

MATHEMETICAL BIOLOGY PROJECT

TOPIC: - S.E.I.R MODEL

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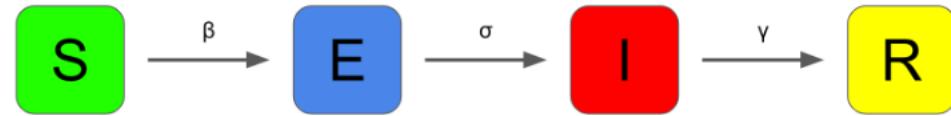
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INTRODUCTION



Susceptible – Individuals who have not been exposed to the virus

Exposed – Individuals exposed but not infected by the virus

Infectious – Exposed individuals who get infected

Recovered – Infected individuals who recovered and became immune to the virus

N = sum of the individuals in the four compartments

PARAMETERS

BETA (β): Transmission Coefficient

SIGMA (σ): Rate at which exposed individuals become infectious.

Gamma (γ): Rate at which infectious individuals recover.

Mu (μ): Optional parameter to describe the mortality rate of infectious individuals.

DIFFERENTIAL EQUATIONS

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

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

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

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

$$\frac{dM}{dt} = \mu I \quad (\text{Mortality})$$

Susceptible

S can not increase overtime. The equation is negative as S can only decrease overtime.

Exposed

Flow in and Flow out of individuals occurs. The flow out of S will be matched to Flow in of E.

Infectious

Individuals from exposed enter this compartment. There are two possibilities for infected individuals,

1. They recover which is at the rate γ
2. They will perish as a result of the virus. The mortality rate μ can be used to model them

Recovered

Here we assume that no individual can move back to susceptible compartment. Individuals flow in at the rate γ .

Mortality

This is the fifth compartment model. This compartment can be excluded when $\mu = 0$.

The R_0 value,

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

The equation gives us an estimated number of people who will be infected by the average infectious individual. Here there are two cases again,

1. When $R_0 > 1$, the outbreak will result in an epidemic
2. When $R_0 < 1$, the outbreak can be controlled / contained

The data and assumptions that go into an epidemic model are only as good as the data and assumptions that go into it.

FEASIBILITY OF THE MODEL

- Mixing is non-uniform in big populations. Individuals are far more inclined to interact with others in their immediate surroundings. More complex compartmental models will take this into consideration.
- The model assumes that the population is isolated. In reality, population mixing allows a virus to be introduced and reintroduced several times.
- Individuals are not generally born immune. When considering longer time periods, more advanced models will take the birth rate into account.
- The basic SEIR model does not take into consideration population age structures. Viruses frequently spread quicker in younger, heavily populated communities. However, it may be more lethal to elderly people outside of such cities.
- The SEIR model solely considers averages for each of its parameters. In practice, there will be a great deal of variety. Some people might be contagious for a long period. A small number of people can make a vast number of contacts. As a result, the model is appropriate for characterizing the pandemic at a high level and over a lengthy period of time. However, it is ineffective at forecasting details on a smaller scale.
- However, the SEIR model is a good place to start when trying to understand the dynamics of an epidemic.
- In general, using differential equations to express flows across compartments to simulate complicated systems is a highly powerful method.
- The SEIR model is one of the most widely used mathematical models for characterizing epidemic dynamics and forecasting potential contagion scenarios.
- It can be beneficial for evaluating the efficacy of various methods such as lock-down.

Math-Bio Project

Hidaya Patel

4/10/2022

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SEIR MODEL IMPLEMENTATION

```
# Using Library Desolve
library(deSolve)

## Warning: package 'deSolve' was built under R version 4.0.5

# Using the SEIR function in the Desolve library
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 - mu*I
    dR <- gamma*I
    dM <- mu*I

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

# Setting the parameters to specific assumed values
params <- c(beta=0.5, sigma=0.25, gamma=0.2, mu=0.001)

# Assuming the susceptible to be 999999, Exposed to 1 and the rest to 0
initial_state <- c(S=999999, E=1, I=0, R=0, M=0)

# Generating vector from 0 to 365 days
times <- 0:365

# Modeling the ordinary equations
model <- ode(initial_state, times, SEIR, params)

# Printing summary of the model
summary(model)
```

```

##          S           E           I           R           M
## Min.   108263.6 3.616607e-07 0.000000e+00      0.00   0.0000
## 1st Qu. 108263.7 5.957435e-03 1.414971e-02  63894.43 319.4721
## Median 108395.7 8.470071e+00 1.273726e+01 886814.36 4434.0718
## Mean   362798.6 9.745754e+03 1.212158e+04 612272.74 3061.3637
## 3rd Qu. 852375.5 1.734331e+03 2.533956e+03 887299.83 4436.4991
## Max.   999999.0 1.092967e+05 1.265161e+05 887299.86 4436.4993
## N       366.0 3.660000e+02 3.660000e+02    366.00 366.0000
## sd     381257.2 2.475783e+04 2.969234e+04 387333.47 1936.6673

```

Analyzing the results we notice that: -

From our assumption of million individuals 108,264 have not been infected whereas 126,516 were infected. As for the recovered, 887,300 individuals were recovered in the end. A total of 4436 resulted to be fatal.

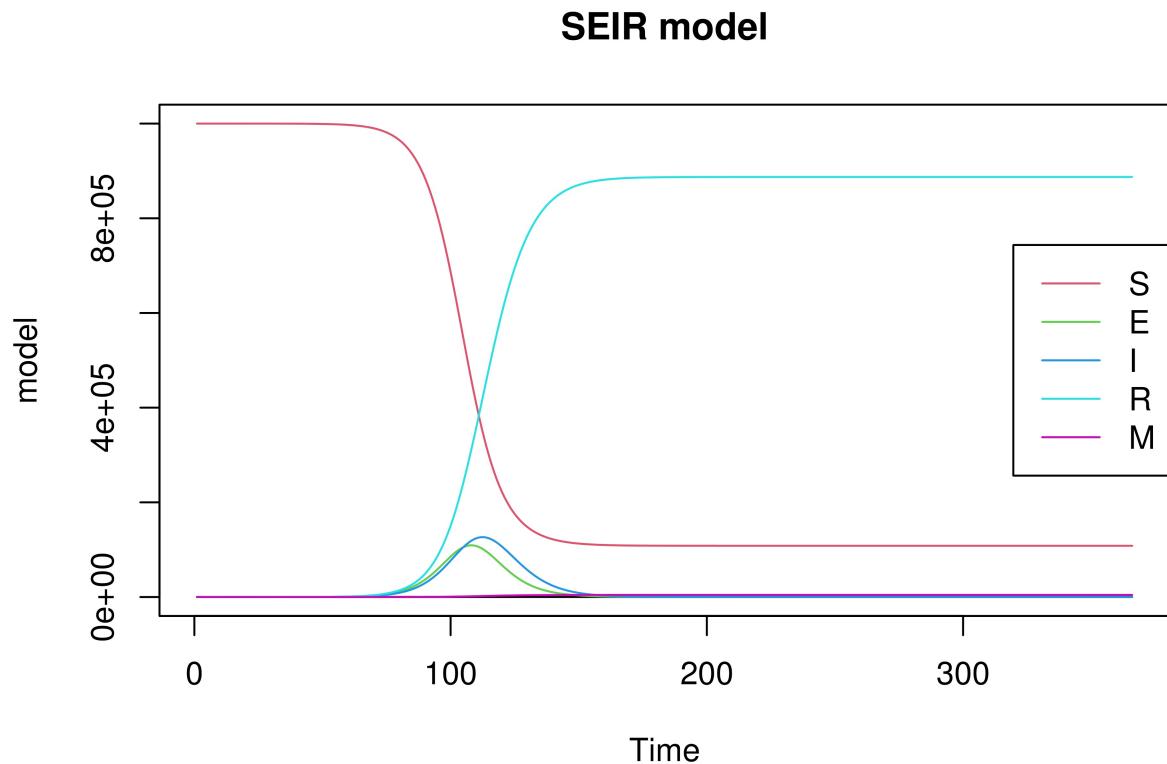
```

# Plotting the model
matplot(model, type="l", lty=1, main="SEIR model", xlab="Time")

legend <- colnames(model)[2:6]

legend("right", legend=legend, col=2:6, lty = 1)

```



```
infections <- as.data.frame(model)$I
```

```
peak <- max(infections)

match(peak, infections)

## [1] 112
```

Here we can see that the number of infections peaked on day 112.

REFERENCES

- Gleeson, P. (2021, March 30). *How to Model an Epidemic with R*. FreeCodeCamp.org; freeCodeCamp.org.
<https://www.freecodecamp.org/news/how-to-model-an-epidemic-with-r/>
- *SEIR Model.* (2020). Uwaterloo.ca.
<https://cs.uwaterloo.ca/~paforsyt/SEIR.html>