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RELIABILITY OF MULTI-AGENT BASED INFECTION SIMULATOR WITH PARAMETERS OF ISOLATION WARDS

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Abstract. *In the spread of virus disease, capacity limitation of isolation wards for admitting infectors of virus to the hospital is important to decrease the number of persons who die and/or total infectors. Therefore, we developed multi agent-based virus spread simulator that has parameter of capacity limitation of isolation wards and reported the effectiveness of it in the previous research. However, the reliability evaluation of this simulator was insufficient. One of the traditional virus spread simulations is the ordinary differential equation-based approach. It is desirable that the output value of the number of total infectors of our multi agent-based simulator is similar to the traditional ordinary differential equation-based simulator. Therefore, in this paper, we discuss this point. As a result, we confirmed the similarity between our simulator and traditional simulator. In conclusion, our simulator has the reliability in this view point.*
Keywords: Infection simulator, Multi-agent simulation, Isolation wards

1. **Introduction.** Virus diseases spread often occurred in the world (e.g., Severe Acute Respiratory Syndrome (SARS) in 2002 [1], and COVID-19 in 2019 [2]). To understand the spread features of viruses, it is important to develop the simulators of spreading virus disease. For example, Hou et al. [3] reported COVID-19 spread simulation in Wuhan in China. Chatterjee et al. [4] reported COVID-19 spread simulation in India and the effectiveness of city lockdown on decreasing infectors. As the other simulations for COVID-19, there are some case studies (e.g., "Hubei Province, China [5, 6]", "Netherlands [7]" and "Korea, Italy, France [8]"). Moreover, Niwa et al. [9] reported the effectiveness of airplane passengers' quarantine in the airports. As the other studies, there are also researches for developing new simulation methods (e.g., [10, 11]) for COVID-19 spread simulation. By their researches, we might understand the features of virus spread, quantitatively.

The infectors of communicable diseases, such as influenza, SARS, and COVID-19, cannot be hospitalized in the ordinary wards because there is possibility that they infect other persons. Therefore, the capacity limitation of isolation wards for admitting infectors of communicable diseases to the hospital is important. If they are in isolation wards, they

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will not infect other persons in the societies and their fatality rate will decrease by being given the adaptive treatment.

Therefore, virus spread simulator that can represent the capacity limitation of isolation wards is important. However, the researches including this point of view are insufficient. Because of the reason, as the previous research, we developed the multi agent-based virus spread simulator (MAS) that has the parameter to represent the capacity limitation of isolation wards [12]. Moreover, we reported the presence of effectiveness on decreasing the total infectors and dead persons of isolation wards.

However, the reliability evaluation of this simulator [12] was insufficient. To evaluate reliability of this simulator, it is required to compare the estimation results with other simulation methods. One of the traditional virus spread simulations is the ordinary differential equation-based approach (ODE). As ODE-based simulators, there is an SEIR model. The ODE-based SEIR model was used to simulate spreading infection (e.g., [13, 14, 15]). The SEIR model for vaccination control is also discussed in [16]. Moreover, there are many researches of COVID-19 spreading simulations by the ODE-based SEIR model (e.g., [10, 11]). Therefore, we consider the ODE-based SEIR model has a high reliability. In this view point, it is desirable that the output value of the number of total infectors of our MAS-based simulator is similar to the traditional ODE-based simulator.

In this paper, we briefly report our MAS-based simulator that can represent capacity limitation of isolation wards and ODE-based simulator. Moreover, we describe the reliability evaluation result of MAS-based simulator by comparison with the number of infectors outputted from ODE-based simulator.

The remainder of this paper is organized as follows. In Sections 2 and 3, we provide an overview of the proposed MAS model and traditional ODE model, respectively. In Section 4, we explain how to verify the reliability of MAS model. In Section 5, we show the results of MAS-based model and traditional ODE-based model, and then discuss the reliability of MAS model. Section 6 concludes the research.

2. **Proposed MAS Model.**

We describe the MAS-based infection simulator that can represent capacity limitation of isolation wards developed by Omae et al. [12]. Because the previous research [12] is written in Japanese, we briefly explain the method here.

2.1. **Infection transition.**

The SEIR model is one of the models to simulate the spread of the virus disease [17]. In the model, there are five states: S, E, I, R and D. The person of state S has a possibility of being an infector by having contact with other infectors. The person of state E means an infector who does not appear symptoms (incubation periods). The person of state I means an infector that appears symptoms (infection periods). The person of state R means the recovered person from the virus disease. The person of state D means the person who was dead.

The infection transition model is shown in Figure 1. The arrows mean that there are the possibilities of the states' transition. To describe the states' transition, we define the transition probability as

$$P\left(X_{t_{\text{step}}+1}|X_{t_{\text{step}}}, C, T, H\right), \tag{1}$$

where C means the variable for having the contact with the persons of state I or E, i.e., $C = 0$ means not-contact and $C = 1$ means contact. T means the number of days elapsed from changing to other states. H means the variable for expressing whether being in hospitalization or not of agents of state I ($H = 0$: nonhospitalization; $H = 1$: hospitalization). t_{step} means the elapsed time units of MAS (In the case of our simulator, 1 step sets 10 minutes). $X_{t_{\text{step}}}$ and $X_{t_{\text{step}}+1}$ mean the states of an agent at step t_{step} and $t_{\text{step}} + 1$, respectively, and they are defined by

$$X_{t_{\text{step}}}, X_{t_{\text{step}}+1} \in \{\text{S}, \text{E}, \text{I}, \text{R}, \text{D}\}. \tag{2}$$

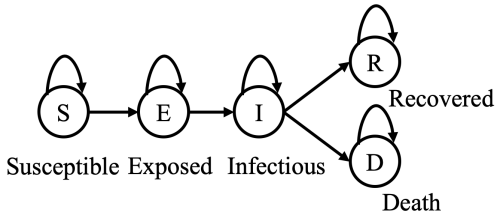

FIGURE 1. Transition model of infection states

The transition probability from the state S to the state S is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{S}|X_{t_{\text{step}}}=\text{S},C\right)=\begin{cases}1 & (C=0)\\ 1-\alpha^{\text{MAS}} & (C=1)\end{cases}, \tag{3}$$

where α^{MAS} means an infection probability of 10 minutes that is minimum time unit of MAS environment. If $C=0$, the persons of state S keep the same state. In contrast, if $C=1$, the probability keeping state S decreases.

The transition probability from the state S to the state E is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{E}|X_{t_{\text{step}}}=\text{S},C\right)=\begin{cases}0 & (C=0)\\ \alpha^{\text{MAS}} & (C=1)\end{cases}. \tag{4}$$

If the agent has contact with infectors (State E or I; $C=1$), the transition probability from state S to state E is α^{MAS}. This is because the state S only changes to state S or E,

$$P\left(X_{t_{\text{step}}+1}=\text{S}|X_{t_{\text{step}}}=\text{S}\right)+P\left(X_{t+1}=\text{E}|X_t=\text{S}\right)=1 \tag{5}$$

is satisfied.

The transition probability from the state E to the state E is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{E}|X_{t_{\text{step}}}=\text{E},T\right)=\begin{cases}0 & \left(T=T^{\text{MAS}}_{\text{E}\to\text{I}}\right)\\ 1 & \left(T\neq T^{\text{MAS}}_{\text{E}\to\text{I}}\right)\end{cases}, \tag{6}$$

and the transition probability from state E to state I is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{I}|X_{t_{\text{step}}}=\text{E},T\right)=\begin{cases}0 & \left(T\neq T^{\text{MAS}}_{\text{E}\to\text{I}}\right)\\ 1 & \left(T=T^{\text{MAS}}_{\text{E}\to\text{I}}\right)\end{cases}, \tag{7}$$

where $T^{\text{MAS}}_{\text{E}\to\text{I}}$ means the period of required transition time [day] (incubation period). If T becomes $T^{\text{MAS}}_{\text{E}\to\text{I}}$, the state of the agents necessarily changes from state E to state I. If T does not reach $T^{\text{MAS}}_{\text{E}\to\text{I}}$, state E is keeping. Because state E only changes to state E or I,

$$P\left(X_{t_{\text{step}}+1}=\text{E}|X_{t_{\text{step}}}=\text{E}\right)+P\left(X_{t_{\text{step}}+1}=\text{I}|X_{t_{\text{step}}}=\text{E}\right)=1 \tag{8}$$

is satisfied.

The transition probability from the state I to the state I is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{I}|X_{t_{\text{step}}}=\text{I},T\right)=\begin{cases}1 & \left(T\neq T^{\text{MAS}}_{\text{I}\to\text{RD}}\right)\\ 0 & \left(T=T^{\text{MAS}}_{\text{I}\to\text{RD}}\right)\end{cases}, \tag{9}$$

and the transition probability from the state I to the state R is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{R}|X_{t_{\text{step}}}=\text{I},T,H\right)=\begin{cases}0 & \left(T\neq T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=0\right)\\ 1-\delta^{\text{MAS}}_0 & \left(T=T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=0\right)\\ 0 & \left(T\neq T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=1\right)\\ 1-\delta^{\text{MAS}}_1 & \left(T=T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=1\right)\end{cases}. \tag{10}$$

Moreover, the transition probability from the state I to the state D is defined as

$$P\left(X_{t_{\text{step}}+1}=\text{D}|X_{t_{\text{step}}}=\text{I},T,H\right)=\begin{cases}0 & \left(T\neq T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=0\right)\\ \delta^{\text{MAS}}_{0} & \left(T=T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=0\right)\\ 0 & \left(T\neq T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=1\right)\\ \delta^{\text{MAS}}_{1} & \left(T=T^{\text{MAS}}_{\text{I}\to\text{RD}}\wedge H=1\right)\end{cases}, \tag{11}$$

where $T^{\text{MAS}}_{\text{I}\to\text{RD}}$ means the period of the required transition time [day] (the infection period). If T that is the elapsed day from changing to the state I becomes $T^{\text{MAS}}_{\text{I}\to\text{RD}}$, the state of the agents translates from the state I to the state R or D. δ^{MAS}_{0} and δ^{MAS}_{1} mean the fatality rates in the case of nonhospitalization ($H=0$) and hospitalization ($H=1$), respectively. In other words, the fatality rate depends on whether the hospitalization of agents or not (In general, we recommend $\delta^{\text{MAS}}_{0}>\delta^{\text{MAS}}_{1}$). Because the state I only changes to the state I, R, or D,

$$\sum_{x\in\{\text{I},\text{R},\text{D}\}}P\left(X_{t_{\text{step}}+1}=x|X_{t_{\text{step}}}=\text{I}\right)=1 \tag{12}$$

is satisfied.

The state R means that the agents acquired immunity and the state D means death. Therefore,

$$P\left(X_{t_{\text{step}}+1}=\text{R}|X_{t_{\text{step}}}=\text{R}\right)=1 \tag{13}$$

and

$$P\left(X_{t_{\text{step}}+1}=\text{D}|X_{t_{\text{step}}}=\text{D}\right)=1 \tag{14}$$

are satisfied, respectively.

More details of the infection transition model considering the effectiveness of hospitalization can be found in Omae et al. [12].

2.2. **Simulation flow.** We explain the artificial society in MAS-based simulator shown in Figure 2. The agents live in a 2-dimensional space (x-y axes) with the minimum and maximum values 0 and 1000. The parameters of simulator are shown in the 1st row of Table 1 (The values of the 2nd row mean the case study described in Section 5. We can set other values.). "Max simulation period" is the maximum simulation term. "The number of houses" is the number of houses which agents live in. The three persons (an office worker, homemaker, and student, respectively) live in a house. In other words, the total population of the agents in artificial society is 3 times of "the number of houses". "The number of initial infectors" means the number of infected persons (state I) of initial timing of simulation. They infect other persons with virus disease.

In the 2-dimensional space, there are the agents' houses and destination facility locations (company, shop, or school, respectively) in the form of (x,y) coordinates. A house means the location that agents live daily. Moreover, an office worker, homemaker or students go to a company, shop, or school, respectively. There are numerous companies,

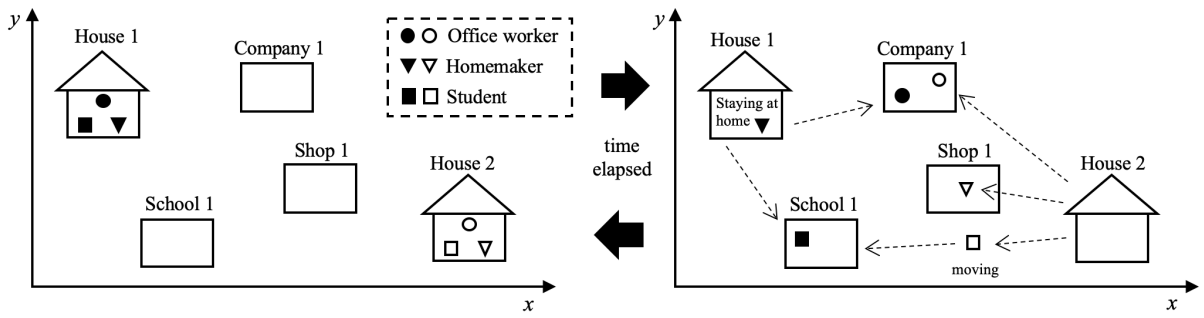

FIGURE 2. MAS-based simulator

Table 1. Simulation conditions of MAS/basic parameters

Parameters	Values
Max simulation period	30 [day]
The number of houses	→ shown in Table 2
The number of initial infectors	10 [ppl.]
Facility locations (companies)	10 places
Facility locations (shops)	10 places
Facility locations (schools)	10 places
Basic going out probability (office worker)	$99.0 \sim 100.0$[%]
Basic going out probability (homemaker)	$50.0 \sim 100.0$[%]
Basic going out probability (student)	$99.0 \sim 100.0$[%]
Going out time (office worker)	$8{:}30 \pm 1{:}30$
Going out time (homemaker)	$10{:}30 \pm 1{:}30$
Going out time (student)	$8{:}30 \pm 1{:}30$
Stay time of facility (office worker)	$6{:}00 \sim 8{:}00$
Stay time of facility (homemaker)	$0{:}10 \sim 0{:}30$
Stay time of facility (student)	$5{:}00 \sim 6{:}00$
Probability of going to a hospital	60.0[%]
Capacity limitation of isolation wards	→ shown in Table 2
Infection probability: α^{MAS}	→ shown in Table 2
Incubation periods (from E to I): $T^{\mathrm{MAS}}_{\mathrm{E}\to\mathrm{I}}$	3, 5, 7 [day]
Infection periods (from I to R, D): $T^{\mathrm{MAS}}_{\mathrm{I}\to\mathrm{RD}}$	8, 10, 12 [day]
Fatality rate (nonhospitalization): $\delta^{\mathrm{MAS}}_{0}$	10.0[%]
Fatality rate (hospitalization): $\delta^{\mathrm{MAS}}_{1}$	1.0[%]

$a \sim b$: a uniform random number from a to b.

$a \pm b$: a Gaussian random number applied mean a and std. b.

shops, and schools. Destination facility location to choose is decided by a uniform random probability at the simulation start timing. The destination facility location is one per agent and after the decision, they do not change.

"Basic going out probability" means the probability of going to destination facility locations. At the start timing of each day, whether the agent goes to destination facility location or not is decided based on "basic going out probability". "Going out time" means the timing that agents go out. They go there in the shortest Euclidian distance from house to facility location in the 2-dimensional space. After arriving at the location, the agents stay there. The stay time is defined as "stay time of facility". Afterward, they go back to their houses.

Then, the agents of the state I go to the hospital based on "probability of going to a hospital". They are isolated there (it means they are hospitalized). In this case, "basic going out probability" becomes zero. If they who could be hospitalized become state R, they leave the hospital and live as usual. However, if the capacity limitation of isolation wards is exceeded, even if the agents are the state I, they cannot be hospitalized. In this case, they can go the outside even if they are state I.

Other parameters in Table 1 (e.g., infection probability α^{MAS}, incubation periods $T^{\mathrm{MAS}}_{\mathrm{E}\to\mathrm{I}}$, infection periods $T^{\mathrm{MAS}}_{\mathrm{I}\to\mathrm{RD}}$ and fatality rate $\delta^{\mathrm{MAS}}_{\{0,1\}}$) are used in the infection transition described in Section 2.1. In this MAS, the minimum unit of time is 10 minutes. Therefore, 1 day of simulation consists of 144 steps (24 hours). After completing their steps, the next day is started. More details of explanation of the simulation flow are shown in [17].

2.3. **Representation of spreading infection disease.** To understand spreading infection disease, we define the number of agents of states S, E, I, R and D of day t_{day} as

$$Z^{\mathrm{MAS}}(t_{\mathrm{day}}) = \text{Observed value, where}$$

$$Z^{\mathrm{MAS}}(t_{\mathrm{day}}) \in \left\{S^{\mathrm{MAS}}(t_{\mathrm{day}}), E^{\mathrm{MAS}}(t_{\mathrm{day}}), I^{\mathrm{MAS}}(t_{\mathrm{day}}), R^{\mathrm{MAS}}(t_{\mathrm{day}}), D^{\mathrm{MAS}}(t_{\mathrm{day}})\right\}, \tag{15}$$

and

$$t_{\mathrm{day}} = \frac{1}{144}\, t_{\mathrm{step}}. \tag{16}$$

Note that because 1 step is 10 minutes, 144 steps is 1 day. $Z^{\mathrm{MAS}}(t_{\mathrm{day}})$ is not calculated by any mathematical functions but it is observed from MAS simulator.

3. **Traditional ODE Model.** We describe one of the traditional infection spread simulation models by ODE-based SEIR model (e.g., [13, 14, 15]). In their models, the number of persons who is each infection state is represented by the instantaneous rate of the change. Therefore, we can know infection spread dynamics with small computational cost.

The forms of ODE-based SEIR model are expressed by

$$\frac{\mathrm{d}S^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}} = -\alpha(t_{\mathrm{day}})S^{\mathrm{ODE}}(t_{\mathrm{day}})\left\{I^{\mathrm{ODE}}(t_{\mathrm{day}}) + E^{\mathrm{ODE}}(t_{\mathrm{day}})\right\}, \tag{17}$$

$$\frac{\mathrm{d}E^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}} = \alpha(t_{\mathrm{day}})S^{\mathrm{ODE}}(t_{\mathrm{day}})\left\{I^{\mathrm{ODE}}(t_{\mathrm{day}}) + E^{\mathrm{ODE}}(t_{\mathrm{day}})\right\} - \beta E^{\mathrm{ODE}}(t_{\mathrm{day}}), \tag{18}$$

$$\frac{\mathrm{d}I^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}} = \beta E^{\mathrm{ODE}}(t_{\mathrm{day}}) - \gamma I^{\mathrm{ODE}}(t_{\mathrm{day}}), \tag{19}$$

$$\frac{\mathrm{d}R^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}} = \{1 - \delta(t_{\mathrm{day}})\}\,\gamma I^{\mathrm{ODE}}(t_{\mathrm{day}}), \tag{20}$$

$$\frac{\mathrm{d}D^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}} = \delta(t_{\mathrm{day}})\gamma I^{\mathrm{ODE}}(t_{\mathrm{day}}), \tag{21}$$

$$Z^{\mathrm{ODE}}(t_{\mathrm{day}}) = \int_0^{t_{\mathrm{day}}} \frac{\mathrm{d}Z^{\mathrm{ODE}}(t_{\mathrm{day}})}{\mathrm{d}t_{\mathrm{day}}}\mathrm{d}t_{\mathrm{day}} + Z^{\mathrm{ODE}}(0), \text{ where } Z^{\mathrm{ODE}}(0) = \text{const.},$$

$$Z^{\mathrm{ODE}}(t_{\mathrm{day}}) \in \left\{S^{\mathrm{ODE}}(t_{\mathrm{day}}), E^{\mathrm{ODE}}(t_{\mathrm{day}}), I^{\mathrm{ODE}}(t_{\mathrm{day}}), R^{\mathrm{ODE}}(t_{\mathrm{day}}), D^{\mathrm{ODE}}(t_{\mathrm{day}})\right\}, \tag{22}$$

where $S^{\mathrm{ODE}}(t_{\mathrm{day}})$, $E^{\mathrm{ODE}}(t_{\mathrm{day}})$, $I^{\mathrm{ODE}}(t_{\mathrm{day}})$, $R^{\mathrm{ODE}}(t_{\mathrm{day}})$, $D^{\mathrm{ODE}}(t_{\mathrm{day}})$ mean the number of day t_{day}'s persons of states S, E, I, R and D calculated by ODE-based simulator, respectively. In MAS-base simulator, the agents of state S translate from state S to E by the contact with the agents of state E or I by shown in Equation (4). Therefore, the sum of the states I and E multiplied by the state S appears in Equations (17) and (18). $\alpha(t_{\mathrm{day}})$ is the day t_{day}'s infection rate.

Because the agents of the state E translate from the state E to I depending on the day elapsed, the number of state E appears in Equations (18) and (19). β is inverse value of the incubation periods. Likewise, because the agents of the state I translate from the state I to R or D depending on the day elapsed, the number of state I appears in Equations (19), (20) and (21). γ is inverse value of the infection periods and $\delta(t_{\mathrm{day}})$ is the day t_{day}'s fatality rate.

Equations (17), (18), (19), (20) and (21) are the derivative coefficients of the number of infection states. Therefore, we get the total number by calculating integral value of them shown in Equation (22). $\alpha(t_{\mathrm{day}})$, β, γ and $\delta(t_{\mathrm{day}})$ are the ODE parameters and we have to decide specific values to perform infection spread simulation.

4. **How to Verify Reliability of MAS Model.** To evaluate the reliability of the MAS-based simulator, it is desirable to the output similarity values by comparison with the ODE-based simulator. MAS-based simulator has many parameters shown in Table 1. On the other hand, ODE-based simulator has simple four parameters of $\alpha(t_{\text{day}})$, β, γ and $\delta(t_{\text{day}})$. Therefore, it is required fitting ODE parameters to MAS.

In the ODE parameters, β is inverse value of the incubation periods and γ is inverse value of the infection periods. Moreover, MAS-based simulator has the incubation and infection periods and they are $T^{\text{MAS}}_{\text{E}\to\text{I}}$ and $T^{\text{MAS}}_{\text{I}\to\text{RD}}$. Therefore, we use

$$\beta^* = \frac{1}{\text{mean}\left[T^{\text{MAS}}_{\text{E}\to\text{I}}\right]}, \quad \gamma^* = \frac{1}{\text{mean}\left[T^{\text{MAS}}_{\text{I}\to\text{RD}}\right]}, \tag{23}$$

as the ODE parameters β, γ, where mean$[\cdot]$ is a mean operator to transform into the scalar value from the multiple values. Because we can set the multiple values as the incubation and infection periods in the case of MAS as shown in Table 1, the mean values are used as the ODE parameters. In other words, mean $\left[T^{\text{MAS}}_{\text{E}\to\text{I}}\right] = 5$, mean $\left[T^{\text{MAS}}_{\text{I}\to\text{RD}}\right] = 10$ in the case of Table 1.

Moreover, we consider the ODE parameters $\alpha(t_{\text{day}})$ and $\delta(t_{\text{day}})$. $\alpha(t_{\text{day}})$ expresses a day t_{day}'s degree of virus spread and $\delta(t_{\text{day}})$ expresses a day t_{day}'s fatality rate. In MAS, the infection probability α^{MAS} exists. However, it is the infection probability in the case of contact with infector during 10 minutes. Moreover, in MAS, the fatality rate $\delta^{\text{MAS}}_{\{0,1\}}$ exists. However, the value is different by whether hospitalization or not. In other words, the ODE parameters $\alpha(t_{\text{day}})$ and $\delta(t_{\text{day}})$ are similar to the MAS parameters $\alpha^{\text{MAS}}, \delta^{\text{MAS}}_{\{0,1\}}$, but different. Therefore, by making fit ODE and MAS outputs, we decide the ODE parameters. Because the ODE parameter $\alpha(t_{\text{day}})$ affects the number of states S and E, we adopt $\alpha(t_{\text{day}})$ leading to be minimum difference between the number of states S and E of ODE and MAS. Likewise, because ODE parameter $\delta(t_{\text{day}})$ affects the number of states R and D, we adopt $\delta(t_{\text{day}})$ leading to be minimum difference between the number of states R and D of ODE and MAS. In other words, we set

$$\begin{aligned}\alpha^*(t_{\text{day}}) = \underset{\alpha(t_{\text{day}})}{\text{argmin}} \big[&\left|S^{\text{ODE}}(t_{\text{day}}+1) - S^{\text{MAS}}(t_{\text{day}}+1)\right| \\ &+ \left|E^{\text{ODE}}(t_{\text{day}}+1) - E^{\text{MAS}}(t_{\text{day}}+1)\right|\big], \end{aligned} \tag{24}$$

$$\begin{aligned}\delta^*(t_{\text{day}}) = \underset{\delta(t_{\text{day}})}{\text{argmin}} \big[&\left|R^{\text{ODE}}(t_{\text{day}}+1) - R^{\text{MAS}}(t_{\text{day}}+1)\right| \\ &+ \left|D^{\text{ODE}}(t_{\text{day}}+1) - D^{\text{MAS}}(t_{\text{day}}+1)\right|\big], \end{aligned} \tag{25}$$

as the ODE parameters $\alpha(t_{\text{day}})$ and $\delta(t_{\text{day}})$. We evaluate the reliability of MAS by comparing the outputs of ODE adopting $\alpha^*(t_{\text{day}})$, β^*, γ^* and $\delta^*(t_{\text{day}})$ as ODE parameters $\alpha(t_{\text{day}})$, β, γ and $\delta(t_{\text{day}})$ with outputs of MAS.

5. Experiment for the Reliability Verification of MAS Model.

5.1. **Simulations condition.** We verify the reliability of MAS-based simulator [12] by comparing with traditional ODE-based simulator. We set the MAS parameters shown in Tables 1 and 2, which are based on Omae et al. [17]. As shown in Table 2, we considered the eight cases that consist of 2 pattern populations, infection probabilities and capacity limitation of isolation wards. The ODE parameters $\alpha^*(t_{\text{day}})$, β^*, γ^* and $\delta^*(t_{\text{day}})$ are solved by Equations (23), (24) and (25).

5.2. **Results and discussions.** The infection spread dynamics are shown in Figure 3. The left side, center and right side figures mean MAS outputs, ODE outputs and optimal parameters of ODE-based simulator calculated by Equations (24) and (25), respectively. We can verify the high similarity between MAS and ODE outputs. Moreover, virus spread speed in the presence of isolation wards is more delayed than the cases in the absence

TABLE 2. Simulation conditions of MAS/variables parameters

Case ID	Case 0	Case 1	Case 2	Case 3	Case 4	Case 5	Case 6	Case 7
The number of houses [units]	1000	1000	1000	1000	1500	1500	1500	1500
The number of agents* [ppl.]	3000	3000	3000	3000	4500	4500	4500	4500
Infection probability α^{MAS}[%]	0.06	0.06	0.09	0.09	0.06	0.06	0.09	0.09
Cap. limit. of isolation wards [beds]	0	15	0	15	0	15	0	15

*: The number of agents is 3 times of number of houses (office worker, homemaker and student).

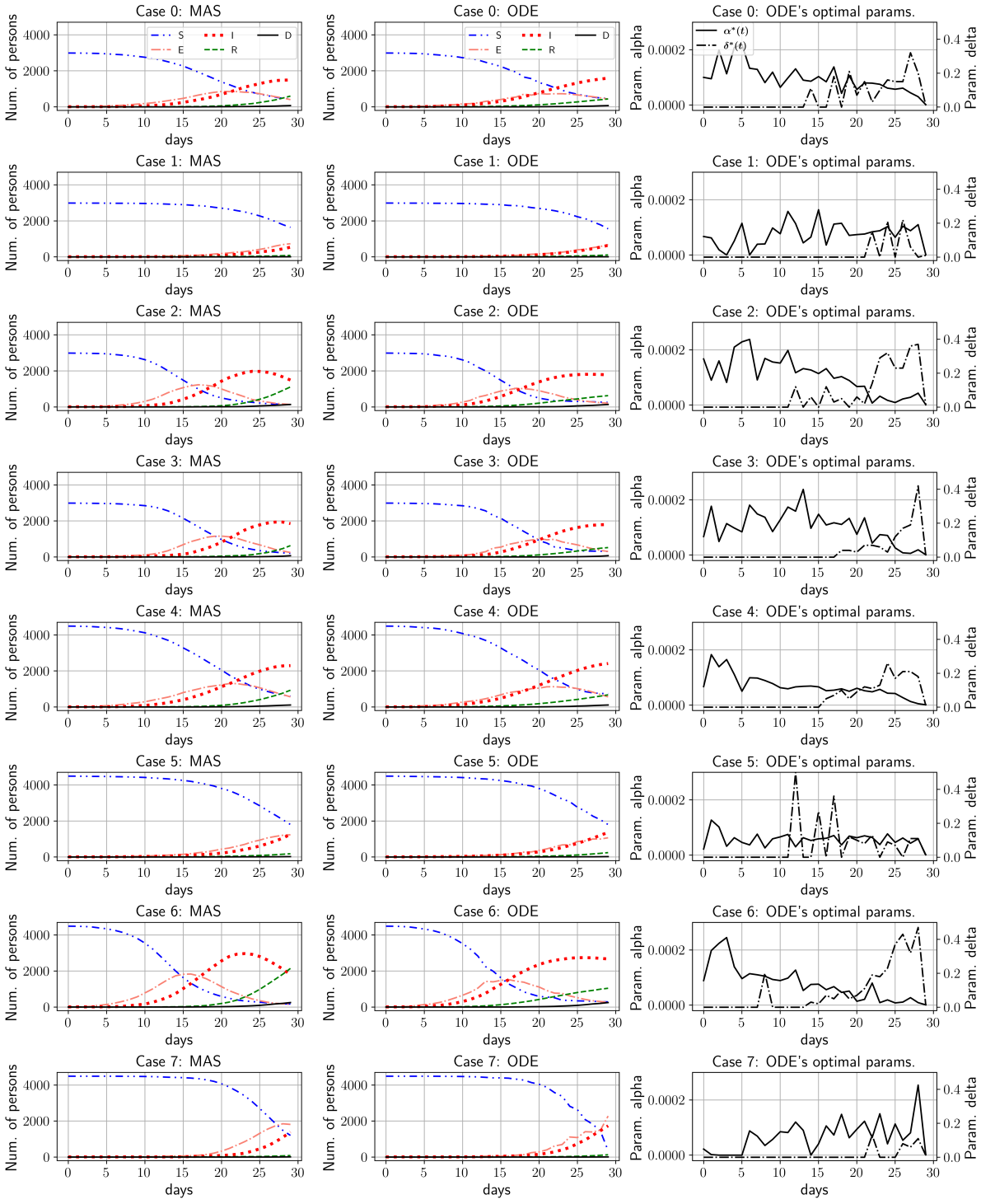

FIGURE 3. The outputs of infection spread dynamics (left: MAS, center: ODE, right: ODE's optimal parameters)

of isolation wards (note that the cases 0, 2, 4, and 6 mean the absence of isolation wards and the cases 1, 3, 5, 7 mean the presence of them). $\alpha^*(t_{\text{day}})$ and $\delta^*(t_{\text{day}})$ in the presence of isolation wards are lower than $\alpha^*(t_{\text{day}})$ and $\delta^*(t_{\text{day}})$ in the absence of them. Because $\alpha^*(t_{\text{day}})$ is the ODE's infection probability and $\delta^*(t_{\text{day}})$ is the ODE's fatality rate, isolation wards have the effectiveness of decreasing infection spread and the number of dead persons. Their results are similar to the results obtained by Omae et al. [12].

To quantitively evaluate MAS-based simulator, we calculated the coefficient of determination r^2 between the MAS and ODE outputs. The definition of r^2 is

$$r^2 = 1 - \frac{\sum_{t_{\text{day}}=0}^{T_{\max}-1} \left(Z^{\text{MAS}}(t_{\text{day}}) - Z^{\text{ODE}}(t_{\text{day}})\right)^2}{\sum_{t_{\text{day}}=0}^{T_{\max}-1} \left(Z^{\text{MAS}}(t_{\text{day}}) - \text{mean}\left[Z^{\text{MAS}}\right]\right)^2},$$

$$\text{mean}\left[Z^{\text{MAS}}\right] = \frac{1}{T_{\max}} \sum_{t_{\text{day}}=0}^{T_{\max}-1} Z^{\text{MAS}}(t_{\text{day}}), \tag{26}$$

where $T_{\max}$ is the maximum simulation period (30 days). If r^2 is similar to 1, MAS outputs are similar to ODE outputs. They are shown in Table 3. On most cases except some of State R (e.g, $r^2 = 0.671$ at case 3), the values of r^2 are high. We also show the outputs of MAS and ODE at the last day in the seven to eight rows of Table 3. Likewise r^2, the last day's MAS outputs are similar to ODE outputs on most cases (except case 7). Therefore, we consider that MAS-based simulator that can represent isolation wards is reliable.

Table 3. Reliability verification of MAS based on comparison with ODE

	Case 0	Case 1	Case 2	Case 3	Case 4	Case 5	Case 6	Case 7
Coef. of determination r^2 of state S	0.999	0.998	0.998	0.999	1.000	0.998	0.999	0.993
Coef. of determination r^2 of state E	0.957	0.970	0.945	0.955	0.959	0.967	0.935	0.963
Coef. of determination r^2 of state I	0.990	0.912	0.981	0.981	0.994	0.933	0.968	0.715
Coef. of determination r^2 of state R	0.922	0.811	0.827	0.671	0.925	0.853	0.781	0.711
Coef. of determination r^2 of state D	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.935
The number of total infectors/MAS	2565.00	1358.00	2872.00	2796.00	3765.89	2696.00	4333.00	3298.00
The number of total infectors/ODE	2535.52	1439.09	2754.71	2694.70	3759.73	2699.37	4212.74	4144.30

6. **Conclusion.** In this paper, we evaluated MAS-based infection simulator that can represent isolation wards and its capacity limitation developed by Omae et al. [12]. The evaluation method is the comparison of MAS-based simulator's outputs with traditional ODE-based approach. As the results shown in Figure 3 and Table 3, MAS-based simulator's outputs were similar to ODE-based simulator. Therefore, we consider that MAS-based simulator is reliable.

In future work, we will consider how many capacity limitation of isolation wards will be required to decrease dead people by COVID-19 infection disease by using the MAS-based simulator.

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