Changing of Spreading Dynamics for Infectious Diseases in an Aging Society: A Simulation Case Study on Flu Pandemic

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Abstract: In this paper, we report some initial results obtained from the agent-based simulation system SimTW about the changing of spreading dynamics, e.g. speed, magnitude and affected people of different ages, when the target society is aging. A disease model of influenza is built and then is invoked with two different social structures, e.g., population and household distribution, and working and schooling patterns based on Census 2000 and Census 2010 of Taiwan. In the 10 years time, the average population age in the country increases from 33.0 to 37.6 while the average household size decreases from 3.19 to 2.94. From the simulation results, we find that in the more aging year-2010 society, the pandemic, if occurred, is smaller, in terms of the total number of infected persons and slower in terms of the date of the peak number of daily new cases, but is more serious both in terms of the numbers of needed hospital beds and death cases. Using this finding, we hope to motivate further discussions on adapting public health policies to this inevitable global trend of aging.

1 INTRODUCTION

The building of an agent-based simulation on modeling the spreading of infectious diseases like influenza or flu has been reported in order to study their spreading dynamics (Adam, 2020; Tsai et al., 2010). We observed from the kernel of simulation systems that vital factors affecting the nature of spreading include the compositions of people in households, communities, work groups and schools. In a typical scenario, virus in an infected person travels through commuting to work places and schools. The virus also has a better chance of propagating in households of larger sizes. Motivated by these observations, and the fact that the world is aging with a growing average population age and smaller household size (World Health Organization, 2020), we want to study and compare disease spreading patterns between two societies with different aging populations. We hope to study changing of spreading patterns and as a result to motivate better adaptation of public health policies reflecting to inevitable demographical changes over time. In order not to deal with parameter aligning across different

societies, we choose to carry the study on the same society, but with a 10-year time-lag. That is, we compare the results between the demography of Taiwan in the year 2000 and that of the year 2010. We also focus on flu which one of the most common infectious diseases (Riley, 2007).

In this paper, we study the spreading patterns between the two populations in year-2000 and year-2010 respectively in Taiwan on influenza pandemic and discuss medical resources requirements if it occurred. We first generate mock populations of year-2000 and year-2010 based on Taiwan census data in years 2000 and 2010 (National Statistics, ROC (Taiwan),). Then we use the disease nature history parameters and system parameters as given in SimTW (Tsai et al., 2010). We then perform simulations on the two models and collect the data on daily newly infected cases. The risk level of people with different ages are different for a disease like flu if infected. Using parameters reported in (Meltzer et al., 1999), we calculate the total hospital beds needed and the death toll. From the simulation results, we find that in the more aging year-2010 society, the pandemic, if occurred, is smaller, in terms of the total number of infected persons and slower, in terms of the date of

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the peak number of daily new cases, but is more serious both in terms of the numbers of needed hospital beds and death cases. Using this finding, we hope to motivate further discussions on adapting public health policies to this inevitable global trend of aging.

The structure of the rest of this paper is as follows. In Section 2, we give a survey of related work. In Section 3, we describe our data source and the methods we used. In Section 4, we describe the experimental results. In Section 5, we give some discussions. Finally, in Section 6, we give some possible future work and conclusions.

2 RELATED WORKS

Simulation models has been widely used in many fields such as epidemiology (Ferguson et al., 2006) and weather forecast (Furrer and Katz, 2008) as an effective tool to understanding characteristic of disease and predicting the future.

The pace of population aging around the world is increasing dramatically. Taiwan became an aging society in 1993, an aged society in 2018 and will become a super aged society in 2025 as projected in (World Health Organization, 2020; Taiwan, National Development Council, Executive Yuan, 2020). A disease has different impacts on different age groups. For example, the death rate of covid 19 among people 70 years older is 100 times more than that of the age group between 20 and 30 years old (Bialek et al., 2020; Richardson et al., 2020; Tsay et al., 2020).

There are two main approaches for simulation work done for epidemiology studies, namely a mathematical one and an agent-based one.

Agent-based stochastic simulation is an approach that widely used for studying infectious diseases (Germann et al., 2006). This approach can be seen as a real world environment that has been simplified and modularized. We can do a lots of experiments that hard to do in real life and get some useful insights from the results. For example, (Tsai et al., 2010) helped government designed intervention methods to prevent the spread of diseases and (Chang et al., 2015) study about the impact of household structure on epidemiology.

In a mathematical modeling of infectious disease, the sensitivity analysis is employed to aid in identifying influential model parameters (Wu et al., 2013). Many domains which utilize simulation softwares have recognized the importance of validation, verification, and uncertainty quantification of simulation outcomes to build trust in interpreting generated results for decision-making processes (Wright et al.,

2020). Relatively few work has been reported on this regard when agent-based disease simulations are used(Venkatramanan et al., 2018; Hunter et al., 2018; Perkins et al., 2019; Hoertel et al., 2020; Ferguson et al., 2020).

3 MATERIAL AND METHOD

In this section, we first describe our data source. Then we describe the architecture of the agent-based simulation system called SimTW that we used. Finally, we give the experimental designs and parameters.

3.1 Data

We briefly describe the difference between the year-2000 and year-2010 societies. The difference in age distribution and household size between year-2000 and year-2010 are shown in Table 1 and Figure 1. The population size of year-2000 is about 22.27 million and year-2010 is about 23.16 million. In Figure 1, the percentage of population below 25 years old drops about 8.7% from year-2000 to year-2010, but the above-45-years-old population increases about 10.5%. The average population age of year-2000 is 33.0 years old and year-2010 is 37.6 years old which means that the whole population in year-2010 is much older than that of year-2000.

Household structure is one of the important factors affects the disease transmission network (Chang et al., 2015). Figure 1 shows the percentages of household sizes from 1 to 8 member in years 2000 and 2010. The total number of households increases from 6.38 million to 7.85 million and the average drops from 3.19 to 2.94. The number of households containing at least 5 members about decreases significantly.
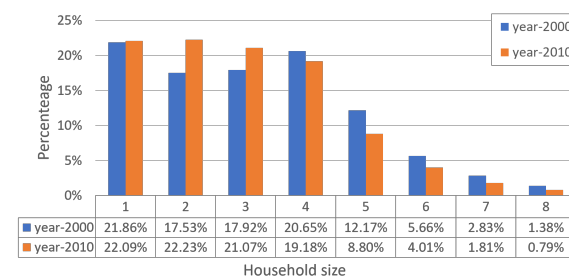

	1	2	3	4	5	6	7	8
year-2000	21.86%	17.53%	17.92%	20.65%	12.17%	5.66%	2.83%	1.38%
year-2010	22.09%	22.23%	21.07%	19.18%	8.80%	4.01%	1.81%	0.79%

Figure 1: Percentage of household sizes from 1 to 8 member in year-2000 and year-2010.

3.2 Simulation System

In this paper, we used the simulation software developed by (Tsai et al., 2010). This software implements

Table 1: Population distribution of year-2000 and year-2010 in five age groups.

		0-4	5-19	20-29	30-64	65+	all
year 2000	number of people	1,489,242	5,089,214	3,780,665	9,996,243	1,921,308	22,276,672
	percentage	6.69%	22.85%	16.97%	44.87%	8.62%	average population age = 33.03
year 2010	number of people	964,093	4,268,372	3,473,436	11,968,329	2,487,893	23,162,123
	percentage	4.16%	18.43%	15.00%	51.67%	10.74%	average population age = 37.62

an agent-based stochastic and heterogeneous discrete time agent-based model.

3.2.1 Mock Population

This software generates a mock population. i.e., the set of agents, based on the national demographics, and then build daily commuting pattern, i.e., worker and student flow, using Taiwan Census Data Year 2000. Each agent in this system has its own attributes, such as person ID, age group, gender, routine type, resident place, work/school place, medical record and so on.

This system uses an approach proposed by (Geard et al., 2013) to generate a mock population with household structure. It separates the whole population into five age groups, namely preschooler children (0-4 years old), school-age children (5-18 years old), young-adults (19-29 years old), adults (30-64 years old) and elders (65+ years old). People in the same age group has similar behaviors such as daily activities and contacts. Routine type is an attribute that describes an individual's activities. There are nine types in the model: household, day-care center, play-group children, kindergarten student, elementary school student, middle school student, high school student, university student and workers.

3.2.2 Social Structures

A mixing group is a daily close association of individuals, where every member is connected to all other members in the same group. There are twelve classes of such mixing groups in the model and they can be divided into three categories: resident areas, routine areas and surrounding areas. Resident areas include household, household cluster, day-care center and play-group which is the location of the agent's home. Routine area is where agents stay for working and studying which include kindergarten, elementary school, middle school, high school, university, work group, dormitory of university and dormitory of work group. Surrounding area are neighborhood and community which represented the places providing occa-

sional casual association such as shopping mall and restaurant around university.

3.2.3 Agent's Behavior

Each simulation day is set as workday, holiday or long holiday which is a holiday lasts for more than 2 days according to the calendar publish by (Directorate-General of Personnel Administration, Executive Yuan, ROC (Taiwan),). Each day is divided into the day time and the night time period with 12 hours each. Agents go to their routine areas in the daytime of a workday except non-schooling preschooler children, dropped out school-age children and young-adults, adults and elders if unemployed and non-schooling. During the night time of workday and the whole day in a holiday, agents who commute to routine area stay at resident area. Those who stay in dormitories go to their resident areas only during long holidays.

3.2.4 Disease Transmission Model

We use the SEIR disease model as described in (Krumkamp et al., 2011). In this model, each individual can be in one of the following four states, susceptible (S), exposed (E), infectious (I), and recovered (R). There are two main parameters in the disease transmission model: contact probability and transmission probability. Contact probability represents the chance of an effective contact between two individuals in the same mixing group. Individuals in the same age group have the same contact probability in any given mixing group. The transmission probability P_{trans} is the chance that an effective contact results in an infection. When a susceptible individual having an effective contact with an infectious individual, the susceptible individual becomes exposed with the probability P_{trans}. An exposed individual will later become infectious and then get recovered according to the embedded disease natural history.

3.2.5 Disease Natural History Model

The model of flu's natural history in (Germann et al., 2006) is used is this system. Latent period refers to the time between E and I, the individual does not have any symptoms or signs of infection in this period, while the incubation period is the time between infection and symptom onset (Park and Ryu, 2018). The time from I to R is called *infectious period*, in which the infected individual can infect others. In this model, the average latent period, incubation period and infectious period are 1.2 days, 1.9 days and 4.1 days respectively, and there are one-third of asymptomatic infectious individual.

3.3 Experiment Design

In this paper, there are a total of twelve experiments consisting of six different P_{trans} from 0.08 to 0.14 and two different mock populations. All others setting besides P_{trans} and mock population are fixed. We note that P_{trans} of a typical seasonal flu is about 0.08 (Fraser et al., 2009; Tsai et al., 2010).

The seeding policy is one index case that randomly picked from the susceptible individuals every five days (Tsai et al., 2010). The duration of a simulation run is set to be 930 days. No intervention strategy such as vaccination, school closure or social distancing policy is involved. We perform 100 runs for each experiment then we take the average.

The mock population is then generated randomly according to the household structure and the population of all age groups. We then dump the age distribution of the generated mock population and check the actual census data from year-2000 and year-2010. They are highly matched with both correlation coefficients being greater than 0.99 which is shown in Figure 2.

The basic reproductive number R_0 is defined as the expected number of new infections caused by a typical infected individual in a susceptible population (Heesterbeek, 2002; Heffernan et al., 2005). We can determine whether an infectious disease will be a pandemic through R_0. Usually, when R_0 is more than 1, then it is called a pandemic. R_0 of twelve experiments mention above are also run by the simulation system in "R_0 mode". When running in "R_0 mode", the system generated the same simulation world (included mock population, mixing groups, flows, agent's behavior and disease transmission model) as "normal mode". The only different part is the seeding and the P_{trans} of non-seeded index cases. In "R_0 mode", the system will only seed one agent in each run. P_{trans} of all non-seeded index cases (cases that infected by
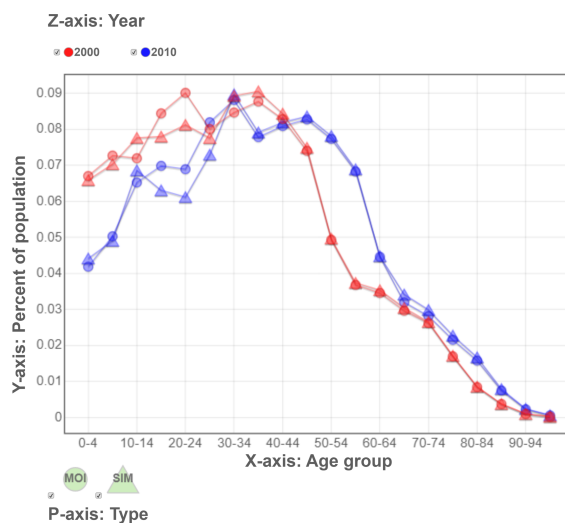

Figure 2: Comparing generated mock population and the actual census data.

the seeded case) is set become 0 to avoid interference. When the seeded case recovered from infectious state, this run of simulation ended and the infected case number beside the seeded case will be recorded, then went to the next run. We carry out 10,000 simulation run and then take the average as the result of R_0.

The average R_0 of each experiment is calculated and summarized in Table 2. We chose those P_{trans}'s for experiments because the calculation result of R_0 is similar to the H1N1 pandemic in year 2009 (Fraser et al., 2009). We note that with the same P_{trans}, year-2000 always have a larger value compared to that of year-2010. The impact of the household structure mention in (Chang et al., 2015) may be a reason because the average household size of year-2010 is smaller than that of year-2000.

Table 2: Relations between P_{trans} and R_0.

P_{trans}	2000	2010
0.08	1.121	1.053
0.09	1.251	1.166
0.10	1.374	1.303
0.11	1.504	1.421
0.12	1.647	1.539
0.13	1.771	1.650
0.14	1.902	1.795

4 RESULTS

One of the advantages of using an agent-based simulation is that we can get a finer resolution during the entire pandemic process, e.g., daily infected cases,

peak day, peak value and the infected cases in each age group.

As shown in Figure 3, the number of total infected cases in both years becomes higher as P_{trans} goes higher, and year-2000 has a larger number comparing to that of year-2010, but the difference gets smaller when P_{trans} increases. This phenomenon is due to the amount of susceptible individuals is fixed, it is harder to find a susceptible individual when most of the population are already in the R state when the pandemic is almost end.
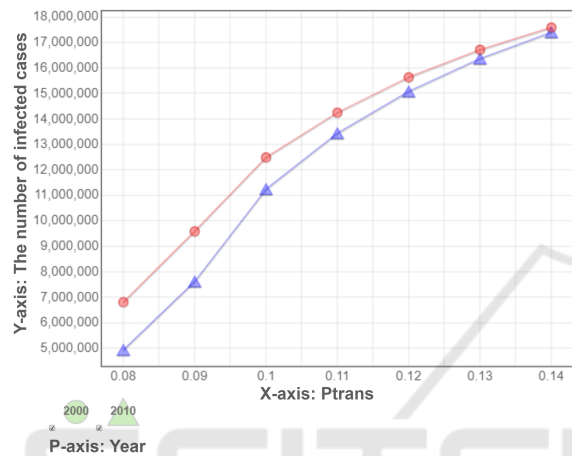
Figure 3: The total number of infected cases against different transmission probabilities (P_{trans}).

Figure 4 and Figure 5 show the peak day and peak value during a pandemic. The peak day of year-2010 is a bit late comparing to year-2000 when P_{trans} is lower than 0.12. There is no significant difference when P_{trans} gets higher. The peak number of daily new cases of year-2000 society is higher than that of year-2010.
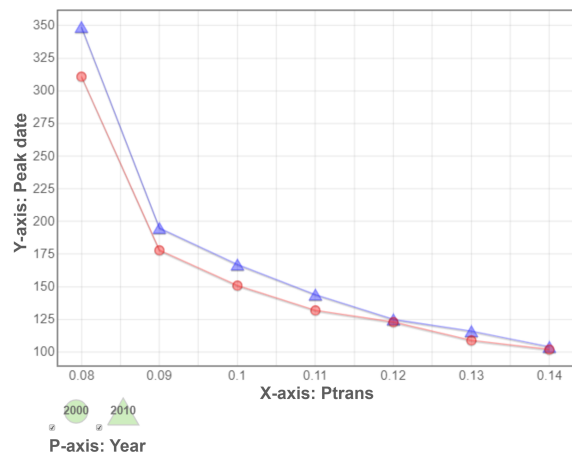
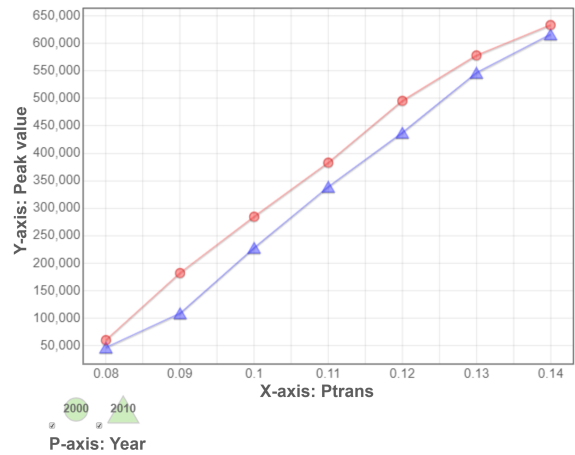

Figure 4: Peak date of daily newly infected cases.

Figure 5: Peak value of daily newly infected cases.

5 DISCUSSION

We note the following interesting points for discussion. The hospitalization rates of different age groups are very different. Elders are likely to have a higher hospitalization rate compared to others. Table 3 shows the hospitalization rates reported by (Meltzer et al., 1999). We use those data to do a post-process calculation and find some interesting results.

Table 3: Hospitalization and Death Rates.

Variable	Rates per 1,000 cases		
	0-19 years old	20-64 years old	65+ years old
Hospitalizations	1.22	7.88	28.83
Deaths	0.87	2.11	12.56

We show the total number of hospitalizations in Figure 6, and hospitalizations separated by age groups in Figure 7. In Figure 6, there is an intersection near the point when P_{trans} is 0.10. We can clearly see that this intersection is mainly caused by the chaning of the number of infected adults and elders in Figure 7. Recall that the total infected cases in the year-2000 society is always higher than that of in the year-2010 society using all combinations of parameters. Due to the differences in hospitalization rates for different age groups, it causes the number of hospitalizations of the year-2010 society to overtake the year-2000 society.

We further show the number of deaths in Figure 8 and deaths separated by age groups in Figure 9. The intersection moved a bit forward comparing to the total hospitalizations.

Figure 10 shows the daily new cases and hospitalizations when P_{trans} is 0.08. We observe that the pandemic in year-2000 is faster and the peak is higher
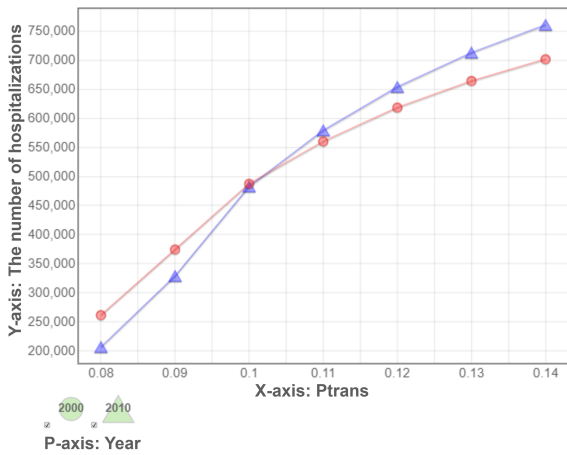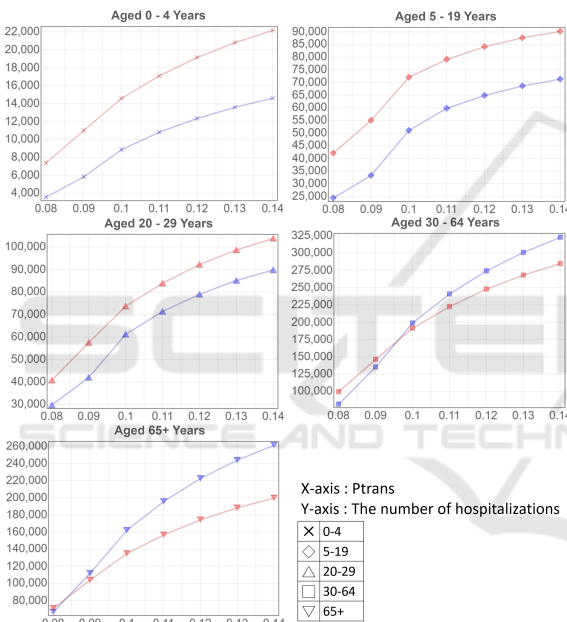
Figure 6: The number of hospitalizations.

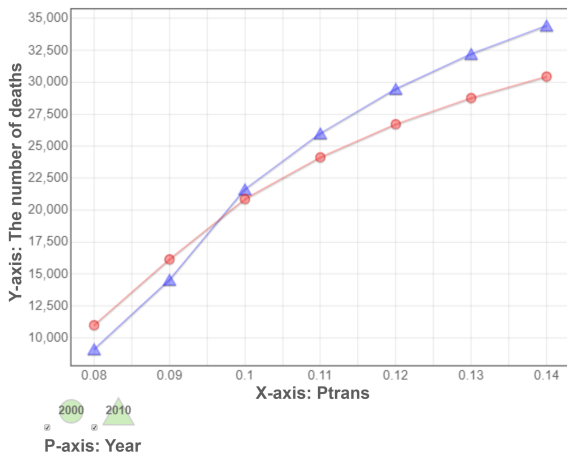Figure 7: The number of hospitalizations by age groups.
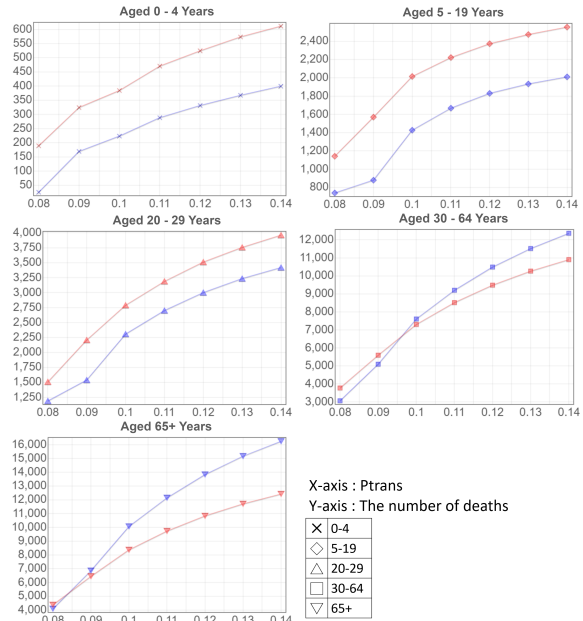

Figure 8: The number of deaths.

Figure 9: The number of deaths by age groups.

compare to year-2010 in terms of daily new cases, but the peak number of hospitalizations is about the same due to having a higher hospitalization rate for the elders.
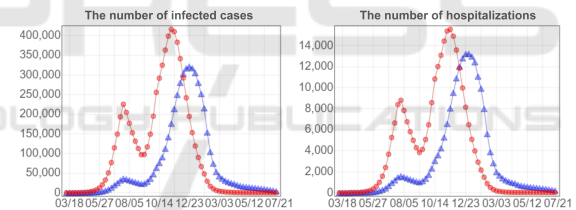

Figure 10: The numbers infected cases and hospitalizations (P_{trans} =0.080).

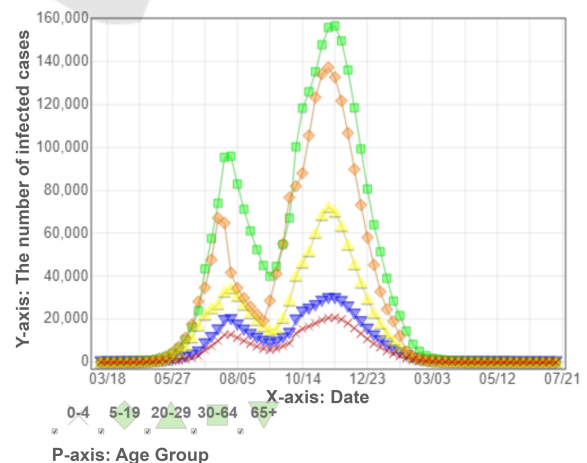Figure 11: The numbers of infected case by age groups (P_{trans} =0.080, year-2000).

As observed from Figure 11, there are two peaks during a pandemic. This phenomenon may be due to the holiday's effect during the summer vacation. We note that the number of infected school-age children significantly drops during the summer vacation and rises quickly when the holiday ends.

6 CONCLUSIONS AND FUTURE WORK

We have reported our simulation results on the changing of spreading patterns in facing a flu pandemic between the year 2000 and the year 2010 in Taiwan. In the 10-year time-lag, Taiwan has shown great signs of aging. The average population age is up 14% from 33.0 to 37.6 while the average household size is down 8% from 3.19 to 2.94. In facing a flu pandemic, year-2010 has less total infected cases and later peak date comparing to year-2000 though the total population is up 4% from 22.27 million to 23.16 million. However, due to the fact having more higher risk population, e.g., people over the age of 65, higher demands of hospital beds and a larger death toll are observed (Meltzer et al., 1999). Though Census 2020 data has yet to be released, the current preliminary data (Dept. of Household Registration, Ministry of the Interior, ROC (Taiwan),) show the tend of aging to get worse, namely the average population age is further 11% up to 41.86 while the household size is plunged another 9% to 2.67. What are seen in this study will get worse. We hope to motivate some further studies in redesigning public health policies to better taking care of this trend.

We remark that the approach we used in this paper is useful for studying how disease spreads in Taiwan, but it has some limitation. First it is impossible to simulate every possible spreading ways in the real world though the validation of this simulation system on a flu model had done by (Tsai et al., 2010). Secondly, we only focus on the trend but not the exact number when we interpret the results.

For future studies, we hope to rerun our experiments when the year 2020 Census data are released. We also want to study efficacy of different intervention mechanisms, such as mask wearing and vaccine strategies, in an aging society. Public health policies designed 20 years ago may not be as effective if used now.

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