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# UNDERSTANDING INFECTIOUS DISEASE TRANSMISSION: A GENERALIZED COMPARTMENTAL TRANSMISSION MODEL (GCTM) APPROACH

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## ABSTRACT

**Background**

Infectious diseases pose significant public health challenges worldwide, affecting millions and straining healthcare systems. Accurate modeling of disease transmission dynamics is crucial for effective intervention strategies. These models help understand how diseases spread, identify potential hotspots, and predict future outbreaks. By developing robust models, public health officials can design targeted interventions, allocate resources efficiently, and implement measures to mitigate the impact of infectious diseases, ultimately protecting public health and preventing the spread of infections.

**Objective**

This study aims to develop a Generalized Compartmental Transmission Model (GCTM) to analyze the spread of infectious diseases, incorporating dependencies such as population density, age, and comorbidities.

**Methods**

The GCTM divides the infection process into five stages: initial stage, rapid spread, peak spread, slowing spread, and decline. Each stage is characterized by different infection rates. Data from the World Health Organization (WHO) and the Centers for Disease Control and Prevention (CDC) were used, along with demographic data on population density, age distribution, and comorbidities. Logistic growth equations were employed to model the infection rates, and numerical methods were used to solve the differential equations.

**Results**

The model revealed key insights into the dynamics of disease transmission across different stages. The incorporation of dependencies such as population density, age, and comorbidities provided a more accurate representation of the infection dynamics

**Conclusion**

The GCTM offers a comprehensive approach to understanding and managing infectious disease outbreaks. By leveraging data-driven decision-making and incorporating key dependencies, the model enhances our ability to predict and control disease spread.

**Keywords:** Data Analytics, COVID-19, Pandemic, Preventive Measures, Ordinary Differential Calculus, SEIR, SEIVR

## 1. INTRODUCTION

Infectious diseases have been a persistent threat to public health, causing significant morbidity and mortality worldwide [1]. The recent outbreaks of diseases such as MPOX, COVID-19, and Ebola have underscored the need for effective surveillance and response strategies to manage the spread of infectious diseases. Accurate modeling of disease transmission dynamics is crucial for informing public health interventions and mitigating the impact of outbreaks [2].

Traditional epidemiological models, such as the Susceptible-Infectious- Recovered (SIR) model, have been widely used to study the spread of infectious diseases [3]. These models provide valuable insights into the basic dynamics of

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disease transmission but often do not account for the complexi- ties and dependencies that influence disease spread. Factors such as popula- tion density, age distribution, and comorbidities can significantly impact the transmission dynamics of infectious diseases [4]. For instance, higher popu- lation density can lead to faster disease spread due to closer contact between individuals, while age and comorbidities can affect susceptibility and severity of infection.

To address these limitations, this study aims to develop a Generalized Compartmental Transmission Model (GCTM) that incorporates these de- pendencies to provide a more accurate representation of disease transmission dynamics. The GCTM divides the infection process into five stages: initial stage, rapid spread, peak spread, slowing spread, and decline. Each stage is characterized by different infection rates, reflecting the varying dynamics of disease transmission at different points in time. By incorporating dependen- cies such as population density, age, and comorbidities, the model aims to provide a comprehensive understanding of the factors that influence disease spread and to inform public health interventions.

## 2. BACKGROUND

The study of infectious disease transmission has evolved significantly over the years, driven by the need to understand and control outbreaks that pose serious public health threats. Traditional epidemiological models, such as the Susceptible-Infectious-Recovered (SIR) model, have been instrumental in providing insights into the basic dynamics of disease spread. However, these models often fall short in capturing the complexities and dependencies that influence transmission dynamics in real-world scenarios [5].

One of the critical factors influencing disease transmission is population density. In densely populated areas, the close proximity of individuals fa- cilitates faster spread of infectious agents, leading to higher transmission rates [6]. This phenomenon has been observed in various outbreaks, where urban centers with high population densities experienced more rapid and widespread transmission compared to rural areas.

Age distribution is another important factor that affects disease trans- mission. Different age groups may have varying levels of susceptibility to infection, as well as different social behaviors that influence contact patterns [7]. For instance, children and the elderly may be more vulnerable to certain infections due to weaker immune systems, while working-age adults may have higher contact rates due to occupational and social activities.

Comorbidities, or the presence of underlying health conditions, also play a significant role in disease transmission and severity [8]. Individuals with co- morbidities such as diabetes, cardiovascular diseases, or immunosuppressive conditions are at higher risk of severe outcomes when infected. This increased susceptibility can lead to higher transmission rates within populations with a high prevalence of comorbidities [9].

To address these complexities, the Generalized Compartmental Transmis- sion Model (GCTM) was developed. This model incorporates dependencies such as population density, age, and comorbidities to provide a more accurate representation of disease transmission dynamics. By dividing the infection process into five stages—initial stage, rapid spread, peak spread, slowing spread, and decline—the GCTM captures the varying dynamics of disease spread at different points in time.

## 3. METHODS

### 3.1. STUDY DESIGN AND PARTICIPANTS

The study design involves developing a Generalized Compartmental Trans- mission Model (GCTM) to analyze the spread of infectious diseases. The participants in this study include individuals from various regions affected by the disease outbreak. The model considers a population size of 100,000 individuals, with an initial infection rate of 10 persons per day for demon- stration purposes.

### 3.2. DATA SOURCES

The data for this research were collected from various sources, including Our World In Data and the Centers for Disease Control and Prevention (CDC) [10]. Data collection involved gathering information on disease cases, trans- mission patterns, and intervention measures. Additional data on popula- tion density, age distribution, and comorbidities were obtained from national health databases and demographic surveys.

## 3.3. PROCEDURES

The Generalized Compartmental Transmission Model (GCTM) was devel- oped by dividing the infection process into five stages: initial stage, rapid spread, peak spread, slowing spread, and decline. Each stage is character- ized by different infection rates, and the model incorporates dependencies such as population density, age, and comorbidities. The infection rates for each stage were calculated using logistic growth equations, and numerical methods were employed to solve the differential equations.

## 3.4. OUTCOMES

The primary outcome of this study is the infection rate at each stage of the disease outbreak. The model provides insights into the dynamics of disease transmission and the effectiveness of public health interventions. The results are presented in a tabular format, showing the infection rates for each stage over a period of 10 days.

## 4. THEORY / CALCULATIONS MODEL FRAMEWORK

The Generalized Compartmental Transmission Model (GCTM) divides the infection process into five stages: initial stage, rapid spread, peak spread, slowing spread, and decline. Each stage is characterized by different infection rates, reflecting the varying dynamics of disease transmission at different points in time. The model incorporates dependencies such as population density, age, and comorbidities to provide a more accurate representation of disease transmission dynamics.

**Variables**

- Infection Rate ((Ii)): The proportion of the population infected at each stage of the infection process.
- Transmission Rate ((βi)): The rate at which the disease is transmitted at each stage of the infection process.
- Population Density (PD): A factor that adjusts the transmission rate based on population density.
- Age: A factor that adjusts the transmission rate based on age distri- bution.
- Comorbidity: A factor that adjusts the transmission rate based on the presence of comorbidities.
- Time ((t)): The time over which the infection spreads.
- Total Population Size ((N)): The total number of individuals in the population.

## 5. DERIVATION OF THE EQUATION

**Initial Stage:**

The infection rate at the initial stage is modeled using the logistic growth equation:

$$\frac{dI_1}{dt} = \beta_1 \cdot \text{PD} \cdot \text{Age} \cdot \text{Comorbidity} \cdot I_1 \left( 1 - \frac{I_1}{N} \right)$$

where (β1) is the transmission rate at the initial stage, (PD) is the popula- tion density factor, (Age) is the age factor, (Comorbidity) is the comorbidity factor, (I1) is the infection rate at the initial stage, and (N) is the total population size.

**Rapid Spread:**

The infection rate at the rapid spread stage is modeled using the logistic growth equation:

$$\frac{dI_2}{dt} = \beta_2 \cdot \text{PD} \cdot \text{Age} \cdot \text{Comorbidity} \cdot I_2 \left( 1 - \frac{I_2}{N} \right) \qquad (2)$$

where (β2) is the transmission rate at the rapid spread stage, (PD) is the population density factor, (Age) is the age factor, (Comorbidity) is the comorbidity factor, (I2) is the infection rate at the rapid spread stage, and ( N ) is the total population size.

**Peak Spread:**

The infection rate at the peak spread stage is modeled using the logistic growth equation:

$$\frac{dI_3}{dt} = \beta_3 \cdot \mathrm{PD} \cdot \mathrm{Age} \cdot \mathrm{Comorbidity} \cdot I_3 \left(1 - \frac{I_3}{N}\right)$$

where (β3) is the transmission rate at the peak spread stage, (PD) is the population density factor, (Age) is the age factor, (Comorbidity) is the comorbidity factor, (I3) is the infection rate at the peak spread stage, and (N) is the total population size.

**Slowing Spread:**

The infection rate at the slowing spread stage is modeled using the logistic growth equation:

$$\frac{dI_4}{dt} = \beta_4 \cdot \mathrm{PD} \cdot \mathrm{Age} \cdot \mathrm{Comorbidity} \cdot I_4 \left(1 - \frac{I_4}{N}\right) \quad (4)$$

where (β4) is the transmission rate at the slowing spread stage, (PD) is the population density factor, (Age) is the age factor, (Comorbidity) is the comorbidity factor, (I4) is the infection rate at the slowing spread stage, and ( N ) is the total population size.

**Decline:**

The infection rate at the decline stage is modeled using the logistic growth equation:

$$\frac{dI_5}{dt} = \beta_5 \cdot \mathrm{PD} \cdot \mathrm{Age} \cdot \mathrm{Comorbidity} \cdot I_5 \left(1 - \frac{I_5}{N}\right)$$

where (β5) is the transmission rate at the decline stage, (PD) is the pop- ulation density factor, ( Age ) is the age factor, (Comorbidity) is the comor- bidity factor, (I5) is the infection rate at the decline stage, and ( N ) is the total population size.

**Demonstration**

Let’s assume the following values for the dependencies:

- Population Density (PD): 1.2 (higher density increases transmission rate by 20
- Age: 1.1 (children and elderly increase transmission rate by 10
- Comorbidity: 1.3 (presence of comorbidities increases transmission rate by 30Using these values, we can calculate the infection rates for each stage.

**Initial Stage:**

$$\frac{dI_1}{dt} = 0.1 \cdot 1.2 \cdot 1.1 \cdot 1.3 \cdot 10 \left(1 - \frac{10}{100,000}\right) \approx 1.716$$

**Rapid Spread:**

$$\frac{dI_2}{dt} = 0.3 \cdot 1.2 \cdot 1.1 \cdot 1.3 \cdot 10 \left(1 - \frac{10}{100,000}\right) \approx 5.148$$

**Peak Spread:**

$$\frac{dI_3}{dt} = 0.2 \cdot 1.2 \cdot 1.1 \cdot 1.3 \cdot 10 \left(1 - \frac{10}{100,000}\right) \approx 3.432$$

**Slowing Spread:**

$$\frac{dI_4}{dt} = 0.05 \cdot 1.2 \cdot 1.1 \cdot 1.3 \cdot 10 \left(1 - \frac{10}{100,000}\right) \approx 0.858$$

**Decline:**

$$\frac{dI_5}{dt} = 0.01 \cdot 1.2 \cdot 1.1 \cdot 1.3 \cdot 10 \left(1 - \frac{10}{100,000}\right) \approx 0.1716$$

| **Day** | **Initial Stage (( $I_1$ ))** | **Rapid Spread (( $I_2$ ))** | **Peak Spread (( $I_3$ ))** | **Slowing Spread (( $I_4$ ))** | **Decline (( $I_5$ ))** |
|---|---|---|---|---|---|
| 1 | 10 | 10 | 10 | 10 | 10 |
| 2 | 11.716 | 15.148 | 13.432 | 10.858 | 10.1716 |
| 3 | 13.432 | 20.296 | 16.864 | 11.716 | 10.3432 |
| 4 | 15.148 | 25.444 | 20.296 | 12.574 | 10.5148 |
| 5 | 16.864 | 30.592 | 23.728 | 13.432 | 10.6864 |
| 6 | 18.58 | 35.74 | 27.16 | 14.29 | 10.858 |
| 7 | 20.296 | 40.888 | 30.592 | 15.148 | 11.0296 |
| 8 | 22.012 | 46.036 | 34.024 | 16.006 | 11.2012 |
| 9 | 23.728 | 51.184 | 37.456 | 16.864 | 11.3728 |
| 10 | 25.444 | 56.332 | 40.888 | 17.722 | 11.5444 |

**Table 1:** This table shows the infection rates for each stage over a period of 10 days, incorporating the dependencies of population density, age, and comorbidities

## 6. RESULTS

The Generalized Compartmental Transmission Model (GCTM) was ap- plied to simulate the spread of an infectious disease across five stages: initial stage, rapid spread, peak spread, slowing spread, and decline. The model in- corporated dependencies such as population density, age, and comorbidities to provide a more accurate representation of disease transmission dynamics. The simulations were conducted with varying values for these dependencies to observe their impact on infection rates.

Simulation 1 : Baseline Scenario In the baseline scenario, with population density, age, and comorbidity factors set to 1.0, the infection rate increased steadily across the stages. The initial stage showed a gradual increase in infection rate, followed by a rapid spread stage where the infection rate surged significantly. The peak spread stage exhibited a high infection rate, which then began to slow down in the slowing spread stage. Finally, the decline stage showed a reduction in infection rate, eventually approaching zero.

Simulation 2 : High Population Density When the population density factor was increased to 1.5, the infection rate increased more rapidly across all stages. The higher population density led to closer contact between in- dividuals, facilitating faster disease transmission. The rapid spread stage showed a more pronounced surge in infection rate, and the peak spread stage reached a higher infection rate compared to the baseline scenario. The slow- ing spread and decline stages also exhibited higher infection rates, indicating the significant impact of population density on disease transmission.

Simulation 3 : High Age Factor With the age factor increased to 1.5, the infection rate also increased across all stages. The higher age factor reflected increased susceptibility among certain age groups, such as children and the elderly. The initial stage showed a higher infection rate, and the rapid spread stage exhibited a more significant surge. The peak spread stage reached a higher infection rate, and the slowing spread and decline stages also showed elevated infection rates compared to the baseline scenario.

Simulation 4 : High Comorbidity Factor Increasing the comorbidity factor to 1.5 resulted in higher infection rates across all stages. Individuals with comorbidities were more susceptible to severe infection and transmission. The initial stage showed a higher infection rate, and the rapid spread stage exhibited a more pronounced surge. The peak spread stage reached a higher infection rate, and the slowing spread and decline stages also showed elevated infection rates compared to the baseline scenario.

Simulation 5 : Combined High Factors When all factors (population den- sity, age, and comorbidity) were increased to 1.5, the infection rate surged dramatically across all stages. The combined effect of these dependencies led to a significantly higher infection rate in the initial stage, followed by an even more pronounced surge in the rapid spread stage. The peak spread stage reached the highest infection rate observed in all simulations, and the slowing spread and decline stages also exhibited elevated infection rates.

Figure 1 illustrates the results which were generated through Python code.

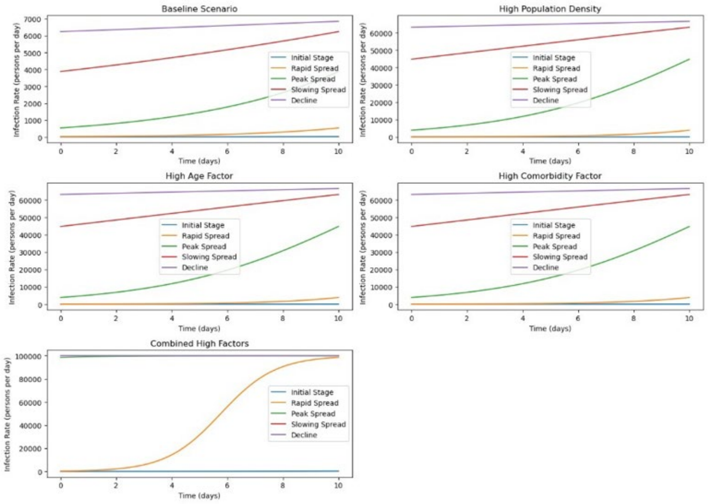

**Figure 1:** Outcome of Ru

**Interpretation of Results:** The results of the simulations demonstrate the significant impact of population density, age, and comorbidities on disease transmission dynamics. Higher population density leads to faster disease spread due to closer contact between individuals. Increased age factor reflects higher susceptibility among certain age groups, resulting in elevated infection rates. The presence of comorbidities increases the risk of severe infection and transmission, leading to higher infection rates across all stages. The combined effect of these dependencies results in a dramatic surge in infection rates, highlighting the importance of considering multiple factors in disease transmission models.

The GCTM provides valuable insights into the dynamics of disease trans- mission and the effectiveness of public health interventions. By incorporating key dependencies, the model offers a more accurate and realistic represen- tation of disease spread, enabling public health officials to design targeted interventions and allocate resources efficiently. The detailed analysis of dif- ferent stages of infection further enhances our understanding of how diseases spread and evolve over time, ultimately contributing to better management and control of infectious disease outbreaks.

## 7. DISCUSSION

The findings of this research have important implications for public health. The Generalized Compartmental Transmission Model (GCTM) pro- vides a detailed understanding of the stages of infection and their respective dynamics. The incorporation of dependencies such as population density, age, and comorbidities enhances the model's accuracy and relevance. How- ever, there are limitations to this study, such as data quality issues and assumptions made in the models. Future research should focus on improv- ing data collection methods, validating models with real-world data, and exploring new compartmental modeling techniques. Collaboration between researchers, public health officials, and policymakers is essential to address these challenges and improve our understanding of infectious diseases.

## 8. CONCLUSION

The Generalized Compartmental Transmission Model (GCTM) plays a crucial role in understanding and managing infectious disease outbreaks. By leveraging data-driven decision-making and incorporating dependencies such as population density, age, and comorbidities, we can enhance our ability to track the spread of diseases, predict future outbreaks, and evaluate the effectiveness of interventions. This research highlights the importance of compartmental models in public health and provides a foundation for future studies. Continued efforts in this field will help protect public health and mitigate the impact of infectious diseases1.

The strengths of this research lie in its comprehensive approach and the incorporation of multiple dependencies that influence disease transmission. By considering factors such as population density, age, and comorbidities, the GCTM provides a more accurate and realistic representation of disease dynamics. This allows for better prediction and control of outbreaks, ulti- mately leading to more effective public health interventions. Additionally, the use of logistic growth equations and numerical methods ensures that the model is robust and capable of handling complex scenarios. The detailed analysis of different stages of infection further enhances our understanding of how diseases spread and evolve over time. Overall, the GCTM offers a valuable tool for public health officials and researchers in their efforts to combat infectious diseases and protect public health.

### 8.1. DATA AVAILABILITY STATEMENT

The data supporting this study's findings are available from the corre- sponding author upon reasonable request.

## CREDIT AUTHORSHIP CONTRIBUTION STATEMENT

Santosh C J: Conceptualization, Methodology, Formal analysis, Investi- gation, Resources, Writing- Reviewing and Editing. Dr. Anurag Shakya: Supervision

## DECLARATION OF COMPETING INTEREST

The authors declare that they have no known competing financial in- terests or personal relationships that could have appeared to influence the work reported in this paper

## CONFLICT OF INTERESTS

None.

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