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System Dynamics Approach to Epidemic Compartment Model: Translating SEIR Model for MERS Transmission in South Korea

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전염병 구획 모형에 대한 시스템다이내믹스 접근법: 국내 MERS 전염 SEIR 모형의 해석 및 변환

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Abstract Compartment models, a type of mathematical model, have been widely applied to characterize the changes in a dynamic system with sequential events or processes, such as the spread of an epidemic disease. A compartment model comprises compartments, and the relations between compartments are depicted as boxes and arrows. This principle is similar to that of the system dynamics (SD) approach to constructing a simulation model with stocks and flows. In addition, both models are structured using differential equations. With this mutual and translatable principle, this study, in terms of SD, translates a reference SEIR model, which was developed in a recent study to characterize the transmission of the Middle East respiratory syndrome (MERS) in South Korea. Compared to the replicated result of the reference SEIR model (Model 1), the translated SEIR model (Model 2) demonstrates the same simulation result (error=0). The results of this study provide insight into the application of SD relative to constructing an epidemic compartment model using schematization and differential equations. The translated SD artifact can be used as a reference model for other epidemic diseases.

Key Words : Compartment Model, Epidemic Disease, SEIR Model, System Dynamics, Model Translation

요 약 수학모형의 한 유형인 구획모형은 전염병의 확산처럼 순차적인 이벤트나 프로세스로 구성된 동적 시스템의 변화를 분석하는 데 폭넓게 활용되어 왔다. 구획모형은 상자와 화살표로 표현되는 구획과 구획 간 관계로 구성된다. 이러한 원리는 stock과 flow로 구성되는 시스템다이내믹스(SD)의 모델링 원리와 비슷하다. 두 모형 모두 미분방정식을 이용하여 구조화된다. 이와 같은 두 모형 간 변환 가능성을 이용하여 국내 MERS 전염의 특징을 분석한 최근 연구의 SEIR 참조모형을 SD 관점에서 해석·변환한다. 변환된 SEIR 모형(Model 2)은 참조모형(Model 1)의 재현 결과와 비교하여 동일한 시뮬레이션 결과를 나타내었다. 본 연구는 전염병 구획모형의 구축에 도식과 미분방정식을 이용한 SD 방법론의 활용에 대한 인사이트를 제공하며, 변환된 SD 모형은 다른 전염병을 위한 참조모형으로 활용 가능하다.

주제어 : 구획모형, 전염병, SEIR 모형, 시스템다이내믹스, 모형 변환

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1. Introduction

When applied to characterizing the spread of epidemic disease, such as influenza, compartment modeling is, in terms of schematization, similar to stocks-and-flows diagramming of system dynamics (SD) [1]. A compartment model comprises boxes, i.e., compartments, and the relations between these compartments are represented by arrows [2]. A compartment stores an accumulative value, such as a reservoir, and an arrow is a flow that adds or subtracts a value to/from a compartment [2,3]. A stocks-and-flows diagram (SFD) comprises stocks and flows depicted as boxes and arrows, and their roles are the same as the elements of a compartment model [1,4]. Consequently, the same equations can be used to translate the elements of a compartment model to those of an SFD [5].

In contrast, compartment models in epidemiology were developed from the reference models of Kermack and McKendrick [6-8]. The basic Susceptible-Infected-Susceptible (SIS) model comprises compartment S (susceptible class or individuals) and compartment I (infected class) without immunity against reinfection of disease, and the Susceptible-Infected-Recovered (SIR) model includes compartment R (recovered class) with immunity against reinfection [9,10]. The Susceptible-Exposed-Infected-Recovered (SEIR) model is an extension of the SIR model with another compartment E (exposed class) representing a delay between susceptible and infected individuals [11].

The variables used in a compartment model to describe an epidemic disease are formed as listed above; however, in an SD model that addresses epidemics [12,13], defining variables is relatively free and informal compared. In addition, the SD approach utilizes an *auxiliary* element that is not used in a compartment model [1,14]. In this sense, translating a compartment model to an SD model can be realized; however, the reverse process is not guaranteed.

When translating a compartment model in SD, the agent-based modeling (ABM) approach is often compared to the SD modeling approach [15,16]. ABM constructs an inductive model that does not have a fixed structure to represent individual behaviors, and SD constructs a deductive model with a fixed structure that represents abstract or summarized behaviors of individuals [17]. Of the two approaches, ABM produces a more natural result in terms of individual behavior, and SD shows similarity with compartment models in terms of schematization because SD and compartment models are both based on differential equations [15,16,18].

Based on the similarity between compartment and SD models, this study attempts to build an epidemic SEIR model using the SD approach by translating a discrete SEIR model into an SD model with sharable schematization and differential equations. To translate an epidemic compartment model, the discrete SEIR model proposed by Kwon and Jung [19] for a Middle East respiratory syndrome (MERS) outbreak in South Korea was used as a baseline model.

2. Baseline: Discrete SEIR Model for MERS Transmission in South Korea

MERS is an illness with a high fatality rate (30%~40%) caused by the MERS coronavirus, which, to date, has been linked to travel or residence in countries in and near the Arabian Peninsula [20]. The first MERS outbreak occurred in Jordan in 2012, and the largest outbreak outside the Arabian Peninsula was recorded in South Korea in 2015, which was associated with a traveler visiting the Arabian Peninsula [20,21].

MERS cases in South Korea showed rapid increase in early days with previously unseen high fatality rates [22]. Related to the rapid transmission of MERS in South Korea, various causes were indicated, e.g., medical conditions (factors) of super spreaders and misleading hospital systems (hospitalization and quarantine) [23-25]. Among them, intra-hospital and

hospital-to-hospital transmissions were considered as a main cause in South Korea [26]. With no MERS vaccine or medicine, the delay of proper quarantine of individuals (susceptible, exposed, and infected) contributed to the fastest spread and largest number of MERS cases outside the Middle East.

Kwon and Jung [19] simulated MERS transmission in South Korea using a discrete SEIR model (Model 1) and identified that transmission rates were reduced sequentially by critical government actions, i.e., the disclosure of names and closure of MERS-transmission hospitals.

Fig. 1 schematizes the SEIR model used by Kwon and Jung [19]. Here, β, ϵ, and γ represent the transit rate from S (susceptible) to E (exposed), from E to I (infected), and from I to R (recovered), respectively; μ^* represents birth rate, μ represents death rate at each compartment, and α is the immunity loss rate of recovered individuals.

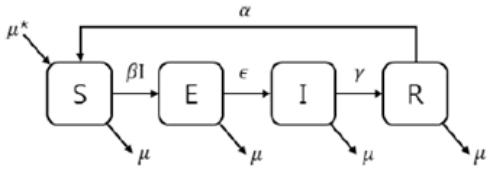


Fig. 1. SEIR Model [19]

S, E, I, and R for time t are Equations (1)-(4) [19].

$$S_{t+1} = S_t - \beta I_t \times S_t / N, \quad (1)$$

$$E_{t+1} = E_t - \beta I_t \times S_t / N - \epsilon E_t, \quad (2)$$

$$I_{t+1} = I_t + \epsilon E_t - \gamma I_t, \quad (3)$$

$$R_{t+1} = R_t + \gamma I_t. \quad (4)$$

Kwon and Jung [19] assumed the following parameters.

- α = 0 (MERS shows a long immunity period)
- μ^*, μ = 0 (the time interval is insufficiently long to consider birth and death)
- Total population $(N) = S_t + T_t + I_t + R_t$
- Population is well mixed
- S_0=16,874, E_0=3, I_0=2, and R_0=0 (approximately estimated with official MERS cases on the first day in Korea)
- Initial susceptible individuals are confined to the people quarantined due to contact with infectious patients

Based on this SEIR model and the clinical MERS data observed by the Korea CDC (See [19]; Table 1), the values of β, ϵ, and γ were estimated using the R programming language from May 20 to Oct 11, 2015, where the entire period was divided into three periods (Period 1, Period 2, and Period 3) relative to critical government action at T1 (disclosure of names of MERS-spread-hospitals) and T2 (closure of MERS-spread-hospitals). Thus, the infectious rate β reduced sequentially (See Table 1).

The estimated SEIR model was used to translate an epidemic compartment model in SD.

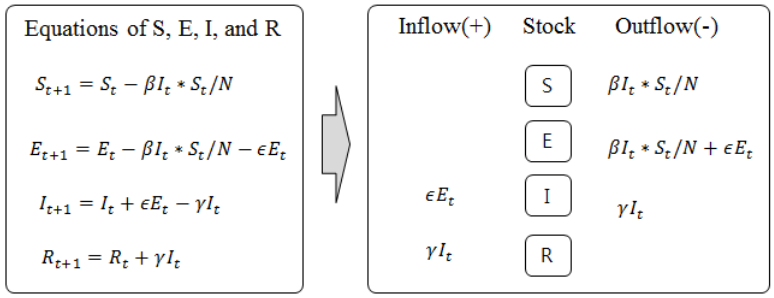
Table 1. Baseline Discrete SEIR Model [19]

Parameters	Period1	Period2	Period3
β	2.0	1.1	0.5
ϵ	0.2	0.2	0.2
γ	0.6	0.7	0.7

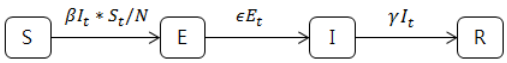
3. SD Approach to Translating Baseline SEIR Model

To represent the reference SEIR model in SD, this study translated the four compartmental equations of S, E, I, and R to stocks and flows (in and out) for an SD model. Fig. 2(a) shows the process of translating the differential equations of the four compartments to the stocks and flows of SD, and Fig. 2(b) shows the concatenated stocks and flows from each compartment.

Based on the findings shown in Fig. 2, this study constructed a discrete SEIR model for MERS transmission in South Korea using the Powersim Studio 8 software (See Fig. 3).



(a) Translating Compartmental Equations to Stocks and Flows



(b) Concatenated Stocks and Flows

Fig. 2. Translated Stocks and Flows from Four Compartmental Equations

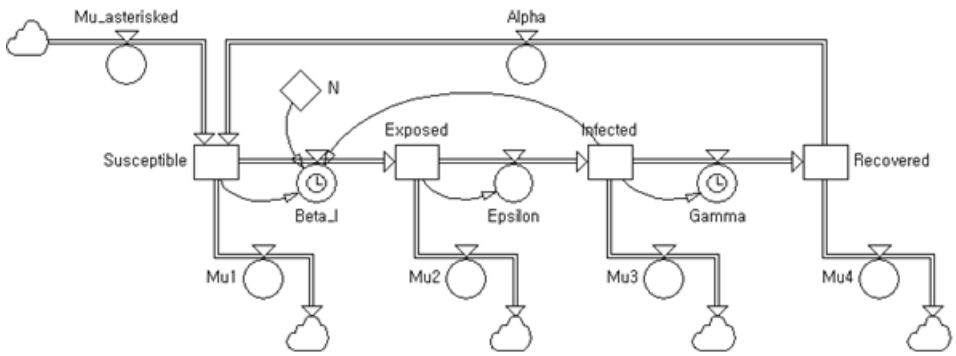


Fig. 3. Translated SEIR Model for MERS Transmission in South Korea to SFD

Table 2. Values and Equations

Name	Definition
Alpha	0/1<<da>>
Beta_I	(IF((TIME-STARTTIME)<=17<<da>>,2,IF((TIME-STARTTIME)<=23<<da>>,1.1,0.5))*Infected*Susceptible/N)/1<<da>>
Epsilon	(0.2*Exposed)/1<<da>>
Exposed	3
Gamma	(IF((TIME-STARTTIME)<=17<<da>>,0.6,0.7)*Infected)/1<<da>>
Infected	2
Mu1	0/1<<da>>
Mu2	0/1<<da>>
Mu3	0/1<<da>>
Mu4	0/1<<da>>
Mu_asterisked	0/1<<da>>
N	16883
Recovered	0
Susceptible	16878

Table 2 shows the variables and equations used in the SD model. Here, the total population N and initial values of S_0, E_0, I_0, and R_0 were assumed as discussed in Section 2, and the estimated values of β, ϵ, and γ referred to those given in Table 1.

The new SEIR model developed in SD (Model 2) was compared to the original discrete SEIR model (Model 1), and Model 2 demonstrated the same results as the replicated model of Model 1 (See Table 3).

This successful translation of the discrete SEIR model for MERS transmission in South Korea demonstrates one application of the SD approach to an epidemic compartment model with a common

theoretical root between a compartment model and SD approaches.

Table 3. Infected Cases of Models 1 and 2

Time	Model1	Model2	Error
0	2	2	0
1	1	1	0
2	2	2	0
3	2	2	0
4	3	3	0
5	4	4	0
6	5	5	0
7	6	6	0
8	7	7	0
9	9	9	0
10	12	12	0
11	15	15	0
12	19	19	0
13	24	24	0
14	30	30	0
15	38	38	0
16	48	48	0
17	60	60	0
18	75	75	0
19	87	87	0
20	94	94	0
21	101	101	0
22	108	108	0
23	116	116	0
24	124	124	0
25	132	132	0
26	127	127	0
27	121	121	0
28	114	114	0
29	107	107	0
30	101	101	0
31	95	95	0
32	90	90	0
33	85	85	0
34	80	80	0
35	75	75	0
36	70	70	0
37	66	66	0
38	62	62	0
39	59	59	0
40	55	55	0
41	52	52	0
42	49	49	0
43	46	46	0
44	43	43	0
45	40	40	0
46	38	38	0
47	35	35	0
48	33	33	0
49	31	31	0
50	29	29	0
51	27	27	0
52	26	26	0
:			

4. Conclusion

This study aimed to translate an epidemic compartment model to an SD model using the sharable differential equations and schematic elements of compartment and SD simulation models. To facilitate procedural verification in terms of schematization and differential equations, this study employed the reference SEIR model produced by a recent study concerning MERS spread in South Korea. The translated SEIR model produced the same result as the replicated simulation result from the reference model.

The successful translation of a compartment model to an SD artifact provides insight into how the SD approach can be applied to building an epidemic compartment model using translatable schematization and differential equations. In addition, the translated SD artifact can be used as a reference model for other epidemic diseases.

However, in this study, a parameter estimation process was omitted to evaluate the translation accuracy of the SD approach from the reference SEIR model under the same environment. Thus, estimating the parameters of a compartment model in the SD approach will be addressed in a future study that will consider randomness for more extendable modeling of the SD approach.

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