

# Compartmentalise, Review, Adapt: Analysing compartmental models suited to model COVID-19

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## **1. INTRODUCTION**

The Coronavirus (COVID-19) pandemic has plagued the world as one of the most widespread and dangerous pandemics. The infectious disease is now a health crisis that has been pushing boundaries and revamping norms for over a year now. It took, and continues to take, the world by surprise owing to its unprecedented and unpredictable nature.

This is where the employment of mathematical compartmental models and the field of epidemiology can assist us understand, predict and combat the effects of this pandemic. Insights obtained from these models help us get a sense of how infectious diseases spread and propagate among different groups of people (here, they are divided into distinct compartments), the effectiveness of various public health interventions and estimate the outcomes of respective public health interventions. It also aids us to forecast healthcare requirements that we might need in the future to deal with further outbreaks (Shekatkar et al. 2).

In this report, I am going to examine a few standard compartmental models for infectious diseases- the [SIR](#), the [SEIR](#), the [SIS](#), the [SEIS](#) and the [SEIRS](#) models and then I will introduce and analyse the [INDSCI-SIM](#) model-a compartmental model designed especially to model COVID-19 in India. All these models are simplistic models, governed by parameters, differential equations and consist of different compartments among which the individuals of the population shift. These compartments typically represent different states or stages with regard to how a given infectious disease progresses.

I will begin with the simplest SIR model and then discuss the rest. I will be critiquing each former model with regard to how that model fails in capturing a certain factor governing COVID-19, and introducing a subsequent model that makes up for that particular factor. All the subsequent models result from modifying or adding compartments to the SIR model.

The aim here is to add compartments and improve each model in such a way that we arrive at a more nuanced and sophisticated, one that can sufficiently capture and represent the specific factors governing the progression of COVID-19 (more specifically, in India).

In the [\*\*MATERIALS AND METHOD\*\*](#) section, I will enumerate the equations governing these models and include coded simulations of these equations in the form of graphs. The code used to generate these graphs is attached in the [\*\*APPENDIX\*\*](#). This will aid our understanding of the models discussed.

In the [\*\*RESULTS AND DISCUSSION\*\*](#) section, I am going to briefly recapitulate why the INDSCI-SIM model best captures COVID-19 in India along with some ways in which even this model fails. Additionally, I will touch upon various challenges and issues with modelling COVID-19 in general.

In the [\*\*IMPLICATIONS\*\*](#) section, I will discuss the ways in which models are useful with respect to understanding the effects, efficiency and validity of various interventions with the use of some *examples*. Along with this, I will enumerate what insights modelling can give us which can help combat the pandemic effectively. I will primarily set forth certain questions that can be answered by extension and robust analysis of the models discussed in this paper.

## **2. MODEL DESCRIPTIONS**

**NOTE:** For the purpose of this report, we ignore natural births and deaths and do not consider vital dynamics: the birth rate or the death rate for any of the standard compartmental models.

Additionally, in all models, we assume the whole population to be equally susceptible and that we are dealing with a well-mixed population where every member of the population can come in contact with every other member of the population (regardless of geographical or social limitations).

### **2.1.1 SIR MODEL**

The population is divided into three compartments: Susceptible (S), Infected (I) and Recovered (R). The total population must remain constant, thus  $S + I + R = N$ , where 'N' is the total population.

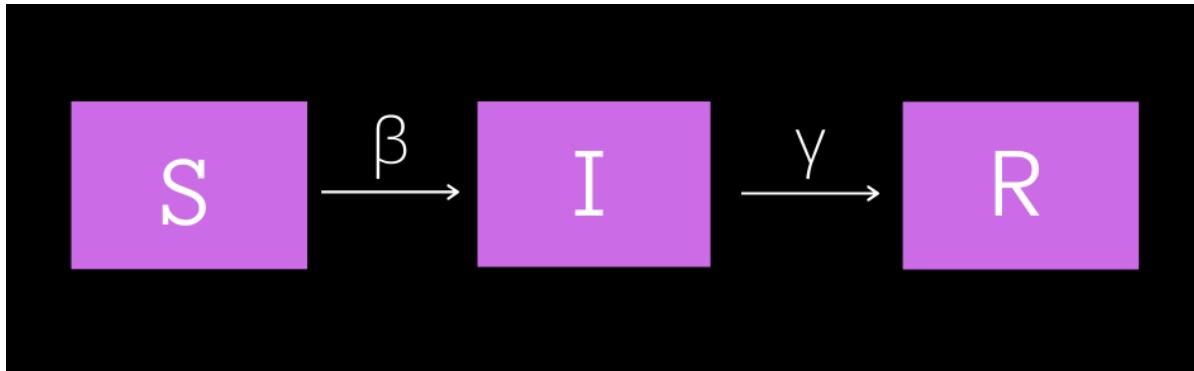
We also assume that the whole population is susceptible to the infectious diseases in the beginning and thus, belongs in the Susceptible (S) compartment.

The Infected (I) compartment contains any and all infected individuals.

The Recovered (R) compartment consists of individuals who cannot be susceptible again and cannot spread the disease any further. This implies two kinds of recovered individuals- the ones

that recovered from the disease and are now immune to it and the ones that couldn't recover from the disease and are now deceased. This also implies that in this model, once an individual recovers from the disease, they gain permanent immunity to the disease as they cannot belong in the susceptible compartment again.

Here we assume that  $\beta$  is the rate of transmission of infectious disease and  $\gamma$  is the recovery rate.  $1/\gamma$  is the average time taken for recovery.



**NOTE:** In the case of COVID-19, we observe that there is a latent period before an infected person becomes infectious ("SEIR And SEIRS Models — HIV Model Documentation"). We call this the "incubation period" of the virus. In the case of COVID-19, the incubation period is 5-6 days ("Coronavirus Disease (COVID-19)").

This delay is incorporated into the SIR model by introducing an additional Exposed (E) compartment where a person who has been infected but is not infectious yet remains, thus making it more representative of COVID-19.

### 2.1.2 SEIR MODEL

The population is divided into four compartments: Susceptible (S), Exposed (E), Infected (I) and Recovered (R). The total population must remain constant, thus  $S + E + I + R = N$ , where 'N' is the total population.

We also assume that the whole population is susceptible to the infectious diseases in the beginning and thus, belongs in the Susceptible (S) compartment.

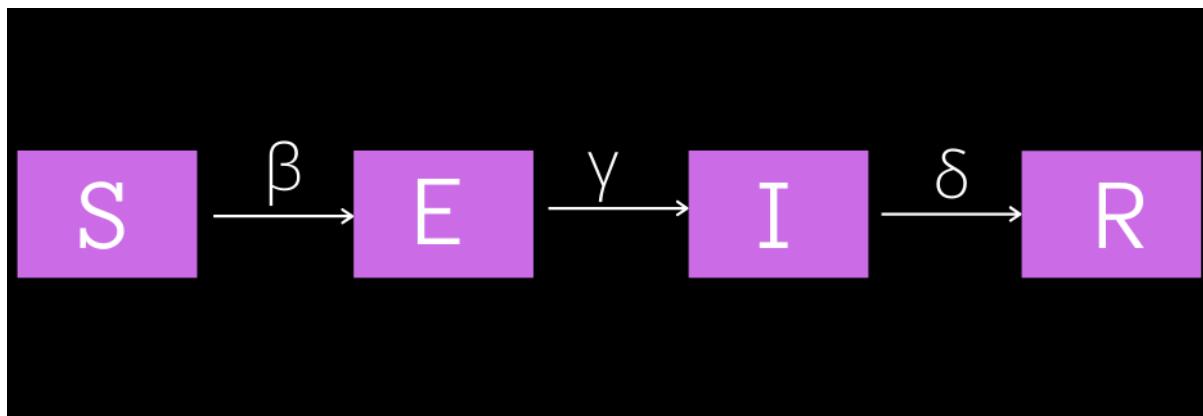
The new compartment here, i.e. the Exposed (E) compartment consists of any individual that has been exposed to the infectious agent but isn't actually infectious yet. Every individual from this compartment will go to the infected compartment.

The Infected (I) compartment contains any and all infected individuals.

**NOTE:** We still have no clear distinction between symptomatic and asymptomatic individuals here and we assume that all infected individuals are definitely capable of spreading the disease, i.e. of infecting others.

The Recovered (R) compartment consists of individuals who cannot be susceptible again and cannot spread the disease any further. This implies two kinds of recovered individuals- the ones that recovered from the disease and are now immune to it and the ones that couldn't recover from the disease and are now deceased. This also implies that in this model, upon recovery, an individual gains permanent immunity to the disease and they cannot belong in the susceptible compartment again.

Here we assume that  $\beta$  is the rate of transmission of infectious disease,  $\gamma$  is the incubation rate ( $1/\gamma$  is the period before which an infected person becomes infectious), and  $\delta$  is the recovery rate.



**NOTE:** In the case of COVID-19, we know that a person, after recovering, can get infected again and the immunity conferred to a COVID-19 patient is not permanent. Thus, we discuss a simple model which captures temporary immunity of infectious diseases.

### 2.1.3 SIS MODEL

In this model, the population is divided into two compartments: Susceptible (S) and Infected (I). The total population must remain constant, thus  $S + I = N$ , where 'N' is the total population.

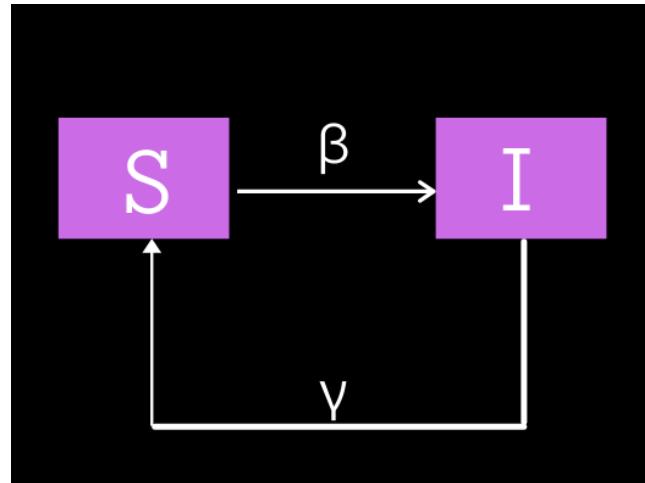
The movement of individuals among compartments is as follows:

The whole population is susceptible to the infectious diseases in the beginning and thus, belongs in the Susceptible (S) compartment. An individual, upon getting infected moves into the Infected

(U) compartment. Upon recovery, the individual once again moves into the Susceptible (S) compartment.

Here, we see that the recovered individuals do not attain permanent immunity. They recover and then shift back to the susceptible category (depending on how long the immunity lasts). But they inevitably shift back to the susceptible category.

Here we assume that  $\beta$  is the rate of transmission of infectious disease,  $\gamma$  is the rate of recovery.



**NOTE:** We combine the SEIR model and SIS model to get the SEIS model (so as to have an Exposed (E) compartment as well as movement of recovered individuals back to the Susceptible (S) compartment/state).

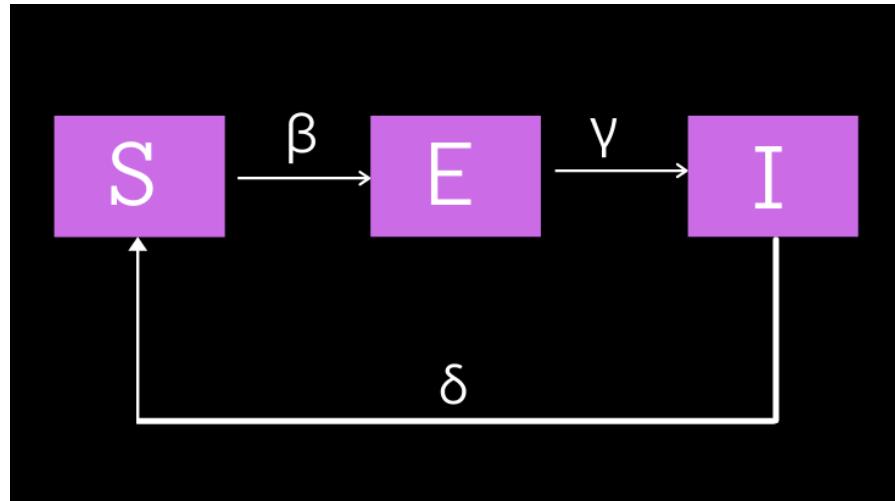
#### 2.1.4 SEIS MODEL

The population is divided into three compartments: Susceptible (S), Exposed (E) and Infected (I). The total population must remain constant, thus  $S + E + I = N$ , where 'N' is the total population.

Here, we see that the recovered individuals do not attain permanent immunity. They recover and then shift back to the susceptible category (depending on how long the immunity lasts). But they inevitably shift back to the susceptible category.

In addition to that, there is a clear distinction between when an individual contracts the disease and when the individual is definitely infectious. We also assume that the asymptomatic category of infected individuals is interwoven in the Infected (I) compartment with the symptomatic individuals.

Here we assume that  $\beta$  is the rate of transmission of infectious disease,  $\gamma$  is the average incubation period and  $\delta$  is the recovery rate.



**NOTE:** Now, we know that recovered individuals can become susceptible to the infection again since we have seen many cases of re-infection in cases of COVID-19. Thus, there must be movement of *some* individuals back to the Susceptible (S) compartment. However, we must consider that there is some period of immunity provided after recovering from COVID-19, which isn't captured by the SEIS model. Let's combine these factors and discuss the SEIRS model.

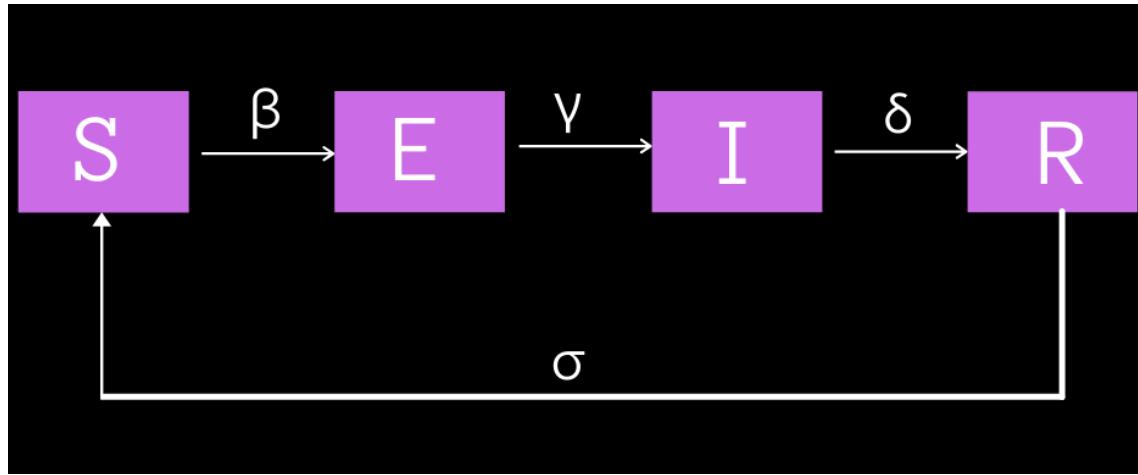
### 2.1.5 SEIRS MODEL

The population is divided into four compartments: Susceptible (S), Exposed (E), Infected (I) and Recovered (R).  $N=S+E+I+R$  is the total population.

The movement of individuals among compartments is as follows:

The whole population is susceptible to the infectious diseases in the beginning and thus, belongs in the Susceptible (S) compartment. An individual, upon getting infected moves into the Exposed(E) compartment until they become infectious. Then, they move to the Infected (U) compartment. Upon recovery, the individual attains a certain period of immunity but upon loss of immunity, the individual once again moves into the Susceptible (S) compartment.

Here we assume that  $\beta$  is the rate of transmission of infectious disease,  $\gamma$  is the period before which an infected person becomes infectious,  $1/\delta$  is the infectious period, and  $1/\sigma$  is the period of immunity.



**NOTE:** We have incorporated the incubation period and loss of immunity and hence return to susceptibility- factors specific to COVID-19. However, we know that every infected person, in the case of COVID-19, does not experience the same kind of infection and different severity of infections lead to varying subsequent results. There are asymptomatic cases, mildly symptomatic and severely symptomatic cases. This distinction is not captured by the singular Infected (I) compartment of the SEIRS model.

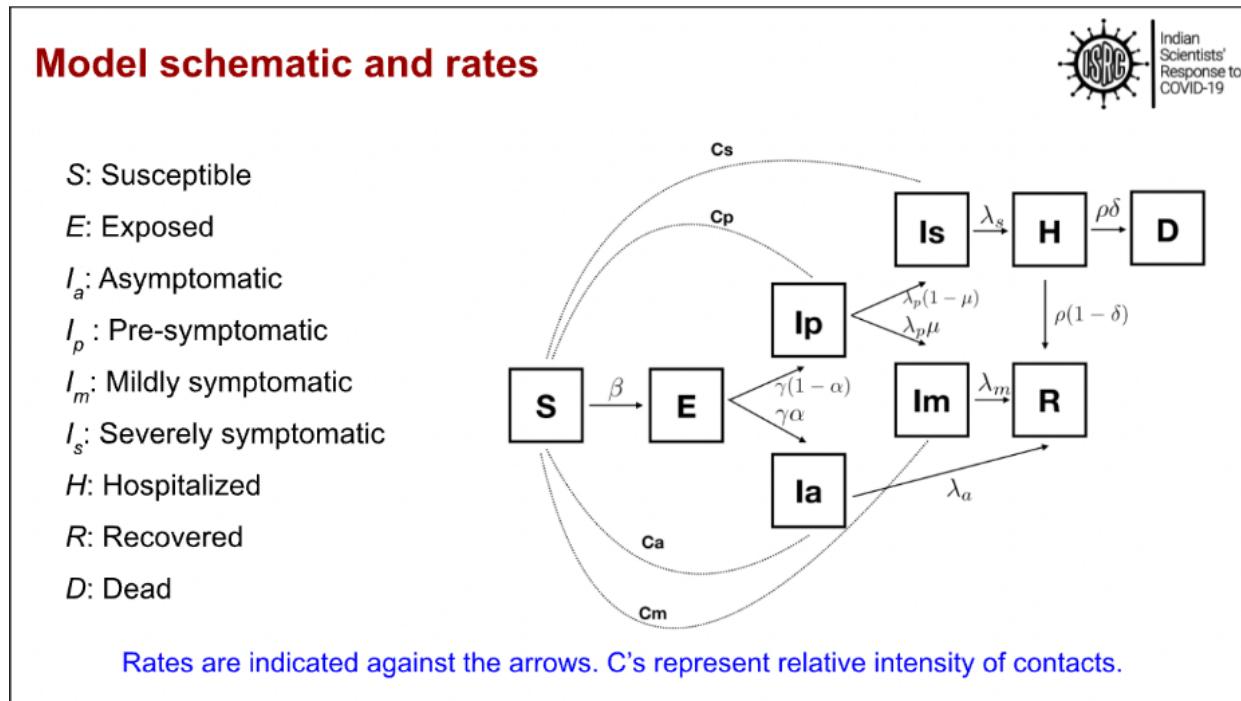
Additionally, COVID-19 is a fatal disease and in the SEIRS model, all recovered individuals move into the Susceptible (S) compartment after loss of immunity. The distinction between deceased and recovered is not made.

Thus, we must add compartments which represent the propagation of COVID-19 more accurately.

## 2.2 INDSCI-SIM

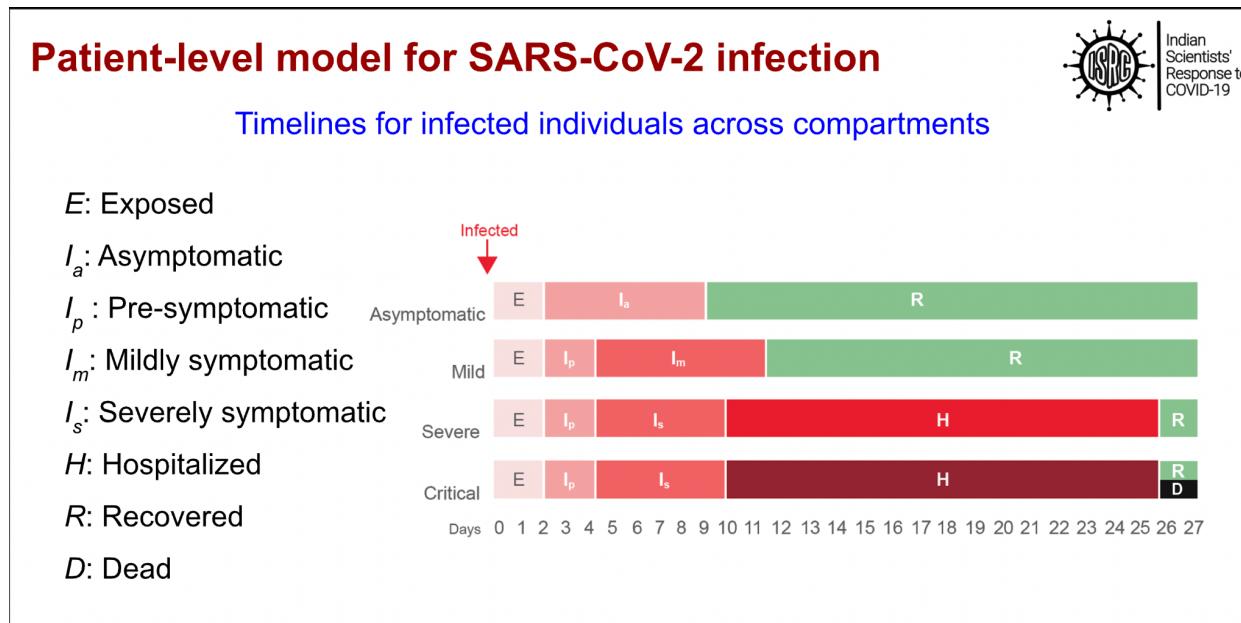
In this model, there are nine compartments- Susceptible (S), Exposed (E), Asymptomatic ( $I_a$ ), Pre-symptomatic ( $I_p$ ), Mildly symptomatic ( $I_m$ ), Severely symptomatic ( $I_s$ ), Recovered (R), Dead (D). The model is further developed to incorporate age structures and effects of migration, but for the purpose of this report, we will ignore that.

The movement of individuals among compartments is as follows:



(Shekatkar et al. 7)

Here the whole population initially belongs in the Susceptible (S) compartment. Once a susceptible individual is infected, they move into the Exposed (E) compartment. The subsequent traversal between compartments is based on the kind of infection.



(Shekatkar et al. 6)

In the case of asymptomatic infections, an individual moves from the Exposed (E) compartment to the Asymptomatic ( $I_a$ ) compartment and upon recovery, into the Recovered (R) compartment.

In the case of mild infections, an individual moves from the Exposed (E) compartment to the Pre-symptomatic ( $I_p$ ) category for a while, then to the mildly symptomatic ( $I_m$ ) compartment and upon recovery, into the Recovered (R) compartment.

In the case of severe infections, an individual moves from the Exposed (E) compartment to the Pre-symptomatic ( $I_p$ ) category for a while, then the severely symptomatic ( $I_s$ ) compartment and then to the Hospitalised (H) compartment. Upon recovery, they move into the Recovered (R) compartment.

In the case of critical infections, an individual moves from the Exposed (E) compartment to the Pre-symptomatic ( $I_p$ ) category for a while, then the severely symptomatic ( $I_s$ ) compartment and then to the Hospitalised (H) compartment. There can be two outcomes in this scenario: the patient can recover and move into the Recovered (R) compartment OR the patient fails to recover and moves into the Deceased (D) compartment.

Here the parameters and their descriptions are:

## Model Parameters and Values



Parameter	Rate (1/day)	Description
$\beta$	0.42	Infectivity
$\gamma$	0.5	Transition rate from exposed to asymptomatic or pre-symptomatic
$\lambda_a$	0.1428	Transition rate from asymptomatic to recovered
$\lambda_m$	0.1428	Transition rate from mild to recovered
$\lambda_p$	0.5	Transition rate from pre-symptomatic to mild and severe
$\lambda_s$	0.1736	Transition rate from severe to hospitalized
$\rho$	0.068	Transition rate from hospitalized to recovered or dead

Parameter	Efficiency	
$C_a$	0.67	Relative intensity of contacts for asymptomatic
$C_p$	1	Relative intensity of contacts for pre-symptomatic
$C_m$	1	Relative intensity of contacts for mild
$C_s$	1	Relative intensity of contacts for severe

Parameter	Fractions	
$\alpha$	0.67	Fraction of exposed that become asymptomatic
$\mu$	0.956	Fraction of pre-symptomatic with mild symptoms
$\delta$	0.2	Fraction of hospitalized that die

$$R_0 \approx \frac{\alpha\beta C_a}{\lambda_a} + (1 - \alpha)\beta C_p \left[ \frac{1}{\lambda_p} + \frac{\mu}{\lambda_m} + \frac{1 - \mu}{\lambda_s} \right]$$

Values are based on the recent literature on epidemiology of COVID-19. See References slides in the end.

### **3. MATERIALS AND METHODS**

**NOTE:**

All models are governed by ODEs and hence all of the compartments are functions of time. In the graphs, the y-axis represents the fraction/number of individuals from the population and x-axis represents the number of days.

The  $\beta SI$  term in the equations can be replaced by  $\beta SI/N$  so that the (S/N) term more accurately represents the fraction of the susceptible population.

The code for all simulations is attached in the [appendix](#).

#### **3.1.1 SIR MODEL**

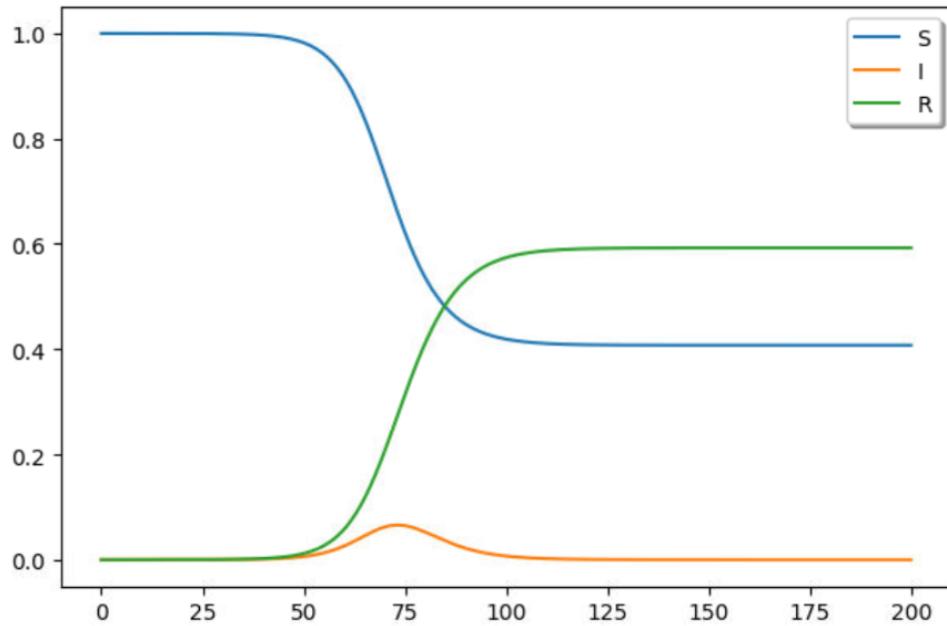
*Mathematical equations:*

$$\frac{dS}{dt} = -\beta SI$$

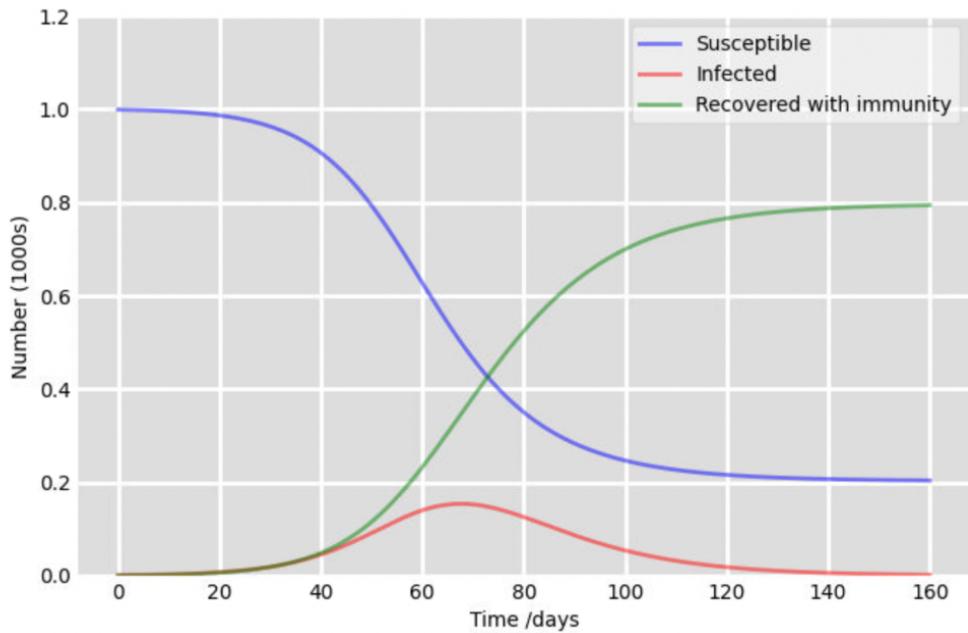
$$\frac{dI}{dt} = \beta SI - \gamma I$$

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

## SIR SIMULATION



Here,  $S(0)=1-1.27 \times 10^{-6}$ ,  $I(0)=1-1.27 \times 10^{-6}$ ,  $R(0)=0$ ,  $\beta=0.5$ ,  $\gamma=0.33$



Here,  $N=1000$ ,  $S(0)=999$ ,  $I(0)=1$ ,  $R(0)=0$ ,  $\beta=0.5$ ,  $\gamma=0.33$ , also  $\beta SI$  is replaced by  $\beta SI/N$

The code for these graphs is included [here](#).

### 3.1.2 SEIR MODEL

*Mathematical equations:*

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$$\frac{dS}{dt} = -\frac{\beta S I}{N}$$


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$$\frac{dE}{dt} = \frac{\beta S I - \gamma E}{N}$$


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$$\frac{dI}{dt} = \gamma E - \delta I$$

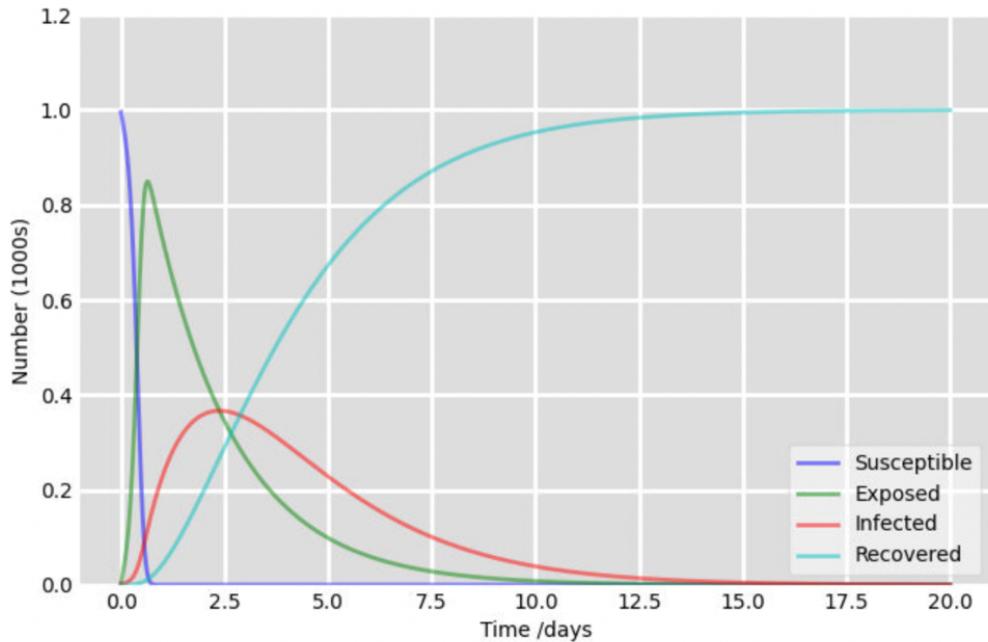

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$$\frac{dR}{dt} = \delta I$$

### SEIR SIMULATION



Here,  $N=1000$ ,  $S(0)=995$ ,  $E(0)=2$ ,  $I(0)=3$ ,  $R(0)=0$ ,  $\beta=1.2$ ,  $\gamma=0.2$ ,  $\delta=0.5$

The code for this graph is included [here](#).

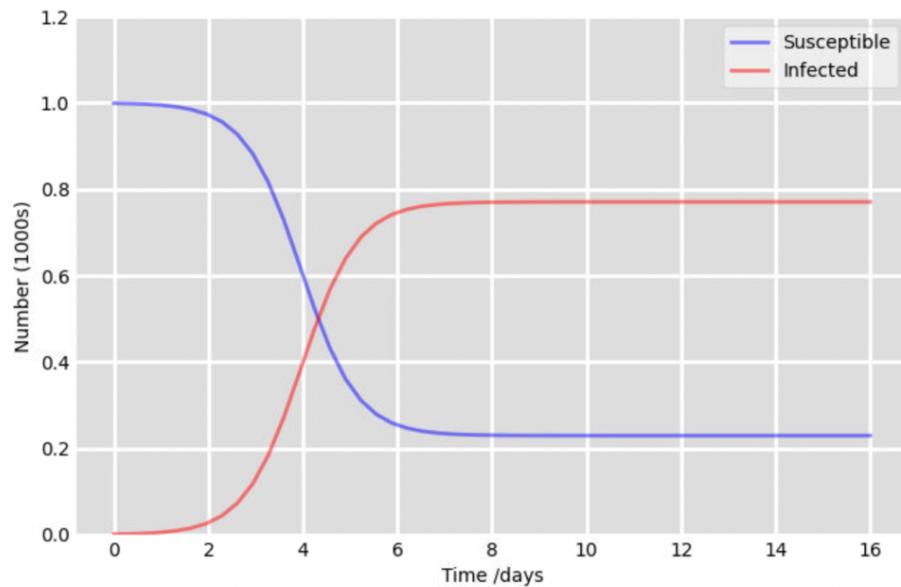
### 3.1.3 SIS MODEL

*Mathematical equations:*

$$\frac{dS}{dt} = -\beta SI + \gamma I$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

### SIS SIMULATION



Here,  $N=1000$ ,  $S(0)=999$ ,  $I(0)=1$ ,  $\beta=2.18$ ,  $\gamma=0.5$

The code for this graph is included [here](#).

#### 3.1.4 SEIS MODEL

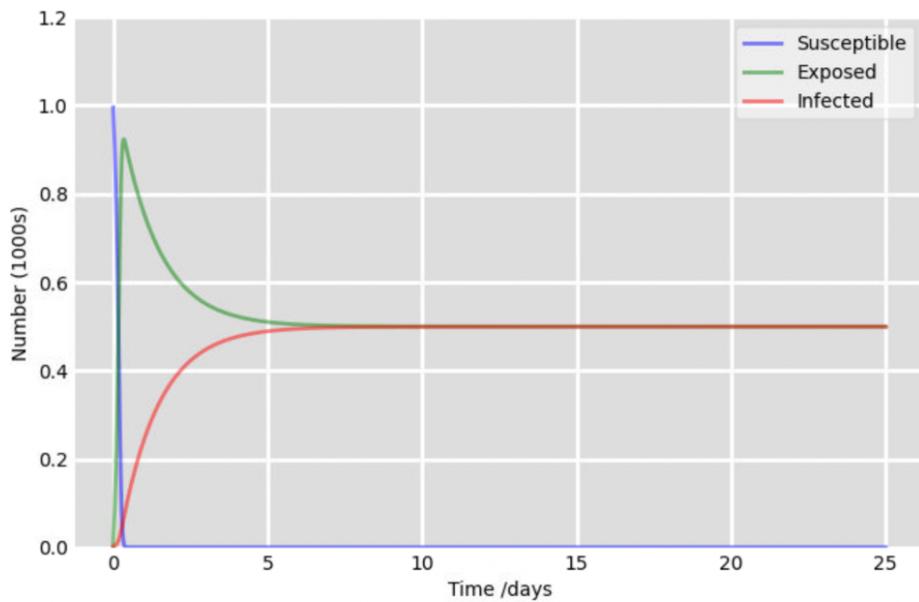
*Mathematical equations:*

$$\frac{dS}{dt} = -\beta SI + \gamma E$$

$$\frac{dE}{dt} = \beta SI - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \beta SI$$

### SEIS SIMULATION



Here,  $N=1000$ ,  $S(0)=995$ ,  $E(0)=2$ ,  $I(0)=3$ ,  $\beta=0.5$ ,  $\gamma=0.3$ ,  $\delta=0.4$

The code for this graph is included [here](#).

### 3.1.5 SEIRS MODEL

*Mathematical equations:*

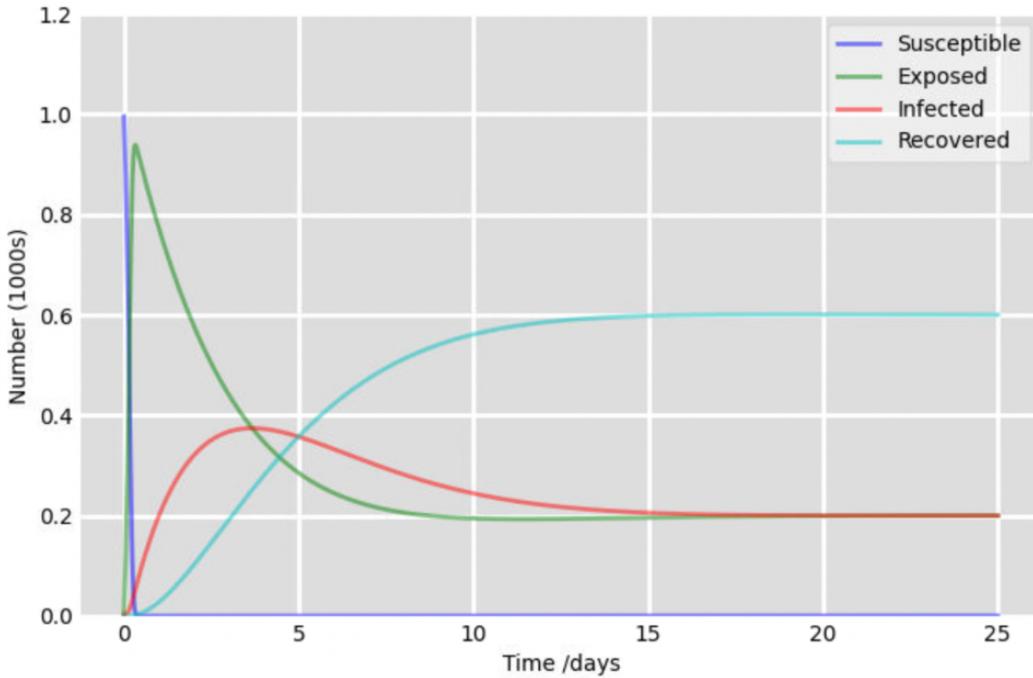
$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dE}{dt} = \beta SI - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \sigma I$$

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

### SEIRS SIMULATION



Here,  $N=1000$ ,  $S(0)=995$ ,  $E(0)=2$ ,  $I(0)=3$ ,  $R(0)=0$ ,  $\beta=0.5$ ,  $\gamma=0.4$ ,  $\delta=0.3$ ,  $\sigma=0.1$

The code for this graph is included [here](#).

### 3.2 INDSCI-SIM

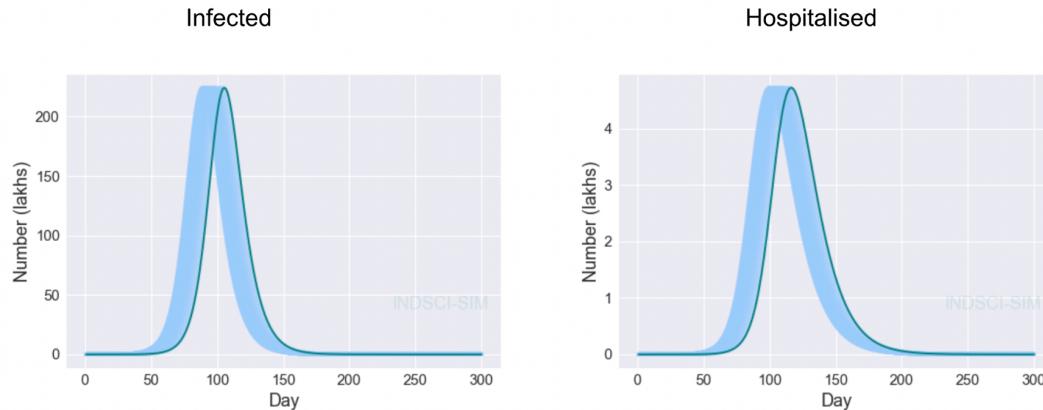
*Mathematical equations:*

$$\begin{aligned}
 \dot{S} &= -\frac{\beta}{N}S(C_p I_p + C_a I_a + C_s I_s + C_m I_m) \\
 \dot{E} &= \frac{\beta}{N}S(C_p I_p + C_a I_a + C_s I_s + C_m I_m) - \gamma E \\
 \dot{I}_p &= (1-\alpha)\gamma E - \lambda_p I_p \\
 \dot{I}_a &= \alpha\gamma E - \lambda_a I_a \\
 \dot{I}_s &= (1-\mu)\lambda_p I_p - \lambda_s I_s \\
 \dot{I}_m &= \mu\lambda_p I_p - \lambda_m I_m \\
 \dot{H} &= \lambda_s I_s - \rho H \\
 \dot{R} &= (1-\delta)\rho H + \lambda_a I_a + \lambda_m I_m \\
 \dot{D} &= \delta\rho H
 \end{aligned}$$

(Shekatkar et al. 8)

## INDSCI-SIM SIMULATION

### Results: No quarantine, no lockdown



The baseline result in the absence of any NPIs: Infected individuals and hospitalisations increase, reach a peak and decline with time.

Qualitative nature of results are insensitive to a **broad range of initial conditions**  
(infected individuals were varied from 10 to 100; with solid line at 10 which is the default initial condition)

(Shekatkar et al. 16)

## 4. RESULTS AND DISCUSSION

The SIR model provides a large-scale overview of infectious diseases. On adding compartments to the SIR model based on missing factors, we arrived at the INDSCI-SIM model which effectively captures the complexities of incubation period, different kinds of infections and severity of infection, temporary immunity and fatality of COVID-19. All other models were unable to capture these elements all at once. However, the INDSCI-SIM model is yet imperfect.

I will not allude to specifics that the advanced version of the model captures (such as age structure, migration, various states as metapopulations). Instead, I want to stress on the unreliability and complexity of the parameters that govern this model (Raju 19). There are nearly 14 parameters, ranging from social parameters based on contact between groups, to clinical parameters such as the fraction of asymptomatic individuals, etc.

Additionally, the pre-symptomatic category is ill-defined. We could instead break the Exposed (E) compartment into symptomatic and asymptomatic individuals and then define consequent compartments, for each, based on severity which would further break into compartments that are defined by the necessary protocol for treatment of an infection of that particular severity.

The model fails to account for the recovered category of people who despite testing negative can remain carriers of the disease and hence, spread infection.

What makes it difficult to quash a pandemic in reality? What are some other factors that make it difficult to accurately model and predict COVID-19? The answer to this is that there are a myriad of factors that we cannot control for. Real life isn't as definitive as models- parameters, factors, etc are dynamic and constantly change to introduce new complexities and thus, cannot be standardised.

Various discrepancies such as false positive or false negatives in COVID-19 testing (unreliable tests), erroneous data, data discrepancies due to government vendettas and strategies, new variants of the virus and its effects, deaths due to lack of resources, slow recovery rates due to lack of resources, etc. cannot be captured by the models but have a very real and critical impact on the way COVID-19 has been modelled, estimated and progressed in India and the world.

In addition to this, the effects of new developments such as vaccines or medicines as well as effects of interventions like lockdowns on social and emotional well-being of humans also have constant influence on the way the disease progresses (Raju 2).

Economic constraints and challenges may hinder governments from imposing lockdowns, financially weaker sections of society may have trouble fetching out money for costly tests and treatments, impact of social media, misinformation and conspiracies and its influence on the decisions of individuals and precautions taken by them are some other aspects that dynamically influence the pandemic and cannot be standardised.

Another poorly understood area is the varied susceptibility of individuals to COVID-19. Age, pre-existing health conditions, innate immunity, frequency of contact with other individuals, the kind of contact with other individuals, effectiveness of sanitisers, social distancing or masks, etc. all influence the way in which any individual would be likely to contract the virus.

Another significant challenge is the variation of the pandemic among and within countries. The spread of the virus, the nature of the virus, the variant of the virus and the effects on the population varies greatly among countries and even within each country. Each government tackles these things differently and strategises measures and interventions best suited to their own country. Additionally, the effect of trade and travel on how individuals might transmit the disease is also not accounted for in these models. It is extremely hard to generalise such nuanced factors.

## 5. IMPLICATIONS

The most fundamental way models help us understand infectious diseases better is that we can observe the peak of infection based on the parameters concerning the disease we are studying. It is important to see projections of the graph upon strategically intervening in order to delay the peak, flatten or change the way in any way.

This helps us choose what kind of interventions and necessary measures we must take in the future based on our needs and the best possible result predicted by the models. Additionally, we can potentially observe the eradication of the disease or at least figure out ways to combat it.

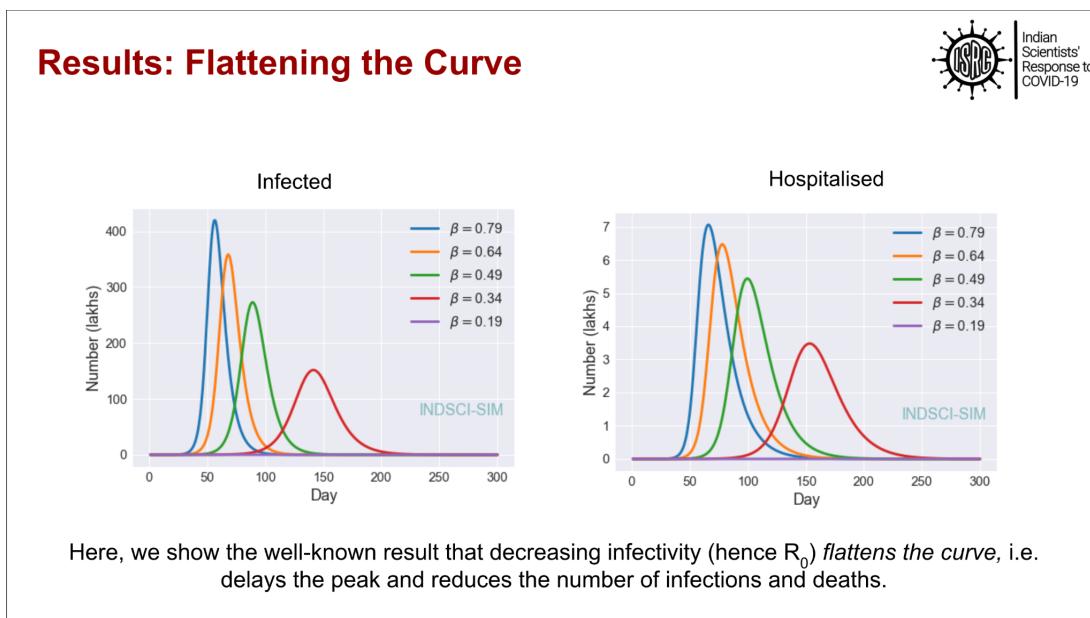
A significant insight that models can provide us with is the **reproductive ratio**. This ratio can help us understand the contagious nature of the disease and also help us visualise the effect of vaccination in combating the disease. The reproductive ratio can also tell us the necessary vaccine threshold required by a given population in order to achieve herd immunity.

Further explanation of these terms and concepts can be found in these videos:

<https://www.youtube.com/watch?v=sMA116kzyK4> ("R Nought and Vaccine Coverage | Health & Medicine | Khan Academy" 03:15–05:21) and

<https://www.youtube.com/watch?v=cEn1PKyBUNc> (Microbiology Society 03:15–05:21).

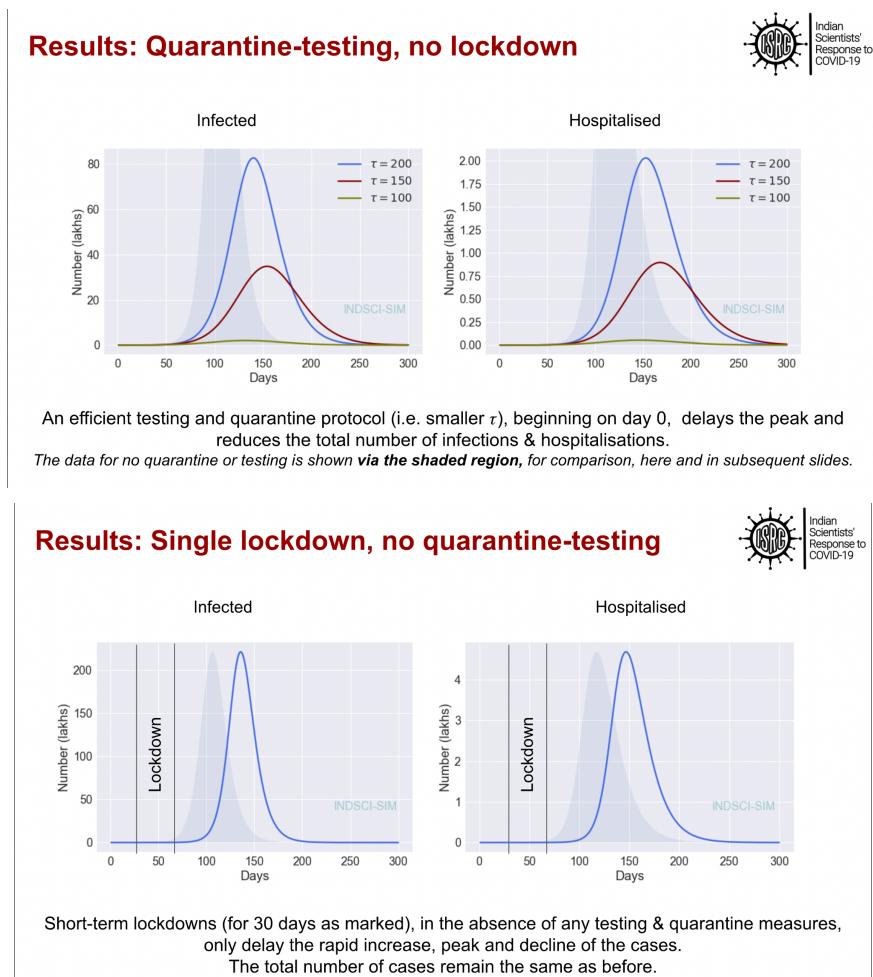
Below is an example from the INDSCI-SIM model where they change the transmission rate (and hence the reproductive ratio) to flatten the curve.



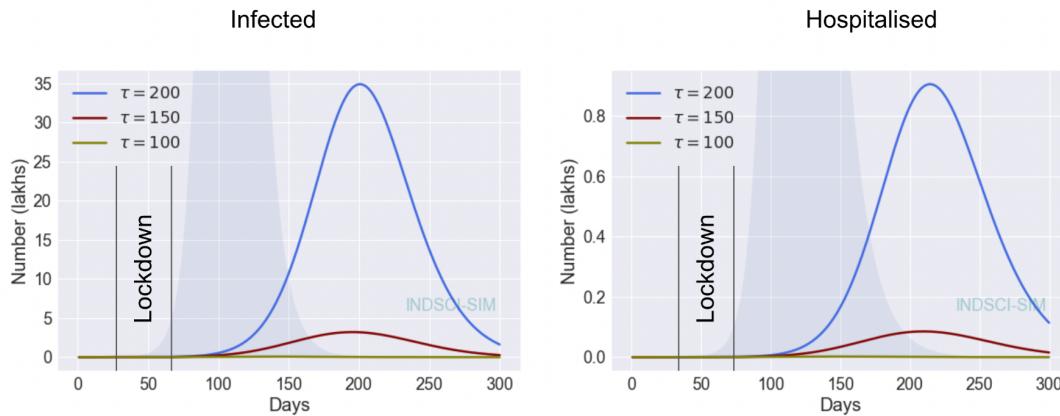
Other insights relate to the effects of (both pharmaceutical and non-pharmaceutical interventions) interventions- immunisation (vaccinations, medicines), different kinds of lockdowns, quarantining, frequent testing, etc.

Models help provide us with overviews and insights that can answer questions which would be very difficult to visualise otherwise. With respect to lockdowns, these questions can be: do lockdowns really work? How do they work? Do they avert deaths or reduce the number of cases? What kind of lockdowns work best- short, long, continuous, dispersed? When should one impose a lockdown? Is it the best strategy we have in combating the pandemic?

Models also provide the ease to compare, contrast and couple the effectiveness of certain intervention strategies. The INDSCI-SIM model yields this to understand the interplay among various non-pharmaceutical interventions and observe how different affect and alter the infection peak. This is an extremely useful tool for policymakers to conclude which measures they must take, which kind of lockdown they should implement, etc. in the future.

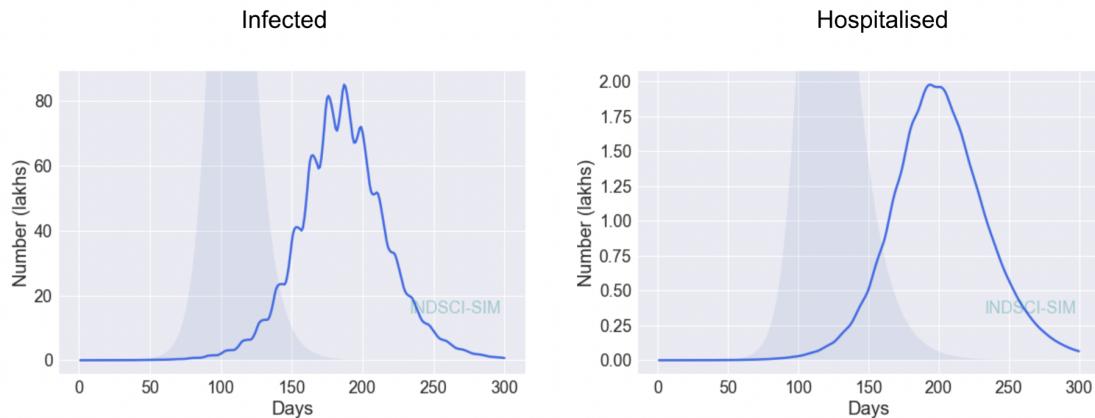


## Results: Single lockdown with quarantine-testing



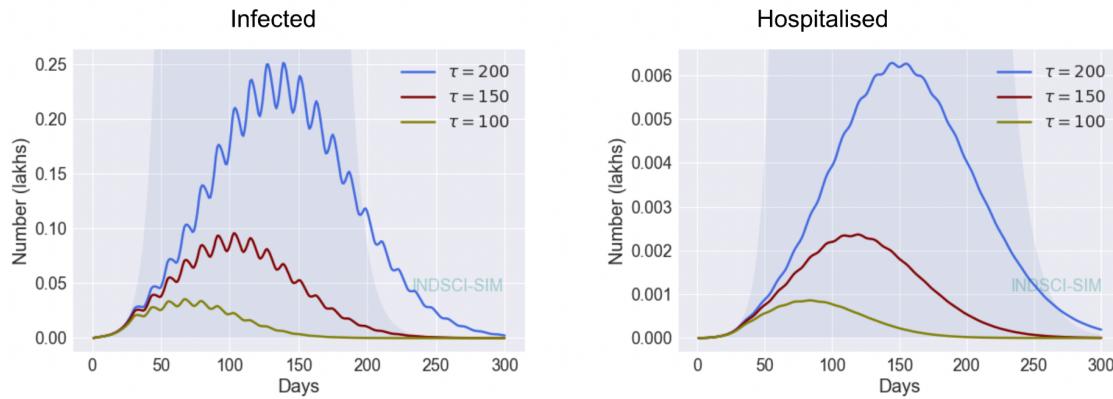
A single short-term lockdown (30 days) together with efficient testing and quarantine protocol (smaller  $\tau$ ), beginning on day 0, can delay the peak and reduce the total number of infections & hospitalisations.

## Results: Periodic lockdown, no quarantine-testing



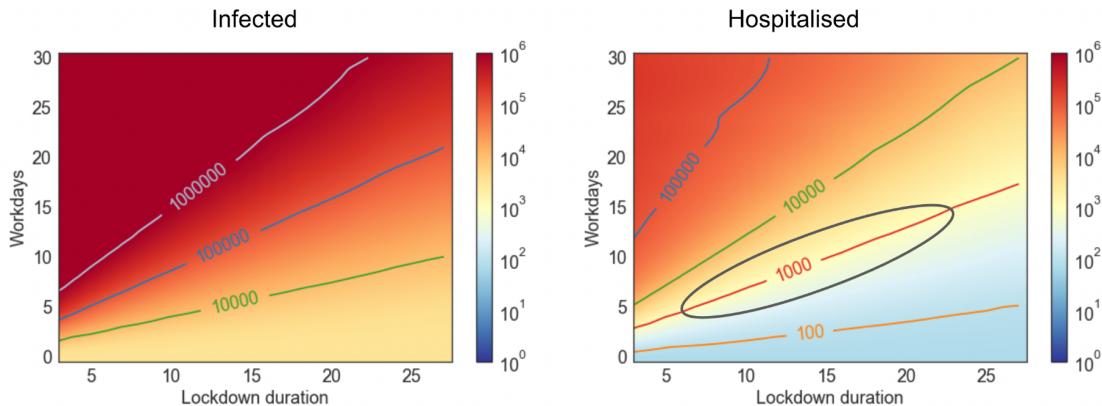
A periodic lockdown (via 7+5 schedule) can also delay the peak and reduce the total number of infections & hospitalisations.

## Results: Periodic lockdown, with quarantine-testing



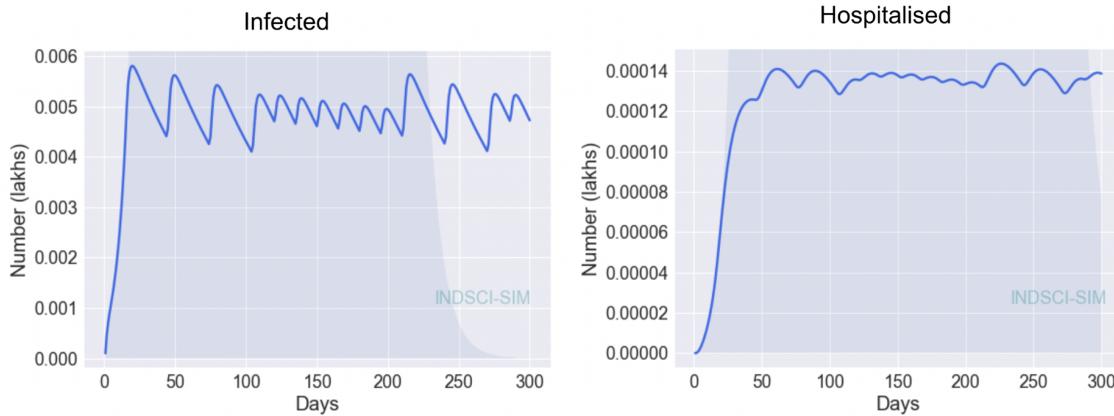
A periodic lockdown (via 7+5 schedule) together with an efficient testing and quarantine protocol can be an effective way to delay the peak and reduce the total number of infections and hospitalisations.

## Results: Periodic lockdown with quarantine-testing



Different combinations of lockdown and workdays can be used to obtain the same hospitalisation numbers. For example, along the highlighted contour (right panel), hospitalised numbers not exceeding 1000 can be achieved by choosing appropriate combinations of lockdown & workday durations.

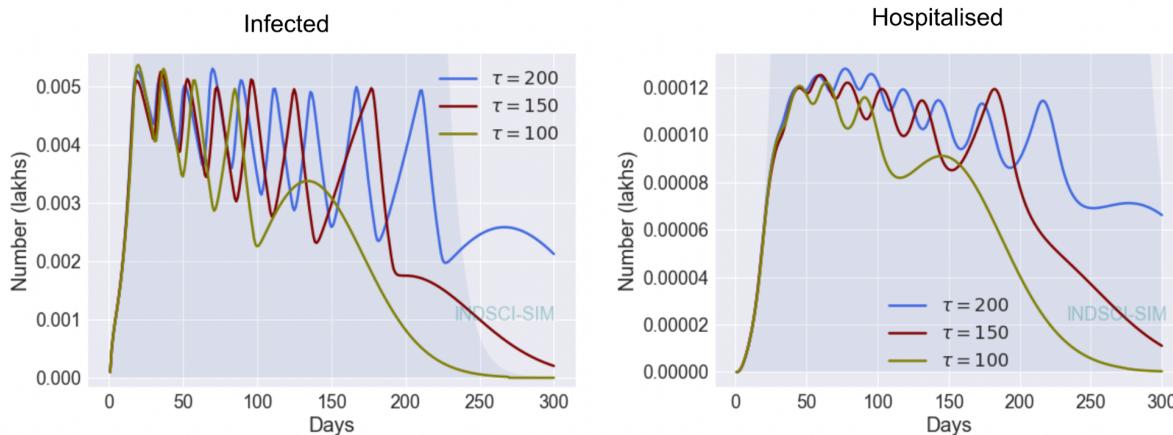
## Results: Lightswitch lockdown, no quarantine-testing



Lightswitch lockdown, where a lockdown begins as soon as a threshold number (500) of total number of infected are reached, can limit the total infections and hospitalisations, but the disease persists.

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## Results: Lightswitch lockdown with quarantine-testing



Substantial decrease in total infections and hospitalisations can be achieved via lightswitch lockdown, if combined with testing and quarantining.

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(Shekatkar et al. 18-25)

Other examples of how models have helped policymakers make choices for implementing measures are:

The UK government used strategies to predict how they could shift the peak of the outbreak such that it would take place in the spring when healthcare services would be less preoccupied with seasonal ailments and have the capacity to combat it efficiently (Kahn, and Dunn).

Additionally, it is believed that the government consulted the projections made by the model developed by MRC Center for Global Infectious Disease Analysis at Imperial College London in collaboration with WHO to implement policies such as strict social distancing and lockdown (Boseley).

The Austrian government is said to have relied on the simulation model developed at Technical University of Vienna to formulate the outbreak strategy (Eker).

## **APPENDIX**

### **I. SIR MODEL**

i.

```
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

def model(z,t,b,g):
    s,i,r=z
    return [-b*s*i, b*s*i-g*i, g*i]

z0=[1-1.27*10**-6, 1.27*10**-6, 0]

t=np.linspace(0,200,1000)

y=odeint(model,z0,t,args=(0.5, 0.33))

plt.plot(t, y)
plt.legend(['S', 'I', 'R'], shadow=True, loc= 'best' )
plt.show()
```

ii.

```

import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Total population, N.
N = 1000
# Initial number of infected and recovered individuals, I0 and R0.
I0, R0 = 1, 0
# Everyone else, S0, is susceptible to infection initially.
S0 = N - I0 - R0
# Contact rate, beta, and mean recovery rate, gamma, (in 1/day).
beta, gamma = 0.2, 1./10
# A grid of time points (in days)
t = np.linspace(0, 160, 160)

# The SIR model differential equations.
def deriv(y, t, N, beta, gamma):
    S, I, R = y
    dSdt = -beta * S * I / N
    dIdt = beta * S * I / N - gamma * I
    dRdt = gamma * I
    return dSdt, dIdt, dRdt

# Initial conditions vector
y0 = S0, I0, R0
# Integrate the SIR equations over the time grid, t.
ret = odeint(deriv, y0, t, args=(N, beta, gamma))
S, I, R = ret.T

# Plot the data on three separate curves for S(t), I(t) and R(t)
fig = plt.figure(facecolor='w')
ax = fig.add_subplot(111, facecolor="#dddddd", axisbelow=True)
ax.plot(t, S/1000, 'b', alpha=0.5, lw=2, label='Susceptible')
ax.plot(t, I/1000, 'r', alpha=0.5, lw=2, label='Infected')
ax.plot(t, R/1000, 'g', alpha=0.5, lw=2, label='Recovered with immunity')
ax.set_xlabel('Time /days')

```

```

ax.set_ylabel('Number (1000s)')
ax.set_ylim(0,1.2)
ax.yaxis.set_tick_params(length=0)
ax.xaxis.set_tick_params(length=0)
ax.grid(b=True, which='major', c='w', lw=2, ls='-')
legend = ax.legend()
legend.get_frame().set_alpha(0.5)
for spine in ('top', 'right', 'bottom', 'left'):
    ax.spines[spine].set_visible(False)
plt.show()

```

## II. SEIR MODEL

```

import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Total population, N.
N = 1000
# Initial number of infected, exposed and recovered individuals, I0, E0
and R0.
I0 = 3
E0 = 2
R0 = 0
# Everyone else, S0, is susceptible to infection initially, and S+E+I+R=N
S0 = N - I0 - E0 - R0
# parameters(in 1/days).
beta, gamma, delta = 1.2 , 0.2, 0.5
# A grid of time points (in days)
t = np.linspace(0, 20, 1000)

# The SEIR model differential equations.
def deriv(y, t, N, beta, gamma):
    S, E, I, R = y
    dSdt = -beta * S * I/N
    dEdt = beta * S * I/N - gamma * E
    dIdt = gamma * E - delta * I

```

```

dRdt = delta * I

return dSdt, dEdt, dIdt, dRdt

# Initial conditions vector
y0 = S0, E0, I0, R0
# Integrate the SEIR equations over the time grid, t.
ret = odeint(deriv, y0, t, args=(beta, gamma, delta))
S, E, I, R = ret.T

# Plot the data on three separate curves for S(t), E(t), I(t) and R(t)
fig = plt.figure(facecolor='w')
ax = fig.add_subplot(111, facecolor="#dddddd", axisbelow=True)
ax.plot(t, S/1000, 'b', alpha=0.5, lw=2, label='Susceptible')
ax.plot(t, E/1000, 'g', alpha=0.5, lw=2, label='Exposed')
ax.plot(t, I/1000, 'r', alpha=0.5, lw=2, label='Infected')
ax.plot(t, R/1000, 'c', alpha=0.5, lw=2, label='Recovered')

ax.set_xlabel('Time /days')
ax.set_ylabel('Number (1000s)')
ax.set_ylim(0,1.2)
ax.yaxis.set_tick_params(length=0)
ax.xaxis.set_tick_params(length=0)
ax.grid(b=True, which='major', c='w', lw=2, ls='-')
legend = ax.legend()
legend.get_frame().set_alpha(0.5)
for spine in ('top', 'right', 'bottom', 'left'):
    ax.spines[spine].set_visible(False)
plt.show()

```

### III. SIS MODEL

```

import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Total population, N.
N = 1000

```

```

# Initial number of infected and recovered individuals, I0 and R0.
I0 = 1

# Everyone else, S0, is susceptible to infection initially.
S0 = N - I0

# parameters (in 1/days).
beta, gamma = 2.18 , 0.5

# A grid of time points (in days)
t = np.linspace(0, 16, 50)

# The SIS model differential equations.
def deriv(y, t, N, beta, gamma):
    S, I = y
    dSdt = -beta * S * I/N + gamma * I
    dIdt = beta * S * I/N - gamma * I
    return dSdt, dIdt

# Initial conditions vector
y0 = S0, I0

# Integrate the SIS equations over the time grid, t.
ret = odeint(deriv, y0, t, args=(N, beta, gamma))
S, I = ret.T

# Plot the data on three separate curves for S(t), I(t).
fig = plt.figure(facecolor='w')
ax = fig.add_subplot(111, facecolor='#dddddd', axisbelow=True)
ax.plot(t, S/1000, 'b', alpha=0.5, lw=2, label='Susceptible')
ax.plot(t, I/1000, 'r', alpha=0.5, lw=2, label='Infected')

ax.set_xlabel('Time /days')
ax.set_ylabel('Number (1000s)')
ax.set_ylim(0,1.2)
ax.yaxis.set_tick_params(length=0)
ax.xaxis.set_tick_params(length=0)
ax.grid(b=True, which='major', c='w', lw=2, ls='-' )
legend = ax.legend()
legend.get_frame().set_alpha(0.5)

```

```

for spine in ('top', 'right', 'bottom', 'left'):
    ax.spines[spine].set_visible(False)
plt.show()

```

#### IV. SEIS MODEL

```

import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Total population, N.
N = 1000
# Initial number of infected and exposed individuals, I0 and E0.
I0 = 3
E0 = 2

# Everyone else, S0, is susceptible to infection initially, and S+E+I=N
S0 = N - I0 - E0
# parameters(in 1/days).
beta, gamma, delta= 0.5 , 0.3, 0.4
# A grid of time points (in days)
t = np.linspace(0, 25, 1000)

# The SEIS model differential equations.
def deriv(y, t, N, beta, gamma):
    S, E, I = y
    dSdt = -beta * S * I/N + delta * I
    dEdt = beta * S * I/N - gamma * E
    dIdt = gamma * E - delta * I
    return dSdt, dEdt, dIdt
# Initial conditions vector
y0 = S0, E0, I0
# Integrate the SEIS equations over the time grid, t.
ret = odeint(deriv, y0, t, args=(beta, gamma, delta))
S, E, I = ret.T

# Plot the data on three separate curves for S(t), E(t), I(t)

```

```

fig = plt.figure(facecolor='w')
ax = fig.add_subplot(111, facecolor='#dddddd', axisbelow=True)
ax.plot(t, S/1000, 'b', alpha=0.5, lw=2, label='Susceptible')
ax.plot(t, E/1000, 'g', alpha=0.5, lw=2, label='Exposed')
ax.plot(t, I/1000, 'r', alpha=0.5, lw=2, label='Infected')

ax.set_xlabel('Time /days')
ax.set_ylabel('Number (1000s)')
ax.set_ylim(0,1.2)
ax.yaxis.set_tick_params(length=0)
ax.xaxis.set_tick_params(length=0)
ax.grid(b=True, which='major', c='w', lw=2, ls='-' )
legend = ax.legend()
legend.get_frame().set_alpha(0.5)
for spine in ('top', 'right', 'bottom', 'left'):
    ax.spines[spine].set_visible(False)
plt.show()

```

## V. SEIRS MODEL

```

import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt

# Total population, N.
N = 1000
# Initial number of infected, exposed and recovered individuals, I0, E0
and R0.
I0 = 3
E0 = 2
R0 = 0
# Everyone else, S0, is susceptible to infection initially, and S+E+I+R=N
S0 = N - I0 - E0 - R0
# parameters(in 1/days).
beta, gamma, delta, sigma = 0.5 , 0.4, 0.3, 0.1
# A grid of time points (in days)
t = np.linspace(0, 25, 1000)

```

```

# The SEIRS model differential equations.

def deriv(y, t, N, beta, gamma):
    S, E, I, R = y
    dSdt = -beta * S * I/N + sigma * R
    dEdt = beta * S * I/N - gamma * E
    dIdt = gamma * E - delta * I
    dRdt = delta * I - sigma * R
    return dSdt, dEdt, dIdt, dRdt

# Initial conditions vector
y0 = S0, E0, I0, R0
# Integrate the SEIRS equations over the time grid, t.
ret = odeint(deriv, y0, t, args=(beta, gamma, delta))
S, E, I, R = ret.T

# Plot the data on three separate curves for S(t), E(t), I(t) and R(t)
fig = plt.figure(facecolor='w')
ax = fig.add_subplot(111, facecolor="#dddddd", axisbelow=True)
ax.plot(t, S/1000, 'b', alpha=0.5, lw=2, label='Susceptible')
ax.plot(t, E/1000, 'g', alpha=0.5, lw=2, label='Exposed')
ax.plot(t, I/1000, 'r', alpha=0.5, lw=2, label='Infected')
ax.plot(t, R/1000, 'c', alpha=0.5, lw=2, label='Recovered')

ax.set_xlabel('Time /days')
ax.set_ylabel('Number (1000s)')
ax.set_ylim(0,1.2)
ax.yaxis.set_tick_params(length=0)
ax.xaxis.set_tick_params(length=0)
ax.grid(b=True, which='major', c='w', lw=2, ls='-' )
legend = ax.legend()
legend.get_frame().set_alpha(0.5)
for spine in ('top', 'right', 'bottom', 'left'):
    ax.spines[spine].set_visible(False)
plt.show()

```

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