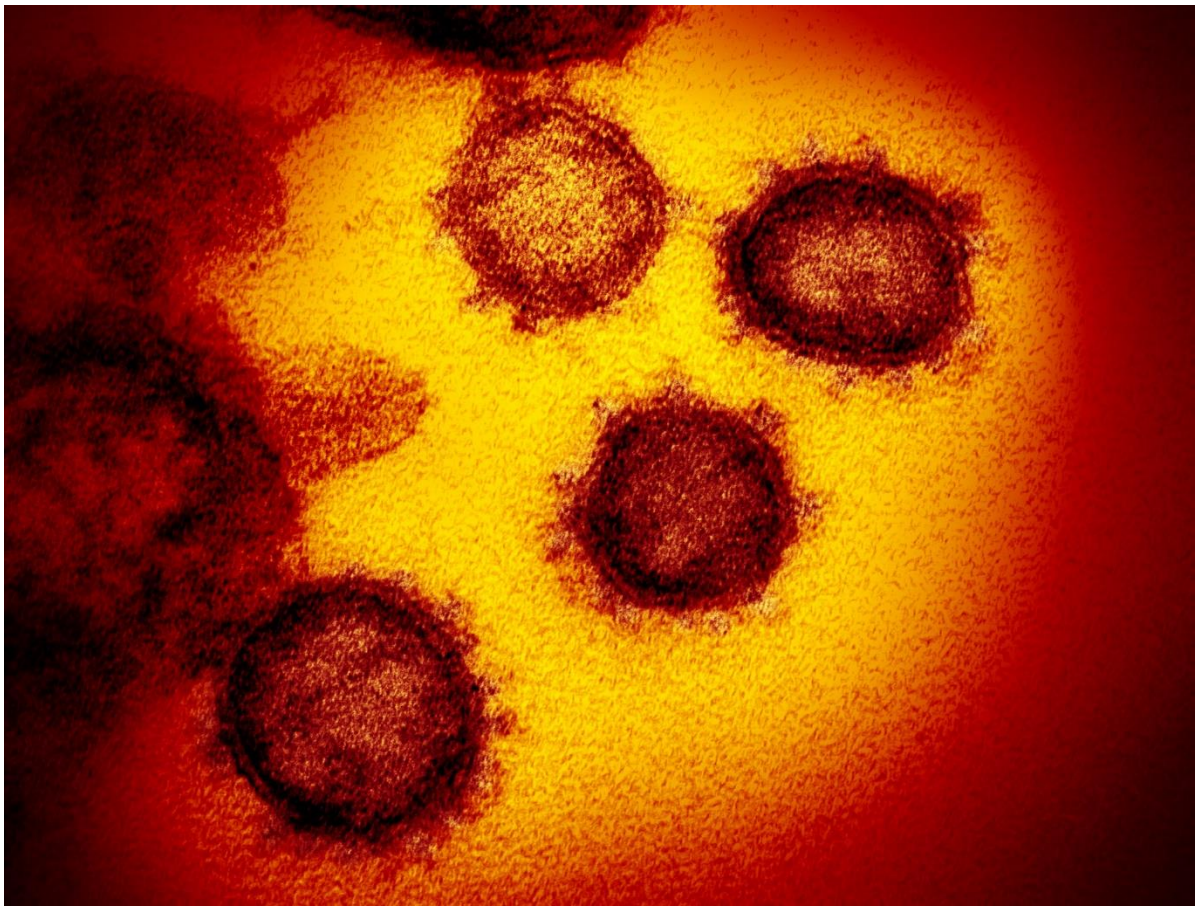

COVID-19 EPIDEMIC SIMULATION

SIMULATION MODELLING PROJECT

Group 8
Anh Viet Doan | BS21DON043
Anh Phuong Dinh | BS21DON037

CONTENT

ACKNOWLEDGEMENT

We want to express our sincere thanks to Dr. Suchismita Das for being such a fantastic supervisor throughout our research journey as well as for her support and encouragement in shaping my overall understanding of simulation modelling. Her guidance and encouragement really made a difference.
We would also like to thank our friends for supporting us with their knowledge and experiences.

1. INTRODUCTION

The COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has posed significant challenges to public health systems. Since its emergence in late 2019, the virus has spread rapidly, leading to widespread illness, overwhelmed healthcare systems, and a staggering loss of life. The complexity of controlling the spread of COVID-19 lies in its highly contagious nature, making traditional public health strategies less effective in hindering transmission.

In response to the challenges posed by COVID-19, the use of mathematical models has proven to be invaluable in understanding the dynamics of the disease and in guiding decision-making processes. Among these models, the Susceptible-Exposed-Infectious-Removed (SEIR) model has gained prominence for its ability to compartmentalize the population based on disease status. This model divides the population into compartments based on their disease status, allowing for the prediction of disease spread over time and the assessment of the impact of intervention strategies.

2. PROBLEM STATEMENT

The COVID-19 pandemic has underscored the limitations of conventional public health approaches in effectively curbing the transmission of a highly contagious virus. To address this, our project aims to leverage the SEIR model as an initial step in comprehensively understanding the dynamics of COVID-19 spread. By utilizing the SEIR model, we intend to explore the intricacies of the disease's transmission patterns and assess the effectiveness of existing intervention strategies.

Recognizing the need for continuous refinement and improvement in our analysis, we propose the integration of the SEIR-D model—a modified and enhanced version of the SEIR model. The SEIR-D model incorporates additional compartments to account for individuals who are removed from the infectious population through factors such as recovery or death. This enhancement allows for a more nuanced exploration of various scenarios and intervention strategies, providing valuable insights that can inform evidence-based public health planning and decision-making.

In essence, our project seeks to bridge the gap between mathematical modeling and real-world implications, offering a holistic understanding of COVID-19 dynamics and contributing to the development of effective strategies for pandemic control. Through the integration of the SEIR-D model, we aim to refine our analytical framework, enabling a more accurate depiction of the ongoing pandemic and empowering public health authorities with actionable insights for strategic planning and response.

3. MODEL FORMULATION

3.1. SEIR MODEL

"Our study applies the SEIRD model, drawing from the insights of Taghizadeh and Mohammad-Djafari [1]. The diagrams and equations closely align with their explanations."

3.1.1 Concept

In the generic SEIR model, population is segmented into four compartments:

- **Susceptible**: Individuals who are susceptible to catching the disease.

- **Exposed**: Individuals who are exposed to virus, but not yet infective.

- **Infective**: Exposed individuals who become infective and are able to infect others.

- **Recovered**: Infective individuals who recover and become immune to the virus.

3.1.2 Attributes

- N = S + E + I + R, where N is the population size.

- At each point in time, each individual of the population belongs to only one compartment (S, E, I, or R).

- An individual can only move from compartment S to E, from E to I, and from I to R.

The figure below illustrates different compartments and the flow of individuals between them:

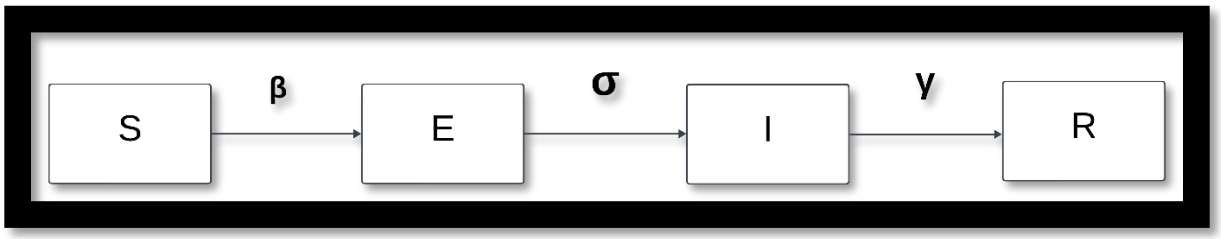

Fig 1. SEIR model flowchart diagram

***β*, σ, γ** are coefficients to construct differential equations in the next section.

3.1.3. Differential Equations

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - \gamma I \quad (3)$$

$$\frac{dR}{dt} = \gamma I \quad (4)$$

The coefficients are:

- $\boldsymbol{\beta}$**:**. the rate of contacts between susceptible and infectious individuals (transmission coefficient)

- **σ:** the rate at which exposed individuals become infective.

- **γ:** the rate at which infective individuals recover.

3.1.4. Derivation of differential equations

Equation (1)

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

- The model indicates that S cannot increase over time, as there are no returns to the compartment. Thus, **equation (1)** should be negative, as S only decreases.

- An individual can move out of compartment S by getting infected from contact with an infective person.

- At any point, the proportion of infective individuals in the population is **I/N**, and the proportion of susceptible individuals is **S/N**. Assuming perfect mixing (where individuals are equally likely to come into contact with any other individual in the population), the probability of any contact being between an infective and susceptible individual is **(I / N) * (S / N)**.

- This is then multiplied by the transmission coefficient $\boldsymbol{\beta}$ to give **equation (1).**

Equation (2)

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

- The individuals that flow in E are matched with individuals who flow out of S.

- Individuals can leave E by transitioning into the Infective compartment. This occurs at a rate determined by two variables – the rate **σ** and the current number of individuals in E.

Equation (3)

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

- The individuals that flow in I are matched with individuals who flow out of E.

- Individuals can leave I by transitioning into the Recovered compartment. This occurs at a rate determined by two variables – the rate **γ** and the current number of individuals in I.

Equation (4)

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

- The individuals that flow in R are matched with individuals who flow out of E.

- No individuals can leave the Recovered Compartment as it is the last compartment in the flowchart diagram.

3.2 SEIR-D MODEL

In our study, we use the SEIRD model, taking guidance from Melo's work (2022) [2]. The diagrams and equations we employed closely resemble those explained by Melo [2]

3.2.1. Concept

So far, we have introduced the concepts of a simple SEIR model, for understanding purposes. We find out that one way that we can improve our model is to incorporate a new compartment (**D**), which denotes for disease-related deaths, into the model. This modification aims to provide a more detailed portrayal of the dynamics involved in the spread of the epidemic.

In SEIR-D Model, population is divided into five compartments:

- **Susceptible**: Individuals who are susceptible to catching the disease.

- **Exposed**: Individuals who are exposed to virus, but not yet infective.

- **Infective**: Exposed individuals who become infective and are able to infect others.

- **Recovered**: Infective individuals who recover and become immune to the virus.

- **Died**: Infective individuals who do not survive the infection.

3.2.2. Attributes

- N = S + E + I + R + D, where N is the population size.

- At each point in time, each individual of the population belongs to only one compartment (S, E, I, R or D).

- An individual can only move from compartment S to E, from E to I, and (from I to R or I to D).

- The flowchart diagram below explains the attributes of the model.

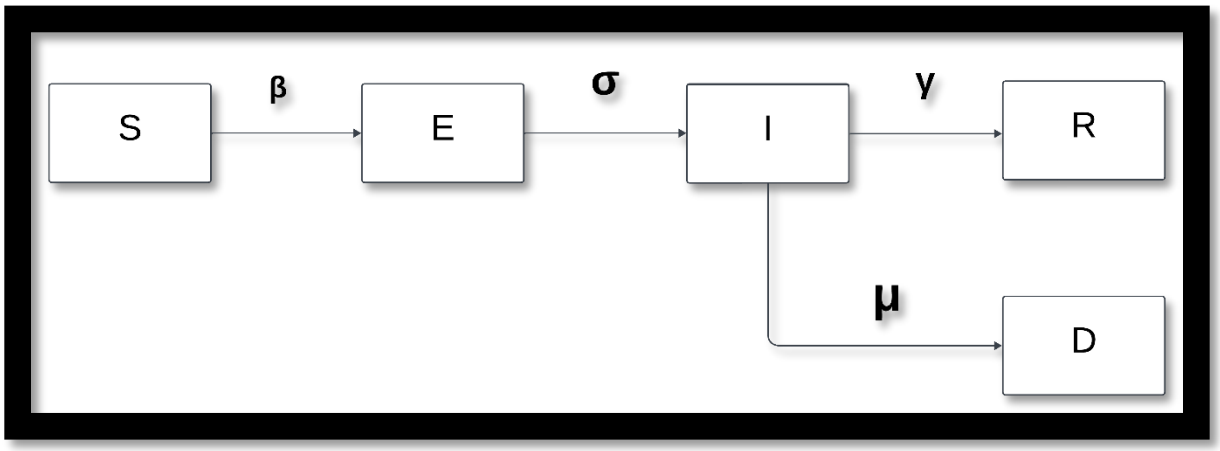

Fig2. SEIR-D model flowchart diagram

3.2.3. Differential Equations

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - \mu I - \gamma I \quad (3)$$

$$\frac{dR}{dt} = \gamma I \quad (4)$$

$$\frac{dD}{dt} = \mu I \quad (5)$$

3.2.4. Derivation of differential equations.

Equation (1), (2) and (4) are explained in section 3.1.3.

Equation (3)

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

- Individuals can flow out of the Infective compartment to either Recovered compartment (at rate of **γ**) or Died compartment (at the rate of **μ**).

Equation (5)

$$\frac{dD}{dt} = \mu I$$

- Individuals who flow out of Infective compartment (at the rate of μ) are moved into Died compartment.

4. R SIMULATION

4.1. DEPENDENCY

4.1.1. Library and Tools

We load all necessary packages, which assist us in solving the differential equations and plotting the graph.

```
# Importing package
library(deSolve) # solve ode
library(ggplot2) # plot graph
library(tidyr) # plot graph
```

4.1.2. Graph function for visualization

```
### FUNCTION TO VISUALIZE THE MODEL
plot_result ← function(model){
model_df ← as.data.frame(model)
# Convert the dataframe to long format for ggplot
model_df_long ← gather(model_df, key = "Group", value = "Value", -time)

# Set the order of levels for the "Group" factor
model_df_long$Group ← factor(model_df_long$Group, levels = c("S", "E", "I", "R", "D"))

# Plotting using ggplot
ggplot(model_df_long, aes(x = time, y = Value, color = Group)) +
  geom_line() +
  labs(title = "Evolution of epidemic",
       x = "Time",
       y = "Population") +
  scale_color_manual(values = c("blue", "yellow", "red", "green", "black")) +
  theme_minimal()
}
###
```

4.2. SEIR MODEL

```
SEIR ← function(time, current_state, params){

  with(as.list(c(current_state, params)),{
    N ← S+E+I+R
    dS ← -(beta*S*I)/N
    dE ← (beta*S*I)/N - sigma*E
    dI ← sigma*E - gamma*I
    dR ← gamma*I

    return(list(c(dS, dE, dI, dR)))
  })
}
```

4.3. SEIR-D MODEL

```
SEIRD ← function(time, current_state, params){

  with(as.list(c(current_state, params)),{
    N ← S+E+I+R+D
    dS ← -(beta*S*I)/N
    dE ← (beta*S*I)/N - sigma*E
    dI ← sigma*E - gamma*I - mu*I
    dR ← gamma*I
    dD ← mu*I

    return(list(c(dS, dE, dI, dR, dD)))
  })
}
```

5. RESULT AND DISCUSSION

Initial state

```
# Initial State
initial_state ← c(S=999997, E=3, I=0, R=0, D=0)
times ← 0:365
```

Our population size is 1,000,000. The population comprises of **999,997 Susceptible** individuals, **3 Exposed** individuals, **0 Infective** individual and **0 Recovered** individual and **0 Died** individual. The time span for the simulation is **365** days

5.1 SEIR MODEL

5.1.1 Parameters

```
## parameters
params ← c(
  beta=0.5,
  sigma=0.25,
  gamma=0.2
)
```

The meaning of these parameters are:

- $\boldsymbol{\beta}$ **= 0.5 :** Transmission rate is 0.5

- $\boldsymbol{\sigma}$ **= 0.25**: On average, an exposed individual becomes infective after 4 (= 1/0.25) days

- $\boldsymbol{\gamma}$ **= 0.2**: On average, an infective individual recovers after 10 (= 1/0.2) days

5.1.2. Result

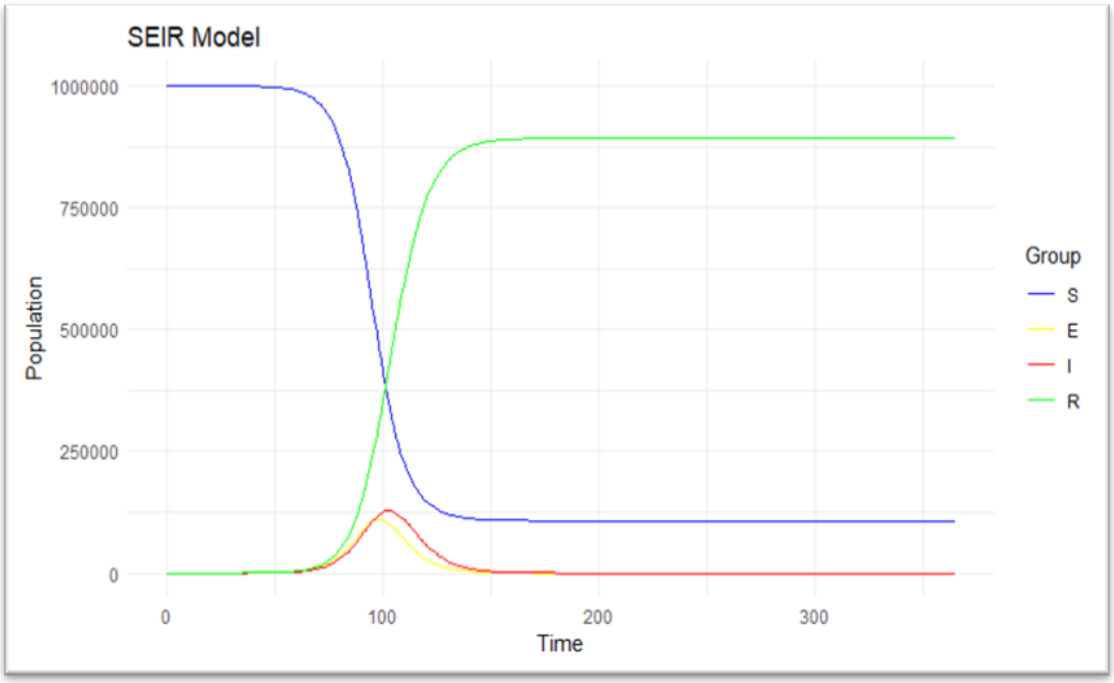

Fig 3. Evolution of epidemic using SEIR model.

	S	E	I	R
Min.	107354.7	1.354875e-07	0.000000e+00	0.0
1st Qu.	107354.7	2.259840e-03	5.431461e-03	168542.5
Median	107405.3	8.269599e+00	1.246747e+01	892456.9
Mean	340516.1	9.755690e+03	1.219461e+04	637533.6
3rd Qu.	656265.8	1.692800e+03	2.529324e+03	892645.3
Max.	999997.0	1.097737e+05	1.276097e+05	892645.3
N	366.0	3.660000e+02	3.660000e+02	366.0
sd	370049.7	2.483184e+04	2.991450e+04	379580.2

Fig 4. Summary of SEIR model

There are some fascinating insights from the model:

- At the end of the simulation, the model predicts that **107,354** individuals who do not become infective. This could indicate a portion of population that has strong immunity to the virus.
- The peak of the epidemic is marked by **127,609** Infective individuals. This could pose the most challenging period for healthcare systems and public health interventions.
- At the end, the model forecasts **892,645** individuals who have recovered. This suggests a significant number of individuals who may potentially contribute to community immunity.

5.2 SEIR-D MODEL

In section 5.1, the SEIR model has provided exciting insights regarding the spread of the epidemic. As previously indicated, a more detailed representation of the epidemic can be achieved by adding new compartments to the SEIR model. Therefore, this section assesses the implementation of the SEIR-D model. Our current focus is on extracting insights from the SEIR-D model and conducting experiments under various scenarios.

5.2.1 Parameters

```
# parameters
params ← c(beta=0.5,
           sigma=0.25,
           gamma=0.2,
           mu=0.001)
```

The meaning of $\boldsymbol{\beta}$, $\boldsymbol{\sigma}$, $\boldsymbol{\gamma}$ are explained in section 5.1.1. Similarly, $\boldsymbol{\mu = 0.001}$ indicates that on average, 1 out of 1000 (= 1/0.01) infective individuals do not survive through the disease.

5.2.2. Result

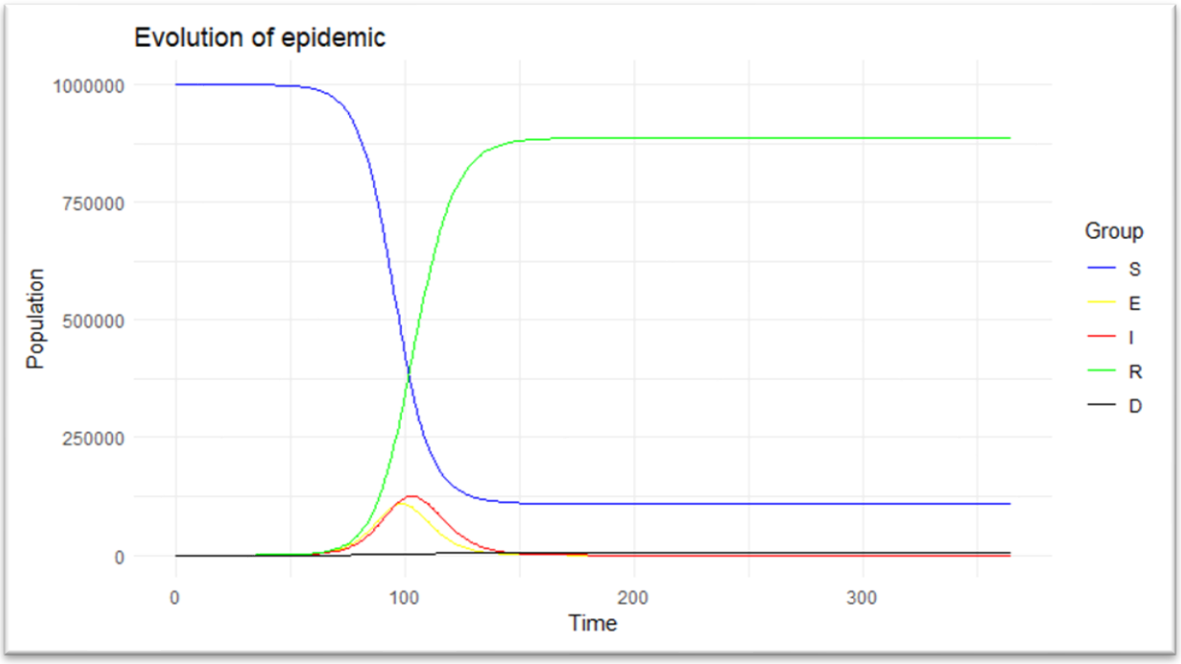

Fig 5. Evolution of epidemic using SEIR-D model

	S	E	I	R	D
Min.	108998.0	1.508341e-07	0.000000e+00	0.0	0.0000
1st Qu.	108998.0	2.457191e-03	5.828795e-03	162645.9	813.2293
Median	109051.9	8.507688e+00	1.273876e+01	886371.3	4431.8565
Mean	342586.6	9.737731e+03	1.211160e+04	632402.0	3162.0101
3rd Qu.	666005.1	1.714111e+03	2.584467e+03	886569.2	4432.8458
Max.	999997.0	1.090569e+05	1.264174e+05	886569.2	4432.8459
N	366.0	3.660000e+02	3.660000e+02	366.0	366.0000
sd	369761.1	2.472779e+04	2.965739e+04	377319.2	1886.5959

Fig 6. Summary of SEIR-D model

Insights from the SEIR-D model:

- According to the model, **108,998** individuals remain uninfected at the end of the simulation.
- The peak of the epidemic is marked by **126,417** active cases.
- At the end, the model predicts **886,569** individuals who recovered from the pandemic.
- Throughout the simulation, **4432** individuals did not survive.

5.3. SEIR-D MODEL WITH VARIANTS OF THE VIRUS

New variants, which are more deadly, could be formed during the epidemic. In this simulation, we suppose that the new variants, which are more severe, will arrive at the middle of the epidemic. This means that the parameters **γ**, **μ** will be affected. Let us observe the dynamic of the epidemic.

5.3.1Setting up code and parameters

```
SEIRD_new_variant ← function(time, current_state, params){

  with(as.list(c(current_state, params)),{

    gamma = ifelse(
      (time ≤ start),
      0.2, 0.07
    )

    mu = ifelse(
      (time ≤ start),
      0.001, 0.015
    )

    N ← S+E+I+R+D
    dS ← -(beta*S*I)/N
    dE ← (beta*S*I)/N - sigma*E
    dI ← sigma*E - gamma*I - mu*I
    dR ← gamma*I
    dD ← mu*I

    return(list(c(dS, dE, dI, dR, dD)))
  })
}
```

```
params ← c(beta=0.5,
           sigma=0.25,
           gamma=0.2,
           mu=0.001,
           start = 90)
```

5.3.2. Result

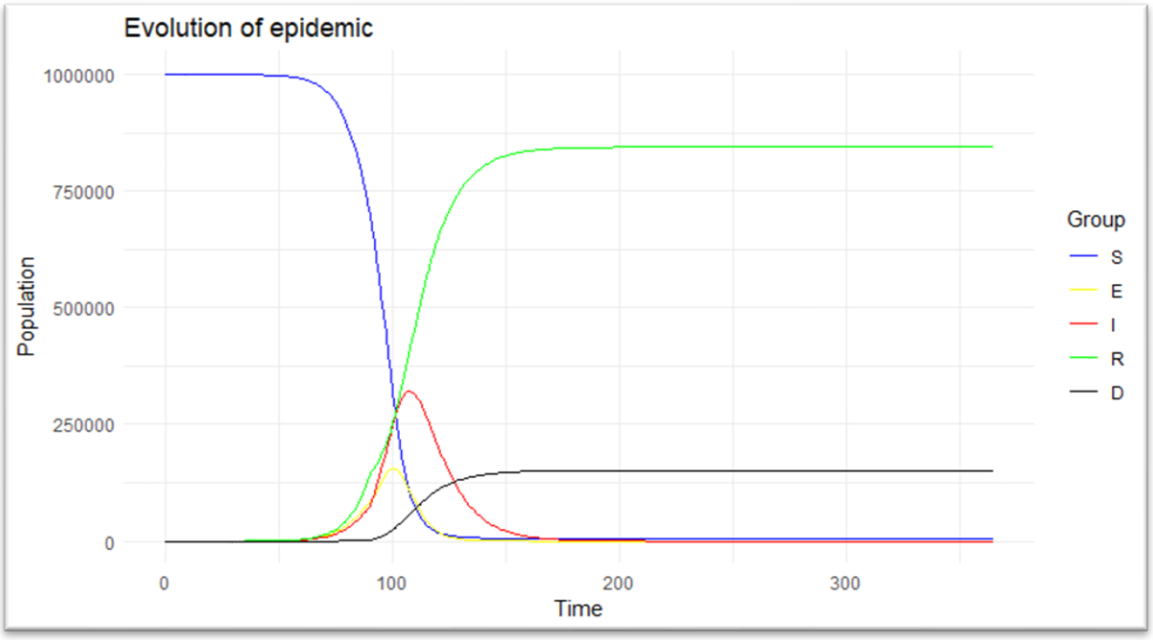

Fig 7. Evolution of epidemic using SEIR-D model with more severe variants

Insights from the graph:

- The population of Susceptible individuals has declined remarkably since the arrival of the new variants.
- Accordingly, the number of infective individuals has significantly increased.
- It is notable that the number of deaths has exceeded 130,000. Compared to roughly 4000 deaths from the previous SEIR-D model in section 5.2, this simulation has underscored the severity of the outbreak and its impact on public health and safety.
- As a consequence, without appropriate intervention measures, the virus may potentially pose far-reaching threats to the community.

5.4. SEIR-D MODEL WITH LOCK-DOWN INTERVENTION

In the previous simulation, we understood that the covid-19 virus can be lethal if we do not have any appropriate prevention. In this section, we will address the efficiency of the lock-down intervention.

During the 2020 coronavirus pandemic, numerous countries implemented various forms of "lockdown" measures. The primary goal of these lockdowns is to change the trajectory of the epidemic by lowering the transmission coefficient, β.

5.4.1 Setting up code and parameters

Assuming the government has implemented a "lockdown" from day 90 to day 150, the transmission coefficient β will be adjusted to 0.1 during this period.

```
# with intervention
SEIRD_lockdown ← function(time, current_state, params){

  with(as.list(c(current_state, params)),{

    beta = ifelse(
      (time ≤ start_lockdown || time ≥ end_lockdown),
      0.5, 0.1
    )

    N ← S+E+I+R+D
    dS ← -(beta*S*I)/N
    dE ← (beta*S*I)/N - sigma*E
    dI ← sigma*E - gamma*I - mu*I
    dR ← gamma*I
    dD ← mu*I

    return(list(c(dS, dE, dI, dR, dD)))
  })
}
```

```
params ← c(
  sigma=0.25,
  gamma=0.2,
  mu=0.001,
  start_lockdown=90,
  end_lockdown=150
)
```

5.4.2 Result

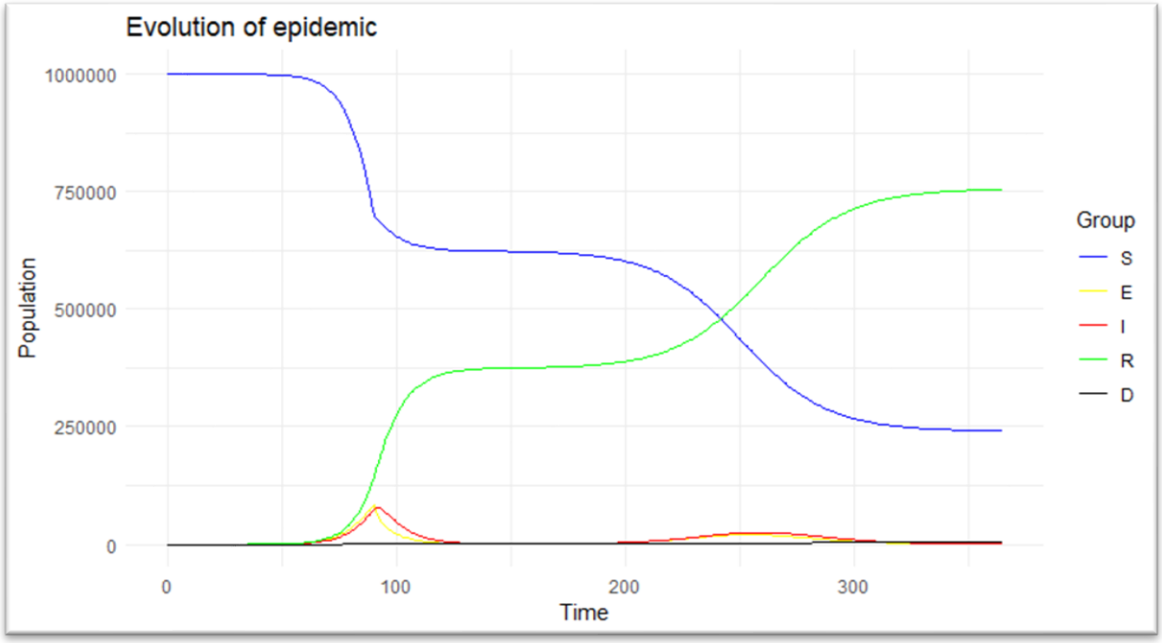

Fig 8. Evolution of epidemic using SEIR-D model with lockdown

Insights from the graph:

- Throughout the lockdown period, the count of susceptible individuals remains stable without a decrease, indicating a horizontal trend.
- Similarly, the number of infective individuals is notably lower compared to the pre-lockdown and post-lockdown periods.
- These findings suggest that the lockdown can potentially hinder the spread of the epidemic.

5.5. SEIR-D MODEL WITH VACCINATION

While lockdowns act as a crucial short-term measure to suppress the virus's transmission, vaccination offers a sustainable and long-term solution to establish community immunity within the population. In this section, we will simulate a vaccination campaign. Our objective is to vaccinate 100% of the population in 365 days. Let us see how the epidemic evolves.

For this simulation, we will introduce the vaccine parameter (v) to the SEIR-D model.

5.5.1 Flow chart and differential equations

In this study, we employed the SEIR-D model as outlined by Annas et al. (2020) [3], the diagram and differential equations used in our analysis closely follow those presented by Annas et al. (2020) [3]

Flow chart

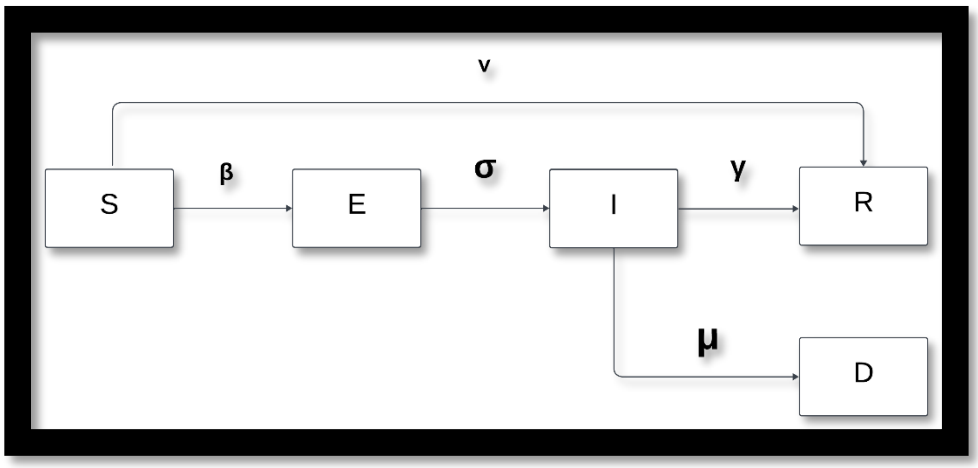

Fig 9. SEIR-D model with vaccine parameter flowchart diagram

Differential Equations

$$\frac{dS}{dt} = -\frac{\beta SI}{N} - \frac{vS}{N} \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - \mu I - \gamma I \quad (3)$$

$$\frac{\boldsymbol{dR}}{\boldsymbol{dt}} = \boldsymbol{\gamma I} + \frac{\boldsymbol{vS}}{\boldsymbol{N}} \quad (\mathbf{4})$$

$$\frac{dD}{dt} = \mu I \quad (5)$$

Equations (1) and (4) describe how the number of susceptible and recovered individuals in a population change over time in response to disease transmission, recovery, and vaccination

5.5.2 Setting up code and parameters.

```
# vaccination

SEIRD_vaccine ← function(time, current_state, params){

  with(as.list(c(current_state, params)),{
    N ← S+E+I+R+D
    dS ← -(beta*S*I)/N - v*S/N
    dE ← (beta*S*I)/N - sigma*E
    dI ← sigma*E - (gamma+mu)*I
    dR ← gamma*I + v*S/N
    dD ← mu*I

    return(list(c(dS, dE, dI, dR, dD)))
  })
}
```

```
# parameters
params ← c(beta=0.5,
           sigma=0.25,
           gamma=0.2,
           mu=0.001,
           v = 3000)
```

v = 3000 means that we will execute vaccination for 3000 people each day. We expect to vaccinate 100% of the population at the end of the simulation.

5.5.3. Results

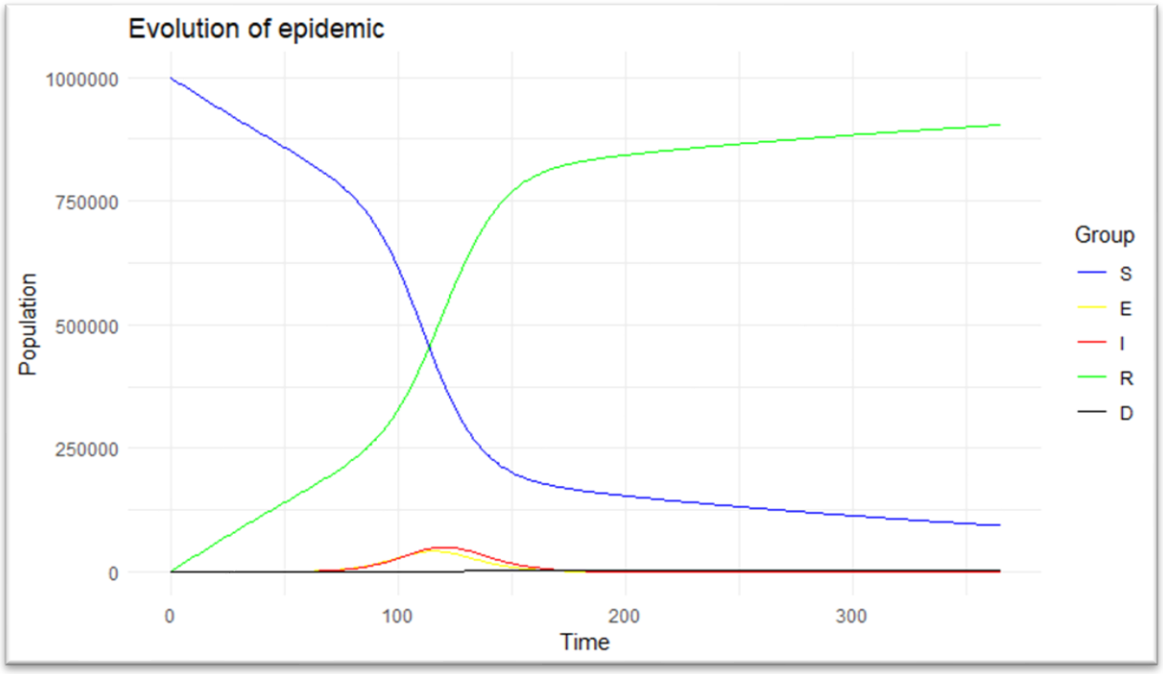

Fig 10. Evolution of epidemic using SEIR-D model with vaccination

Insights from the graph:

- Under the vaccination campaign, people recovered from COVID-19 at a faster rate. On day 250, nearly 90 percent of the population has recovered.
- In the context of the lockdown strategy, the reduction in the number of infective individuals is only observed during the actual lockdown period. Yet, the number of recovered individuals remains approximately constant. This implies that achieving community immunity requires a more prolonged effort.
- On the other hand, the vaccination approach, although not as rapidly reducing the number of infective cases as seen in the lockdown strategy, proves to be more effective in the long run.

6. CONCLUSION

In conclusion, our project focused on simulating the dynamics of the COVID-19 epidemic using the SEIR and SEIR-D models.

The primary objective of our project was to utilize mathematical models to understand the spread of the pandemic and provide valuable insights for public health planning and decision-making by exploring different scenarios and interventions.

The SEIR model provided insights into the population's peak infective cases, recovery rates, and potential immunity. The SEIR-D model, enhanced with a compartment for disease-related deaths, offered a more detailed portrayal of the epidemic's impact. Experimentation with severe virus variants highlighted increased susceptibility and emphasized the potential severity of outbreaks. Additionally, implementing a lockdown intervention demonstrated its potential to stabilize susceptible individuals and reduce infective cases. Lastly, in the vaccination approach, the model is expected to provide further insights into maintaining immunity and achieving long-term control over the epidemic.

However, it is essential to acknowledge that there is still room for the models to improve. Model refinement is essential, particularly in parameter estimation, where aligning model parameters with real-world data becomes crucial. The precision of the model parameters, achieved by validating with the actual data, can enhance the reliability and practicality of our simulation.

Still, the models have provided a concrete foundation for comprehending epidemic dynamics. Our next step involves applying the SEIR-D model to real-world data for more accurate parameter estimation. This practical application will contribute valuable insights to the understanding and management of the COVID-19 pandemic based on real-world conditions.

7. REFERENCE

[1]. Taghizadeh, E., & Mohammad-Djafari, A. (Y). "SEIR Modeling, Simulation, Parameter Estimation, and Their Application for COVID-19 Epidemic Prediction." Phys. Sci. Forum, 5(1), 18. https://doi.org/10.3390/psf2022005018

[2]. Melo, Luz (2022) "Modeling COVID-19 Spread through the SEIRD Epidemic Model and Optimal Control," Proceedings of GREAT Day: Vol. 2021, Article 19. Available at: https://knightscholar.geneseo.edu/proceedings-of-great-day/vol2021/iss1/19

[3]. Annas, S., Pratama, M. I., Rifandi, M., Sanusi, W., & Side, S. (2020). Stability analysis and numerical simulation of SEIR model for pandemic COVID-19 spread in Indonesia. Chaos, Solitons and Fractals: Nonlinear Science, and Nonequilibrium and Complex Phenomena. From: https://www.sciencedirect.com/science/article/pii/S0960077920304690?fbclid=IwAR1HZj2-YZjEdZtmy5Sf2qjnwzrxlAqgo9sYZK-vbLRpa7j10BHfrecjzSw