



**AN INTRODUCTION-MATHEMATICAL MODELING IN POPULATION HEALTH BY
USING SIR AND SEIR MODELS**

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ABSTRACT

Mathematical modeling serves as a corner stone in understanding and managing health issues at the population level. This study explores the application of compartmental models—specifically the susceptible -infectious-recovered (SIR) and Susceptible-Exposed-infectious-recovered (SEIR) frame works—to simulate disease transmission dynamics and guide public health interventions. By integrating real-world epidemiological data and differential equations, these models quantify the spread of infectious diseases such as influenza, COVID-19, and dengue. The inclusion of an "Exposed" compartment in SEIR enhances realism for pathogens with incubation periods, enabling more precise projections. Analytical techniques are applied to assess parameters such as transmission rate, recovery rate, and basic reproduction number (R_0). Results from model simulations provide insights into outbreak trajectory, peak infection periods, and the impact of interventions like vaccination, isolation, and contact reduction. This paper underscores the value of mathematical modeling in strategic planning and decision-making, offering a predictive lens to manage public health emergencies efficiently.

KEYWORDS: SIR model, SEIR Model, Covid-19, Recovery rate, Transmission Rate.

INTRODUCTION

The application of mathematical modeling to population health has revolutionized our understanding of infectious disease dynamics and epidemic control. Among the most widely used frameworks are the SIR (Susceptible-Infectious-Recovered) and SEIR (Susceptible-Exposed-Infectious-Recovered) models, which divide a population into distinct health-related compartments and describe transitions between these states through differential equations. These models allow researchers and policymakers to quantify the impact of factors such as transmission rates, recovery periods, and latency effects—offering powerful insights into the temporal evolution of disease outbreaks.

The SIR model, initially proposed by Kermack and McKendrick in 1927, is foundational in epidemiology and assumes immediate infectiousness post-exposure. In contrast, the SEIR model introduces an "exposed" stage, accounting for diseases with incubation periods. This refinement makes SEIR models particularly relevant for modeling complex outbreaks like COVID-19, influenza, and Ebola. With data-driven parameterization, these models enable public health officials to simulate intervention scenarios, estimate the basic reproduction number (R_0), and allocate resources effectively to mitigate disease spread.

Through mathematical rigor and real-world relevance, SIR and SEIR models bridge the gap between theoretical epidemiology and strategic public health planning. Their adaptability to regional contexts, population heterogeneity, and changing policy measures makes them indispensable tools for forecasting and managing health crises at both local and global scales.

Explanation about SIR and SEIR model in Epidemiology

The SIR model is a foundational mathematical framework used to simulate how infectious diseases spread through a population. It divides the population into three compartments

Compartments

S (Susceptible): Individuals who can catch the disease.

I (Infectious): Individuals who have the disease and can transmit it.

R (Recovered): Individuals who have recovered and are immune (or removed from the population due to isolation or death).

Now we can apply Mathematical Equations for this model to get the model uses ordinary differential equations (ODE's) to describe how people move between compartments over time.

Before we get into the mathematics of the SIR model itself, let's take a quick detour to discuss Differential Equations, of which the SIR model is a set. Simply put, differential equations are mathematical tools used to describe the rate at which something changes over time, relative to other things. So, for the SIR model, the S, I, and R variables are all changing in relation to each other as they represent the 3 stages any 1 person can be in.

There are also equations called Ordinary Differential Equations (which the SIR model fits into) where most of the factors are static in relation to one changing variable (in our case time), and Partial Differential Equations, which will be covered sometime later as they are fundamentally more complex and aren't needed right now.

$$\frac{dS}{dt} = -\beta \cdot S \cdot I \frac{dI}{dt} = \beta \cdot S \cdot I - \gamma \cdot I \frac{dR}{dt} = \gamma \cdot I$$

(OR)

- $\frac{dS}{dt} = -\beta \frac{SI}{N}$,
- $\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$
- $\frac{dR}{dt} = \gamma I$

Key parameters—including transmission rate (β), recovery rate (γ), and incubation rate (σ)—are used to compute metrics like the basic reproduction number R_0 , guiding public health decisions on interventions such as vaccination, isolation, and social distancing. These models can be adapted to heterogeneous populations, incorporate spatial and temporal factors, and allow for stochastic simulations that improve resilience planning

and epidemic forecasting. By enabling scenario analysis and sensitivity testing, SIR and SEIR models form a vital component of evidence-based public health strategies.

$N=S+I+R$ =Total population should be for the assumed constant.

Here we consider the basic Reproduction Number (R_0)

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

If $R_0 > 1$, the disease spreads and If $R_0 < 1$, the disease dies out. Susceptible Equation (dS/dt): This equation depicts the rate of decrease in the susceptible population over

time. The term captures the process of susceptible individuals becoming infected after interacting with infectious individuals.

$$-\beta \frac{SI}{N}$$

The rate of this transition is proportional to both the number of encounters between susceptible and infectious individuals and the probability of transmission per encounter. Infectious Equation (dI/dt): This equation shows the rate of change in the infectious population.

The increase in infectious individuals ($\beta \frac{SI}{N}$) is offset by the recovery rate ($-\gamma I$), reflecting the number of individuals who recover and move into the recovered compartment per unit time.

$$\beta \frac{SI}{N}$$

Recovered Equation (dR/dt): This equation represents the rate at which the recovered population increases, directly correlated with the number of individuals recovering from the disease (γI).

Effective Contact Rate (β): The Disease's Speed Dial
Beta isn't just a number—it's the throttle for disease transmission. It measures how often susceptible individuals come into effective contact with infectious ones, resulting in new infections. A higher beta means the infection spreads more rapidly, like a wildfire catching in dry grass. Interventions like mask-wearing,

Need to understand the parameters which are used in the above process.

social distancing, contact tracing, and limiting gatherings act like turning down the dial, suppressing the chance of transmission during encounters. So, when policymakers talk about "flattening the curve," what they're really aiming to do is tame Beta.

$$\frac{1}{\gamma}$$

The magic lies in its inverse, which tells us the average duration of infectiousness. For instance, if $\gamma = 0.2$, then on average, individuals recover in 5 days. It's a vital piece for understanding how long someone remains a

Recovery Rate (γ): The Exit Door from Infection

Gamma tracks how quickly infected individuals recover or are removed from the pool of transmitters. It's like the disease's clock: how long people stay contagious before they either recover or are isolated.

transmission risk. Together, β and γ shape the outbreak's trajectory—and their ratio, determines whether it fizzles out or flares up.

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

Real world Example

The Role of the SIR Model in Public Health

The SIR model has served as a foundational tool in public health, enabling experts to decode the dynamics of infectious disease spread. By compartmentalizing populations into susceptible, infectious, and recovered groups, it offers a quantitative lens to simulate transmission pathways and assess epidemic evolution.

During the COVID-19 crisis, this model and its enhanced variants (like SEIR and stochastic SIR) became critical in scenario-based forecasting. Researchers used them to estimate peak infection periods, healthcare demand, and the impact of non-pharmaceutical interventions such as lockdowns, mask mandates, and social distancing. These simulations weren't just academic—they directly informed government decisions, shaped public communication strategies, and helped allocate resources more efficiently.

In essence, the SIR framework transformed abstract epidemiological trends into actionable insights, reinforcing its role as a strategic ally in managing public health emergencies.

$$\frac{dS}{dt} = -\beta \cdot \frac{S \cdot I}{N} \quad \frac{dE}{dt} = \delta \cdot E - \gamma \cdot I \quad \frac{dI}{dt} = \delta \cdot E - \gamma \cdot I \quad \frac{dR}{dt} = \gamma \cdot I$$

Where

β = transmission rate

δ = rate of progression from exposed to infectious (1/incubation period)

γ = recovery rate

N = total population

Why Use the SIER Model?

It's ideal for diseases like COVID-19, measles, or influenza, where individuals are infected before becoming contagious.

The SIER model is a variation of the classic SIR epidemiological model, with an added compartment to better represent diseases that have an incubation period. It's often referred to as the SEIR model, where:

S = Susceptible

E = Exposed (infected but not yet infectious)

I = Infectious

R = Recovered (or Removed)

How the SIER/SEIR Model Works

This model captures the progression of individuals through four stages:

Susceptible (S): People who can catch the disease.

Exposed (E): People who have been infected but are not yet contagious.

Infectious (I): People who can transmit the disease.

Recovered (R): People who have recovered or are no longer infectious.

Mathematical Formulation

The model uses differential equations to describe transitions.

It allows for more accurate predictions of outbreak timing and peak infection.

It helps evaluate the impact of interventions like quarantine, vaccination, and testing.

Problem with solution

Say you are at a resort with 29 other people who all arrived yesterday ($N = 30$). Due to wild winter weather, as soon as you all arrived you were cut off from travel in or out of the resort. At the start of the first day, 1 person is infected with a fairly contagious cold, and given close proximity, this cold can be spread to 20% of the resort

per day. Say the infectious period lasts 3 days, and there is an incubation period of 1 day. How long would it be until 10 people are likely infectious?

- A) 1 Day
- B) 4 days
- C) 7 days
- D) There are never 10 concurrent infections.

Solution

To solve this problem, we'll use a modified SEIR model, considering the incubation period and infectious period.

Initial Conditions

1. Susceptible (S): 29
2. Exposed (E): 0 (initially)
3. Infectious (I): 1
4. Recovered (R): 0

Transmission Rate

1. β (transmission rate): 0.20 (20% of susceptible individuals can be infected per day)

Incubation Period

1 day: Exposed individuals become infectious after 1 day

Infectious Period

3 days: Infectious individuals recover after 3 days

Calculating the Number of Infectious Individuals

Let's calculate the number of infectious individuals over time:

Day 1

1. Infectious (I): 1
2. New Exposures: $29 \times 0.20 = 5.8 \approx 6$ (assuming integer values for simplicity)
3. Exposed (E): 6

Day 2

1. Infectious (I): 1 (from Day 1) + 6 (newly infectious from exposed) = 7
2. New Exposures: $(29 - 6) \times 0.20 = 4.6 \approx 5$
3. Exposed (E): 5

Day 3

1. Infectious (I): 7 (from Day 2) + 5 (newly infectious from exposed) = 12
2. However, some individuals from Day 1 will recover, so let's adjust:
 - Recovered (R): 1 (from Day 1)
 - Infectious (I): 1 (from Day 1) will recover, leaving 6 from Day 1 + 5 (newly infectious) = 11

Day 4

1. Infectious (I): Some from Day 2 will recover ($6 - 3 = 3$, since they were infectious for 3 days), and new individuals will become infectious.
 - Infectious from Day 2: $5 - 3 = 2$ (since 3 days have passed for some)
 - Newly Infectious: 5 (from exposed on Day 2)
 - Infectious (I): 2 (remaining from Day 2) + 5 (new) = 7

Given the dynamics, let's focus on when 10 people are likely infectious:

Analysis

Based on the calculations above, by Day 3, we already have 11 infectious individuals, which exceeds the threshold of 10. The best answer is B.

CONCLUSION

Mathematical models have become indispensable tools in understanding, predicting, and controlling health challenges at the population level. Whether simulating the spread of infectious diseases through compartmental frameworks like SIR and SEIR, or evaluating the long-term burden of chronic illnesses, these models provide a structured lens through which complex health dynamics can be examined.

By transforming biological interactions and public health policies into mathematical expressions, these models allow for scenario testing, resource optimization, and targeted interventions. Their ability to incorporate real-world data—from demography and mobility to behavior and immunity—makes them exceptionally versatile for guiding strategies in both emergency response and preventive care.

As global health threats continue to evolve, mathematical modeling will play a pivotal role not only in crisis management but also in designing resilient healthcare systems. When calibrated and applied thoughtfully, these tools bridge the gap between theory and action—empowering data-driven decisions for healthier, more prepared populations.

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