# Mathematical Modeling
# Extension of the SEIR Model

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## Introduction

In the field of infectious disease modeling, compartmental models such as SEIR are fundamental for studying the dynamics of disease transmission. However, to capture more realistic scenarios, extensions to the basic SEIR model are often necessary. This project involves designing and analyzing two extended SEIR models: one incorporating a mildly symptomatic class and another introducing a hospitalized class. These models aim to better represent the transmission characteristics of diseases where individuals may experience different stages of infection, with varying levels of infectiousness.

## Model 1: Extended SEIR Model with Mildly Symptomatic Class

We need to modify the simple SEIR model to incorporate a class of infected individuals who are mildly symptomatic and infectious (compartment M) before they progress to a fully symptomatic and infectious class (compartment I). In this model, all latent individuals progress to the M-compartment before moving to the I-compartment. Mildly symptomatic and infectious individuals have reduced infectiousness relative to the fully infectious and symptomatic I-individuals. The average time spent by infected individuals in the M-compartment is not necessarily the same as that in the I-compartment..

### Compartmental Diagram of the Model

The compartmental diagram of model 1, clearly showing the rates of flow between compartments is given below.
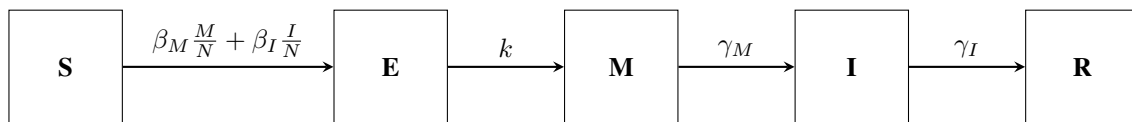


From the model above, the variables are defined as:

- $S(t)$: number of susceptible individuals at time $t$

- $E(t)$: number of exposed individuals at time $t$

- $M(t)$: number of mildly symptomatic individuals at time $t$

- $I(t)$: number of infected individuals at time $t$

- $R(t)$: number of recovered individuals at time $t$

The SEMIR Differential equations for the model is given below

$$\frac{dS}{dt} = -S\left(\beta_M \frac{M}{N} + \beta_I \frac{I}{N}\right)$$
$$\frac{dE}{dt} = S\left(\beta_M \frac{M}{N} + \beta_I \frac{I}{N}\right) - kE$$
$$\frac{dM}{dt} = kE - \gamma_M M$$
$$\frac{dI}{dt} = \gamma_M M - \gamma_I I$$
$$\frac{dR}{dt} = \gamma_I I$$

## Model Parameters Overview

The model 1 parameter symbols, their definitions, and units is given in the table below.

| Parameter Symbol | Definition | Units |
|:---:|:---|:---:|
| $\beta_M$ | Transmission rate from mildly symptomatic (M) individuals | per day |
| $\beta_I$ | Transmission rate from fully symptomatic (I) individuals | per day |
| $k$ | Rate of progression from exposed (E) to M | per day |
| $\gamma_M$ | Rate of progression from M to I | per day |
| $\gamma_I$ | Recovery rate from I | per day |
| $N$ | Total population size (S + E + M + I + R) | Individual |

Table 1: Parameter Table for the SEMIR Model

## Derivation of the Basic Reproduction Number

The basic reproduction number $R_0$, represents the average number of secondary infections caused by a singled infected individual during their entire infectious lifetime. It is a measure of how quickly a disease spreads in its initial phase and can predict whether a disease will become endemic or whether it will die out. For this model, $R_0$ can be split into contributions from both mildly symptomatic individuals and fully symptomatic individuals. The expression for the derivation is given below:

$$R_0 = R_{0M} + R_{0I}$$
$$= \left(\frac{\beta_M}{\gamma_M}\right) + \left(\frac{\beta_I}{\gamma_I}\right)$$
$$= \beta_M \left(\frac{1}{\gamma_M}\right) + \beta_I \left(\frac{1}{\gamma_I}\right)$$

Note from the expression that:

$\frac{1}{\gamma_M}$ represents the average time spent in the mildly symptomatic state and,
$\frac{1}{\gamma_I}$ represents the average time spent in the fully symptomatic state.
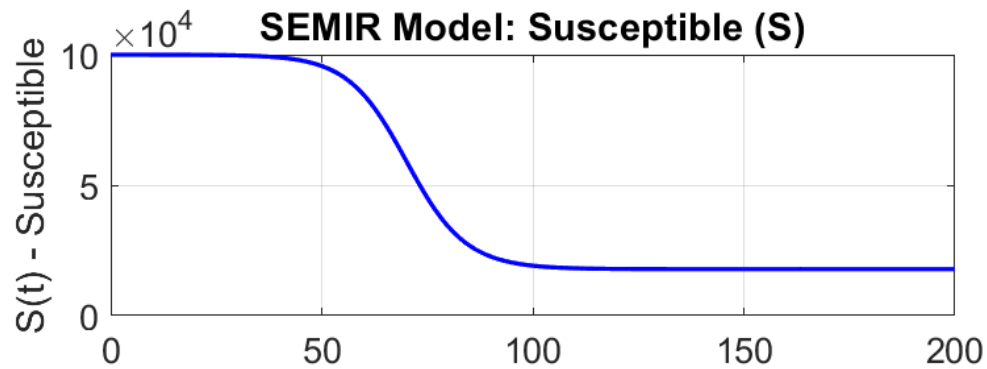
## Simulation of Epidemic Dynamics

In this simulation, the parameters for the SEMIR model are:

$\gamma_M = \frac{1}{2}$, $\gamma_I = \frac{1}{3}$, N= 100000, K= $\frac{1}{2}$, $\beta_M = \frac{3}{10}$, $\beta_I = \frac{1}{2}$, and, the time span for the simulation is 200 days.

The graph of each variable after the simulation is given below.

The susceptible population decreases over time as individuals become exposed to the disease and move into the $E(t)$ compartment.

By around day 50, the sharp decline indicates a substantial portion of the population has moved to the exposed category, and by day 100, most of the population is no longer susceptible.

The exposed population initially increases around day 50 as individuals transition from susceptible to exposed.
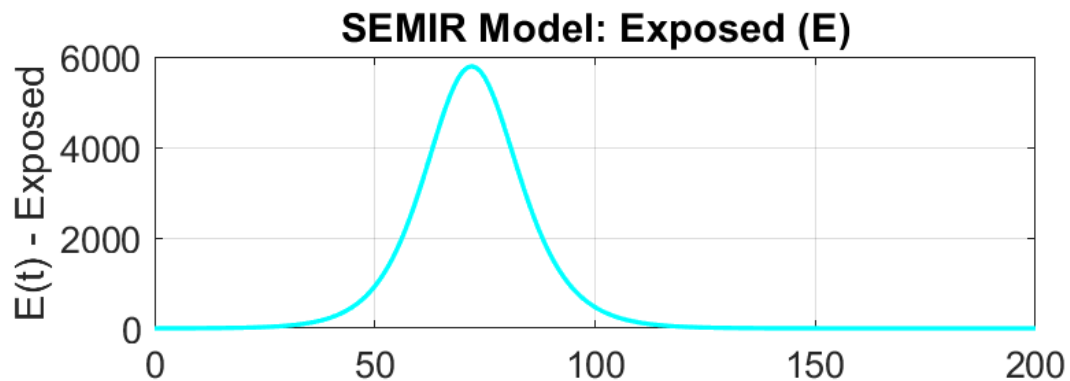


The exposed population peaks near day 70 before gradually decreasing as individuals progress to the mildly symptomatic stage.

This group represents individuals who show mild symptoms and are less infectious.
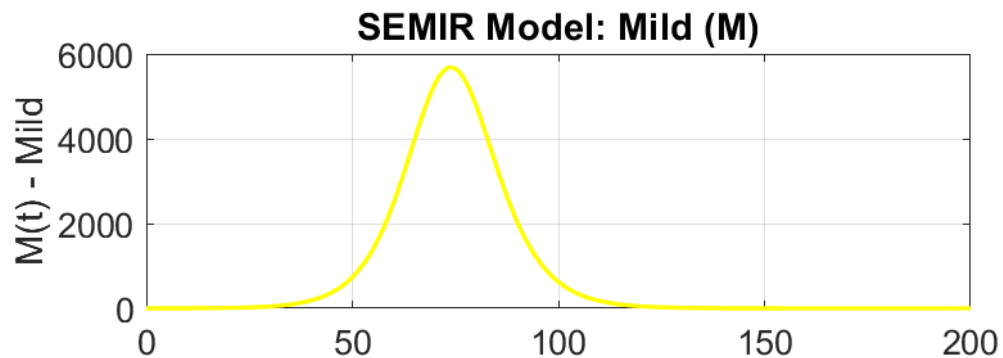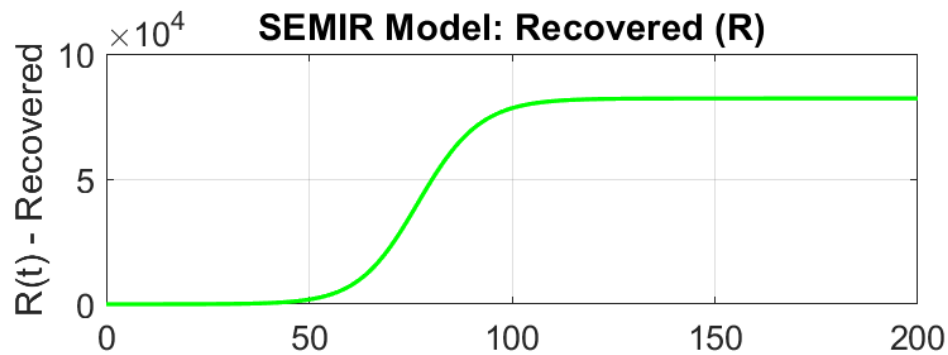


The population of mildly symptomatic individuals increases after the exposed population begins to transition into this compartment and peaks around day 70 before declining.

The infectious population grows after the mildly symptomatic individuals transition into the infected compartment, peaking around day 77.
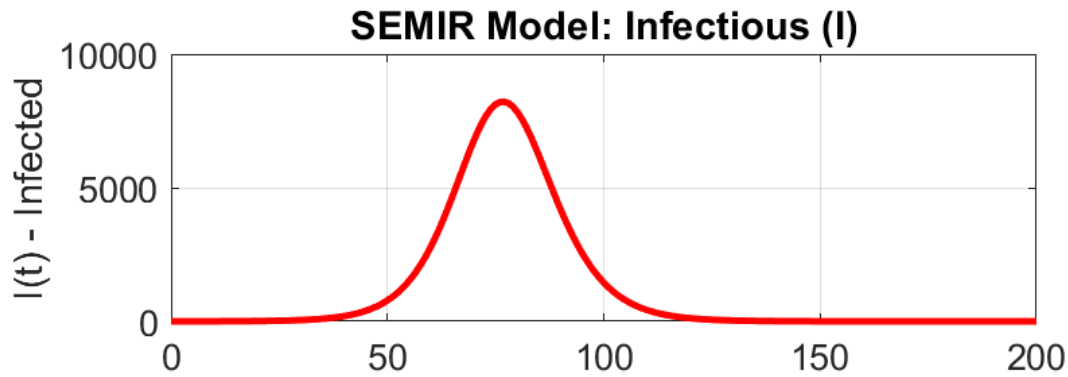


As the mildly symptomatic individuals become more infectious, they contribute to the epidemic spread. However, $\gamma_M = \frac{1}{3}$ ensures that the infected individuals recover or die, leading to the decline of the infectious population after the peak.

The recovered population grows steadily and levels off after day 100, indicating that the majority of individuals have recovered by that time.



Recovery occurs from both mildly symptomatic and infectious individuals. The graph shows that by day 200, most of the population has recovered, aligning with the decline in both the exposed and infectious compartments.

The cumulative number of infections grows rapidly, particularly during the first 90 days, and then stabilizes after day 110.
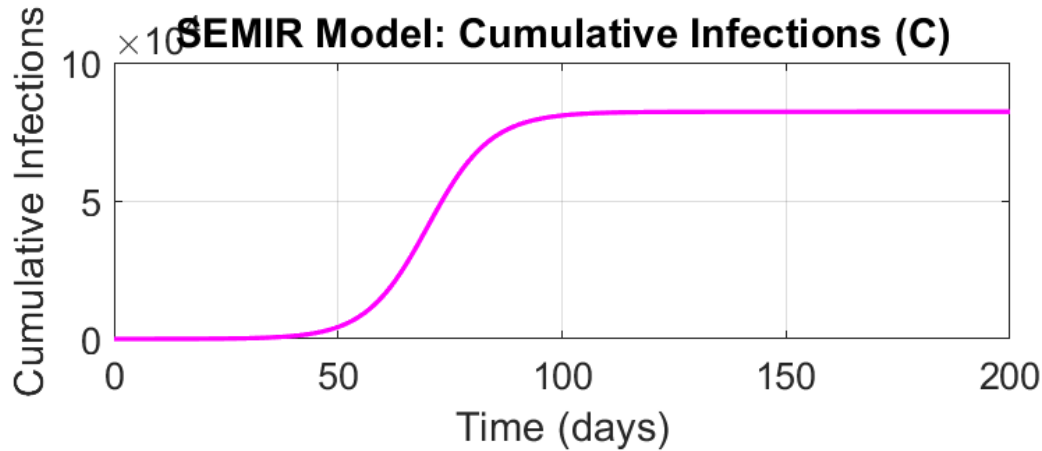


The graph of the cumulative infections follows an S-shaped curve, indicating that the number of new infections rises rapidly at first and then levels off as most of the population either recovers or becomes immune.

## Impact of Infectiousness on $R_0$

As the infectiousness of $M$ individuals increases, meaning $\beta_M$ increases, the term $R_{0M}$ also increases. This is because more individuals are being exposed due to the increased rate of mild transmission. This means that the overall $R_0$ will increase because more people are getting infected by each mildly symptomatic individual.

## Example

Assume initially that $\gamma_M = \frac{1}{10}, \quad \gamma_I = \frac{1}{5}, \quad \beta_M = \frac{1}{5}, \quad \beta_I = \frac{2}{5}$, then calculating for $R_0$ yields:

$$R_0 = R_{0M} + R_{0I}$$
$$= \left(\frac{0.2}{0.1}\right) + \left(\frac{0.4}{0.2}\right)$$
$$= 2 + 2 = 4$$

Now, if the infectiousness of mildly symptomatic individuals increases $\beta_M$ from $\frac{1}{5}$ to $\frac{9}{10}$, then
$\gamma_M = \frac{1}{10}, \quad \gamma_I = \frac{1}{5}, \quad \beta_M = \frac{1}{5}, \quad \beta_I = \frac{2}{5}$,

$$R_0 = R_{0M} + R_{0I}$$
$$= \left(\frac{0.9}{0.1}\right) + \left(\frac{0.4}{0.2}\right)$$
$$= 9 + 2 = 11$$

Thus, increasing the infectiousness of $M$ individuals leads to a higher $R_0$, which indicates that the disease spreads more quickly and affects a larger number of people.

## Model 2: Extended SEIR Model with Hospitalized Class

We need to modify the the simple SEIR model, incorporate a class of hospitalized and infectious individuals (compartment H). In this model, all latent individuals progress to the symptomatic and infectious compartment I. Individuals in the I-compartment either become hospitalized or recover without hospitalization. Hospitalized and infectious individuals recover at a different rate than those in the I-compartment. Due to infection control measures in hospitals, hospitalized infected individuals have reduced infectiousness relative to the fully infectious and symptomatic I-individuals.

### Compartmental Diagram of the Model

The compartmental diagram of model 2, clearly showing the rates of flow between compartments is given below.
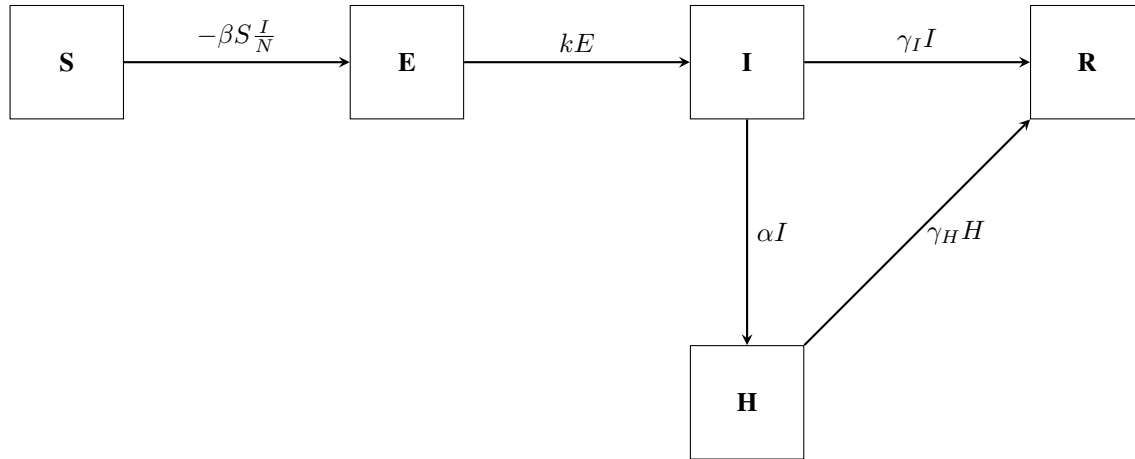


From the model, the variables are defined as:

- $S(t)$: number of susceptible individuals at time $t$
- $E(t)$: number of exposed individuals at time $t$
- $I(t)$: number of infected individuals at time $t$
- $H(t)$: number of hospitalized individuals at time $t$
- $R(t)$: number of recovered individuals at time $t$

The SEIHR Differential equations for the model is given below

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta S \frac{I}{N} \\
\frac{dE}{dt} &= \beta S \frac{I}{N} - kE \\
\frac{dI}{dt} &= kE - \gamma_I I - \alpha I \\
\frac{dH}{dt} &= \alpha I - \gamma_H H \\
\frac{dR}{dt} &= \gamma_I I + \gamma_H H
\end{aligned}
$$

## Model Parameters Overview

The model 2 parameter symbols, their definitions, and units is given in the table below.

| Parameter Symbol | Definition | Units |
|:---:|:---|:---:|
| $\beta$ | Transmission rate from infected (I) individuals | per day |
| $k$ | Rate of progression from exposed (E) to infected (I) | per day |
| $\alpha$ | Rate of progression from infected (I) to hospitalized (H) | per day |
| $\gamma_I$ | Recovery rate from infected (I) individuals | per day |
| $\gamma_H$ | Recovery rate from hospitalized (H) individuals | per day |
| $N$ | Total population size (S + E + I + H + R) | Individual |

Table 2: Parameter Table for the SEIHR Model

## Derivation of the Basic Reproduction Number

To derive the basic reproduction number $R_0$, we need to focus on the transmission potential of both infected individuals in the $I$- compartment and hospitalized individuals in the $H$- compartment. Let $\beta$ and $\alpha$ represent the transmission rate from infected individuals and hospitalized individuals, and $\gamma_I$ and $\gamma_H$ represent the recovery rate for these individuals respectively. The expression for the derivation is given below:

$$R_0 = R_{0I} + R_{0H}$$

$$= \left(\frac{\beta}{\gamma_I + \alpha}\right) + \left(\frac{\beta}{\gamma_H}\right)$$

$$= \beta \left(\frac{1}{\gamma_I + \alpha} + \frac{1}{\gamma_H}\right)$$

Note from the expression that:

$\frac{1}{\gamma_I}$ represents the average duration of infection for symptomatic infected individuals in the $I$- compartment and,

$\frac{1}{\gamma_H}$ represents the average duration of hospitalization for individuals in the $H$- comoartment.

## Simulation of Epidemic Dynamics

In this simulation, the parameters for the SEIHR model are:

$\gamma_I = \frac{1}{3}$, $\quad \gamma_H = \frac{1}{2}$, $\quad$ N= 100000, $\quad$ K= $\frac{1}{2}$, $\quad \beta = \frac{3}{10}$, $\quad \alpha = \frac{1}{20}$, $\quad$ and, the time span for the simulation is 200 days.

The graph of each variable after the simulation is given below.

The susceptible population steadily declines as more individuals are exposed to the infection.
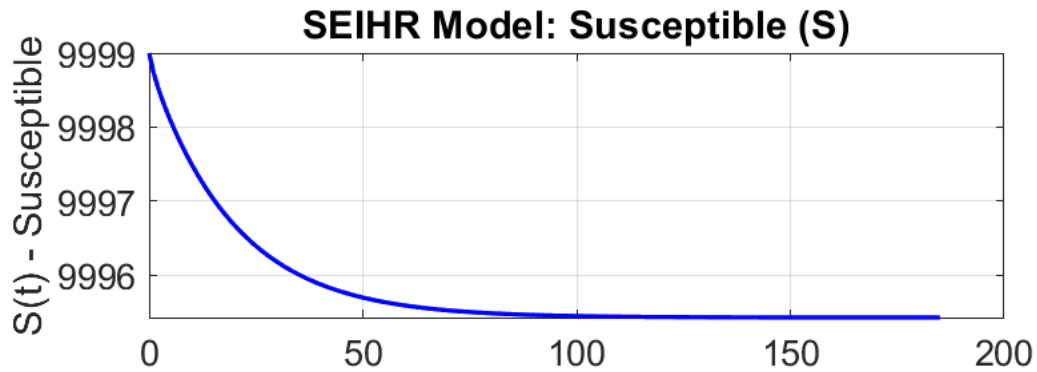


The sharp initial decrease represents the start of the epidemic, where many individuals become exposed and infected. As the epidemic progresses, fewer people remain susceptible because they either get infected or recover, reducing the rate of new infections.

The exposed compartment rises initially as susceptible individuals contract the infection but are not yet

9

infectious.

## SEIHR Model: Exposed (E)
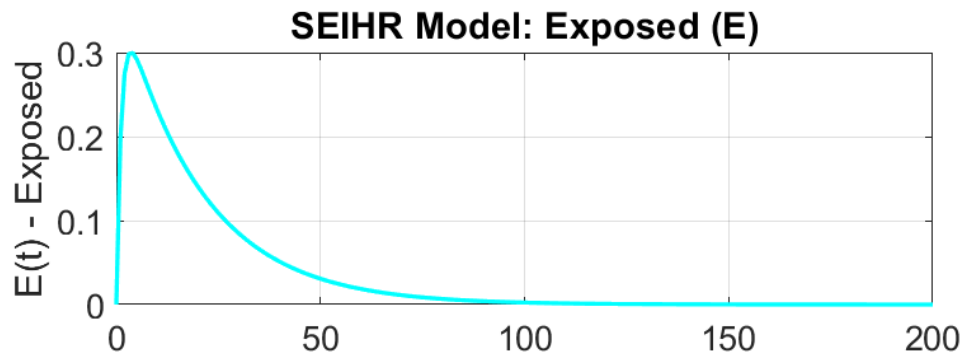


The peak occurs early in the outbreak, around day 10, indicating the maximum number of individuals who are exposed but not yet infectious. After the peak, the exposed population declines as individuals transition to the infectious ($I$).

The number of infectious individuals spikes early in the epidemic as exposed individuals progress to become infectious.

## SEIHR Model: Infectious (I)
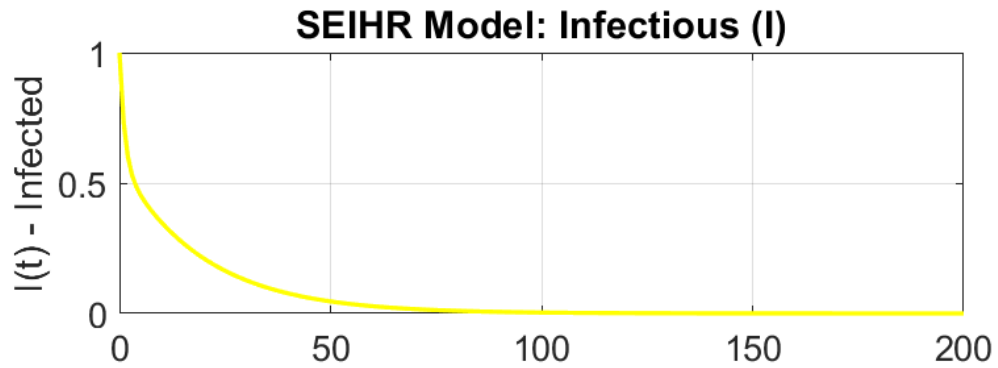


The curve shows that the infectious population reaches a peak and then declines as infected individuals either recover or are hospitalized. The relatively quick decline suggests that the average time spent in the infectious state is short.

The number of hospitalized individuals rises initially, reaching a peak around day 10.
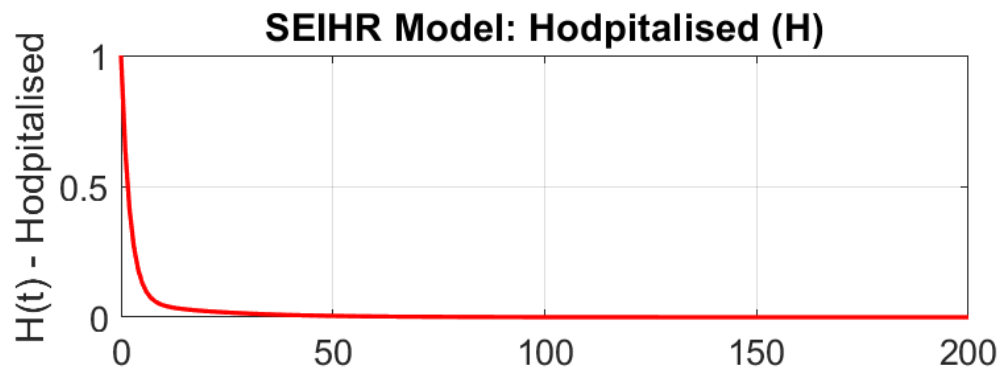


The plot represent hospitalizations at each time point, showing how the hospitalization rate decreases over time. Hospitalized individuals reduces infectiousness due to infection control measures in hospitals.

The recovered population steadily increases as infectious and hospitalized individuals recover.
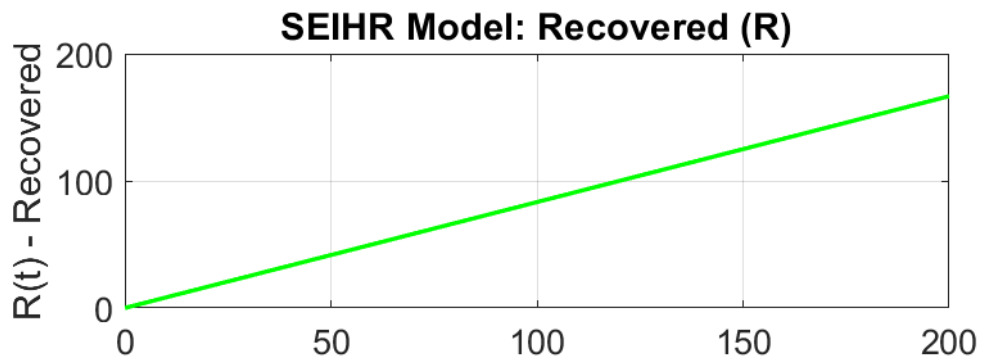


By the end of the simulation (200 days), a significant portion of the population has recovered, leading to herd immunity and the cessation of new infections.

This plot shows the cumulative number of infections increasing initially and then leveling off.
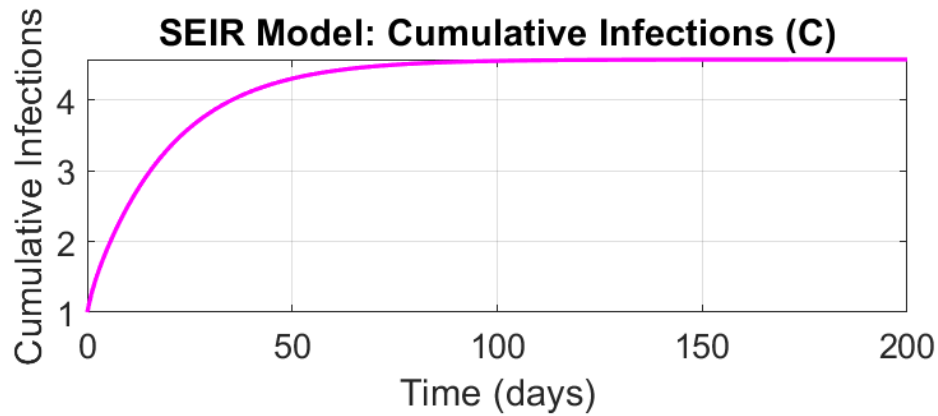


The curve levels off around day 70 as the epidemic runs its course. The rapid increase at the beginning shows how the spreads, but as fewer people are susceptible, the graph flattens. The number of new infections decreases as no new infections are happening.

## Impact of Infectiousness on $R_0$

As the infectiousness of hospitalized individuals decreases, the term $\gamma_H$ in the expression for $R_0$ will increase. This means that the overall $R_0$ will decrease because the contribution of hospitalized individuals to the spread of the infection becomes smaller.

## Example

Assume initially that $\gamma_I = \frac{1}{10}, \quad \gamma_H = \frac{1}{10}, \quad \beta = \frac{1}{2}, \quad \alpha = \frac{1}{5}$, then calculating for $R_0$ yields:

$$R_0 = R_{0I} + R_{0H} = \beta \left( \frac{1}{\gamma_I + \alpha} + \frac{1}{\gamma_H} \right)$$
$$= 0.5 \left( \frac{1}{0.1 + 0.5} + \frac{1}{0.1} \right)$$
$$= \left( \frac{0.5}{0.6} \right) + \left( \frac{0.5}{0.1} \right)$$
$$= 0.83 + 5 = 5.83$$

Now, if infection control measures increases $\gamma_H$ from $\frac{1}{10}$ to $\frac{5}{2}$, then

$$
\begin{aligned}
R_0 = R_{0I} + R_{0H} &= \beta \left( \frac{1}{\gamma_I + \alpha} + \frac{1}{\gamma_H} \right) \\
&= 0.5 \left( \frac{1}{0.1 + 0.5} + \frac{1}{2.5} \right) \\
&= \left( \frac{0.5}{0.6} \right) + \left( \frac{0.5}{2.5} \right) \\
&= 0.83 + 0.2 = 1.03
\end{aligned}
$$

Thus, the decrease in $R_0$ from 5.83 to 1.03 shows that controlling the infectiousness of hospitalized individuals significantly reduces the overall reproduction number, thereby slowing the epidemic spread.

## Conclusion

Through simulation and parameter variation, both extended SEIR models demonstrate the critical role of mildly symptomatic and hospitalized individuals in disease transmission.
Model 1 shows that increasing the infectiousness of mildly symptomatic individuals accelerates the epidemic's spread and increases the basic reproduction number $(R_0)$, while decreasing it slows the spread.
Model 2 highlights that reducing the infectiousness of hospitalized individuals, through infection control measures, lowers the peak and slows the epidemic.
These findings underscore the importance of targeting these stages with public health interventions to effectively control disease transmission.