


# A Theoretical Linguistic Fuzzy Rule-Based Compartmental Modeling for the COVID-19 Pandemic

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## ABSTRACT

The COVID-19 pandemic has affected the whole world quite seriously. The number of new infectious cases and death cases are rapidly increasing over time. In this study, a theoretical linguistic fuzzy rule-based susceptible-exposed-infectious-isolated-recovered (SEIIR) compartmental model has been proposed to predict the dynamics of the transmission of COVID-19 over time considering population immunity and infectiousness heterogeneity based on viral load in the model. The model's equilibrium points have been calculated, and stability analysis of the model's equilibrium points has been conducted. Consequently, the fuzzy basic reproduction number,  $R_0$ , of the fuzzy model has been formulated. Finally, the temporal dynamics of different compartmental populations with immunity and infectiousness heterogeneity using the fuzzy Mamdani model are delineated, and some disease control policies have been suggested to get over the infection in no time.

## KEYWORDS

COVID-19, Epidemiological Compartmental Model, Fuzzy Basic Reproduction Number, Fuzzy Mamdani Model, Population Heterogeneity

## 1. INTRODUCTION

The novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), well-known as COVID-19, has become the single-most burning issue all over the world right now. As of September 08, 2020, from 213 countries and regions throughout the world along with 2 international transportations, the total number of reported coronavirus cases is 27,510,544, and the number of deaths till now is

DOI: 10.4018/IJFSA.285553

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897,231 whereas only 19,605,017 recovered from the disease (Worldometer, 2020). The number of positive infected cases and death cases has been increasing so rapidly throughout the world that this outbreak of COVID-19 was notified as a pandemic by the World Health Organization (WHO) on March 11, 2020 (WHO, 2020). On December 31, 2019, this outbreak was first detected and reported in Wuhan, China (Yang & Wang, 2020). Controlling the outbreak of this disease has become so much strenuous for several reasons (Chatterjee et al, 2020; Yang & Wang, 2020). One of the major reasons for this is that the scientific world still lacks all the necessary biological and clinical information regarding this new virus. Again, no vaccine for this disease is still available (Chatterjee et al, 2020). The responses of the antibody or the immune protein against the virus are not yet understood well and also the clinical efficacy of the serological testing has remained ambiguous (Tang et al, 2020). At this moment, it has become very urgent to realistically recognize the transmission process of COVID-19 with known clinical information and predict the temporal infection dynamics accordingly to contain this epidemic with the help of strict and correct intervention measures.

Different research works are being conducted on COVID-19 in countries all over the world. Jia et al (2020) developed a spatio-temporal risk source model to statistically derive the geographic spread of COVID-19 and the growth pattern based on the population outflow from Wuhan. In another study, Wu et al (2020) forecasted national and global spread of COVID-19 in Wuhan and estimated that large cities outside China could also become outbreak epicentres. Wu et al (2020) later extended his research to estimate clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. Various classical compartmental epidemiological models (Brauer et al, 2019; Daley & Gani, 1999; Martcheva, 2015) have been proposed for predicting and understanding the temporal transmission dynamics of COVID-19. In these classical models, the entire population is split into different compartments of specific groups of individuals distinguished by the infection. To model the infection of the asymptomatic carriers (Rothe et al, 2020), the exposed ( $E$ ) compartment is typically used in the compartmental models for SARS-CoV-2 predictive studies (Yang & Wang, 2020). Using the Susceptible-Exposed-Infected-Recovered (SEIR) model, Wang et al (2020) estimated the transmission dynamics in Wuhan with respect to the number of infected cases. Another compartment, which is Viral Concentration ( $V$ ), has been appended to this SEIR model in a study by Yang et al (2020) to model multi-transmission channels of SARS-CoV-2. Chatterjee et al (2020) executed the Susceptible-Infected-Recovered-Death (SIRD) model to predict the infection dynamics in India and other countries. Giordano et al (2020) performed the predictive study for the transmission dynamics of SARS-CoV-2 in Italy using the Susceptible-Infected-Diagnosed-Ailing-Recognized-Threatened-Healed-Extinct (SIDARTHE) model.

However, all these classical models exploiting the system of ordinary differential equations (ODE) that belongs to the crisp set disregarded the different uncertainties or variabilities associated with the transmission dynamics of SARS-CoV-2. One main assumption in all these classical models is population homogeneity that indicates that all infectious individuals have the identical capacity or possibility of transmitting the disease to the susceptible individuals. As a result, many studies assumed the transmission rate,  $\beta$  as a constant value which is the most significantly influential parameter in the system of ODE of the classical compartmental models. Many studies exploited phase-based  $\beta$  in the classical system using phase-based effective reproduction number,  $R_t$  (Chatterjee et al, 2020; Giordano et al, 2020; Wang et al, 2020) values although  $R_t$  is a dynamic parameter. Moreover, no population heterogeneity was incorporated into these models. In reality, transmission rate might change from place to place and time to time depending on different complex population heterogeneities, such as population immunity, infectiousness etc. Again, the infectiousness of the disease may or may not depend on the viral load of a given viral infection or disease. However, a study on SARS-CoV-2 conducted by He et al (2020) delineated that both infectiousness and viral load change as population transit from asymptomatic exposed through symptomatic infected to recovered state over time. Long et al (2020) studied the antibody or the immune protein (immunoglobulin-G and immunoglobulin-M) responses to COVID-19 in the patients. Denning et al (2020) recently studied the temporal dynamics

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