



An interaction-oriented multi-agent SIR model to assess the spread of SARS-CoV-2

Koray Altun^{*1} , Serkan Altuntas² , Turkey Dereli³ 

¹Department of Industrial Engineering, Bursa Technical University, 16330, Bursa, Turkey

²Department of Industrial Engineering, Yildiz Technical University, 34349, Istanbul, Turkey

³Office of the President, Hasan Kalyoncu University, 27410, Gaziantep, Turkey

Abstract

It is important to recognize that the dynamics of each country are different. Therefore, the SARS-CoV-2 (COVID-19) pandemic necessitates each country to act locally, but keep thinking globally. Governments have a responsibility to manage their limited resources optimally while struggling with this pandemic. Managing the trade-offs regarding these dynamics requires some sophisticated models. “Agent-based simulation” is a powerful tool to create such kind of models. Correspondingly, this study addresses the spread of COVID-19 employing an interaction-oriented multi-agent SIR (Susceptible-Infected-Recovered) model. This model is based on the scale-free networks (incorporating 10,000 nodes) and it runs some experimental scenarios to analyze the main effects and the interactions of “average-node-degree”, “initial-outbreak-size”, “spread-chance”, “recovery-chance”, and “gain-resistance” factors on “average-duration (of the pandemic last)”, “average-percentage of infected”, “maximum-percentage of infected”, and “the expected peak-time”. Obtained results from this work can assist determining the correct tactical responses of partial lockdown.

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1. Introduction

Although it is known that life after the COVID-19 pandemic will not continue where it left off, it is still a matter of debate when (and how) the outbreak will end. Preparing for life during and after this pandemic has the highest priority in the to-do list of each country. The dynamics of each country (e.g. economic, political, social, and cultural dynamics) are different and therefore this uncharted territory necessitates them to act locally, but keep thinking globally. “COVID-19 Act Local Think Global” concept needs learning from the (global) experiences and doing some (local) trial-and-error (and then observing the reactions).

*Corresponding Author.

Email addresses: koray.altun@btu.edu.tr (K. Altun), serkan@yildiz.edu.tr (S. Altuntas), turkay.dereli@hku.edu.tr (T. Dereli)

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Modeling this pandemic by using some sophisticated methods may be vital while executing these trial-and-error processes. Understanding the spreading mechanism of this pandemic is the main prerequisite for these modeling works. Modeling these spread process by dividing the population into distinct compartments indicating the status is known as “compartmental modeling” in the literature. One of the simplest and earliest contributions to these modeling attempts is Kermack and McKendrick [16] model, which is the “SIR (Susceptible-Infected-Recovered) model”, and yields important results for epidemics [13]. This model consists of three compartments as “Susceptible”, “Infected”, and “Recovered”. The transition process in the SIR model is illustrated in Figure 1. While $S(t)$ is the compartment of “Susceptible” individuals, $I(t)$ and $R(t)$ are the compartments of “Infected” and “Recovered” individuals, respectively. The initial state includes one (or more) “infected” individual. The disease spreads from any “infected” individual to any “susceptible” individual by contact infection. The individuals of the “recovered” compartment were “infected” in their previous states, and their actual status is either “gain-resistant” or “removed/dead”.

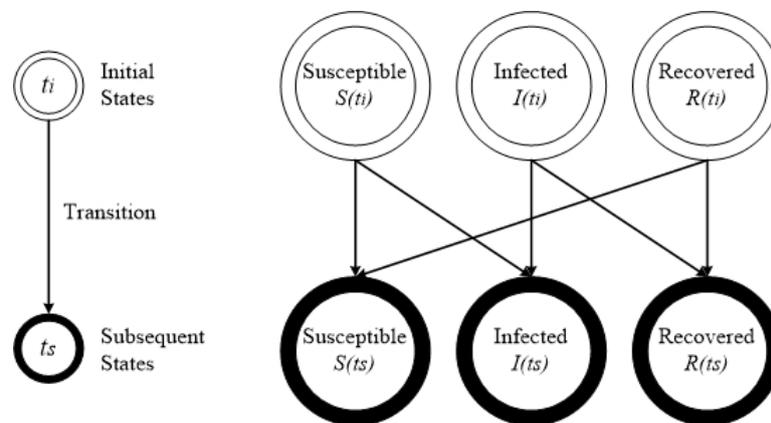


Figure 1. The transitions in the SIR model.

An extension of this simple SIR model is the SEIR (Susceptible-Exposed-Infected-Recovered) model [9, 26]. It includes an additional compartment so-called Exposed. This compartment covers infected individuals who are not infectious. This simple SIR model can also be extended by considering birth, mortality, and vaccination rate. QSEIR, which is proposed by [19], can be used to consider the unprecedented strict QSEIR (Quarantine-Susceptible-Exposed-Infected-Recovered) measures.

The basic reproduction number (R_0) is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual [11]. Further discussions corresponding to its computation can be found in [6, 8, 11]. General compartmental disease transmissions have been modelled by a system of ordinary differential equations by using this reproduction number. Early analytical approaches for modeling these transitions among compartmental states are some mathematical models involving ordinary differential equations and nonlinear analysis [9, 13, 16, 20, 26]. The use of differential equations and nonlinear analysis (commonly known as EBM - Equations-Based Modeling in the literature) is still a common way in epidemiology. There are also many works trying to model the spread of this new coronavirus (SARS-CoV-2) by using differential equations (e.g. [5, 14, 19, 29]).

Parker and Epstein [24] claim that EBM is ill-suited to representing complex modern social networks and contacts between distinct individuals, interacting with another (not in a well-mixed population) as they move about spatially, adapting their behaviors-perhaps irrationally-based on disease prevalence. The EBM focuses on the overall system behavior

instead of the individuals. Focusing on the individual level of behavior necessitates the use of more advanced modeling approaches such as Agent-Based Modeling (ABM). According to Parunak et al. [25], the ABM and the EBM differ in two ways; the fundamental relationships among entities that they model, and the level at which they focus their attention. While EBM uses some equations derived from system level of observables (measurable characteristics of interest), the ABM focuses the observables of the individuals (so-called; “agents”), supporting the system-level information.

The effect of contact pattern [23] and the network structure of contacts [3, 10, 22] on the disease spreading are also considered in the epidemiology literature. A Network-Based compartmental model (NB-SEIR) is proposed and implemented for the spread of “Whooping Coughby” in Nebraska by [1]. According to the findings of this study, the NB-SEIR model shows a good improvement on the standard SEIR model, and can also find the peak of infection of disease successfully in the demonstrated case studies. Recent advances in network modeling make it possible to model of epidemic spread. Statistical network analysis is especially useful to guide policies regarding partial lockdown and design of sufficient contact tracing programs. In a recent study, Loyal and Chen [21] reviews the network modeling techniques and their applications to the SARS-CoV-2.

Two ABM approaches are discussed in the literature; task-centric modeling (also known as content-centric) and interaction-oriented modeling [4]. While the task-centric modeling approach focuses on the task of agents and the data required, the interaction-oriented approach focuses on the interactions in multi-agent environments. The interaction-oriented ABM approach models each behavior as a part of an interaction. Kubera et al. [17] propose IODA (Interaction Oriented Design of Agent simulations) for modeling the influences and the interactions between the entities of an ABM. In this model, interactions can be modeled independently and an interaction matrix is used to assign all interactions to the agents. Representing these interactions by using graph theory and network analysis enables conceptualizing their frequency, strength, etc. Although the use of the ABM approach has been studied by several authors in the literature of epidemiology (e.g. [15, 24]), according to the authors best knowledge, no previous research has investigated the use of interaction-oriented ABM approach for the spread of this new coronavirus. Correspondingly, this study presents an experimental analysis of the spread of SARS-CoV-2 by using an interaction-oriented multi-agent SIR model. This study analyzes the main effects and the interaction effects of “average-node-degree”, “initial-outbreak-size”, “spread-chance”, “recovery-chance”, and “gain-resistance” factors on “average-duration (of the pandemic last)”, “average-percentage of infected”, “maximum-percentage of infected”, and “the expected peak-time”. The ultimate goal of this study is to provide an in-depth understanding of the spread and to produce knowledge that may help policy makers to plan the degree of partial lockdowns, to design sufficient contact tracing programs, and to determine effective vaccination strategies.

The rest of the paper is organized as follows. Section 2 describes the methodology in more detail. The results of the experiments are provided in Section 3. Finally, the conclusion is given in Section 4.

2. Methodology

2.1. Network design for the interactions

This study simulates the spread of SARS-CoV-2 by using an interaction-oriented ABM. This model uses a network structure to model the interactions among individuals of different compartments. The chosen network structure is important while modeling the interactions among individuals of different compartments.

The SIR consists of three compartments as, “Susceptible”, “Infected”, and “Recovered”. The transition process in the SIR model is illustrated in Figure 1. While $S(t)$ is

the compartment of Susceptible individuals, $I(t)$ and $R(t)$ are the compartments of “Infected” and “Recovered” individuals, respectively. The initial state includes one (or more) “infected” individual. The disease spreads from any “infected” individual to any “susceptible” individual by contact infection. The individuals of the “recovered” compartment were “infected” in their previous states, and their actual status is either “gain-resistant” or “removed/dead”.

The SIR model provides a theoretical framework to investigate a pandemic spread within a community [7]. The disease dynamics equations for standard SIR Model are given as follows based on [2]. Further details of the SIR model can be found in [27].

$$dS/dt = \beta(S.I/N) \quad (2.1)$$

$$dI/dt = \beta(S.I/N) - v.I \quad (2.2)$$

$$dR/dt = v.I \quad (2.3)$$

where, N stands for the total number of people in the population. β implies the rate of spread of infection by an infected person per day when he/she interacts with the susceptible population. The number of people recovering is indicated by the rate of recovery v .

Solé and Valverde [28] define three relevant characteristics of complex networks. These characteristics are “randomness”, “heterogeneity”, and “modularity”. “Randomness represents the degree of randomness of the network building process. “Heterogeneity” is the measure for the diversity of the degree distribution. “Modularity” is the measure of the strength of division into clusters/groups/compartments.

The design of a network indicating how individuals contact each other during this pandemic is crucial. Standard compartmental models consider that people are homogeneously mixed. For this reason, in these models, any pair of individuals has equal chance to interact. This assumption does not reflect the real-life routine. However, network models provide a powerful tool for understanding the spread of disease in the presence of heterogeneous mixing by coding heterogeneous contact patterns [21]. Moreover, in a recent study, a stochastic cellular automata approach has also been employed to evaluate the presence of superspreaders in COVID-19 infection scenarios with reduced mobility [18].

Mossong et al. [23] provide an analysis of population-based contact patterns aiming to help inform the structure and parameterization for close-contact infectious diseases. They record approximately 100,000 contacts with different persons. They observe that mean of the daily contacts is 13.4 per individual. While the German participants have the fewest daily number of contacts with mean 7.95, Italians have the highest number with mean 19.77. As it is stated in [5], Turkey and Italy are the two countries that have a similar collective life typical of the Mediterranean region. While modeling the initial phase of the spread of an epidemic disease, considering these levels of contact is reasonable. Loyal and Chen [21] simulate an SEIR epidemic on a mathematical network model developed for the SARS-CoV-2 spread. They chose the parameters of this model that the networks roughly shared an average degree of 6. However, our initial screening design findings indicate that it is possible to struggle with SARS-CoV-2 without infecting all individuals if the daily number of the contact is less than 5 per individual.

It should be noted here that this work considers the interactions as they are “contacts”, transmitting the virus by depending on the virus-spread chance. An interaction may occur through direct, indirect, or close contact in real environment. However, while modeling these interactions, this study does not differentiate them, just concerns whether an interaction exists. As it is stated in [23], many issues regarding contact patterns remain unexplored in the literature. Above mentioned contact rates are based on epidemiologically relevant social contact patterns. They are useful data to assess how an emerging infection could spread by the social contacts.

The definition of a complex network also involves patterns of “decentralized autonomous interactions” [12]. Since the ABMs are inherently dynamic and they permit the desired richness of behaviors, these decentralized autonomous interactions can easily be modelled through the agent-based approaches. Correspondingly, traditional network analysis has been enhanced by cross-fertilization with ABM. NetLogo is one of the well-known agent-based modeling environments and it is well suited for modeling complex systems. NetLogo Virus on a Network Model [30] demonstrates the spread of a virus through network. This study employs and extends this agent-based network model to assess the spread of SARS-CoV-2. Further details regarding the multi-agent system’s structure can be found in [30].

This study generates the networks by randomly chosen a node and connecting the nearest neighbor node that is not already connected. This process repeats until the average node degree satisfied. It is believed that such a network may represent the interactions during disease. Figure 2 illustrates the generated networks for the average-node-degree are 1 and 4 with the population size is 10,000.

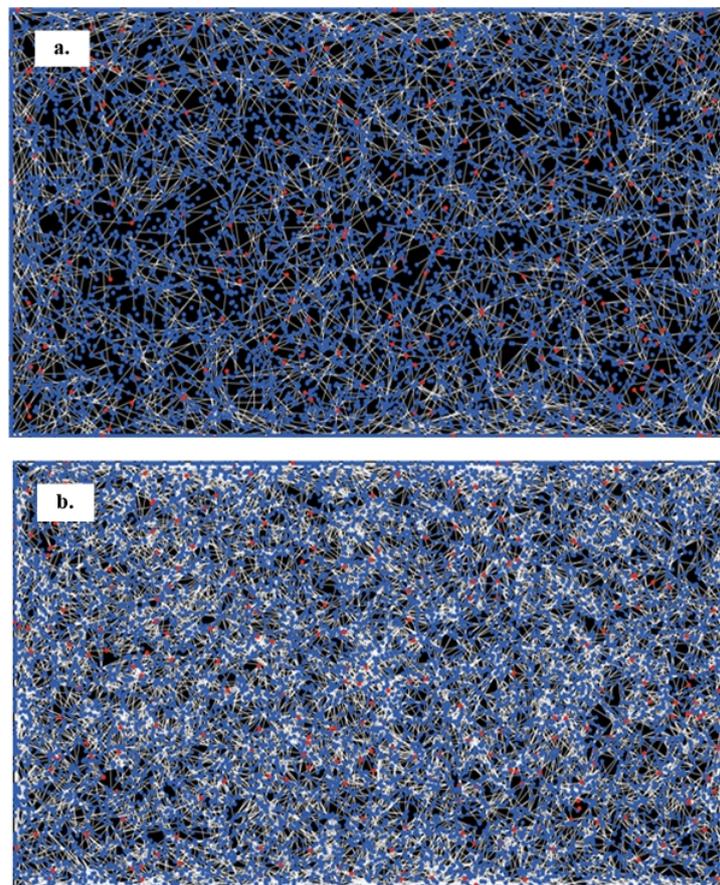


Figure 2. The generated networks with population size 10,000 and average-node-degree are 1 (Figure 2a) and 4 (Figure 2b).

2.2. The spreading mechanism

The behavior of the individuals specifies their subsequent states. In the spread model under consideration, when there exists an interaction between a “susceptible” individual and an “infected” individual, the “susceptible” transforms into the “infected” one or stays “susceptible” by depending on the “virus-spread-chance”. Figure 3 illustrates this interaction. An interaction between “susceptible” individual and recovered” individual does

not change their status. Similarly, an interaction between an “infected” individual and a “recovered” individual does not change their states. On the one hand, the “infected” individuals transform into a “recovered” one or stay still in the state of “infected” depending on the “recovery-chance”. Additionally, the “gain-resistance-chance” specifies the states of “recovered” individuals as “susceptible” or still “recovered”. These new subsequent states of each individual are updated in the network with a period of 14 days (the incubation period of the COVID-19).

Transition from the initial states to the subsequent states depends on the assumptions of the spreading on a network summarized as the followings:

- Transmission from an infectious node to a susceptible node occurs across an edge as a Poisson process with the infection rate, the virus-spread-chance.
- An infectious node recovers as a Poisson process with the recovery-chance.
- By depending on the gain-resistance-chance, transmission from a recovered node to a susceptible node occurs across an edge as a Poisson process.

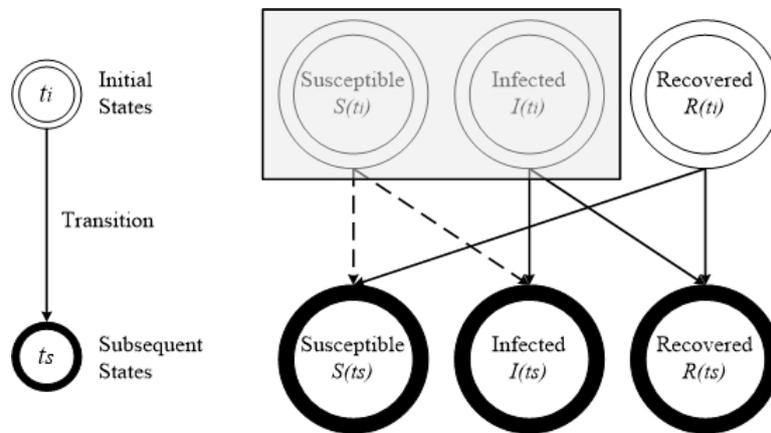


Figure 3. The interaction between a “susceptible” individual and an “infected” individual.

2.3. Design of the experiments

This study aims to analyze the main effects and their interactions of five decisive factors on the duration of the pandemic last and the spectrum of the infected individuals during this disease period. While some of these factors are controllable, some of them are considered because of their uncertain conditions to see the results of what-if scenarios.

The first factor under consideration is “average-node-degree”. It represents the mean of the daily contacts per individual. It greatly depends on the partial lockdown tactics regulated by countries. This factor has four levels as 0.5, 1, 2, and 4 in this study. The second factor is initial-break-size. It indicates the percentage of the total “infected” individuals in the population. The amount of the infected compartment is generally uncertain in practice. Four levels of this factor (as 3%, 5%, 10%, and 20%) are considered to see different scenarios. The third one is “spread-chance”. This is chance of contracting virus per contagious interaction. It is around 3%, but to analyze its effect, 2.8% is also considered in this study. Another factor under consideration is the “recovery-chance”. Its two levels (90% and 95%) are taken into account in this study. The last factor is gain-resistance. It is also uncertain in practice. If there is no gain-resistance, its level can be considered as about 3% because of the mortality rate. To analyze the effect of the gain-resistance factor, its 50% level, and the 80% level are considered as well. By considering these factors and their levels, a full factorial experiment has designed. 240 different experiments have been executed with 5 replications. Factors and level of design experiment are given in Table 1.

Table 1. The considered factors and their levels.

Factors	Number of levels	Level 1	Level 2	Level 3	Level 4
Average-node-degree	4	0.5	1	2	4
Initial-break-size	4	3%	5%	10%	20%
Spread-chance	2	3%	2.8%	NA	NA
Recovery-chance	2	90%	95%	NA	NA
Gain-resistance	3	3%	50%	80%	NA

3. Results

This section summarizes and discusses the main findings of the work. The main effects and the interactions of these factors on “average duration (of the pandemic last)”, “average-percentage of infected”, “maximum-percentage of infected”, and “the expected peak-time” are examined in detail. The main effect plots and the interaction plots are given in Figure 4-7. The main effect plots illustrate the mean response of each level factors. Having a horizontal trend means there is no main effect present. The greater magnitude of the main effect exists when there is a steeper slope. The interaction plots can help to understand the interactions among factors under consideration. Parallel lines indicate that there is no interaction effect.

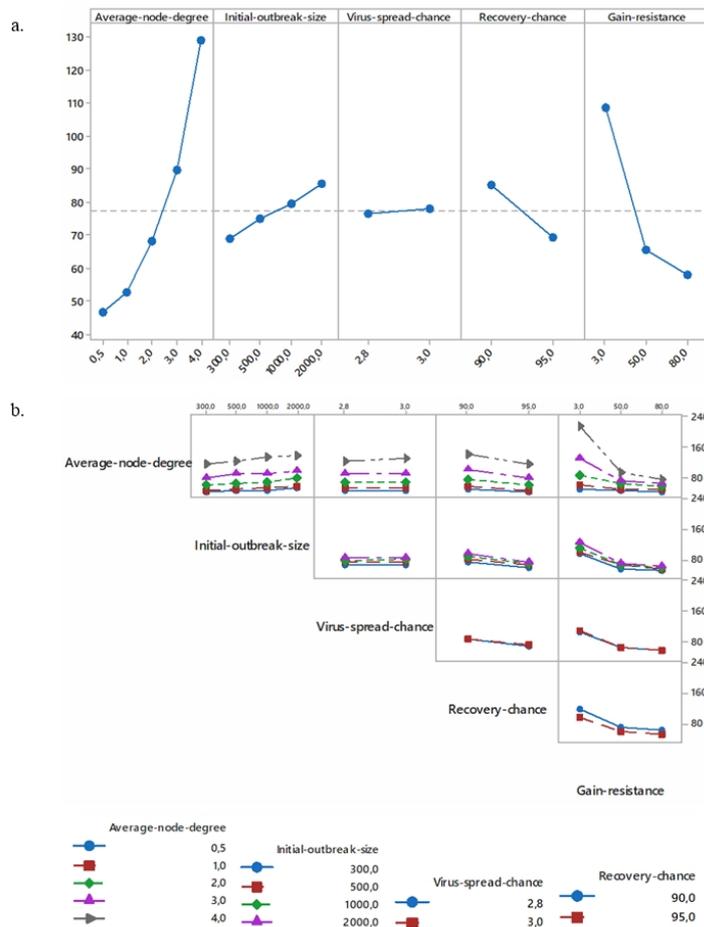


Figure 4. Data means of the main effects (a) and the interaction effects (b) for the “average-duration”.

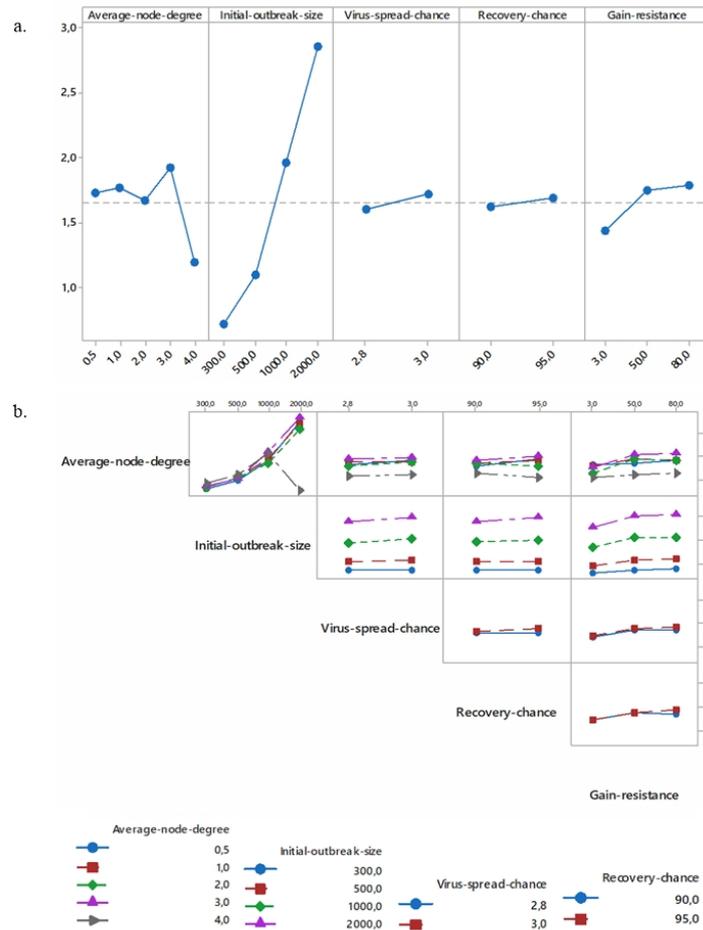


Figure 5. Data means of the main effects (a) and the interaction effects (b) for the “average-percentage of the infected individuals”.

Based on the results, we make the following observations.

- As seen in Figure 4, one of the key findings is that the “average-node-degree” (representing the daily average number of contacts per individual) has the highest main effect on the average-duration. It is pretty obvious that the “average-node-degree” is more influential than the “initial-outbreak-size”.
- If community immunity is 3% (gain-resistance) and the “average-node-degree” is 4, the end time of the pandemic reaches the highest value. Therefore, it can be concluded that these factors are very critical factors that determine the duration of the pandemic.
- It is also obvious (see Figure 5) that “initial-outbreak-size” is the factor with the greatest effect on the “average-percentage of the infected individuals”. “Recovery-chance” is the least variable factor affecting the average number of people infected.
- The average percentage of infected individuals reaches the highest level if the number of individuals interacting is 3 and initial-outbreak-size is 20%.
- The average percentage of infected people is at the lowest level if “initial-outbreak-size” is 20% and the gain-resistance value is 3%.
- The effect of variability in “virus-spread-chance”, “recovery-chance” and “gain-resistance” factors on “maximum-percentage of the infected individuals” and “the expected peak-time” is extremely limited (see Figure 6 and Figure 7).

- One of the interesting results is that if the “average-node-degree” changes from 3 to 4, “the day of the highest infected person” is delayed quite a lot.
- As it can be seen from Figure 4b, the effect of “average-node-degree” is not consistent across all the remaining factors for the “average-percentage of the infected individuals”.
- It should be noted that there is no interaction between “initial-outbreak-size” and the remaining factors at all levels for the “maximum-percentage of the infected individuals”. Additionally, there is no interaction between “virus-spread-chance” and “recovery-chance” and is between “virus-spread-chance” and “gain-resistance” for the “expected peak-time as well.
- The effect of “virus-spread-chance” on “recovery-chance” at all levels is consistent for the “expected peak-time”.

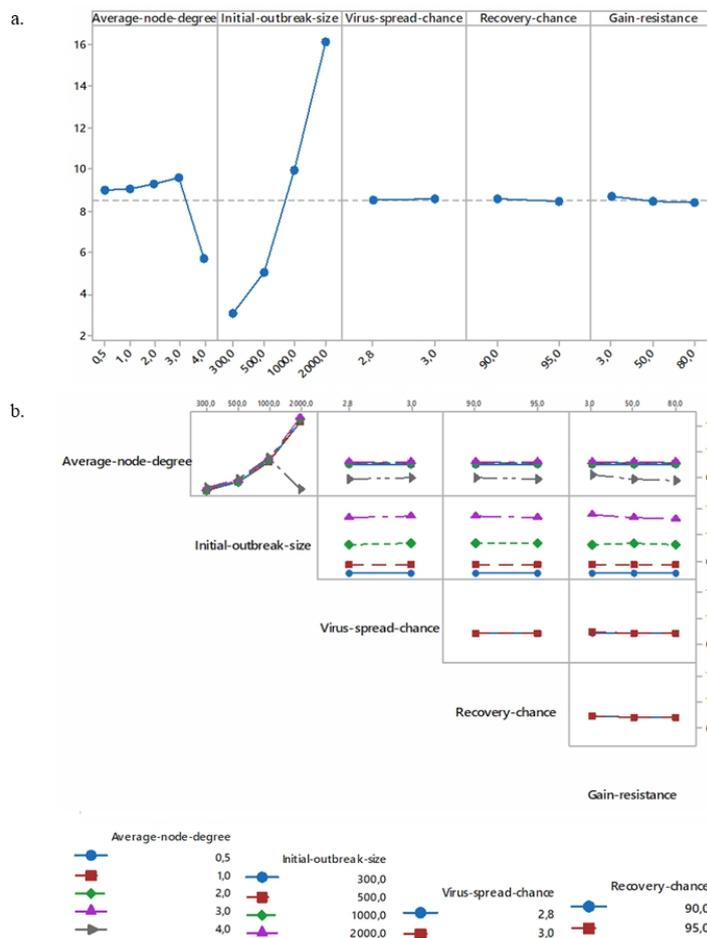


Figure 6. Data means of the main effects (a) and the interaction effects (b) for the “maximum-percentage of the infected individuals”.

4. Conclusion

This study provides a network understanding of the spread of SARS-CoV-2 by using an interaction-oriented multi-agent SIR model (with the NetLogo environment). The main results obtained from this agent-based simulation should be considered to minimize the potential negative effects of this disease in practice. One limitation of this work is that it generates a model with the population size 10,000. This is because of the limitations of

our modeling environment. Although, this size is reasonable to assess the dynamics when considered the previous small-world cases as in [21], it is intrinsically true that higher population is better. Future work can address this issue as to be more realistic.

Interaction-oriented models are required to determine correct tactical responses of partial lockdown. The ranges of the considered factor levels are reasonably large, and therefore what-if scenarios can be executed by using the result of these experiments. Obtained main effect plots may be helpful for decision-makers and policymakers. If other realistic factors affecting the spread of COVID-19 disease are identified, the number of factors to be considered in future studies can be increased. Vaccines and some specific anti-viral treatment are currently available for COVID-19 disease. Future works can consider these advancements as a new compartment as well.

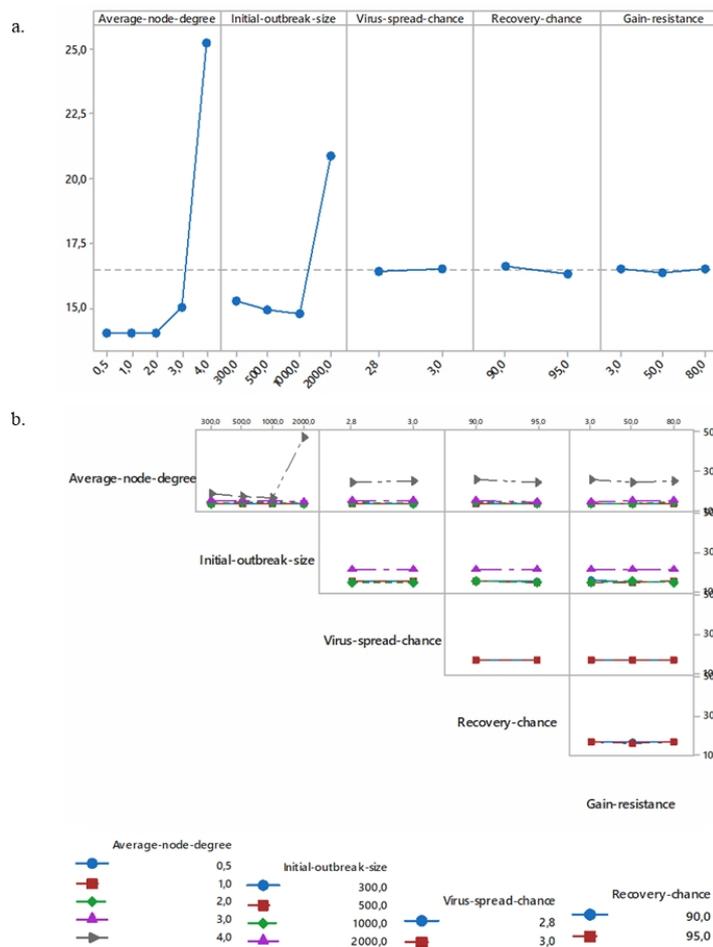


Figure 7. Data means of the main effects (a) and the interaction effects (b) for the “expected peak-time”.

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