

Forecasting Hospitalization Demand in England during COVID-19 Pandemic: A Mathematical Modeling Approach

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Abstract—

Index Terms—

B. Differential Equations

I. INTRODUCTION

THIS paper delves into the mathematical modeling of infectious diseases, specifically focusing on the COVID-19 pandemic. The primary objective is to understand the dynamics of COVID-19 transmission and to forecast the demand for mechanical ventilators in England, a critical healthcare resource during the peaks of the pandemic.

II. PROBLEM STATEMENT

The outbreak of the COVID-19 pandemic has posed significant challenges to healthcare systems worldwide. One of the major concerns during the pandemic's peaks has been the potential overwhelming demand on healthcare resources, particularly the demand for intensive care units (ICUs) and mechanical ventilators. This study aims to develop a mathematical model to understand the dynamics of COVID-19 transmission and forecast the demand for mechanical ventilators in England.

III. MODEL ASSUMPTIONS

- 1) The population is constant, i.e., no births or non-COVID-related deaths are considered.
- 2) The disease transmission occurs only between the susceptible and the infected (both asymptomatic and symptomatic) individuals.
- 3) Individuals progress from being exposed to the virus to being infected (either asymptomatic or symptomatic).
- 4) Symptomatic infected individuals may require mechanical ventilation if their condition deteriorates.
- 5) Ventilated patients either recover or die.
- 6) Recovered individuals can lose immunity and become susceptible again.

IV. MODEL DEFINITION

A. Compartments

- $S(t)$: Susceptible individuals at time t .
- $E(t)$: Exposed individuals at time t .
- $I_a(t)$: Asymptomatic infected individuals at time t .
- $I_s(t)$: Symptomatic infected individuals at time t .
- $V(t)$: Individuals on ventilators at time t .
- $R(t)$: Recovered individuals at time t .
- $D(t)$: Deceased individuals at time t .

$$\begin{aligned}\frac{dS}{dt} &= -\beta S(I_a + I_s) + \omega R \\ \frac{dE}{dt} &= \beta S(I_a + I_s) - \sigma E \\ \frac{dI_a}{dt} &= p\sigma E - \gamma_a I_a \\ \frac{dI_s}{dt} &= (1-p)\sigma E - \gamma_s I_s - \rho I_s \\ \frac{dV}{dt} &= \rho I_s - (v + \alpha)V \\ \frac{dR}{dt} &= \gamma_a I_a + \gamma_s I_s + (1-\delta)\alpha V - \omega R \\ \frac{dD}{dt} &= \delta\alpha V + vV\end{aligned}$$

C. Parameters

- β : Transmission rate.
- σ : Rate of progression from exposed to infected.
- γ_a : Recovery rate for asymptomatic individuals.
- γ_s : Recovery rate for symptomatic individuals.
- ρ : Rate at which symptomatic individuals require ventilation.
- α : Recovery rate for ventilated individuals.
- v : Death rate for individuals on ventilators.
- δ : Proportion of ventilated patients who die.
- ω : Rate at which recovered individuals lose immunity.
- p : Proportion of exposed individuals who become asymptomatic infected.

V. MATHEMATICAL PROOF OF THE MODEL

The model is a system of ordinary differential equations (ODEs) derived from the law of mass action. The sum of all compartments at any time t is equal to the constant population N , ensuring the conservation of mass:

$$S(t) + E(t) + I_a(t) + I_s(t) + V(t) + R(t) + D(t) = N$$

The non-negativity of the solutions is ensured by the non-negative initial conditions and the structure of the ODEs, which prevents negative values in any compartment.

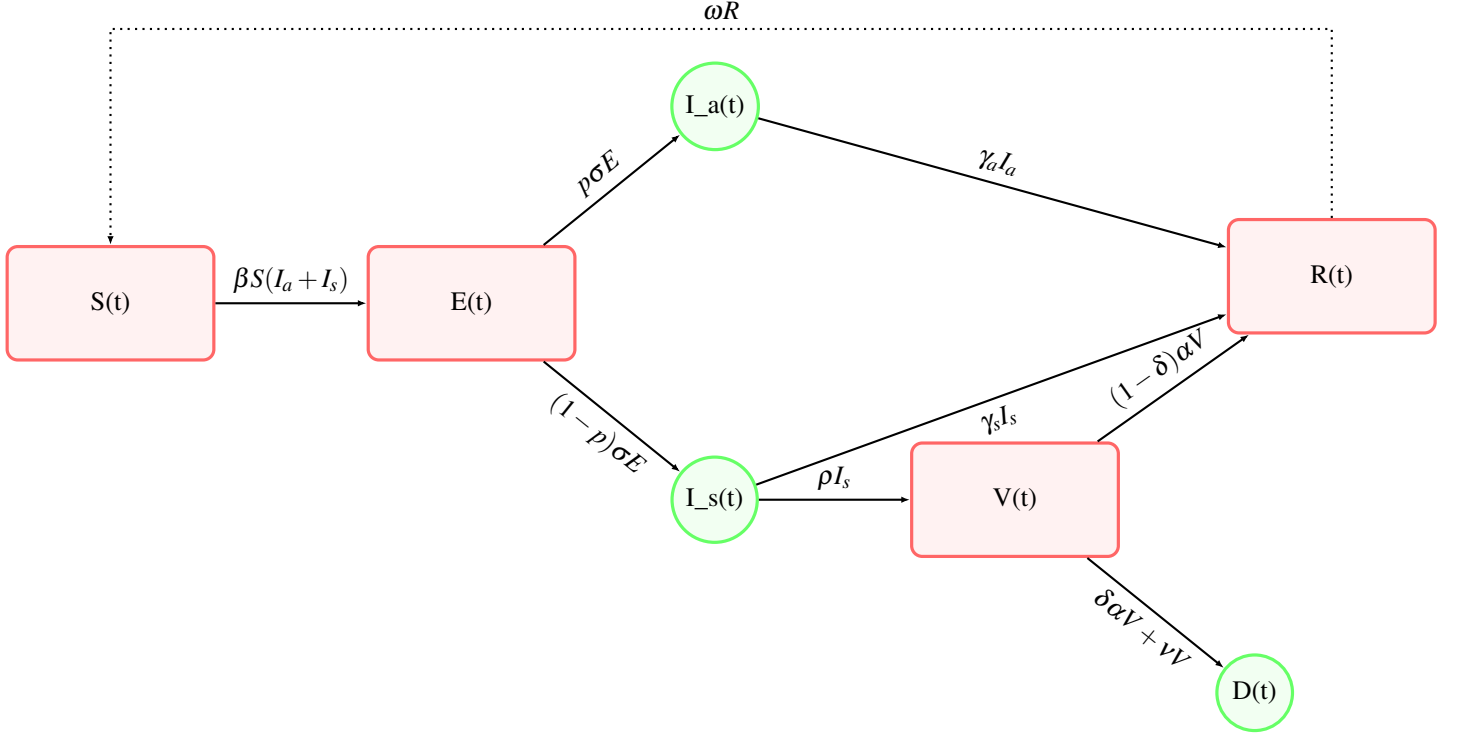


Fig. 1: Compartmental flow of the COVID-19 Transmission Dynamics Model.

VI. REPRODUCTION NUMBERS FOR THE EPIDEMIC MODEL

In this section, we derive the basic reproduction number R_0 and the effective reproduction number R_t using the Next-Generation Matrix (NGM) method.

A. Basic Reproduction Number R_0

The basic reproduction number, R_0 , represents the average number of secondary infections produced by a single infected individual in a completely susceptible population. Using the NGM method, R_0 is derived as:

$$R_0 = \frac{\beta N(\rho - \sigma + p\sigma + \gamma_s)}{p\sigma(\rho + \gamma_s)}$$

B. Effective Reproduction Number R_t

The effective reproduction number, R_t , represents the average number of secondary infections produced by one infected individual at time t in a population that is not entirely susceptible. It is formulated as:

$$R_t = \frac{\beta S(t)(\rho - \sigma + p\sigma + \gamma_s)}{p\sigma(\rho + \gamma_s)}$$

VII. REAL-WORLD APPLICATION

This model serves as a tool for understanding and predicting the demand for critical healthcare resources