Mathematical Epidemiology: Compartmental Models and Equilibrium Stability Analysis

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Background

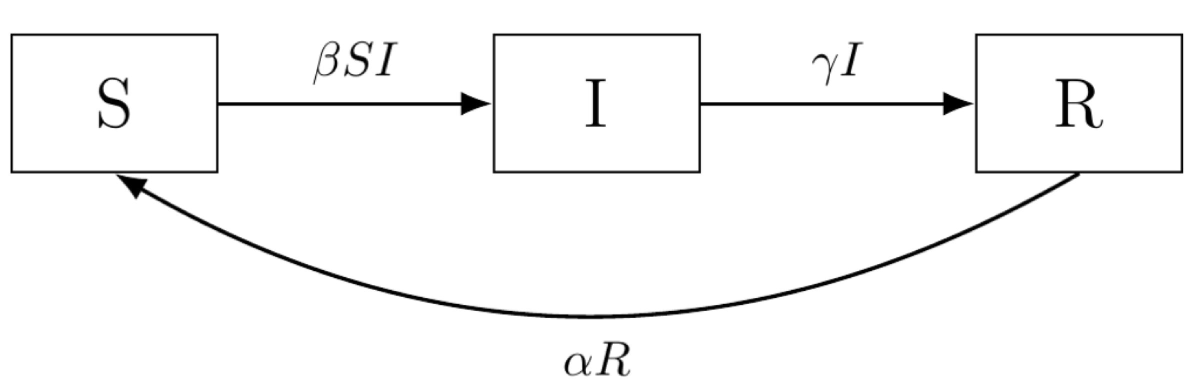
Infectious diseases have historically impacted populations, such as the COVID-19 Pandemic for a recent example, which infected 779 million people and caused 7 million deaths.

Epidemiology exists to understand the cause of diseases, predict how diseases are transmitted, and develop effective intervention strategies. Compartmental models are the modern strategy for defining the flow of diseases, utilizing Ordinary Differential Equations and dynamical systems to depict movements in a population. Transmission is defined by a transmission rate β, and the rate of recovery is defined by γ.

Current theoretical models do not fully account for social dynamics within a population that can alter the spread of disease. These do not address the behavior of infectious individuals. Our research aims to overcome this shortcomings by developing compartmental models and analyzing. The goal is to understand disease spread and evaluate different strategies to reduce it.

Objectives: Understand the stability of diseases at Disease Free and Endemic Equilibria, Understand different effects upon models depending on differing differential equations and parameters, and
Explore how real-world data be integrated into these models to provide accurate predictions

Figure 1.1: The SIR Compartmental Model



Methodology

- Subjects are theoretical populations in compartments defined by the specific model used
- Measures transmission rate β and recovery rates γ as well as the basic reproduction number R_0 to understand the potential threat of an outbreak
- Define different SIR-type compartmental models to describe rates within specific systems
- Create ODEs to define systems and relationship between compartments within a model
- Identify where the disease-free equilibrium and endemic equilibrium, or where the disease dies out or persists, respectively.
- Derive eigenvalues from matrix processes to determine the stability of equilibria
- Apply matrix processes to solve for R_0
- Utilize real-world variables to the equations to simulate differing outcomes based on changing parameters and variables.

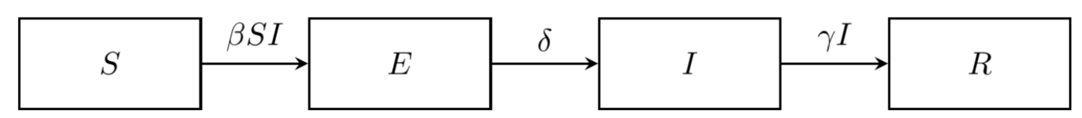


Figure 1.2: The SEIR Compartmental Model

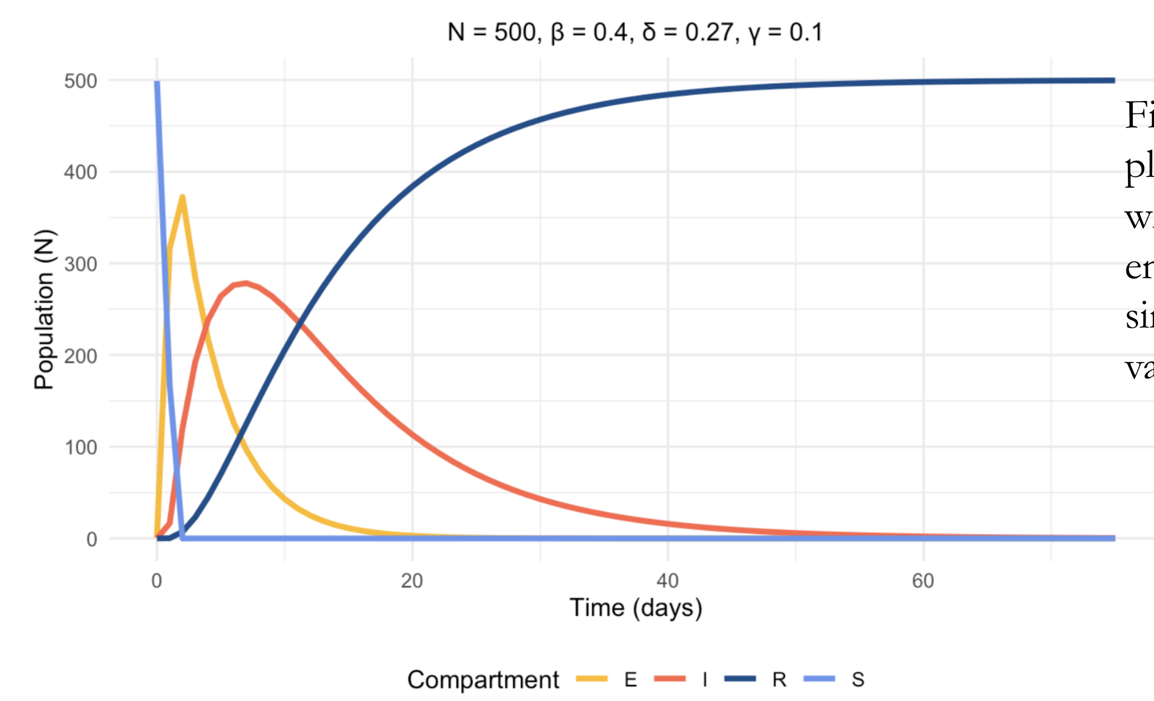


Figure 1.3: Time series plot of SEIR model without vital dynamics at endemic equilibrium, simulated with parameter values.

Results/Conclusions

Multiple models were derived and analyzed at depth; the SEIR and SAIR model will serve as examples showcasing the varying complexities that theoretical and real-world application

SEIR Model

- Population is assumed constant (No Births/Natural Deaths)
- Using Next Generation Matrix processes, R_0 derived:
  - $R_0 < 1 \longrightarrow$ Stable DFE, Disease dies out
  - $R_0 > 1 \longrightarrow$ Unstable DFE, Outbreak/Epidemic occurs
- Integration of the exposed compartment introduces a latent period before exposed individuals become infectious
- Figure 1.3 showcases this relationship:
  - Rise in Exposed Compartment
  - Delayed Peak in Infected Compartment
    - Latent Period
- Without vital dynamics, infections decline to zero; system reaches Disease Free Equilibrium after outbreak

SAIR Model w/ Vital Dynamics

- Vital Dynamics (Birth and Natural Death Rates) integrated
- Transmission can occur from Susceptible and Asymptomatic Compartments
- Using Next Generation Matrix processes, a complex R_0 derived:
  - In Essence:
    - $R_0 < 1 \longrightarrow$ Stable DFE, Disease dies out
    - $R_0 > 1 \longrightarrow$ Stable EE, Outbreak/Epidemic occurs
- Figure 1.5 highlights relationship between compartments:
  - Rapid rise in Infected Compartment; Sharp Decline in Susceptible Compartment
  - Infection Growth slows; All compartments stabilize
  - Convergence to Endemic Equilibrium $\longrightarrow$ Disease persists at steady level

Figure 1.4: The SAIR Compartmental Model

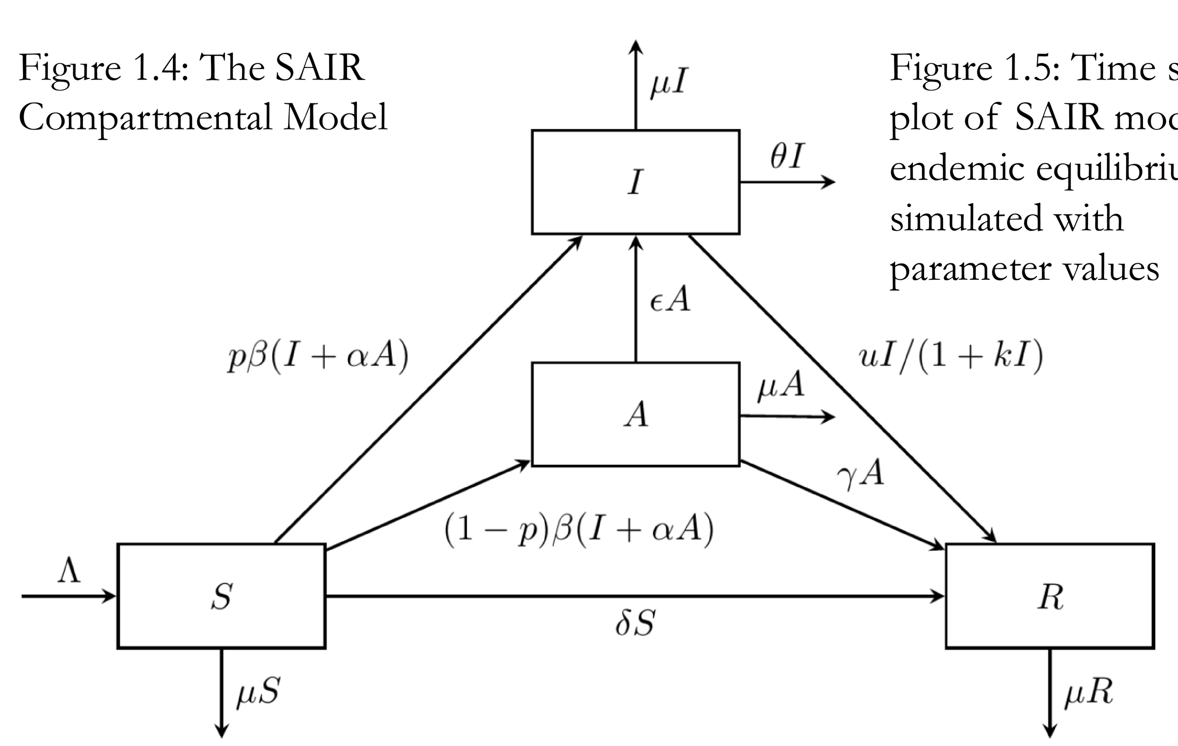
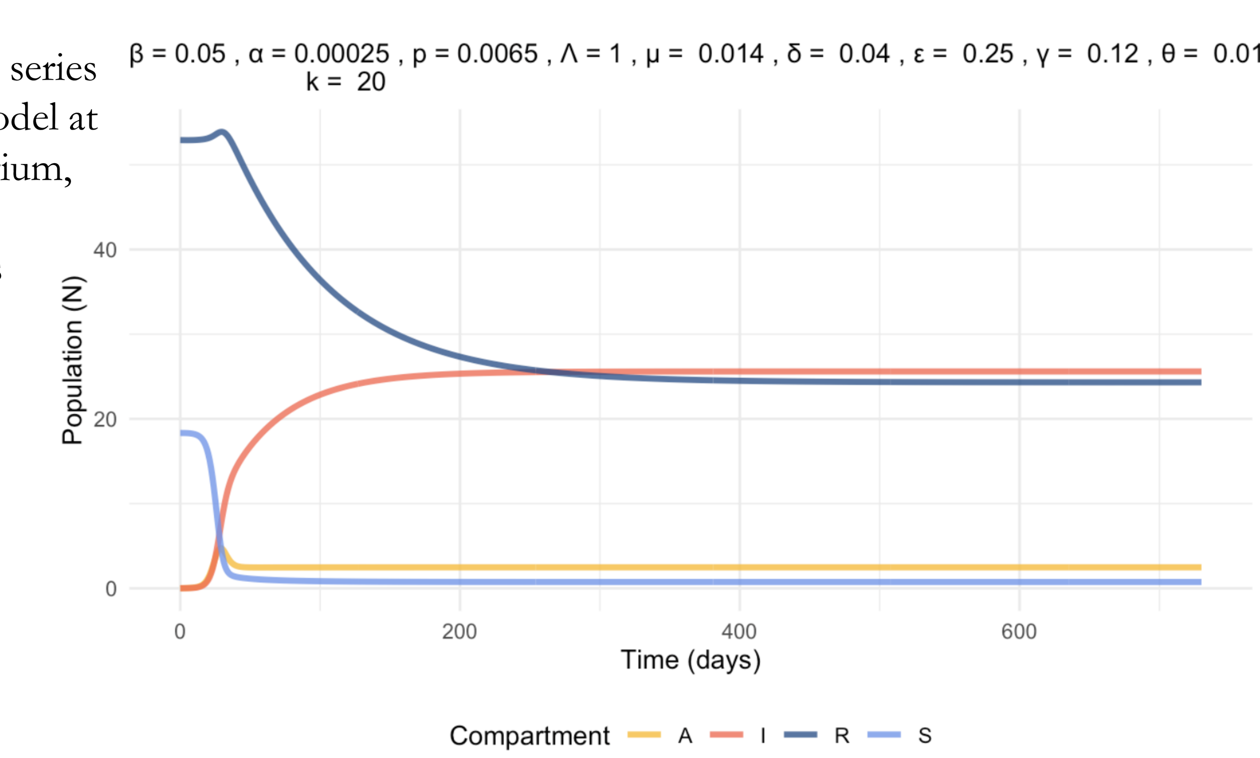


Figure 1.5: Time series plot of SAIR model at endemic equilibrium, simulated with parameter values



Discussion

These results establish a core principle of mathematical epidemiology: the equilibrium in which a disease converges is defined by R_0. In varying models, the relationship between R_0 and the respective derivation designate the persistence or termination of a disease within a population.

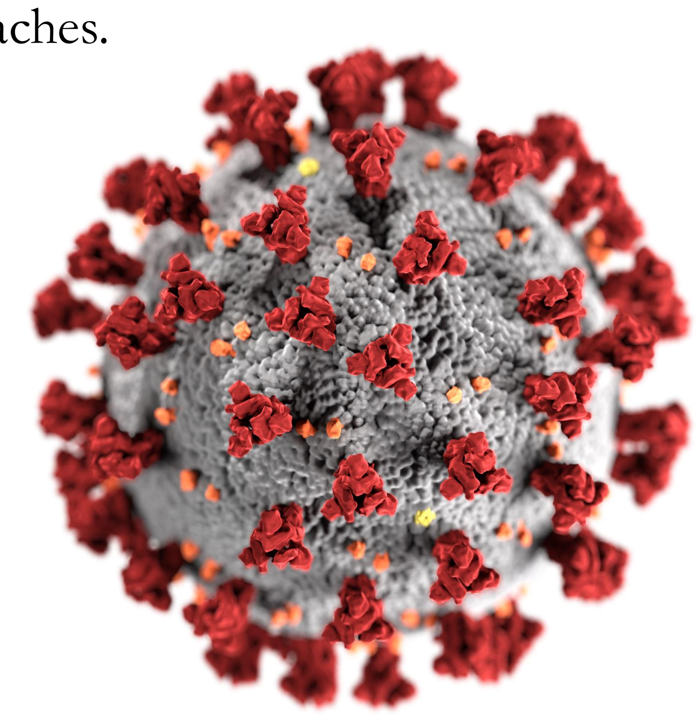
Compartmental models can accurately estimate the dynamics of a disease within a population, capturing the flow of individuals between specific compartments over time. These are presented through the rise and declines of time series plots, which are mathematically determined by specific ODEs.

These models while accurate are limited by social dynamics within a population. Populations in models are assumed to mix uniformly, where susceptible individuals are equally probable to encounter infected individuals. However, this does not account for heterogeneity, in which individuals in a population have differing number of contacts. Additionally, every population is assumed as one; in reality, metapopulations may have varying characteristics. These limitations prevent a perfect model of diseases.

Implications and Future Work

Real-world applications of compartmental models include efficient targeted intervention methods based on quantitative results. Public health officials can utilize compartmental models, adjusting parameters to reflect distinct results within a local population, allowing for intervention and prevention based on probable outcomes. These models prove to be useful and accurate tools that can justify strategic intervention regarding the spread of infectious diseases.

Currently diseases, such as measles, are causing significant complications globally and domestically. Personal future research involves an SAIQR model of measles, focusing on how social dynamics affect the adherence to quarantine Complex theories and concepts within psychological, economic, law, and mathematical fields will be incorporated to accurately assess the spread of measles during quarantine breaches.



References: