

Paper:

Agent-Based Simulation and Modeling of COVID-19 Pandemic: A Bibliometric Analysis

Jing Tang^{*1,*2}, Sukrit Vinayavekhin^{*3,†}, Manapat Weeramongkolkul^{*1}, Chanakan Suksanon^{*1}, Kantapat Pattarapremcharoen^{*1}, Sasinat Thiwathittayanuphap^{*1}, and Natt Leelawat^{*2,*4}

^{*1}International School of Engineering, Faculty of Engineering, Chulalongkorn University

254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

[†]Corresponding author, E-mail: sukrit@tbs.tu.ac.th

^{*2}Disaster and Risk Management Information Systems Research Unit, Chulalongkorn University, Bangkok, Thailand

^{*3}Thammasat Business School, Thammasat University, Bangkok, Thailand

^{*4}Department of Industrial Engineering, Faculty of Engineering, Chulalongkorn University, Bangkok, Thailand

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The coronavirus disease has caused an ongoing pandemic worldwide since 2019. To slow the rapid spread of the virus, many countries have adopted lockdown measures. To scientifically determine the most appropriate measures and policies, agent-based simulation and modeling techniques have been employed. It can be challenging for researchers to select the appropriate tools and techniques as well as the input and output parameters. This study conducted a bibliometric analysis, especially a co-word network analysis, to classify relevant research articles into five clusters: conceptual, economic-based, organizational, policy-based, and statistical modeling. It then explained each approach and point of concern. Through this, researchers and modelers can identify the optimal approaches for their agent-based models.

Keywords: agent-based modeling, agent-based simulation, COVID-19, bibliometric analysis, literature review

1. Introduction

COVID-19 is an ongoing global pandemic that began in late 2019. To slow the rapid spread of this pandemic, many countries have adopted lockdown measures. To scientifically determine the most appropriate measures and policies, many studies using modeling techniques, especially agent-based models (ABMs), have been published. However, it can be challenging for researchers to select the appropriate tools and techniques as well as the input and output parameters. Thus, this study conducted a bibliometric analysis of 194 articles using relevant keywords to classify them into five clusters: conceptual, economic-based, organizational, policy-based, and statistical modeling. This primary framework was used to classify over 50 articles, whose methodologies used to model the transmission dynamics, agents' mobility, population spread, and many more were studied in detail. Thus, the differ-

ent aspects of the modeling approach in each stage can be highlighted to other researchers interested in creating their own ABMs. This research can serve as a valuable guide for the creation of ABMs related to COVID-19 or another pandemic in the future. Researchers interested in creating their own ABMs can start by determining which cluster is the most applicable and studying the methodologies previously used, as summarized in this article. The tuning and calibration process for geographic and demographic data, however, depends on researchers' discretion. Nevertheless, even if the model to be developed is supposed to be independent of the study area, this study would still prove valuable for determining the most suitable approaches for modeling each dynamic of an ABM.

2. Literature Review

COVID-19 is an ongoing outbreak that began in late 2019. On March 11, 2020, the World Health Organization declared the outbreak a pandemic [1]. Numerous academic researchers have studied the spread of the pandemic to identify quantitative patterns and estimate their impact. Many countries have attempted to contain the outbreak using non-pharmaceutical interventions, with varying success. With a diverse range of lockdowns possible, each adversely impacting the economy and level of social activities, it can become challenging to scientifically determine the most appropriate non-pharmaceutical interventions to contain the outbreak. ABMs are one of the most common tools used to aid the decision-making process in this regard.

Simulation modeling is an important method for predicting the potential impact of non-pharmaceutical interventions. Some of the most popular modeling techniques include discrete events, system dynamics, and ABMs. ABMs identify objects or agents and define their behavior within a domain. As the extensiveness of lockdowns varies with the infection rate and fatalities as well as the economic and degree of social activities, ABMs can un-

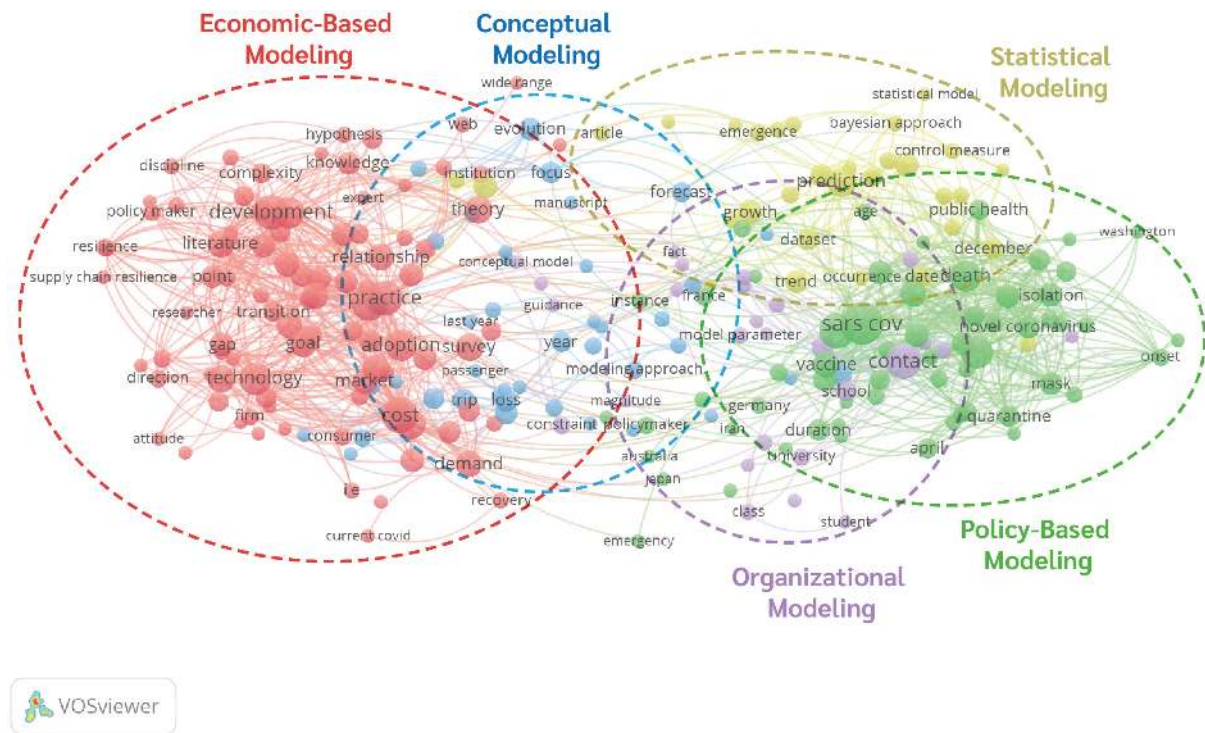


Fig. 1. Results of the bibliometric analysis.

cover numerous insights into the effectiveness and impact of each intervention. To date, 194 articles have been published that use ABMs to study COVID-19. However, it can be challenging for researchers to select the appropriate tools and techniques as well as the input and output parameters. To the best of our knowledge, research analyzing all the articles and providing an overview of the application of ABMs related to COVID-19 or any other pandemic remains lacking.

3. Methodology

In this study, we adopted a bibliometric analysis – a quantitative method – to provide a comprehensive overview of the literature [2]. There are three types of bibliometric analyses: statistical, citation, and content analyses [3]. As our aim was to analyze and categorize articles based on their content, we used a co-word network analysis following a previous study [4]. First, we initially searched for “*agent-based model**” and “*COVID-19*” appearing in the titles, abstracts, and keywords in ScienceDirect on August 4, 2021. After checking for relevant and non-duplicate articles, we downloaded the bibliographic data of 194 articles, including their authors, publication years, journals, abstracts, and keywords. We then used the VoS Viewer program to conduct the co-word network analysis [5]. This helped visualize the network of key terms commonly populated in articles, consisting of the terms shown in nodes and their co-occurrences shown in links [6]. To increase exposure and remove irrelevant

terms, terms with at least three occurrences and in the 60% highest relevance ratings were extracted and clustered into research streams [7]. To optimize quality, the investigators independently read the analysis results and synthesized the findings by consensus and discussion [8].

4. Results

The bibliometric clustering shows five clusters: conceptual, economic-based, organizational, policy-based, and statistical modeling, as presented in **Fig. 1**.

For the conceptual modeling cluster, some important labels include “*modeling approach*,” which has a high linkage with “*model parameter*.” This signifies the importance of appropriately parameterizing the model. The presence of “*conceptual model*” also confirms the trend of adopting ABMs using conceptual modeling. Lastly, “*policy maker*” again highlights how valuable ABMs can be to policymakers as assets.

The economic-based modeling cluster shows a high occurrence of research works related to “*development*” and “*policy maker*.” It also contains other labels such as “*knowledge*,” “*theory*,” and “*technology*,” which shows that these are pivotal to the decision-making processes of policymakers. It also consists of “*cost*,” which shows that policymakers consider the economic impact of these policies.

The organizational modeling cluster indicates several trends of existing ABMs. The “*university*,” “*class*,” “*school*,” and “*student*” labels have high linkages with

“contact,” which implies that contact among students may have been the approach to model the virus spread in educational institutions.

Two interpretations can arise from the policy-based modeling cluster. First, considering that each label had to be present in more than three articles, the presence of the country and city labels strongly suggests that many ABMs are already calibrated to the demographic- and geographic-specific data of these areas. Next, the “isolation,” “quarantine,” “duration,” and “vaccine” labels imply that these are common strategies to contain the spread of “SARS CoV.” This can be useful when considering scenario analysis under an ABM.

The statistical modeling cluster suggests that “statistical model” and “Bayesian approach” are commonly used to make a “prediction.” This cluster includes mathematical and statistical approaches to modeling.

4.1. Conceptual Modeling

Conceptual modeling is a theoretical model used to predict the impacts of changing various input parameters. It behaves similar to a “what if” analysis in which researchers may keep changing the input parameters to find the most suitable decisions. In other words, the results can be used to make decisions. In this case, to analyze the COVID-19 model, conceptual modeling can be used to evaluate many aspects of the pandemic.

Researchers have mainly conducted conceptual modeling to investigate the impact of strategies that may reduce the severity of the COVID-19 pandemic. Li et al. [9] evaluated the effectiveness of various strategies to reduce the spread of diseases, such as the effectiveness of masks, social distancing, lockdown, and self-isolation, by setting grid blocks and generating agents that have different states such as having a mask, quarantine status, and hospitalization status. The behavior of an agent differs according to its state. Agents are set to move around, and transmission occurs during this activity. They found that a lockdown policy may not be needed because social distancing interventions and surgical mask usage are more effective. Durán-Polanco and Siller [10] evaluated the efficiency of a crowd management system. They investigated the point-of-interest recommendation system in shopping centers, which suggests the nearest points having the lowest crowd, and quantified the number of contacts of COVID-19 infections by generating agents with different parameters and changing the number of populations that can access the recommendation system. Castro et al. [11] proposed a multi-agent simulation model to analyze the spread of diseases in open regions using a simulator in MATLAB named “M2 CovidSim.” This model can represent heterogeneity, environmental diversity, and social interaction and it allows agents to move around regions with different risks of infection. The findings from the model showed that a social distancing policy explicitly decreases pandemic severity. Zhang et al. [12] predicted the impact of mask-wearing and shelter-in-place strategies to understand the implications of COVID-19 mitigation strategies. The model population was based on

US demographic data. The daily number of interactions between the same and different age groups were based on a negative binomial distribution and empirically determined contact network. The results showed that mask-wearing and shelter-in-place strategies can significantly reduce the spread of disease when both strategies are employed. Gharakhanlou and Hooshangi [13] studied the impact of several interventions such as school and educational closures, social distancing, and office closures in Urmia City, Iran. They simulated spatial temporal data using NetLogo. In this model, agent movement was classified into two modes: moving by personal vehicles and public transportation. After that, a day in the model was divided into four intervals: moving from the agent’s home to the workplace, working or studying, leaving the workplace and returning home, and staying at home. Agents using public transportation have a chance of being infected during the first and third intervals. By contrast, agents that have personal vehicles are unaffected by this condition. In addition, the model was validated by comparing the results with actual data using the chi-square test.

Conceptual modeling can also be used to assess the impact of factors other than strategies. Du et al. [14] investigated the effects of social media and people’s adoption of disease prevention behaviors along with changes in infection risk in a population. They generated discrete lattice cells and randomly assigned agents to a particular cell. In addition, the model was validated by comparing the original susceptible/exposed/infectious/recovered (SEIR) model with their ABM. They found that social media influences the public’s awareness of infection risk if people can access accurate information at the beginning of pandemics. However, their model cannot represent the effects of disease transmission from mixed data sources. Lu et al. [15] investigated the relationship between outbreak and food trade activities in the Xinfadi wholesale food market in Beijing, China using QGIS and NetLogo. They simulated a city divided into a grid of cells and assigned an estimated number of agents. When agents trade over grid cells, they have a chance of being infected. The findings indicated that the movements of people explicitly caused the Xinfadi market outbreak. Bouchnita and Jebrane [16] attempted to quantify the effects of each level of lockdown measures by developing a multi-scale model with random movement and calibrated it to data from Calabria, Italy. In this model, there were direct and indirect ways for a susceptible agent to be infected. The direct way is coming into contact with an infected individual and the indirect way is infected individuals contaminating the areas through which they move.

4.2. Economic-Based Modeling

A range of research has focused on examining the impact of COVID-19 interventions on economic aspects. Tatsukawa et al. [17] investigated the effect of three policies (i.e., free tickets, flat discounts, and degree-dependent subsidies) on the average social payoff, which

considers the cost of vaccination and infection by implementing the susceptible/infected/recovered/vaccinated (SIR/V) dynamic model. They compared the three subsidy policies based on three criteria (i.e., vaccination coverage, final epidemic size, and average social payoff) to determine the socially optimal one for suppressing the spread of the disease. The multi-agent simulation approach with a finite population size and Albert scale-free networks are used for population modeling. Silva et al. [18] evaluated the epidemiological effects and implemented the COVID-ABS, a new SEIR ABM of the COVID-19 epidemic that aims to simulate the pandemic dynamics by matching people, businesses, and governments. The research focused on seven measures of social distancing interventions: do nothing, lockdown, conditional lockdown, vertical isolation, partial isolation, use of face masks, and use of face masks together with a 50% adherence to social isolation. Agents were initialized based on a percentage distribution of each socioeconomic class, which has different occupations and tasks to which they will have to attend in a day; thus, agents' movements can be traced. Moreover, the model considered the economic relationships between agents (e.g., salary, income, and expenses) and allowed for an economic analysis. Wang et al. [19] focused on human activity patterns and aimed to develop and maintain effective strategies for diminishing the serious and unpleasant socioeconomic side effects. They proposed an extended ABM as a new transmission dynamics simulation. The model integrated census data, postal addresses, and longitudinal employer/household dynamic data for agent generation and integrated it with human activity patterns gathered from the American Time Use Survey data to generate and characterize travel trajectories and activity patterns. They also integrated exposure/agent geographical distributions to estimate total human exposure in large populations. However, the classification of agents was limited to workers, students, or both. Zhang et al. [20] aimed for measures with the least disturbance to socioeconomic activities by implementing the probability infection model. The results of this model, which considers that an agent can exist in multiple disease states concurrently with a varying probability, were compared with those obtained by stochastic SEIR models and Monte Carlo models. A university's class enrollment data were used to model the population of agents that do not move. General data on influenza and measles outbreaks were also used as input parameters. D'Orazio et al. [21] implemented NetLogo and R scripts to create the SIR model to evaluate the effectiveness of risk mitigation measures. They determined the best solutions from a socioeconomic perspective for activities restarting. Sustainable and resilient strategies for tourist cities were the focus of their study.

4.3. Organizational Modeling

This cluster focuses on determining the risk of the spread of viruses in all types of organizations. In the early stage in which working from home and online meetings

were not yet familiar to users, high contact rate places were studied by researchers to understand the risk of infection. The transmission rate in groups of people was assigned by the probability of meeting value [22], along with identifying the crucial elements that may strengthen or weaken the transmission dynamics. In facilities, simulating spatiotemporal transmission processes between the public was considered [23]. The method started by randomly assigning an individual profile to each agent, which defined its main social characteristics and health conditions used during its interactions. All susceptible agents may be infected if an infected agent is within the circle. The model included two movement types: local and long distance. Local displacements represent the most frequent movements when individuals interact in their workspaces. On the contrary, long-distance displacements refer to movements by individuals far from their previous position. In public transportation, Ding et al. [24] proposed the early-stage transportation lockdown and quarantine problem, which can help determine which parts of the transportation infrastructure of a country should be restricted in the early stages. They used effective distance SEIR, which is a dynamic spreading process dominated by a set of the shortest spreading paths, to consider a generic epidemic network composed of a set of populated vertices and a set of transportation edges connecting the vertices.

During the pandemic, most countries were under lockdown; supermarkets were the only place allowed by the government for people to buy their personal care products and food. Hernandez-Mejia and Hernandez-Vargas [25] explored the potential spread of COVID-19 in a small supermarket by diversifying social distancing rules and the number of simultaneous customers in an ABM. They considered potential contagion from an infectious agent to have a 50% probability of spreading, using a binomial distribution governed by the Euclidean distance between the infectious and uninfected agents. This finding resulted in potentially newly infected customers going into supermarkets. After a period, many organizations continued their businesses while managing the risk to their staff. This research finding plays a vital role for decision-makers. Araya [26] explored how COVID-19 can spread among construction workers to help construction project managers create adequate conditions for workers to perform their jobs, while minimizing the chance of contracting COVID-19. The study followed an iterative process from the model formulation to a model simulation in which the computerized model validation was performed by running sensitivity analyses on the model parameters.

In the air travel industry, one of the most damaged sectors from the emergence of the virus, Milne et al. [27] presented six new boarding methods and compared them with the two best boarding methods used to date, with the risks of each seat position calculated using a formula. Then, they compared the risk in all seats (e.g., window seats and aisle seats) using actual airline data on the percentage of passengers and their amount of luggage using NetLogo.

Many researchers have implemented models for educational institutions. At the university level, Gressman and Peck [28] developed a full-scale stochastic ABM to determine whether in-person instruction could safely continue. They used an ABM and viral dynamics to approach the problem to incorporate precise information about the contact heterogeneity between populations (i.e., instructors and students) and even among students at different stages of their university careers. The model simulated an interaction on a daily basis with the following sequences: illness testing, quarantining, status update, contact tracing, infection transmission, and outside transmission. They used Poisson contact as a method generated by a Poisson point process whose rate is determined by a detailed scoring system that considers whether two individuals share any common activities on a given day and the nature of their roles in those activities. Similarly, a simulation of classrooms in four European countries [29] used a social network-based cohort system to reduce the spread of SARS-CoV-2 in secondary schools, finding satisfactory results. Zafarnejad and Griffin [30] also provided guidance on which school policies would be most effective at reducing the risk given local costs and constraints. The simulation model in the COVID-19 agent-based simulator (Covasim) [31] showed the results of six scenarios that represented the combination of two school reopening strategies (full-time and part-time, with 50% of students attending school on alternate weeks) and three testing scenarios in the United Kingdom.

4.4. Policy-Based Modeling

Many models for simulating the dynamics of the COVID-19 pandemic in various scenarios have been proposed. These articles aim to provide policymakers with guidelines or useful insights and data to verify their decisions on enforcing governance measures. Shamil et al. [32] proposed an SIR ABM implemented using Python3. Various scenarios focusing on the inhabitants of a city were analyzed, including no intervention, contact tracing, and lockdown. Each agent had their tasks, behaviors, and actions grouped in the model into stay at home, commute, work or attend school, attend events, or stay in hospital. The states of contagious and asymptomatic agents were also considered for infected individuals. Each agent was associated with a family and assigned to one of the following four generic professions: doctors and nurses, students, service holders, and the unemployed. For each profession, the agents performed specific behaviors or tasks. Two categories of data were used: location-specific data and physiological data. Wallentin et al. [33] explored long-term disease management for forecasting the qualitative behavior of the outbreak after the first wave. Four scenarios were explored: continued severe lockdown until the virus is regionally eradicated, gradually relax the lockdown, slowly relax the lockdown using technologically supported contact tracing (low, medium, or high level of contact tracing), and gradually relax the lockdown using an adaptive response strategy. The author implemented the virus spread model from the GAMA

modeling library along with the model of the mobility of citizens from the bicycle model for agent movement. Moreover, the overview, design concepts, and details protocol was used to report ABMs. Pham et al. [34] calibrated an ABM for transmission in Vietnam and evaluated the risk of upcoming outbreaks upon the reopening of international borders in the country. Three scenarios were considered: constant high compliance, increased complacency, and self-regulating behavior. The models used epidemiological, behavioral, demographic, and policy data on testing, COVID-19 cases, and quarantine breaches in Da Nang, Vietnam. The testing and patient data were obtained from the National Institute of Hygiene and Epidemiology and the General Department of Preventive Medicine, respectively. Covasim's inbuilt methods were used to construct individual interactions over four distinct contact networks: households, schools, workplaces, and communities based on age; however, they did not explicitly model large gatherings that could become super-spreading events. Seven interventions were analyzed by Zhang et al. [35]: delay from symptom onset to hospital admission, temperature detection in public places, screening for incoming individuals, ratio of mask wearing, mandatory quarantine for arrivals from Hubei Province, China, school closures and work stoppages, and probability of symptomatic patients staying at home. Individuals were divided into four groups: students, workers, people without mobility, and people with mobility who did not need to go to work or school. They used the susceptible/exposed/symptomatic infectious/asymptomatic infectious/recovered (SEIIR) model and SEIR model with a differentiated infectious stage based on demographic data from the Shenzhen Municipality, China. The model assumed that infection can only spread through close contact routes. In an urban region, Tatapudi et al. [36] evaluated the effect of full and partial stay-at-home orders, face mask usage, and contact tracing using a modified version of the force of infection equation given by Ferguson et al. [37] and including demographic, epidemiological, and social intervention parameters. Agents were individually generated according to the census data of Miami-Dade County, Florida, USA, which provides population attributes. Thereafter, the model generated the households based on their composition, characterized by the number of adults and children; it also generated schools, workplaces, and other community locations. A daily schedule was assigned to every individual, chosen from a set of alternative schedules based on their attributes. Moreover, agents' schedules varied on weekdays and weekends.

The modified multi-agent model proposed by Vyklyuk et al. [38] implemented classic SIR models, which were integrated into the calibrated social force models of Bobashev et al. [39] using molecular dynamics along with the program code presented by Allen [40] and Volpert et al. [41]. The results depended on a random number generator, which led to different simulation results under the same initial conditions. The effects of lockdown and exit strategies were examined by Dickens et al. [42] in Singapore using the geographical, demographic, and epi-

demological model for respiratory diseases, an epidemic simulation ABM consisting of a synthetic and calibrated population, integrated with the SEIR model. The model's population was constructed using census data based on a sample of 200,000 households. A sample of 3.77 million Singaporeans by age, ethnicity, and gender was then generated using a heuristic search algorithm. All these agents' households were geolocated inside discrete areas named subzones according to the spatial characteristics summarized in the census, and individuals were allocated to workplaces and schools based on commuting time data from Singapore's household interview travel study and EZ-Link data. Vilches et al. [43] evaluated the effect of mitigation measures for the control of COVID-19 outbreaks in long-term care facilities in Ontario, Canada, including frequently testing staff and vaccinating staff and residents. The SEIR model was used with the following agent states: susceptible, latently infected (not yet infectious), asymptomatic (and infectious), pre-symptomatic (and infectious), symptomatic with either mild or severe or critical illness, recovered, and dead. The interactions within and between staff and resident populations were parameterized using the distributions derived from close-range movement and contact network data collected through wearable sociometric tags. The authors parameterized the model with disease-specific estimates and data from initial outbreaks in similar facilities in Ontario and used the movement and contact network data collected from the largest veterans' care facility in Canada [44, 45]. The model was coded in Julia. Chiba [46] modified Covasim to assess the efficiency of mobility control, shortening of restaurants' opening hours, and working from home in Japan. Altogether, 25,000 people were randomly selected as agents from census data. Thereafter, each agent was assigned family members and other attributes such as age, which was used to determine the probability of virus transmission and transition probability and duration in each stage of symptoms. The distortion created in the previous stage and attribute distribution were then organized. Agents' attributes were used to determine the pattern of daily contact, movement behavior, and probability of catching the virus.

4.5. Statistical Modeling

Statistical approaches are also common among ABMs. Bisina and Moro [47] proposed a spatial-SIR of epidemic diffusion to study how the dynamics of an epidemic scale in relevant geographical characteristics: the number and distribution of outbreaks, population size, density, and agents' movements. The method used in this study was the ABM in which spatial-SIR individuals were placed in a two-dimensional space and traveled in this space at a given speed. When infected, they can only infect their neighbors with a probability interpreted as the strength of the virus. The model showed the number of infected patients over time by adjusting various parameters accordingly. Qian et al. [48] applied a probabilistic infection model to study contagion processes in contact networks,

which provided a deeper understanding of the dynamics of the outbreak at individual levels. This allowed users to estimate the value of the basic reproduction number at individual vertices and provided the probability of each infected state of an agent. Additionally, using this probabilistic approach, the overall trajectories of outbreaks can be computed in one simulation as opposed to the numerous repeated simulations required for the Monte Carlo process. The model used general data on influenza and measles outbreak parameters for the simulation's inputs, creating a contact network built from a university's class enrollment data, which showed a number of infectious individuals' graphs over time compared with the results generated from both the Monte Carlo model and the probabilistic infection model. Winkelmann et al. [49] presented a mathematical model of spatio-temporal population dynamics and application to epidemic spreading with two metapopulation approaches (i.e., stochastic and piecewise deterministic). They retained the characteristic properties of the detailed ABM, while significantly reducing the computational effort for the simulation and analysis. They considered the continuous space for agent movements and the discrete status space, whereas the movement of a single agent is defined as a diffusion process and is given by the stochastic differential equation. The model chose parameters based on recent publications. The results showed that for a large number of agents, stochastic metapopulation models, particularly, piecewise-deterministic metapopulation models, represent good approximations of the ABM, but use much less computational power by comparing the different variables and scenarios of the model.

Before vaccines were widely used, Markovi et al. [50] studied the sociodemographic and health factors that drive epidemic progression and guide vaccination strategies for containing COVID-19. They explored how heterogeneity in health status along with spatial distribution patterns within the population influence the progression of the epidemic using a social network model and random geometric graphs in hyperbolic spaces. Their ABM used a group of people with different health risks along with hospitalization rate and their immune periods to represent the impact of COVID-19 in terms of infection, severity, and mortality; the agent can become infected when a susceptible node interacts with an infected node in the underlying network structure given a constant probability. Zachresona et al. [51] studied how mass vaccination would change COVID-19 lockdown requirements in Australia by adapting a previously developed and validated high-resolution ABM for the mitigation and control of the COVID-19 pandemic in the country. They used a discrete-time simulation scenario that progressed by updating agents' states over time from an initial distribution of infection seeded by imported cases in Australia with the attributes of an anonymous individual (e.g., age, residence, gender, workplace, susceptibility, and immunity to diseases) and contact rates within different social contexts, including commuting patterns between places of residence and work or study to represent the coverage and

Table 1. Summary of the models used in COVID-19 ABMs.

Model	Key characteristics/main points	Applied examples
SEIR (susceptible/exposed/infectious/recovered)	Polished and more biologically realistic modeling than SIR, as incubation and infectiousness are considered.	[20, 22, 42, 43]
SEIIR (susceptible/exposed/symptomatic infectious/asymptomatic infectious/recovered)	This follows the concept of the SEIR with two types of infectious agent: symptomatic and asymptomatic infectious agents.	[35]
SEIRD (susceptible/exposed/infected/recovered/deceased)	Similar to SIRD, but considers incubation.	[13, 49]
SEIRS (extended stochastic SEIR)	A modified SEIR model with an extra transmission rate of converting from the susceptible to the infectious phase. Accordingly, it is more stable and realistic.	[50]
SIR (susceptible/infectious/recovered)	A classic simple and easy-to-use model, as it can be run in a relatively short time.	[15, 21, 28, 32, 38]
SIRD (susceptible/infected/recovered/dead)	Similar to SIR, but instead of recovery, some infected people are considered to have died because of the impact of the disease.	[9]
SIR/V (susceptible/infected/recovered/vaccinated)	Using the concept of SIR with the vaccination factor considered, too.	[17]

Pie Chart Distribution of Modeling

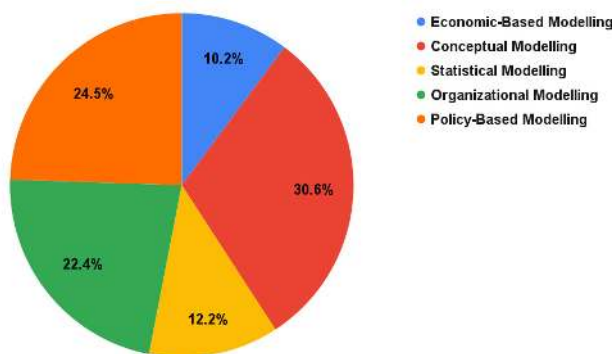


Fig. 2. Pie chart of the modeling types.

efficacy of herd immunity requirements, effects of hybrid mass vaccination on epidemic growth, and effects of mass vaccination with lockdown requirements.

5. Conclusion

The analysis of the methodologies used can be adapted to create new ABMs for COVID-19 or any pandemic spread analysis in the future. **Table 1** summarizes the key models used in COVID-19 simulation research. When considering the distribution of each cluster in **Fig. 2**, we see significantly fewer economic-based and statistical models. For researchers interested in the other three clusters, it may be useful to build their models from existing work rather than starting from scratch. Researchers could also consider new methodologies and modeling approaches when developing economic and statistical models in the future.

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Name:
Jing Tang

Affiliation:

Lecturer, International School of Engineering,
Faculty of Engineering, Chulalongkorn University
Lecturer, Risk and Disaster Management Program,
Graduate School, Chulalongkorn University

Address:

254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:

2013-2017 Enterprise System Transformation Consultant, based in Japan
2017-2019 Lecturer, Sirindhorn International Institute of Technology,
Thammasat University
2019- Lecturer, Chulalongkorn University

Selected Publications:

- J. Tang, L. G. Pee, and J. Iijima, "Investigating the effect of business process orientation on organizational innovation performance," *Information & Management*, Vol.50, No.8, pp. 650-660, 2013.
- M. Fachrizal and J. Tang, "Forecasting annual solar PV capacity installation in Thailand residential sector: A user segmentation approach," *Eng. J.*, Vol.23, No.6, pp. 99-115, 2019.
- T. Katato, N. Leelawat, and J. Tang, "Antecedents of the outsourcing relationship: A systematic review," *Eng. J.*, Vol.24, No.4, pp. 157-169, 2020.

Academic Societies & Scientific Organizations:

- Asia Oceania Geosciences Society (AOGS)
- Association for Computing Machinery (ACM)
- Institute of Electrical and Electronics Engineers (IEEE)



Name:
Manapat Weeramongkolkul

Affiliation:

Undergraduate Student, International School of
Engineering, Faculty of Engineering, Chulalongkorn University

Address:

254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:

2019- Undergraduate Student, Chulalongkorn University



Name:
Chanakan Suksanon

Affiliation:

Undergraduate Student, International School of
Engineering, Faculty of Engineering, Chulalongkorn University

Address:

254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:

2018- Undergraduate Student, Chulalongkorn University
2021 Intern, Business Consulting – Technology and Innovation, KPMG



Name:
Sukrit Vinayavekhin

Affiliation:

Thammasat Business School, Thammasat University

Address:

2 Prachan Road, Pranakorn, Bangkok 10200, Thailand

Brief Career:

2017- Lecturer, Thammasat Business School, Thammasat University

Selected Publications:

- S. Vinayavekhin, R. Phaal, T. Thanamaitreejit, and K. Asatani, "Emerging trends in roadmapping research: A bibliometric literature review," *Technol. Anal. Strateg. Manag.*, doi: 10.1080/09537325.2021.1979210, 2021.
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Name:
Kantapat Pattarapremcharoen

Affiliation:

Undergraduate Student, International School of
Engineering, Faculty of Engineering, Chulalongkorn University

Address:

254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:

2018- Undergraduate Student, Chulalongkorn University
2021 Business Consultant Intern, KPMG
2021 Business Analyst Intern, Pomelo Fashion
2021 Management Consultant Intern, Bluebik Group



Name:
Sasinat Thiwathittayanuphap

Affiliation:
Undergraduate Student, International School of Engineering, Faculty of Engineering, Chulalongkorn University

Address:
254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:
2018- Undergraduate Student, Chulalongkorn University
2021 Software Engineer Intern, ABB Automation (Thailand)



Name:
Natt Leelawat

Affiliation:
Assistant Professor, Department of Industrial Engineering, Faculty of Engineering, Chulalongkorn University
Head of Disaster and Risk Management Information Systems Research Unit, Chulalongkorn University
Assistant Dean, Faculty of Engineering, Chulalongkorn University
Director of Risk and Disaster Management Program, Graduate School, Chulalongkorn University

Address:
254 Phayathai Road, Pathumwan, Bangkok 10330, Thailand

Brief Career:
2007-2009 System Analyst, Bank of Thailand
2016-2017 Assistant Professor, Tohoku University
2017-2018 Lecturer, Chulalongkorn University
2018- Assistant Professor, Chulalongkorn University

Selected Publications:

- K. Saengtabtim, N. Leelawat, J. Tang, W. Treeranurat, N. Wisittiwong, A. Suppasri, K. Pakoksung, F. Imamura, N. Takahashi, and I. Charvet, "Predictive analysis of the building damage from the 2011 Great East Japan tsunami using decision tree classification related algorithms," IEEE Access, Vol.9, pp. 31065-31077, 2021.
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Academic Societies & Scientific Organizations:

- Asia Oceania Geosciences Society (AOGS), Regional Advisory Committee
 - Association for Computing Machinery (ACM)
 - Association for Information Systems (AIS)
 - Institute of Electrical and Electronics Engineers (IEEE), Senior Member
 - The Business Continuity Institute (BCI), MBCI
-