A Comparison Between a Deterministic, Compartmental Model and an Individual Based-stochastic Model for Simulating the Transmission Dynamics of Pandemic Influenza

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Keywords: Agent-based Model, Equation-based Model, Model Comparison, Parameter Calibration.

Abstract: Simulation models are often used in the research area of epidemiology to understand characteristics of disease outbreaks. As a result, they are used by authorities to better design intervention methods and to better plan the allocation of medical resources. Previous work make use of many different types of simulation models with an agent-based model, e.g., Taiwan simulation system, and an equation-based model, e.g., AsiaFluCap simulation system, being the two most popular ones. Some comparison studies has been attempted in the past to understand the limits, efficiency, and usability of some model. However, there was little studies to justify why one model is used instead of the other. In this paper, instead of studying the two most popular models one by one, we try to do a comparative study between these two most popular ones. By observing that one model can outperform the other in some cases, and vice versa, we hence study conditions that which one should be used. Furthermore, previous studies show little results in the issue of allocating medical resources. Our paper studies and compares the two models using medical resources allocation as one of our primary concerns. As a conclusion, we come out with a general guideline to help model designers to pick one that fits the given needs better.

1 INTRODUCTION

Simulation models are often used in the research area of epidemiology estimating the characteristics of a specified disease outbreak, such as outbreak day, peak day and prevalence rate (Diekmann and Heesterbeek, 2000). Simulation results can support governments in designing intervention methods to prevent the spread of diseases (Tsai et al., 2010) or to estimate the amount of medical resources needed (Krumkamp et al., 2011; Rudge et al., 2012; Stein et al., 2012). There are many different types of simulation models, such as homogeneous (Diekmann and Heesterbeek, 2000; Krumkamp et al., 2011) or heterogeneous (Garnett, 2002; Keeling and Danon, 2009; Lunelli et al., 2009), deterministic (Diekmann and Heesterbeek, 2000; Keeling and Danon, 2009) or stochastic (Britton and Lindenstrand, 2009; Lunelli et al., 2009), equation-based (Diekmann and Heesterbeek, 2000; Garnett, 2002) or agent-based (Berger, 2001; Davidsson, 2002; Macal and North, 2005; Moss and Davidsson, 2001; Parker et al., 2003). The major difference between homogeneous and heterogeneous model is a homogeneous model treats all the people exactly the same way but in a heterogeneous model, people are partitioned into different groups according to their characteristic. In a deterministic model, the number of newly infected people is always the same for a given number of susceptible people and infectious people. But in a stochastic model, the number of newly infected people is often different as this number is chosen based on a random distribution. An equation-based model is the one that utilizes numerical time-stepping procedures to simulate the behaviors over time. And an agent-based models focuses on the actions and the interactions among autonomous agents.

Chang H., Chuang J., Chern T., Stein M., Coker R., Wang D. and Hsu T..
A Comparison Between a Deterministic, Compartmental Model and an Individual Based-stochastic Model for Simulating the Transmission Dynamics of Pandemic Influenza.
DOI: 10.5220/0005040905860594
In *Proceedings of the 4th International Conference on Simulation and Modeling Methodologies, Technologies and Applications* (SIMULTECH-2014), pages 586-594
ISBN: 978-989-758-038-3

In 2009, the novel influenza H1N1 spread from Mexico and caused over 18,000 deaths worldwide.[1] The AsiaFluCap project (AFC) (AsiaFluCap, 2009) has focused on the medical resources issue in the southeast Asia where infectious diseases similar to H1N1 may break out. AFC has built a homogeneous deterministic equation-based model (the AsiaFluCap Simulation, AFC model) to simulate the disease transmission behavior. This simulator has the same basis as the SEIR model described in Krumkamp et al.(Rudge et al., 2012; Stein et al., 2012). In the same time, Institute of Information Science (IIS) of Academia Sinica cooperates with CDC in Taiwan (Tsai et al., 2010) has developed a heterogeneous individual based model (the Taiwan simulation model, TW model) to simulate the disease transmission behaviors in order to design effective intervention policies. Although the AFC model and the TW model are different in design, they both model the same disease namely pandemic influenza. Since the two models modeled the same disease, a natural question raised: How different are these two models and how well does each model describe the same disease?

Previous studies have mentioned the relationship between agent-based models and equation-based models (Ajelli et al., 2010; Bobashev et al., 2007; Connell et al., 2009; Rahmandad and Sterman, 2008). These works focused on comparing the simulation results between the compartment model and individual-based model (Connell et al., 2009; Rahmandad and Sterman, 2008), trying to hybrid these two approaches (Bobashev et al., 2007) and giving the principle of which models should be used based on the policy designed (Rahmandad and Sterman, 2008), but none of them focused on how to calibrate different model by calibrating the parameters.

In this paper, we construct a series of methods to calibrate parameters between these two models. In order to compare and analyze the simulation results of these two models, we use the same parameters setting after calibration. We also give a guideline in choosing a simulation model that best fits a user's needs.

2 METHODS

2.1 AsiaFluCap Simulation Model

The AFC model (AsiaFluCap, 2009) is a homogeneous and deterministic model which is base on the fundamental SIR model with three additional compartments, *Prophylaxis* (*P*), *Exposed* (*E*) and *Asymptomatic* (*A*). The detail of the model is described in the supporting text.

In this model, the setting of parameters is the same for all people. The number of people being transited from one compartment to the next compartment in each time slice are given with differential equations. For example, if the latency between E and A is x days and the time slice is y steps per day then in every time slice $1/(x \times y)$ of the people in E are transited to A.

2.2 Taiwan Simulation Model

The TW model (Tsai et al., 2010) is a stochastic and heterogeneous model. Each individual has his own personal attributes such as age, gender, contact probability and daily activities. People with the same daily actives are called in the same mixing group. The duration that an infected individual stays in a disease state is selected according to a probability distribution and individuals may have different disease courses.

2.2.1 Social Structure

In the TW model, the age of a person is the major factor that affects his behaviors such as daily activities and contacts. The social structure basically follows the one given in (Tsai et al., 2010). There are five age groups in the TW model, namely c_0 (0-4 years), c_1 (5-18 years), a_0 (19-29 years), a_1 (30-64 years) and a_2 (above 64 years). At the beginning of the simulation, the age and gender of each person are stochastically generated based on the demographic distributions according to the real census data.[2]

There are ten mixing groups in the TW model, *household* (HH), *household cluster* (CL), *neighborhood* (NB), *community* (CM), *daycare center* (DC), *play group* (PG), *elementary school* (ES), *middle school* (MS), *high school* (HS) and *work group* (WG). Each household contains 1 to 7 people. The age, gender and number of people in each household are also generated according to the Taiwan census data. A household cluster contains four households. A neighborhood contains about 500 people, and a community is formed by four neighborhoods i.e., about 2000 people. Each community has one high school, one middle school and two elementary schools. Each high school and each middle school are shared by all four

[1] Pandemic (H1N1) 2009 - update 112, published by WHO and available at http://www.who.int/csr/don/2010_08_06/en/index.html

[2] 2000 Taiwan census data published by Directorate-General of Budget, Accounting and Statistics, Executive Yuan, Republic of China (Taiwan), available at http://eng.stat.gov.tw/lp.asp?CtNode=1627&CtUnit=777&BaseDSD=7&mp=5

neighborhoods in the same community. Two neighborhoods share one elementary school. Each neighborhood has several daycare centers, playing groups and working groups. The numbers of those groups depend on the number of people in those groups in that neighborhood.

Each day is divided into two periods, the *day time period* (DP) and the *night time period* (NP). Each period has 12 hours. In DP, the young children (c_0) either go to the daycare center or stay close to home in a playing group with an equal probability. The school age children (c_1) go to schools, either ES, MS or HS, depending on their ages with preset drop out rates. The working adults (a_0 and a_1) go to work in DP with a given unemployment rate. All the elder adults (a_2), the drop out students and the unemployed adults stay at home during DP. In NP, people stay at home within the corresponding household cluster, neighborhood and community.

2.2.2 Disease Transmission Model

Disease transmission behavior is mainly controlled by two epidemiological parameters: *contact probability* (CP) and *transmission probability* (P_{trans}). Contact probabilities are given for people of specific age group in a social mixing group, i.e., people in the same age group and same mixing group have the same contact probability. In any time period, a susceptible person may be infected by an infectious person in the same mixing group.

The TW model has four main states S, E, I and R. Each state comprises several compartments. There are two different compartments in E, namely *Latency* (L) and *incubation* (In). For all people in E, only people in In can infect others. I also contains two different compartments, namely *asymptomatic* (I_a) and *symptomatic* (I_s). People in any compartment are transited to the next compartment after one DP and one NP, and they will be transited to either Recover (R) or Death (D) after then.

3 CALIBRATION

We now provide a case study of the calibration between the AFC model and the TW model. We will first group parameters according to they are used in only one model or in both models. For the parameters used in both models, they are grouped according to their representation.

3.1 General Descriptions of the Parameters

In this subsection, parameters are classified according to their attributes. The first step is to distinguish between *shared parameters* and *individual parameters*. Shared parameters are those used by both models such as the transmission probability, the total number of people in the region. Individual parameters are those only used by either one model. In the TW model individual parameters are personal information such as age, gender, household structure etc. Since the individual parameters only appear in one model, in the calibration phase we only focus on the shared parameters. The shared parameters can also be classified into three groups according to the possible range of their values: *fixed-value*, *fixed-probability* and *probability distribution*. The tree structure of the parameter groups is shown in Figure 1.

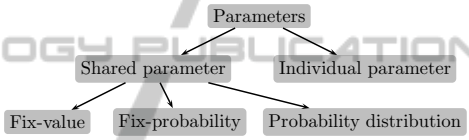

Figure 1: **Parameter usage and type of representation.**

Shared parameters may use the same representation method, to calibrate them we simply assign the same value. For shared parameters that belong to different groups in different models, we need to design a method to transliterate their values.

Before we introduce how to calibrate shared parameters between the AFC model and the TW model, we first describe the different types of parameters and how to group the parameters.

3.2 Individual Parameters

Individual parameters are those only used by either one model. They describe details about the nature of the disease and the human behavior. For example, the compartment expose only appears in the AFC model and the corresponding parameter also only appears in the AFC model. Similarly, the TW model uses mixing group to describe the social structure, so the corresponding parameters which denotes the distribution of household structure and the distribution of age only appear in the TW model.

3.3 Shared Parameters

Shared parameters are those used in both models. They usually refer to *the natural history of disease*

Table 1: Distribution of onset days.

Onset days	3	4	5	6
P_{days}	0.3	0.4	0.2	0.1

Table 2: Distribution of latency and incubation days.

Incubation (Latency) days	1 (1)	2 (1)	3 (2)
$P_{Latency,Incubation} = P_{Latency}$	0.3	0.5	0.2

and *the human behavior*. For example, the number of days of each state of disease and the transmission probability and the efficacy of vaccination belong to the disease natural history. And the reduction of social contact due to government intervention measures and the availability of medical resources belong to the human behavior.

Parameters represented as fixed values include the parameters such as the total number of people, the number of simulation days and the amount of available medical resources.

A parameter represented as a fixed probability means the probability of a particular event will happen e.g., the transmission probability of two people have made an effective contact. Another example is the probability that a patient becomes symptomatic or asymptomatic.

Parameter represented as a probability distribution contains two parts: its sample distribution and the probability space. For example in the section of Taiwan Simulation Model, the number of infectious days are 3-6 days with the corresponding probability of 0.3, 0.4, 0.2 and 0.1 respectively. See Table 1 for an illustration. Another example is shown in Table 2 to illustrate the numbers of latency and incubation days in the TW model.

3.4 Methods of Calibration

For each shared parameter, we first decide whether it belongs to the same group in the two models. We reassign an equal value if they do. If the parameter belongs to different groups, we design a formula to transliterate the 'values' between the two models.

We first consider how to transliterate between a fixed-value parameter in one model and a probability-distribution one in another model. For example, the number of incubation days is 1 day in the AFC model, and it is from 1 to 3 days with probabilities 0.3, 0.5 and 0.2 respectively, in the TW model. To calculated the expected number of incubation days in the TW model, we simply sum the product of the number of days and the corresponding probability, that is:

$$\sum D \times \Pr\{\text{Incubation is } D \text{ days}\}. \quad (1)$$

The expected number of incubation days is $1 \times 0.3 + 2 \times 0.5 + 3 \times 0.2 = 1.9$, and the expected number of onset days is $3 \times 0.3 + 4 \times 0.4 + 2 \times 0.5 + 6 \times 0.1 = 4.1$. See Table 1 and Table 2 for details.

Now we consider the case of transliterating from an expected value parameter in one model to a probability distribution in another model. We use either a scaling or a geometric distributed methods.

In scaling method, the value of probability events of a given distribution is multiplied with the ratio of the given expected value over the expected value of the given probability distribution. Consider a distribution has expected number D_E and sample space $D_1, D_2, \ldots, D_n$ with corresponding probability $P_1, P_2, \ldots, P_n$ respectively. If we want to scale this distribution's expected value to $D_E^{'}$, we first calculate the ratio $RATIO = D_E^{'}/D_E$. Next, we multiply each sample space D_i with $RATIO$ and we have a new distribution with expected value $D_E^{'} = D_E \times RATIO$. For example, the number of latency and incubation days in the AFC model is 1.0 and the expected latency and incubation days in the TW model is 1.9. We can scale down the value of the probability distribution $D_{latency}$ in the TW model with $1.0/1.9 = 0.526$.

In the above case, if we treat the number of days as the expected number of a simple probability distribution, then we can reconstruct the distribution by fitting a probability distribution to that expected value. In the AFC model, each period of the disease course is described as a geometric distribution. For example, the number of latency day is 1.0, and the number of time interval in a day is 15, then in each time interval, $1/15$ of the people in E transit to A. Then we can calculate the corresponding probability of the number of day that a person remain in the same compartment by

$$P(t) = p(1-p)^{t-1} \quad (2)$$

where t is the number of time intervals and p is the probability that person transits to the next compartment. For example, the time interval in the TW model is 2 and the latency period is 1.0 in the AFC parameter setting, then $1.0/2 = 0.5$ of the people transit from E to A in one time interval, and the corresponding probability of people remain in the E is 0.5, 0.25 and 0.125 with 0.5, 1.0 and 1.5 day respectively.

3.5 Experiment design

In order to observe the outputs of the two models under different data settings, we design two experiments. One simulation comprises three major parts, the simulation model, either the AFC model or the TW model, the parameter setting, either the AFC data setting or the TW data setting, and the size of regions.

Table 3: Experiment scenarios for basic experiment.

Model	Regions Size	Parameter Setting
AFC	Large	AFC-setting
AFC	Large	TW-setting
AFC	Small	AFC-setting
AFC	Small	TW-setting
TW	Large	AFC-setting
TW	Large	TW-setting
TW	Small	AFC-setting
TW	Small	TW-setting

Table 4: Experiment scenarios for small region experiment.

Model	Region Size	Parameter Setting
TW	1…100	AFC-setting
TW	1…100	TW-setting

The experiment scenarios is detailed in Table 3 and Table 4.

In the first experiment, we examine the behaviors of both models using different sizes of regions. We denote the whole Taiwan as the large region and 1 CM as the small region. For each model we run the simulation twice in both region sizes with the TW data setting and the AFC data setting respectively. Note that the AFC data setting has longer periods of states in the disease course, the number of days one patient is hospitalized is 12 days and the number of day one patient uses a ventilation is 13 days, and also has a larger number of expected contacts, 7.0, than that of using the TW data setting, 4.19.

Since the prevalence of the AFC model is not affected by changing the region size, and the TW model is sensitive to the size of the region, the second experiment focuses on observing the behavior of the TW model with different sizes of regions. This experiment uses both the AFC and the TW data settings as parameter settings. The size of the region, i.e., the number of CM variates from 1 to 100.

4 EXPERIMENTAL RESULTS

In this section, we introduce the experiment environments for implementing the AFC model and the TW model. We show the data settings and the corresponding experiment results.

The TW model is implemented using C++ (Tsai et al., 2010) and the AFC model is implemented using an Excel spreadsheet (Krumkamp et al., 2011). The experiments were run on a server with dual Intel Xeon X5482, quad-cores, 3.20 GHz CPU and 64GB DDR3 memory. Since TW is an agent-based simulation, for each simulation of TW model we run 30 times and take the average.

The first experiment includes eight scenarios for the combination of the AFC model and the TW model, the AFC setting and the TW setting, and the large region (entire Taiwan) and the small region (1 CM). The experiment results are shown in Figure 2 and the detail values are shown in Table 5. Figure 2 shows the number of daily cases with different size of regions and different parameter settings. The first three columns in Table 5 denote the model used, the data settings and the size of each region, respectively. The three columns followed are the prevalence of symptomatic cases, asymptomatic cases, and their total. The last two columns denote the peak day and the R_0 of each experiment. The peak day is the day with the maximum average number of people that are currently symptomatic. We first calculate the average number of symptomatic cases of all 30 simulations and then choose the day with the largest number of symptomatic cases as the peak day.

The basic reproduction number R_0 is derived for each model. The AFC model calculates R_0 by multiplying the number of contacts with the transmission probability and the number of days of the disease course (Krumkamp et al., 2011).

The TW model calculates R_0 using a formula that is similar to the one used in calculating the expected number of contacts (Tsai et al., 2010). In each simulation, we sample 2,000 individuals, i.e., the number of people in 1 CM. We then calculate the expected number of peoples that can be infected by each of the sampled individuals. We calculate the probability that one susceptible is infected by the indicated infectious person minus the probability that this susceptible individual is not infected by that infectious person in all of the mixing groups they shared.

Table 6: Simulation result in TW model with different numbers of CM.

	AFC			TW		
CM	All(%)	Sym(%)	Peak Day	All(%)	Sym(%)	Peak Day
1	74.09	56.88	24	79.70	59.73	31
2	62.61	46.75	29	66.37	47.36	38
3	56.87	41.52	31	61.70	43.18	45
4	56.01	40.58	33	59.22	41.19	46
5	53.65	38.49	35	56.54	39.16	47
6	52.34	37.50	35	55.20	37.92	50
7	51.34	36.60	37	54.83	37.58	53
8	50.22	35.77	35	53.65	36.65	53
9	49.94	35.40	39	53.87	36.81	55
10	49.38	35.07	38	52.65	35.89	55
20	48.89	34.58	40	51.39	34.76	63
30	48.77	34.49	39	50.38	33.99	66
40	47.27	33.11	48	50.01	33.68	70
50	47.11	33.02	48	50.18	33.74	72
60	47.08	32.94	49	50.09	33.68	72
70	46.77	32.73	53	49.76	33.43	75
80	46.52	32.50	50	49.79	33.45	77
90	46.58	32.58	54	49.56	33.23	77
100	46.66	32.64	53	49.46	33.18	79
Taiwan	46.25	32.29	86	49.39	33.09	130

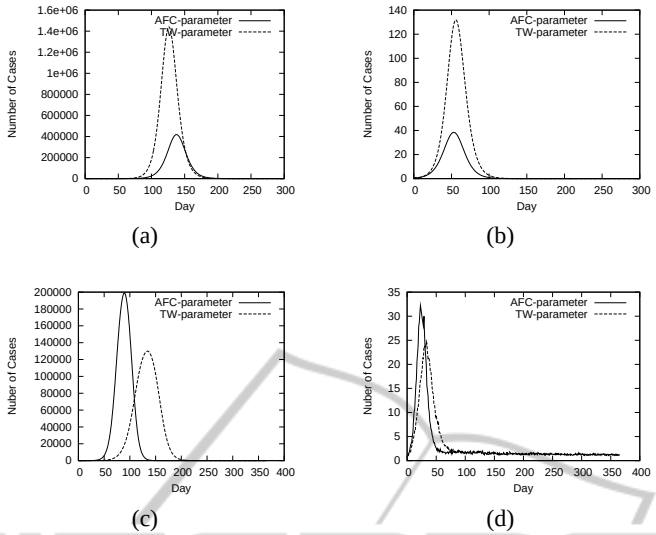

Figure 2: **Basic experiments with two models, two parameter settings and different size of regions.**

Table 5: Basic experiments with two models, two parameter settings and different size of regions.

Model	Parameters	Size	Symptomatic	Asymptomatic	Prevalence All	Peak Day	R_0
AFC	AFC	large	31.32%	13.43%	44.75%	137	1.32
	AFC	small	31.41%	13.44%	44.85%	52	1.32
	TW	large	48.84%	24.42%	73.26%	125	1.78
	TW	small	48.71%	24.33%	73.04%	55	1.78
TW	AFC	large	32.29%	13.97%	46.25%	90	1.38
	AFC	small	56.88%	17.22%	74.09%	24	1.36
	TW	large	33.09%	16.30%	49.39%	136	1.43
	TW	small	59.28%	20.20%	79.48%	34	1.41

5 DISCUSSION

5.1 The Baseline Experiment

The first observation is that the prevalence is not affected by the region size in the AFC model and is affected by the region size in the TW model. In the AFC model, the region size affects the prevalence only slightly, namely 0.1% for the AFC data setting and 0.2% for the TW data setting. In the TW model, experiments using a large region size have much lower prevalence than that of using a small region size. It is 46.25%, greatly reduced from 76.25%, for the AFC data setting and from 79.48% down to 49.39% for TW data setting.

Peak day in a large region setting is later than that of the setting for a small region even using the same model. When using the AFC model with the AFC data setting, the peaks day for a large region setting and a small region setting are 137 and 52 respectively, and when using the AFC model with the TW data setting, the peak day for a large region setting and a small region setting are 125 and 55 respectively. When using the TW model with the AFC data setting, the peak day for a large region setting and small region setting are 90 and 24 respectively, and when using the TW model with the TW data setting, the peaks day for large region setting and small region setting are 136 and 34 respectively.

R_0 of the AFC data setting is almost identical using all 4 different settings, namely 1.32, 1.32, 1.38 and 1.36, but R_0 of the TW data setting deviates a lot, namely 1.78, 1.78, 1.43 and 1.41.

The experiment results show the prevalence is sensitive to the region size in the TW model and is not sensitive in the AFC model with either data settings. This is because AFC model is homogeneous, i.e., contact probability is the same for all individuals. The TW model is, on the other hand, heterogeneous based on demographic statistics for the entire nation, i.e., an individual with in a given mixing group and has a distinct contact probability with another individual in another mixing group.

Both the AFC and TW data settings have a larger prevalence in the TW model when using a smaller region setting, and a smaller prevalence when using a larger region setting. The TW model has similar behaviors when regions of similar size are used even when the values of other parameter are different.

Another important factor is that worker flow is not considered in the AFC model but may affect the accuracy of simulation if there are a large number of people commuting. Worker flow is the only way two

people in different communities may have a chance to contact in the TW model. It takes more time for the disease to spread to other CM when the number of CM's increases. This factor affects the peak day and the prevalence in the TW model.

Although the AFC model is homogeneous, when the size of regions increases, the peak day also delays. This is because when the initial condition is the same, the increasing rate of newly infected people remains the same. As the number of susceptible people increases, more time is needed to infect the same percentage of people.

The values of R_0 are similar for AFC model and the TW model using the AFC data setting, but are quite different when using the TW data setting. The main reason is the disease courses used in the two models are different. The TW model assumes that asymptomatic patients and patients in the incubation period only have half of the original transmission probability. But in the AFC model, the transmission probability is the same in all states. If we apply the formula in the AFC model for the TW data setting and replace the transmission probability for the asymptomatic case and patients in incubation with half of the original probability, then R_0 is 1.40. This value is close to the R_0 values in the TW model using the TW data setting which are 1.41 and 1.43, respectively.

5.2 The Small Region Experiments

This experiment focuses on the behavior of the TW model using the AFC data setting and the TW data setting when the size of regions is small.

The prevalence decreases as the region size increases. The AFC data setting has a prevalence of 74.09% when the number of CM's is 1, and becomes 46.66% when the number of CM's is 100. The TW data setting has a prevalence of 79.70% when the number of CM's is 1, and 49.46% when the number of CM's is 100. In the case of having 100 CM's, the prevalence is very close to that of the simulation result with the entire nation.

The peak day of using a larger region setting is later than the peak day of using a smaller region setting. Although the peak day does not increase monotonically as the number of CM's increases, the peak day of the AFC data setting increases from 24 to 53 and the peak day of the TW data setting increases from 31 to 79 as the number of CM's increases from 1 to 100.

Note there is no direct relationship between the region size and the expected number of contacts. However, when the number of CM's increases, the disease needs more time to transmit to other CM's due to the worker flow being that the only way for people to travel between CM's. Since the worker flow describe the probability that a worker lives in a particular town and works in other town, it only assigns workers to the level of a town not to the level of a CM. The probability of a CM in the same town being chosen as a worker works is uniformly distributed over all CM in this town. As the number of CM's in a town increases, the probability of patients working in some indicated CM decreases. Hence it is harder to spread over the whole town and therefor the prevalence decreases.

Due to reasons similar to the above, as the number of CM's increases, the disease needs more time to spread from the original CM where the index cases are to all other CM's. Hence the peak day is further delayed as the number of CM's increases.

6 CONCLUSION

To analyze the trade-off between various simulation models and establish a guideline for model selection, we first introduced two different real instances, namely the AFC model and the TW model. We grouped the parameters used and introduced procedures to transliterate parameters. We also described procedure to perform calibration. We ran both models with the data settings calibrated between them. We then analyzed the simulation results and gave the advantages and disadvantages of these models and provided a principle of model selection.

As a by-product of our study, we conclude the following recommendations when there is a choice between using a aggregative model and an agent based one to study the same disease. According to the analysis result, we should select the model depending on user requirements. Generally, if we want to build a simulation model to observe the high-level disease transmission behavior, to get a immediate simulation results, or we have only a limited information about the disease course, e.g., the average time of each duration, we should choose the AFC model since it can be built using relatively little information. If we want to study how the heterogeneous social structure, e.g., schools and day care centers, affects the disease transmission behavior, to predict the effect of intervention policy on an individual basis, or to observe the spatio-temporal spreading behaviors of the disease, we should choose the TW model since it is geographic based and can easily contain detail individual information.

ACKNOWLEDGMENTS

The AsiaFluCap project is coordinated by the London School of Hygiene and Tropical Medicine with collaborators from the Hamburg University of Applied Sciences (HAW), Netherlands National Institute for Public Health and the Environment (RIVM), International Health Policy Programme -Thailand (IHPP), Taiwan Centers for Disease Control, University of Indonesia Faculty of Public Health, Vietnam Ministry of Science and Technology, Vietnam Military Medical University, Lao PDR National Emerging Infectious Diseases Coordination Office, Lao PDR University of Health Sciences, Mahidol University Faculty of Tropical Medicine, Cambodia Department of Communicable Disease Control, and Cambodia National Institute of Public Health. We are grateful to the many collaborators within this project consortium for their contribution towards resource characterization, data collection, and discussions at consortium meetings. These include: Ly Khunbunn Narann and Chau Darapheak (Cambodia); Sandi Iljanto, Noviyanti Liana Dewi, Kamaluddin Latief, Amir Suudi, Lilis Muchlisoh (Indonesia); Nyphonh Chanthakoummane, Sing Menorath and Rattanaxay Phetsouvanh (Lao PDR); Yu-Chen Hsu, Yi-Ta Yang, Steve Kuo (Taiwan); Pornthip Chompook, Jongkol Lertiendumrong and Viroj Tangcharoensathien (Thailand); Le Minh Sat and La Thanh Nhan (Vietnam). Excellent administrative support from Nicola Lord and Wasamon Sabaiwan is greatly appreciated. We also thanks for James W. Rudge for revising this paper.

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