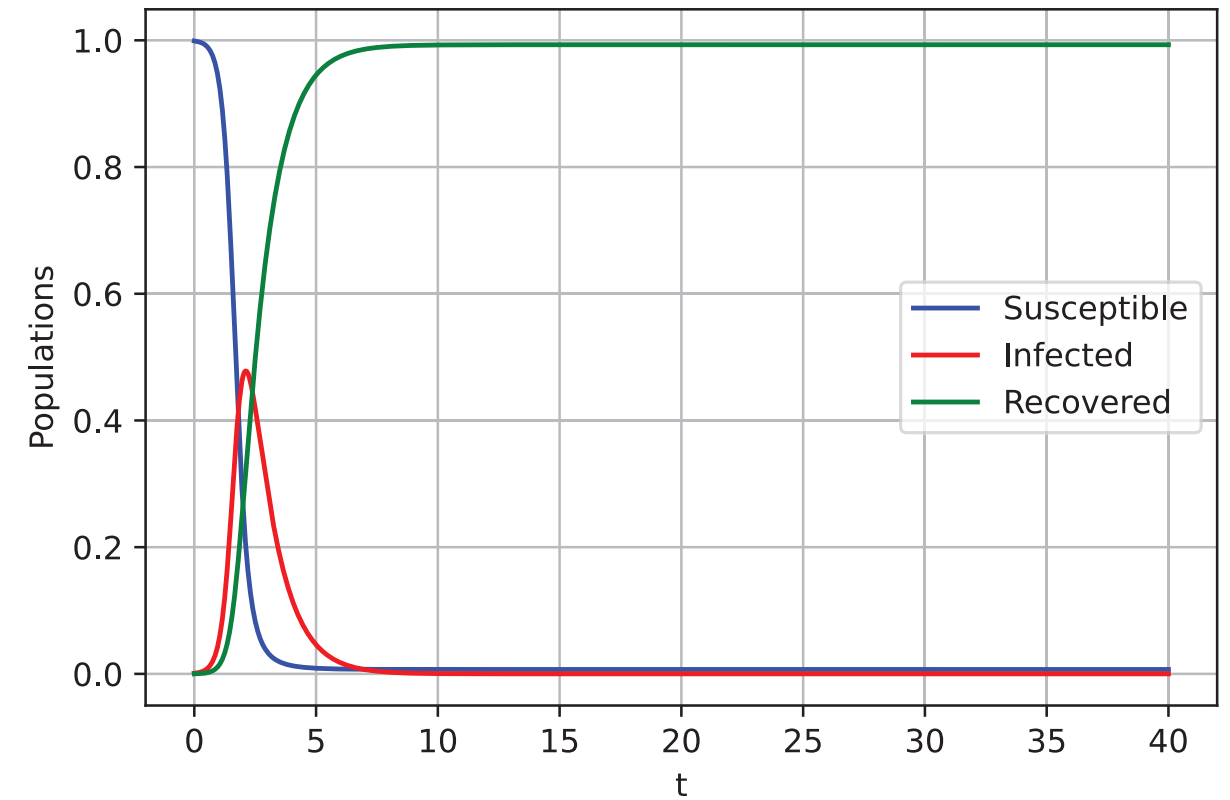# Some computational plots
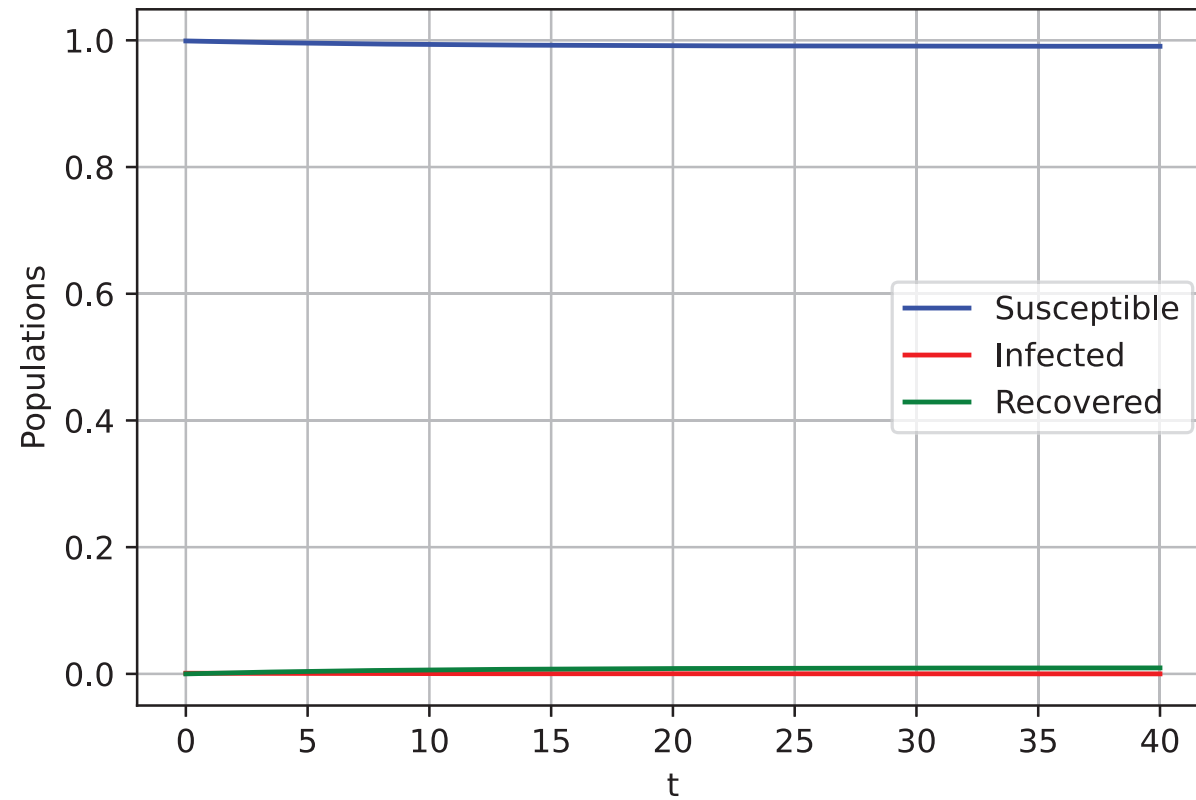
$$R_0 = 0.9,\, r = 1.0,\, I_0 = 0.001$$

$$R_0 = 1.2,\, r = 1.0,\, I_0 = 0.001$$

$$R_0 = 2.0, r = 1.0, I_0 = 0.001$$

$$R_0 = 5.0, r = 1.0, I_0 = 0.001$$

Intervention - vaccinations

Vaccination can prevent the infection of an individual.

In addition, it can also protect a population from epidemics, even if not all individuals are vaccinated.

How would one implement vaccination into the model?

Vaccination is equivalent to removal (or transfer to the Recovered compartment): a vaccinated individual cannot infect or be infected.

SIS Model
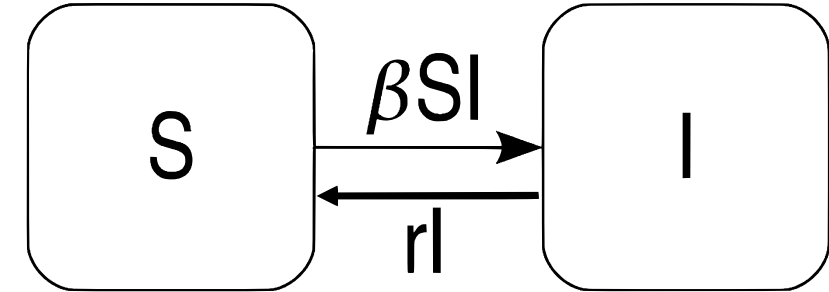
The SIS model

In this type of model, the Recovered is once again subject to infection, so the dynamics is described by

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta S I + r I$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta S I - r I$$

Notice that we have once again $N = S + I$ being a constant:

$$\frac{\mathrm{d}N}{\mathrm{d}t} = \frac{\mathrm{d}S}{\mathrm{d}t} + \frac{\mathrm{d}I}{\mathrm{d}t} = 0$$

Solving for S automatically gives us I

"Normalizing" the populations ...

Again, with $S' \equiv S/N$ and $I' \equiv I/N$, the SIS equations become

$$\frac{\mathrm{d}S'}{\mathrm{d}t} = -rI'(R_0 S' - 1),$$
$$\frac{\mathrm{d}I'}{\mathrm{d}t} = rI'(R_0 S' - 1)$$

with $0 \leq S' \leq 1$ and $0 \leq I' \leq 1$, and the constant population expression becomes
$S' + I' = 1$

Replacing I' in the first equation with $1 - S'$, we simply have

$$\frac{\mathrm{d}S'}{\mathrm{d}t} = -r(1 - S')(R_0 S' - 1)$$

ONE differential equation describing the dynamics

Since this is a single differential equation dynamics, we could do some simple analysis.

Would there be a sustained (i.e. constant in time) non-zero Infected population $I'^{\star}$?

This situation corresponds to

$$\frac{\mathrm{d}I'}{\mathrm{d}t} = 0, \quad \text{or, equivalently,} \quad \frac{\mathrm{d}S'}{\mathrm{d}t} = 0$$

From the differential equation for S' [ie $\dfrac{\mathrm{d}S'}{\mathrm{d}t} = -r(1 - S')(R_0 S' - 1)$], we see that this requires (a) $S'^{\star} = 1$, or (b) $S'^{\star} = 1/R_0$. The first option leads to $I'^{\star} = 0$, and the second

$$I'^{\star} = 1 - \frac{1}{R_0}$$

Notice that $I'^{\star}$ exists only for $R_0 > 1$

Some analytical deductions cont'd

At the beginning of the potential epidemics, it is to be expected that the susceptible population must decrease.
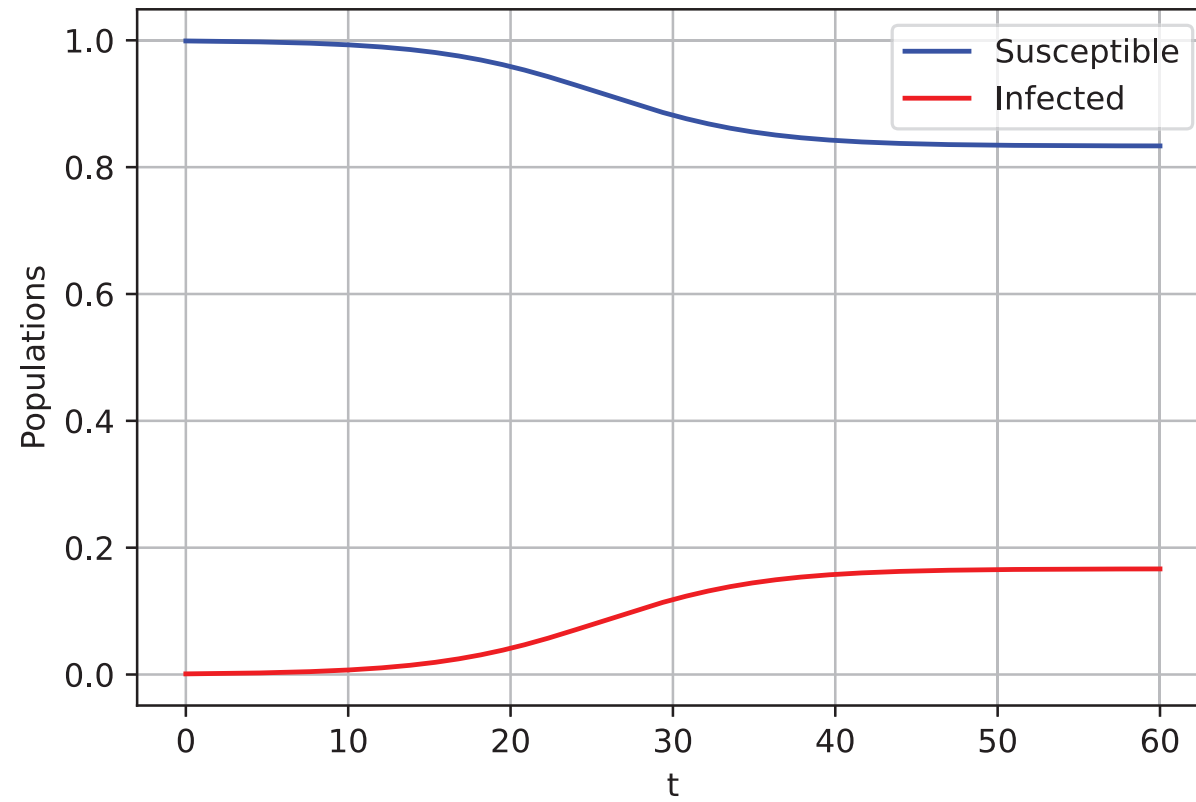
So

$$\frac{dS'}{dt} < 0$$

Again, from the differential equation for S' [ie $\frac{dS'}{dt} = -r(1 - S')(R_0 S' - 1)$], this restricts the R_0 parameter to have values such that $(R_0 S' - 1) > 0$. Or
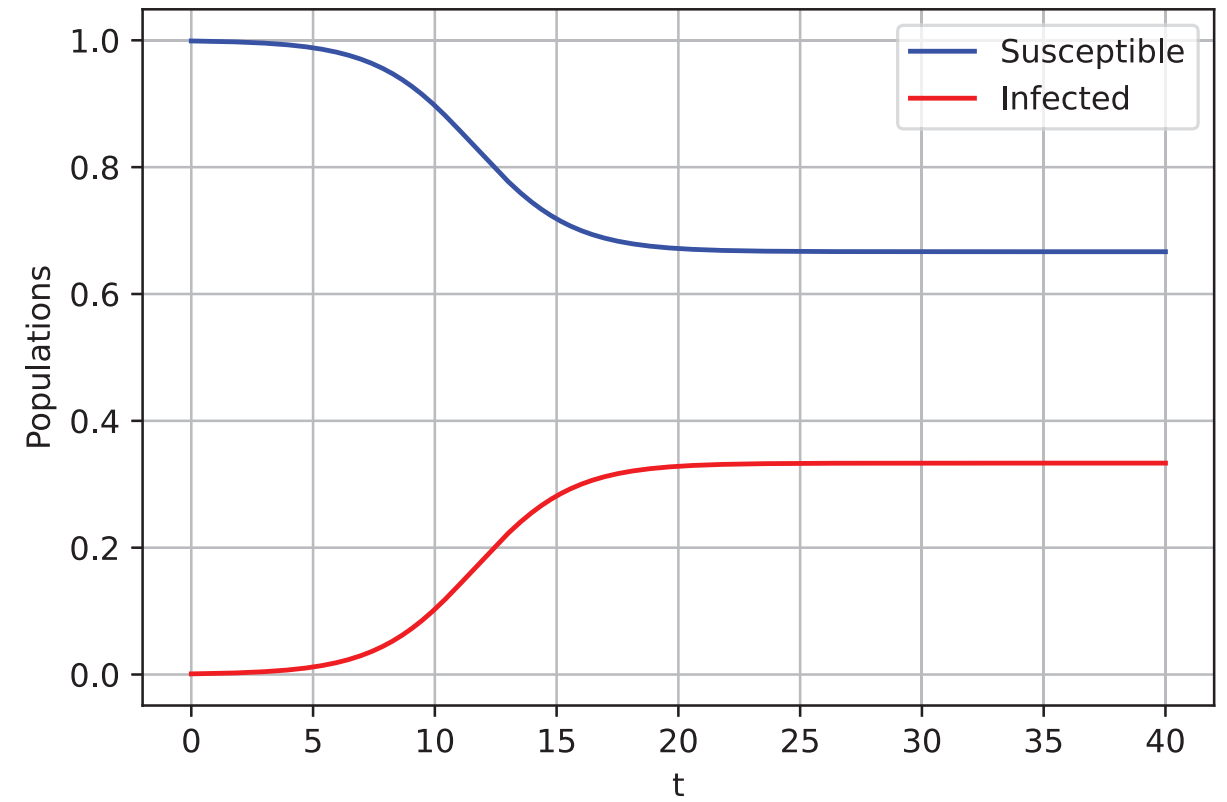
$$R_0 > \frac{1}{S'} \geq 1$$

since we must have $S' \leq 1$.

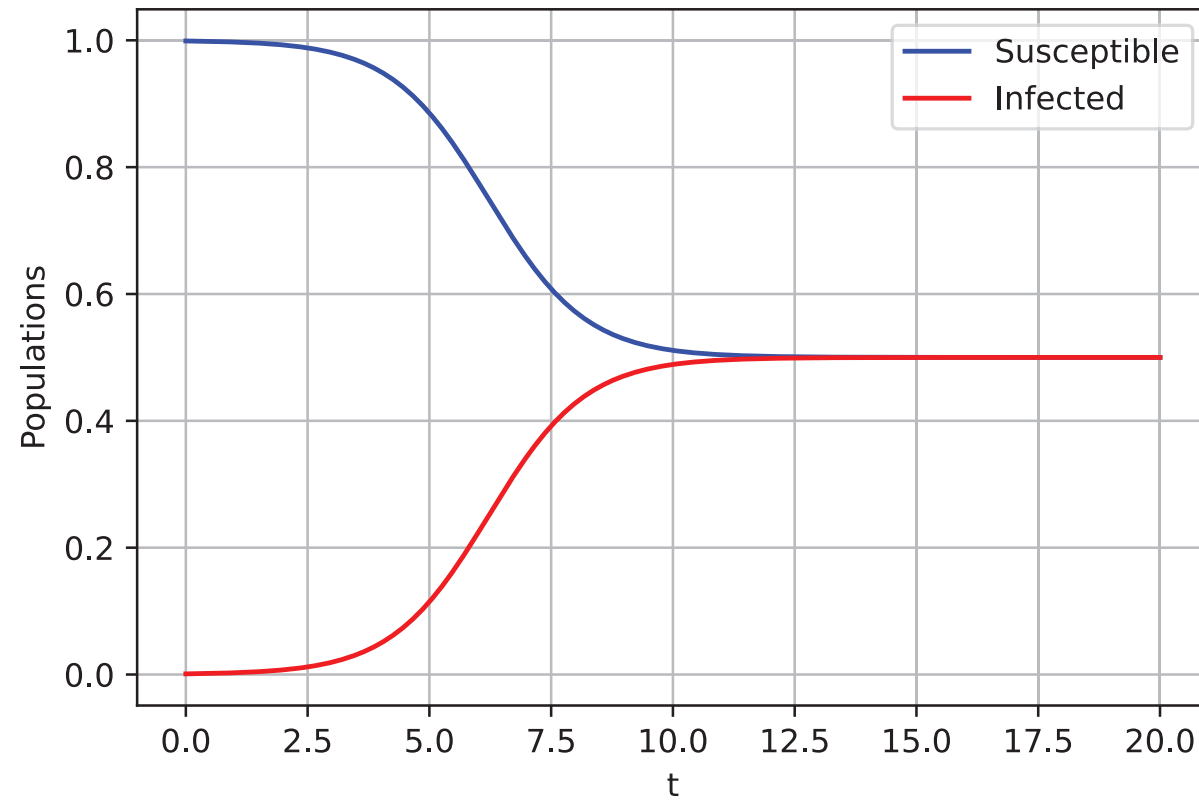$$R_0 = 1.2, \, r = 1.0, \, I_0 = 0.001 \qquad\qquad R_0 = 1.5, \, r = 1.0, \, I_0 = 0.001$$
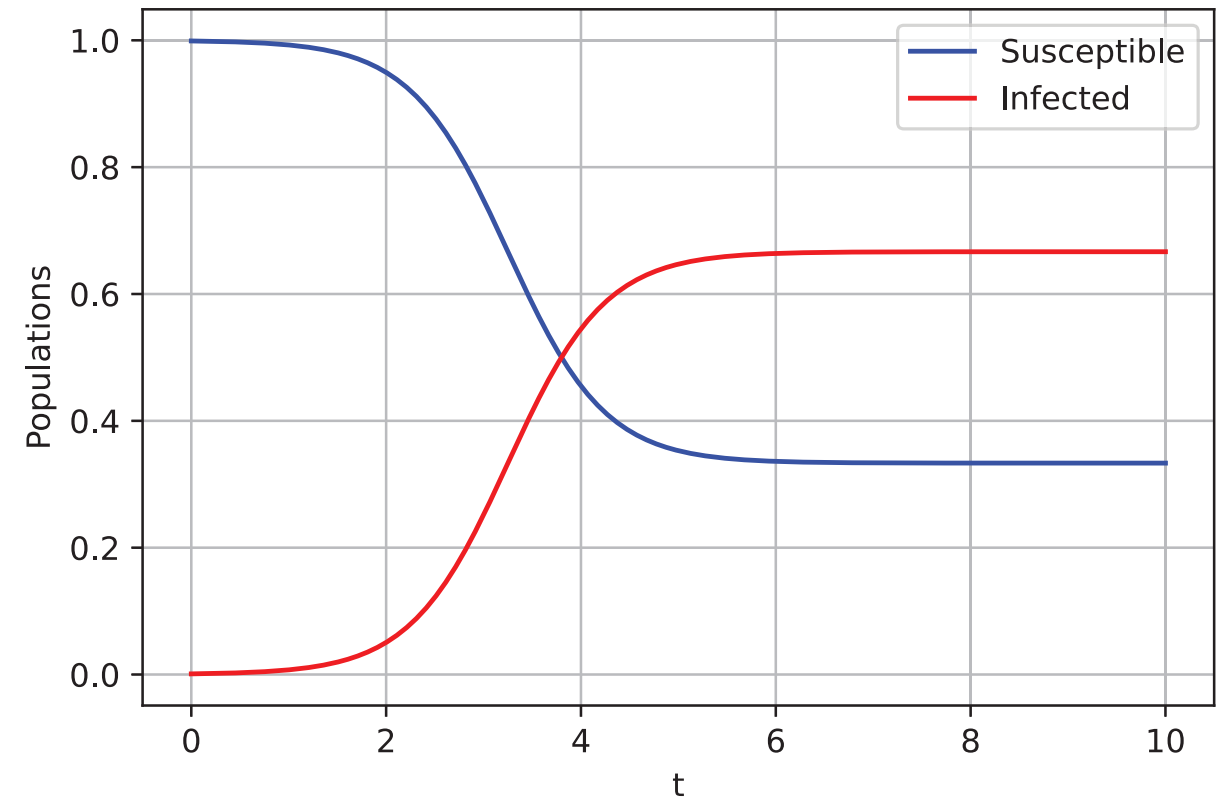
$$R_0 = 2.0, \; r = 1.0, \; I_0 = 0.001$$

$$R_0 = 3.0, \; r = 1.0, \; I_0 = 0.001$$

SEIR model

Epidemics with an incubation period: the SEIR model

In many infectious diseases, a person exposed to the disease may not be infectious (i.e. do not infect others) for a period of time. Then the compartment/group that we called Infected before will have to be divided into two sub-groups: the Exposed and the Infectious

In the Exposed group, the individuals are infected but are not infectious as there is an incubation period

This is the SEIR model

This model is applicable, for example, to measles and rubella

Epidemics with an incubation period: the SEIR model cont'd

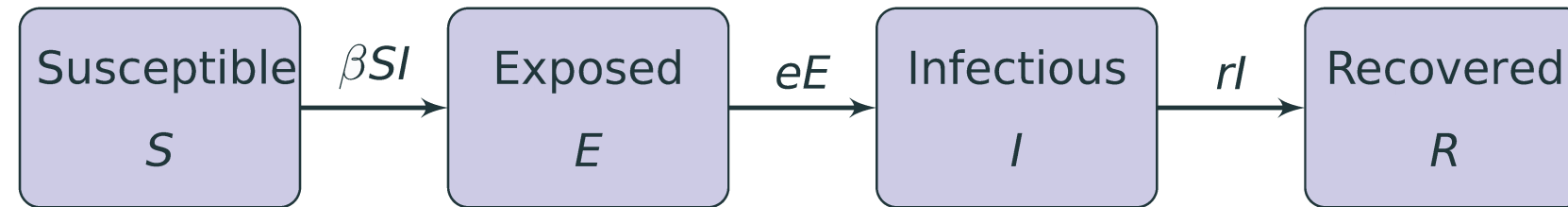$$S \Rightarrow E : \quad -\beta SI,$$
$$E \Rightarrow I : \quad eE,$$
$$I \Rightarrow R : \quad rI$$

$$N = S + E + I + R \quad \text{(constant)}$$

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta SI$$
$$\frac{\mathrm{d}E}{\mathrm{d}t} = \beta SI - eE$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = eE - rI$$
$$\frac{\mathrm{d}R}{\mathrm{d}t} = rI$$

For this model, we will have 3 system parameters: β (or R_0), r, and e.