

2020 Chemical Engineering Undergraduate Research Internship




SEIR Model for COVID-19

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OUTLINE



- PREDICTING AN END TO COVID-19

- MODELLING OF INFECTIOUS DISEASE

- SEIR MODEL & ITS PARAMETERS

- MATHEMATICAL EQUATIONS OF SEIR

- KEY PREDICTIONS OF SEIR MODEL

- SEIR MODEL FOR INDIA

- KANTOR'S CODE

- SEIR MODEL FOR HYPOTHETICAL IIT ROPAR CAMPUS & GRAPHICAL ANALYSIS

- LEARNING OUTCOMES

PREDICTING AN END TO COVID-19

- COVID-19, originated in Wuhan, China is spreading across the globe at an alarming rate.
- Given the current situation, predicting the future path of this pandemic has become of utmost interest to epidemiologists.
- Scientists are in need of a model that can help predict the growth rate of COVID to get an idea about what steps need to be taken in order to bring this pandemic to an end.

COVID-19 INDIA as on :
15 August 2020, 08:00
IST (GMT+5:30)

Active (26.45%)

668220 (6625↑)

Discharged (71.61%)

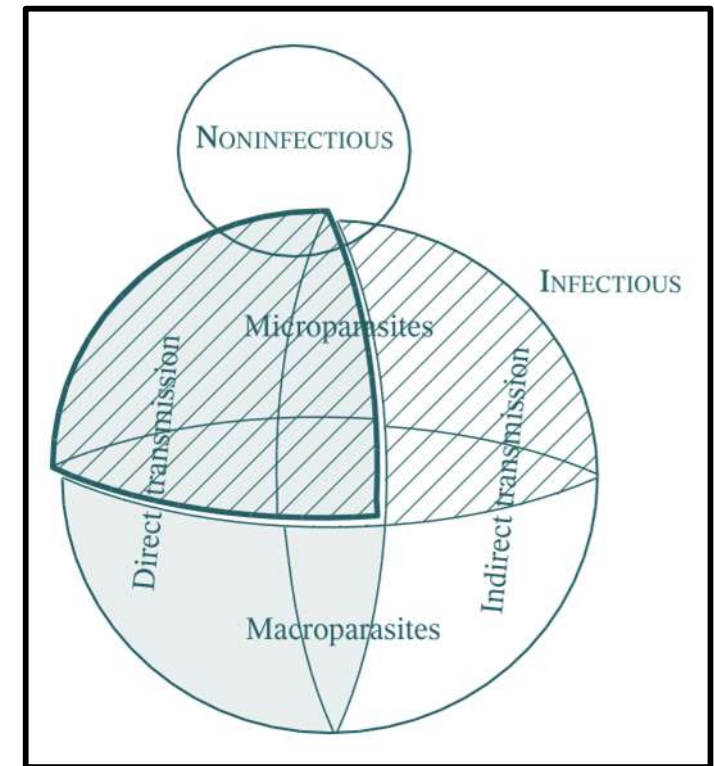
1808936 (57381↑)

Deaths (1.94%)

49036 (996↑)

MODELLING OF INFECTIOUS DISEASE

- During the emergence of a novel pandemic, predictive modelling is important in public health planning and response.
- However, prior to the modelling of infectious disease, many decisions regarding the nature of the disease need to be made.
- For the models in the upcoming slides, COVID -19 is classified as a **directly transmitted, micro parasitic infectious disease**.

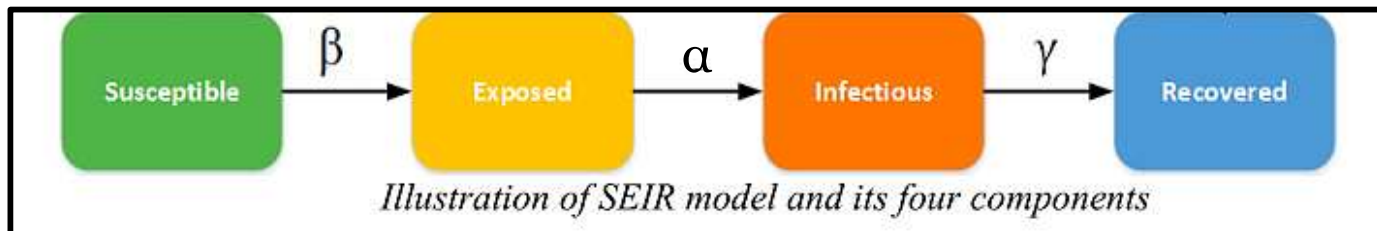


Types of Disease

Reference: Modeling Infectious Diseases in Humans and Animals by Matt J. Keeling and Pejman Rohani, Chapter 01, Figure 1.1

INTRODUCTION TO SEIR MODEL

- The SEIR model is an example of a very basic epidemiological model used for studying the growth of COVID-19.
- In the SEIR model, the population is divided into **4 non-overlapping groups** corresponding to stages of the disease:
 1. **Susceptible (S).** The subpopulation susceptible to acquire the disease.
 2. **Exposed (E).** The subpopulation that has been infected with the virus, but not capable of transmitting the virus to others.
 3. **Infectious (I).** The subpopulation that has acquired the virus and can infect others.
 4. **Recovered (R).** The subpopulation that has recovered from infection and presumed to be no longer susceptible to the disease.



PARAMETERS OF SEIR MODEL

1. **Incubation Period, α** : The average period of time in the exposed state is called the incubation period of the disease, and equal to reciprocal of α

$$\tau_{incubate} = \frac{1}{\alpha}$$

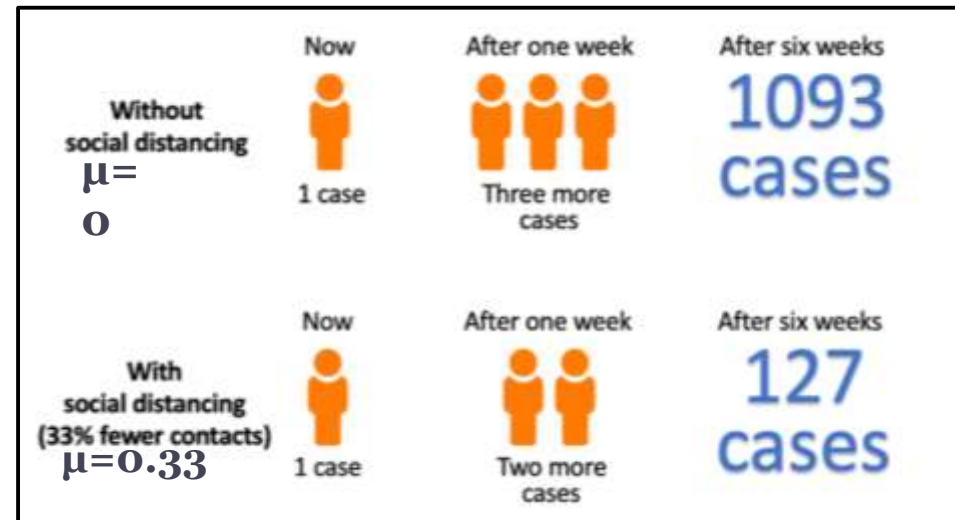
2. **Recovery Period, β** : The average time taken for recovery is called the recovery time period and is equal to reciprocal of β .

$$\tau_{recovery} = \frac{1}{\gamma}$$

3. **Reproduction Number (R_0)** : R_0 describes the transmissibility of an infectious disease. It is equal to the average number of secondary cases that arise from a primary case.

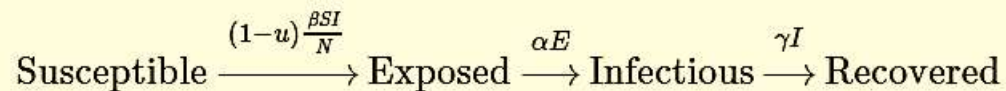
$$R_0 = \frac{\beta}{\gamma}$$

1. **μ** : It describes the effectiveness of any public health interventions to control transmission of the disease.



SEIR MODEL

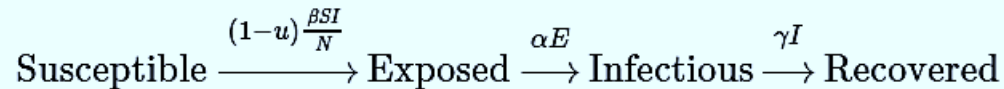
- Neglecting demographic processes of birth and death from other causes, the progression of an epidemic can be modeled as follows:



The features of the model are as follows:

- $(1-\mu)\beta SI$** is the rate at which susceptible population encounters the infected population resulting in transmission of the disease.
- αE** is the rate at which exposed population becomes infective, where E is the size of the exposed population.
- γI** is the rate at which infected population recovers and becomes resistant to further infection.

MATHEMATICAL EQUATIONS: SEIR MODEL



$$s = \frac{S}{N} \quad e = \frac{E}{N} \quad i = \frac{I}{N} \quad r = \frac{R}{N}$$

From the model shown above, the following differential equations can be determined for the calculation of s, e, i, r variables defined above:

$$\begin{aligned} \frac{ds}{dt} &= -(1-u)\beta si \\ \frac{de}{dt} &= (1-u)\beta si - \alpha e \\ \frac{di}{dt} &= \alpha e - \gamma i \\ \frac{dr}{dt} &= \gamma i \end{aligned}$$

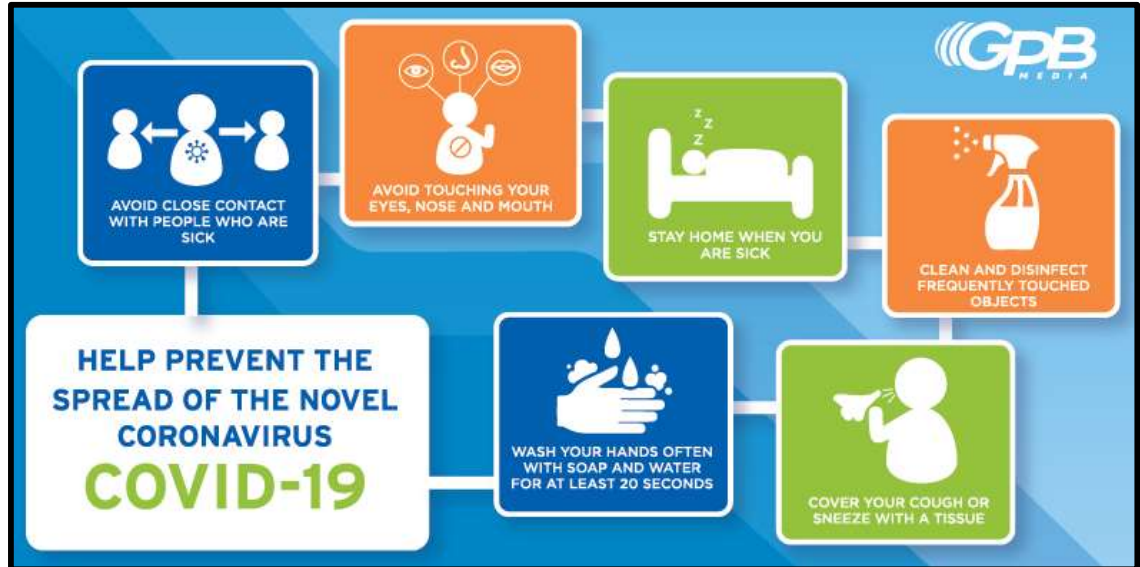
It is also important to note that $s + e + i + r = 1$

KEY PREDICTIONS OF SEIR MODEL

- The key predictions made by the SEIR Model concerning the outbreak and eventual recovery from an epidemic are as follows:

1. The infectious population grows only if $\beta s > \gamma$, that is the rate of infection is greater than the rate of recovery.

- The infectious population can grow only if $R_0 s > 1$.
- The infected population, that is number of people in the subpopulations E and I, decreases if $s R_0 < 1$.



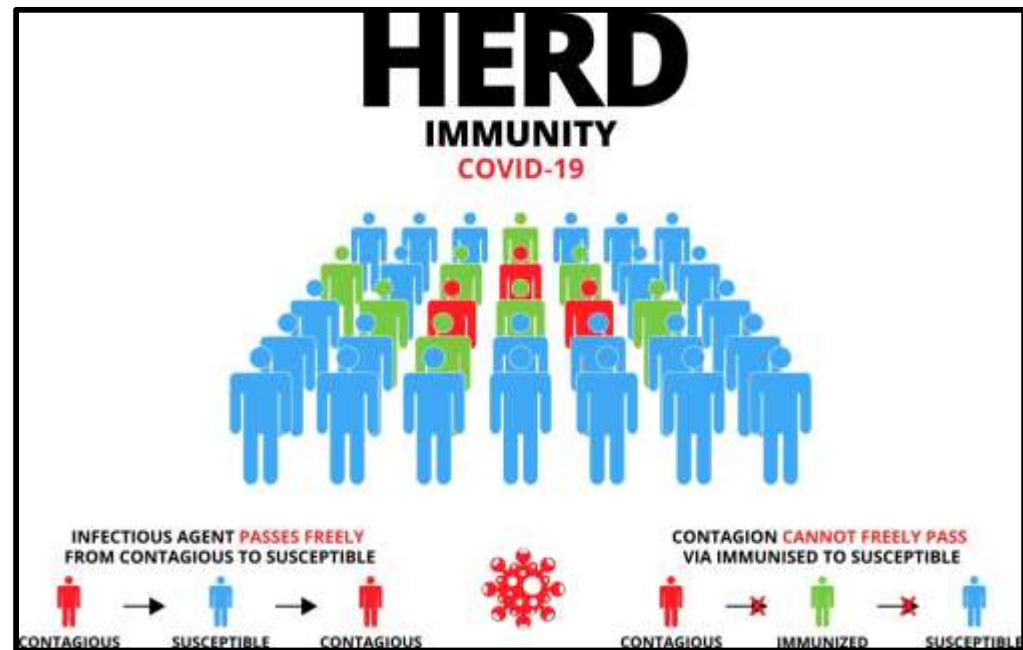
Reference: <https://www.gpb.org/news/2020/03/19/tips-stop-covid-19-spread>

KEY PREDICTIONS OF SEIR MODEL

2. The population has '**herd immunity**' when a sufficient number of individuals are immune to the virus.

➤ People can become immune to certain viruses after surviving infection or being vaccinated. Typically, at least 70% of a population must be immune to achieve herd immunity.

This condition is achieved when the fraction of susceptible(s) is less than $1/R_o$.



Reference: <https://www.narayanahealth.org/blog/herd-immunity-what-is-means-for-covid-19/>

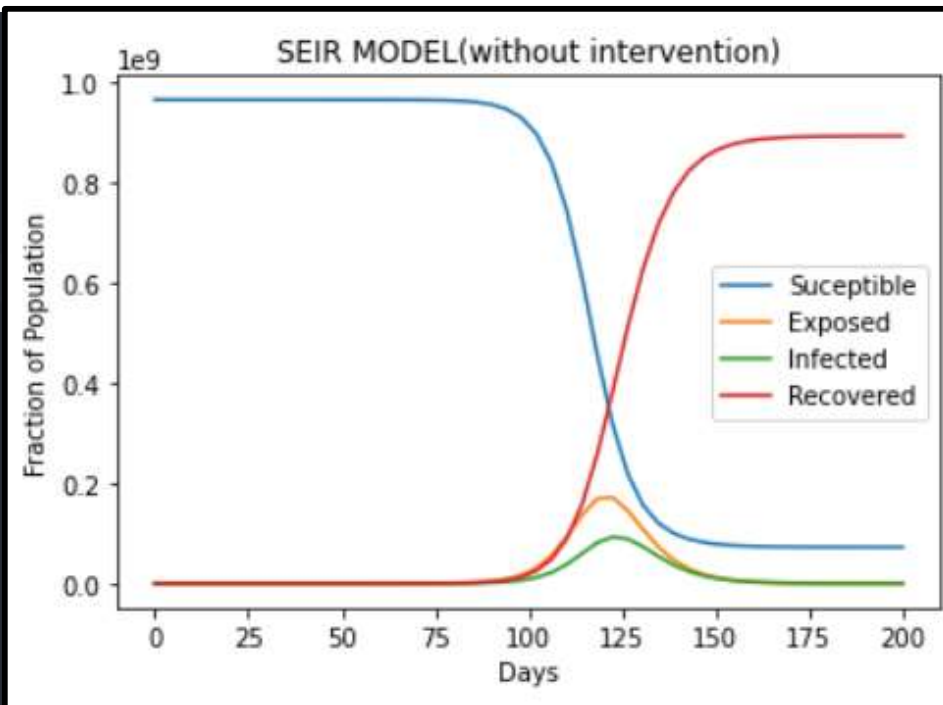
SEIR MODEL FOR INDIA

- The values of various parameters in Kantor's Code were changed according to the available data to build a **SEIR Model for India**. (Reference: SEIR and Regression Model based COVID-19 outbreak predictions in India by Rajan Gupta, Gaurav Pandey, Poonam Chaudhary, Saibal Pal; page4)
- The pictures below depict these changes and the outcome of the model.

```
#Reproduction number
R0 = 4
t_incubation = 5.2 #in days
t_infective = 2.9 # in days
u = 0

#Population Size
N = 1380000000

# initial number of infected and recovered individuals
e_initial = 0
i_initial = 1
r_initial = 0
s_initial = 966000000 #70% of the total population
```



KANTOR'S CODE

- The solution of the SEIR Model can be determined by the Kantor's Code. The entire code can be accessed from https://colab.research.google.com/drive/1ddb_oswsq9MRKyHrzflCzeF8Tqqmp24H#scrollTo=F8ZTZEtVr4Py
- The picture below shows the solving of differential equations in Kantor's Code using odeint function.

```
def step(t):
    return 1 if t >= 7*t_social_distancing else 0 #checking if t is greater than t_social_distancing

# SEIR model differential equations.
def deriv(x, t, u, alpha, beta, gamma):
    s, e, i, r = x
    dsdt = -(1-u*step(t)/100)*beta * s * i
    dedt = (1-u*step(t)/100)*beta * s * i - alpha * e
    didt = alpha * e - gamma * i
    drdt = gamma * i
    return [dsdt, dedt, didt, drdt]

t = np.linspace(0, 210, 210)
x_initial = s_initial, e_initial, i_initial, r_initial
s, e, i, r = odeint(deriv, x_initial, t, args=(u_social_distancing, alpha, beta, gamma)).T

s0, e0, i0, r0 = odeint(deriv, x_initial, t, args=(0, alpha, beta, gamma)).T
```

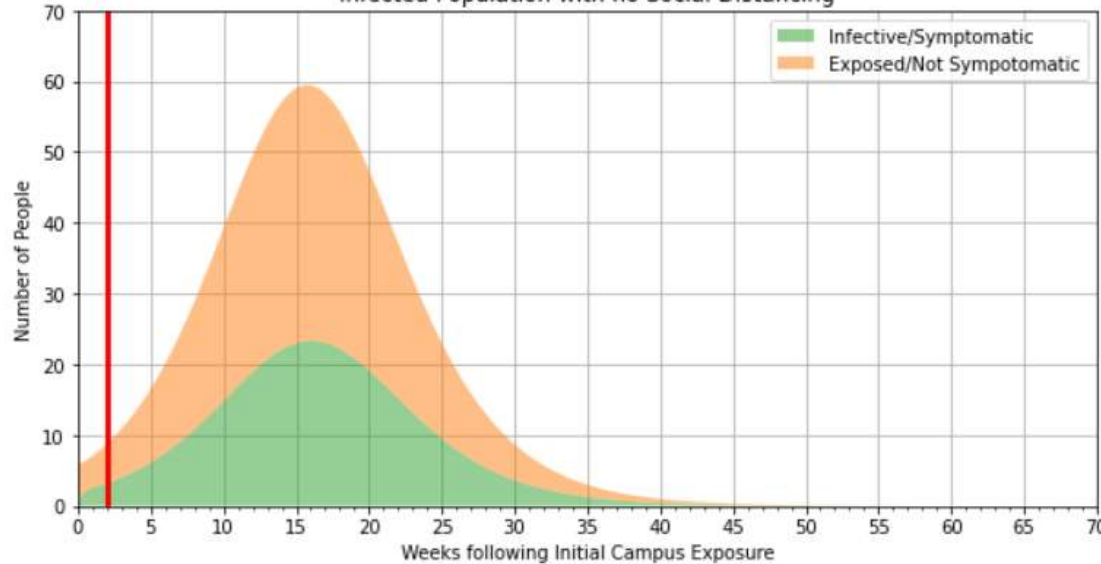
SEIR MODEL FOR IIT ROPAR CAMPUS

- We consider a **hypothetical IIT Ropar Campus** of 2,000 people and construct a SEIR Model as shown below.
- The values of R_0 , incubation time and recovery time have been set as the average values for India in the Kantor's Code

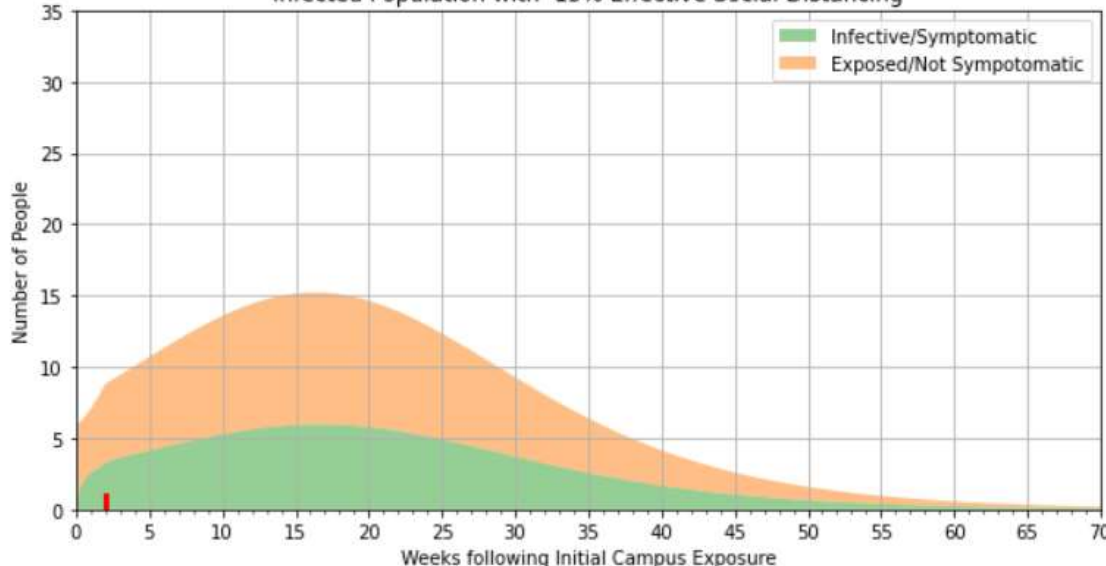
```
#SEIR Model with Social Distancing { run: "auto" }  
R0 = 1.29 #average reproduction number in India  
t_incubation = 5.1  
t_infective = 3.3  
N = 2000 #assumed population of IIT Ropar  
n = 6 #Initial number exposed  
#Start of social distancing following exposure (weeks)  
t_social_distancing = 2  
#@markdown Effectiveness of social distancing (0 to 100%)  
u_social_distancing = 15 |
```

GRAPHICAL ANALYSIS

Infected Population with no Social Distancing



Infected Population with 15% Effective Social Distancing



- From the graph it is clearly possible to predict the course of the pandemic like the time of maximum infected population and also the possible end.
- Also, from the graph we can observe that on introducing public interventions like social distancing, the maximum infected and exposed population decreases multiple times.

This is termed as flattening of the curve.

LEARNING OUTCOMES

1. After careful analysis of SEIR Model, one may implement it to real life scenarios, making necessary assumptions regarding demographic changes, etc. beforehand.
2. Using the SEIR Model, it is possible to formulate mathematical equations for figuring out the exact fraction of infected, exposed, susceptible and recovered population at any point of time under study. These values may be computed in python with the help of **Kantor's Code**.
3. Analysis of the effects of social distancing on the pandemic is feasible which may be summarised as slowing the infection rate or equivalently "**flattening of the curve**".

THANK YOU !

A series of horizontal lines in teal and light blue colors, some solid and some dashed, extending across the bottom of the slide.