# Mathematical Analysis of COVID-19 using SEIR model and vaccination effect

02-712: Biological Modeling and Simulation

**GROUP 13** 

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#### **Problem and Motivation**



**PANDEMIC** 











**GLOBAL TRENDS** 

**Total Cases:** 6,50,127,543

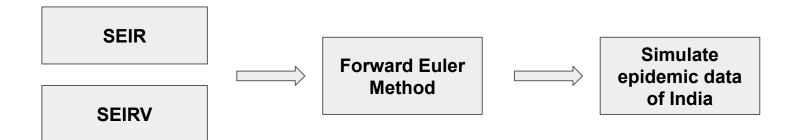
**Deaths:** 6,647,001



### Aim

- To enhance the SEIR Model with effect of different versions of severity
- To predict the susceptibility, infection and recovered percentages using model considering effects of vaccination
- Compare trends for vaccinated and unvaccinated populations

# Methodolgy



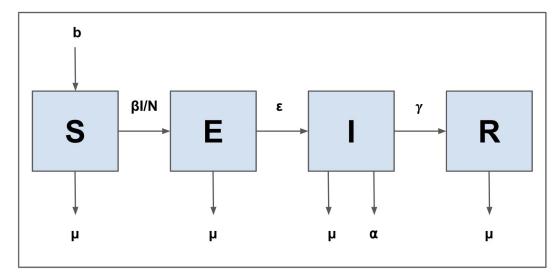
MATHEMATICAL MODEL

**NUMERICAL ALGORITHM** 

ANALYSIS FOR INDIAN COVID DATA

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#### SEIR model



# Differential Equations are as follows:

$$1. S = b - (\mu + \frac{\beta I}{N})S$$

$$E = \frac{\beta IS}{N} - (\mu + \varepsilon)E$$

3. 
$$I = \varepsilon E - (\mu + \alpha + \gamma)I$$

$$4. R = \gamma I - \mu R$$

Parameter	Description	
b	Birth rate	
$\mu$	Natural death rate	
β	Probability of infection	
α	Death due to COVID	
$\epsilon$	Rate of exposed individuals getting infecte	
$\gamma$	Rate of recovery	

#### SEIR model

#### Forward Euler equations are:

1. 
$$S^{t+1} = S^t + dt(b - (\mu + \frac{\beta I^t}{N^t}))$$

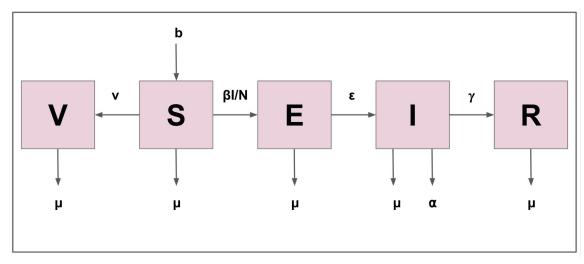
2. 
$$E^{t+1} = E^t + dt(\frac{\beta I^t S^t}{N} - (\mu + \varepsilon)E^t)$$

3. 
$$I^{t+1} = I^t + dt(\varepsilon E^t - (\mu + \alpha + \gamma)I^t)$$

4. 
$$R^{t+1} = R^t + dt(\gamma I^t - \mu R^t)$$

Parameter	Description		
b	Birth rate		
$\mu$	Natural death rate		
β	Probability of infection		
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$\epsilon$	Rate of exposed individuals getting infected		
$\gamma$	Rate of recovery		

#### SEIRV model



Parameter	Description	
b	Birth rate	
$\mu$	Natural death rate	
$\beta$	Probability of infection	
α	Death due to COVID	
$\epsilon$	Rate of exposed individuals getting infected	
$\gamma$	Rate of recovery	
$\dot{v}$	Rate of vaccination	

Differential Equations are as follo:

1. 
$$S = b - (\mu + v + \frac{\theta I}{N})S$$

2. 
$$E = \frac{\beta IS}{N} - (\mu + \varepsilon)E$$

3. 
$$I = \varepsilon E - (\mu + \alpha + \gamma)I$$

4. 
$$R = \gamma I - \mu R$$

5. 
$$V = vS - \mu V$$

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#### SEIRV model

#### Forward Euler equations are:

1. 
$$S^{t+1} = S^t + dt(b - (\mu + v + \frac{\theta I^t}{N^t}))S^t)$$

2. 
$$E^{t+1} = E^t + dt \left( \frac{\beta I^t S^t}{N^t} - (\mu + \varepsilon) E^t \right)$$

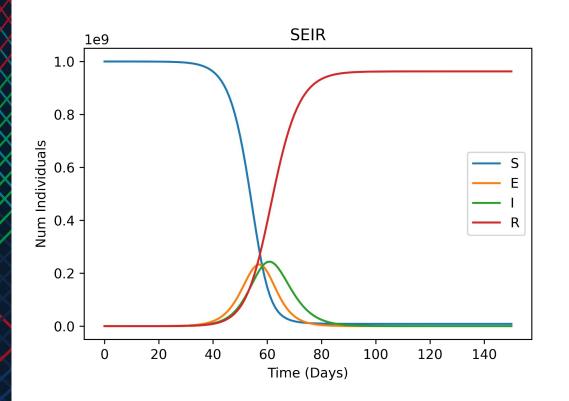
3. 
$$I^{t+1} = I^t + dt(\varepsilon E^t - (\mu + \alpha + \gamma)I^t)$$

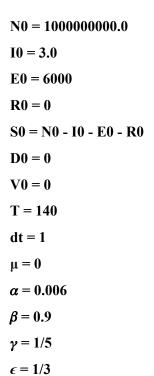
4. 
$$R^{t+1} = R^t + dt(\gamma I^t - \mu R^t)$$

5. 
$$V^{t+1} = V^t + dt(vS^t - \mu V^t)$$

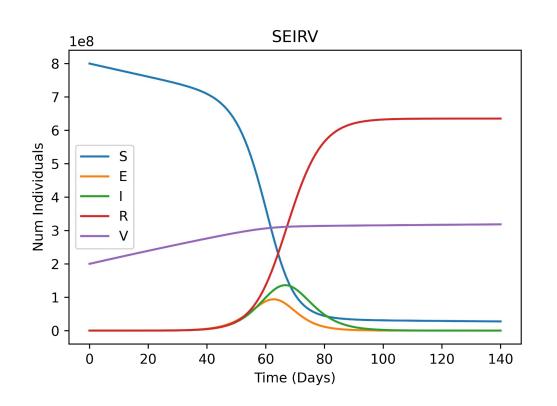
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### **SEIR Model**





#### SEIRV Model - 20% vaccination rate

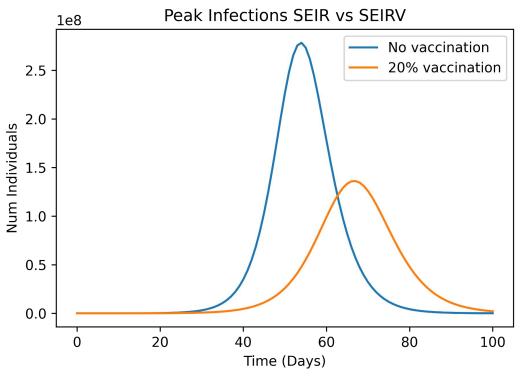


N0 = 1000000000.0I0 = 3.0E0 = 6000R0 = 0S0 = N0 - I0 - E0 - R0 $\mathbf{D0} = \mathbf{0}$ V0 = 0T = 140dt = 1 $\mu = 0$  $\alpha = 0.006$  $\beta = 0.9$  $\gamma = 1/5$ 

 $\epsilon = 1/3$ 

v=0.025

# Infected individuals: Vaccination vs No Vaccination



Peak is delayed and smaller with vaccination

# Reproduction Ratio (Ro)

- Reproduction Ratio is the average number of secondary cases of infection generated by an infectious individual
- It is used to determine the spreadability of the disease in the population

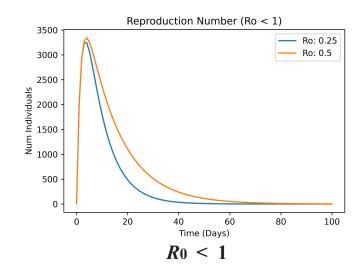
 $R_0 < 1$ : Disease dies out

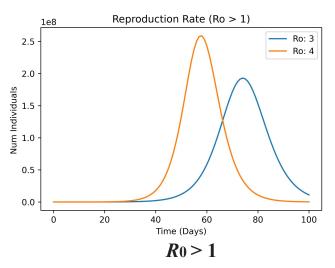
*R*₀>1: An epidemic occurs

$$\beta \approx (\gamma + \alpha)Ro$$

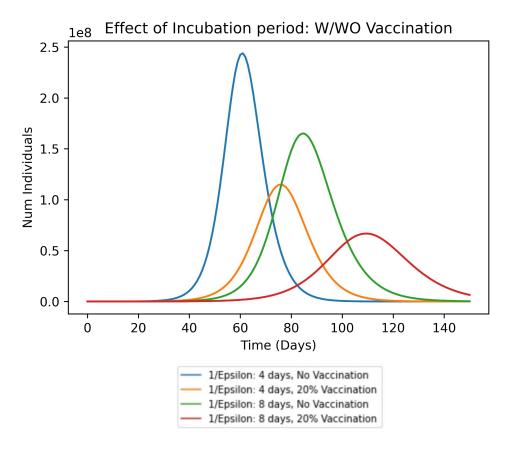
# Effect of Reproduction Rate (Ro)

- For Ro < 1 : Peak location does not change, indicating an effective "suppression" of the epidemic
- For Ro > 1: Curve is wider and moves to later time.
- Significant reduction in the number of infected individuals for Ro < 1 suggests that strict home isolation can be very effective



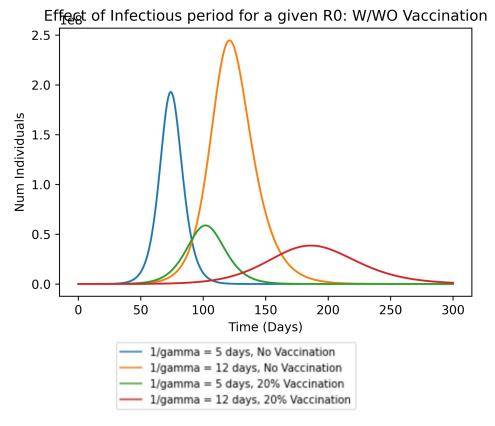


#### Effect of Incubation Period



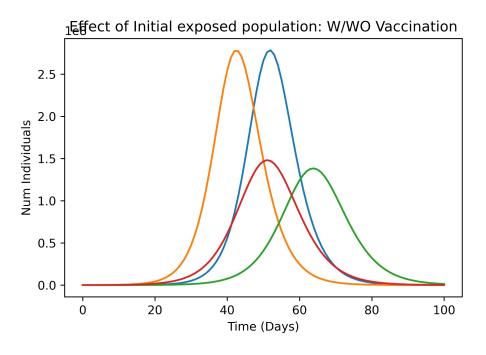
- Increasing the incubation period from 4 to 8 days decreases the maximum number of infected individuals and delays the spread of the epidemic
- Vaccination reduces and delays the peak for same incubation period

#### Effect of Infectious Period



- Increasing the infectious period delays the epidemic
- Vaccination reduces the number of infected individuals

# Results - Effect of Initial Exposed Population

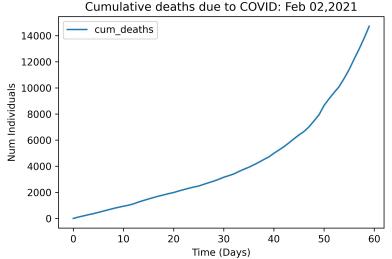


- The initial number of infectious individuals has no apparent effect on the maximum number of infected individuals.
- Decrease in initial exposed population delays the peak

E0: 10,000, No Vaccination
E0: 50,000, No Vaccination
E0: 10,000, 20% Vaccination
E0: 50,000, 20% Vaccination

# Fitting to Indian data - SEIR, Delta Wave

- As per a Science Article, the reported numbers on Covid-19 in India are grossly underestimated, particularly the death/capita (death/million) which is 1/7th of what is reported in the US
- To validate this, and for testing other hypothesis we have to start from a ground truth for fitting the model
- We chose the cumulative death numbers from the delta wave for the first 60 days

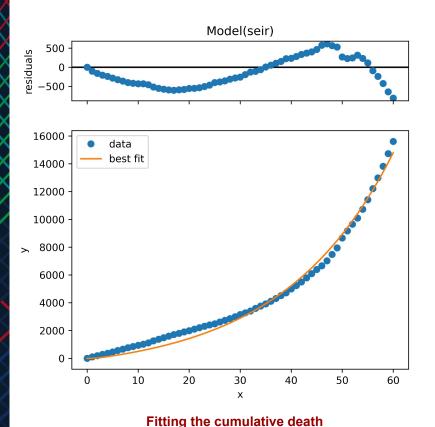


# Levenberg-Marquardt Nonlinear Least Square optimizer

Parameter	Vary	Min	Max	Initial
Е0	True	0	30000	1
β	True	0.25	0.75	0.25
γ	False	-	-	1/5
$\epsilon$	False	-	-	1/3
α	False	-	-	0.006

N0 = Population - total recovered - total dead, <math>I0 = 3.0, E0 = 1, R0 = 0, S0 = N0 - I0 - E0 - R0

# Fitting to Indian data - SEIR, Delta Wave



Using the Levenberg-Marquardt
Nonlinear Least Square optimizer,
implemented in python using a library
lmfit

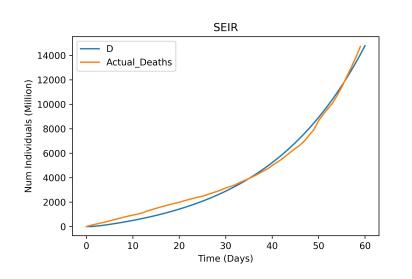
Final values obtained from fitting:

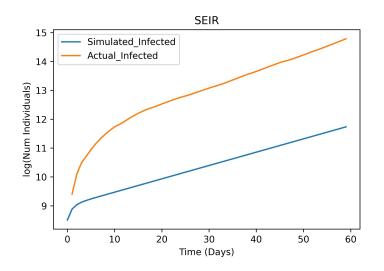
$$E0 = 14862.24$$

$$\beta = 0.2892632$$

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## Fitting to Indian data - SEIR, Delta Wave





- If we assume the reported Beta is correct, (which seems low for Indian Population) and the cumulative death numbers are accurate, the simulated infected individuals must be low. This is what is not reported by India.
- This suggests that number of deaths in India are severely underestimated.

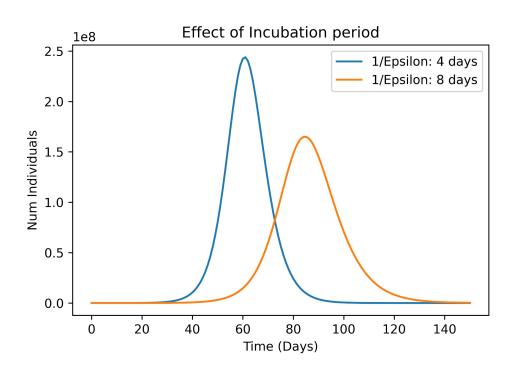


- Mathematical representation of biological processes enables transparency and accuracy regarding the epidemiological assumptions
- Test our understanding of the disease epidemiology by comparing model results and observed patterns
- Assist in decision-making by making projections regarding important issues such as intervention-induced changes in the spread of disease
- Model fitting is sensitive to initial conditions
- The current fitted data, reveals lapse in reporting of India Covid Number.



- Mathematical representation of biological processes enables transparency and accuracy regarding the epidemiological assumptions
- Test our understanding of the disease epidemiology by comparing model results and observed patterns
- Assist in decision-making by making projections regarding important issues such as intervention-induced changes in the spread of disease
- Therefore, when models fail to predict, this failure can provide us with important clues for further research

# Supplementary - Effect of Incubation Period



# Supplementary - Effect of Recovery Rate

