Household Structure Projection: A Monte-Carlo based Approach

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Abstract: The kernel of an agent based simulation system for spreading of infectious disease needs a so called household structure (HSD) of the area being simulated which contains a list of households with the age of each member in the household being recorded. Such a household structure is available in a Census that is usually released every 10 years. Previous researches have shown the changing of the household structure has a great impact on disease spreading patterns. It is observed that the changing of the household structure e.g., the average citizen ages and household size, is at a faster speed. However, serious infectious diseases, such as SARS (year 2002), H1N1 (year 2009) and COVID-19 (year 2019), occur with a higher frequency now than previous eras. For example, it would be bad to use HSD_{2010} built using Census 2010 to simulate COVID-19. In view of this situation, we need a better way to obtain a good household structure in between the Census years in order for an agent-based simulation system to be effective.

Note that though a detailed Census is not available every year, aggregated information such as the number of households with a particular size, and the number of people of a particular age are usually available almost monthly. Given HSD_x, the household structure for year x, and the aggregated information from year y where $y > x$, we propose a Monte-Carlo based approach "patching" HSD_x to get an approximated HSD_y. To validate our algorithm, we pick x and $y = x + 10$ which both Censuses are available and find out the root-mean-square error (RMSE) between Census's HSD_y and generated HSD_y is fairly small for $x = 1990$ and 2000. The spreading patterns obtained by our simulation system have good matches. We hence obtain HSD_{2020} to be used in your system for studying the spreading of COVID-19.

1 INTRODUCTION

The corona virus disease 2019 (COVID-19) has been around the world since late 2019. According to World Health Organization (2022), COVID-19 has infected over 400 million and killed nearly 6 million people (World Health Organization, 2022). The numbers are still rising. Clinical trial reports and researches show that available vaccines have high efficacy against symptomatic infection and viral variants (Voysey et al., 2021; Baden et al., 2021; Thomas et al., 2021; Gilbert et al., 2022; Tregoning et al., 2021). One of the most effective ways to let us get back to the "normal" live as before is to increase the vaccination coverage. While vaccine supply is still limited, developing an effective vaccination strategy becomes an important work.

We try to use a stochastic agent-based simulation called SimTW developed by (Tsai et al., 2010) to find out the best vaccination strategy for Taiwan. The mock population is the kernel of SimTW. Simulation results with a vaccination intervention strategy using a mock population generated from Census 2010 may not be effective because of the dramatic demographic changes over years (Lin et al., 2021). As shown in Figure 1, the population from 5 to 18-year-old drop nearly 25% and the population above-65-year-old is 36.8% higher comparing year 2010 and year 2020. Moreover, the total number of households has increased about 14%. The households containing 1 member, and 8 or more members have huge increases. However, the number of households containing 4 to 6 members are decreasing. An up-to-date

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mock population is highly needed in this research. Census is carried out once per ten years, which leaves the detailed information relevant to build a mock population lacking in non-Census years. However, some high level aggregated data, such as the age distribution and household statistics are available almost yearly. Hence it is desirable to "patch" the mock population built from Census with recent updates.

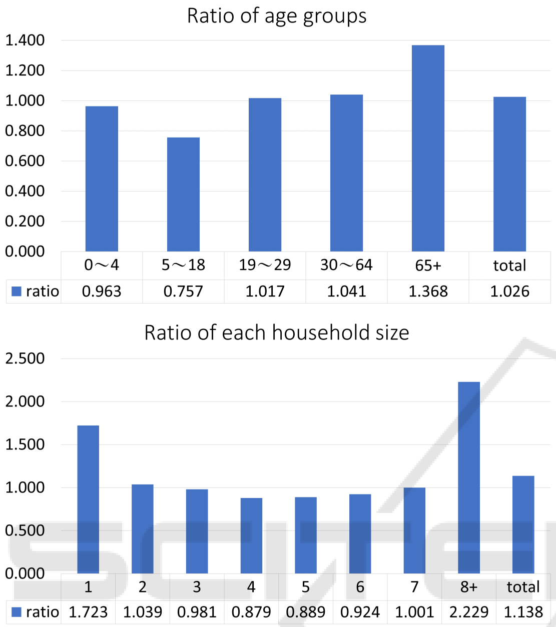


Figure 1: The ratio of age groups and household size in year 2020 over year 2010.

A simulation approach to generate a household structure distribution (*HSD*) with Census data, proposed by Geard et al. (Geard et al., 2013), was used in SimTW. This approach generates *HSD* for a given mock population by a probability distribution over the household patterns. The probability distribution of the household pattern can be obtained from raw data of Census released by (National Statistics, Taiwan,). Although the survey and report of Census 2020 were done and released, the raw data are yet to be released. To make sure having a relatively correct *HSD* and age distributions at any specific year, we formulate the probability distribution of the household pattern building problem as a constrain satisfaction problem and purpose a Monte-Carlo based method to solve it using available aggregated data.

The structure of the rest of this paper is as follows. In Section 2, we describe our data source and the simulation system we used. Then we describe the problem and our algorithms in Section 3. Section 4 will describe the experimental design. In Section 5 and Section 6, we show the validation and experimental results. Finally, in Section 7, we give some discussions and conclusions.

2 PRELIMINARY

In this section, we first describe related work and method. Second, we introduce an agent-based simulation system called SimTW. Then we describe and compare the data sources.

2.1 Related Work

Our needs can be said as a detailed version of the population projection problem (United Nations, 1946). There are a total of 23 manuals and guides of demographic related methods issued by the United Nations (United Nations, 1946). Especially in Manual 1, there are several methods and discussion about estimating the total population in years later. This manual states that the estimation based on incomplete enumerations and non-Census data are clearly more reliable than simply conjectures. In addition, six methods including the arithmetic rate, the geometric rate, the parabola of second/third degree and the second/third-degree on logarithms are also given in this manual. However, none of them are accurate in all aspects (UN DESA, 1952). Manual IV also gives methods on estimating demographic from aggregate and incomplete data and also methods to appraisal the result (United Nations, 1967). Also, several dimensions including population size, educational attainment, etc..., need to be considered when projecting the global population (Lutz and KC, 2010). Methods of estimating population based on grouping population by similarity of fertility, mortality and migration are used in multiple researches (United Nations, 1956; Gleditsch et al., 2021). Research by (Dion, 2012) shows that valid assumptions of the future proximate behavior may lead to a better approximate result. These previous researches are classical but fail short to generate the household structure we needed within regions of a country.

2.2 Simulation System

SimTW is an agent-based stochastic and heterogeneous discrete time agent-based model developed in (Tsai et al., 2010). This system uses a highly connected network model representing daily interaction between 23 million people living in Taiwan. Below is a brief description of SimTW.

In this system, the entire population is classified 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), which denoted as G_1, G_2, G_3, G_4 and G_5 respectively. In addition, each family living together is tagged with the total number of people in the family and the number of people in each age group. This family tag is called household pattern (HHP). An HHP, represents the number of family members in each of the five age groups by gender, and is encoded in five digits. These five digits encode the number of members in each group from elders to preschooler. For example, $HHP = 20120$, is a household containing 2 elders, 0 adult, 1 young-adult, 2 school-age children, 0 preschooler child. We set an upper bound of no more than eight members in any pattern for practical reason. Although there are 6^8 possible patterns, but there are only 18,176, 18,293 and 15,322 different patterns in Taiwan according to Censuses 1990, 2000 and 2010 respectively. The mock population of SimTW was built based on the Taiwan Census Data at a granularity so called regions. A region is a nature division of geographical area in which people work and live. There are 368 regions in the system and each region is characterized by an age group distribution (AGD) which describes the number of people in each age group, and a household structure distribution (HSD) which are the numbers of HHP's among all possible HHP combinations.

The social structures were built based on (Germann et al., 2006) with local modification. A mixing group is a daily close association of individuals, where every member is connected with all other members in the same group. The mixing groups in the model can be divided into three categories: resident areas, routine areas and surrounding areas.

Each simulation day is set as either workday, holiday or long holiday according to the calendar publish by (DGPA, Taiwan, 2016). Each day is divided into the daytime and night-time periods containing 12 hours each. During the daytime of a workday, individuals with work or studying go to their routine areas. During the night-time of workday and holiday, only individual who commute to routine area go back to the resident area and those who live in dormitory remain in the routine area. Those who stay in dormitories remain in routine area and they will go back to their resident areas only during long holidays. All individuals also active at the surrounding area in the region where they stay.

SimTW uses the SEIR disease model as described in (Krumkamp et al., 2011). There are two parameters in this disease transmission model: contact probability ($P_{contact}$) and transmission probability (P_{trans}). $P_{contact}$ represents the probability of an effective contact between two individuals in a mixing group. The details of $P_{contact}$ in each mixing group is derived from a contact diary study of (Fu et al., 2012). P_{trans} can be said to be the infectivity of a pathogen when an effective contact occurs.

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, in which the individual does not have any symptoms or signs of infection, while the incubation period is the time between infection and symptom onset (Park and Ryu, 2018). In this model, FLU's average latent period, incubation period and infectious period are 1.2 days, 1.9 days and 4.1 days respectively. One-third of the infectious individual appear to be asymptomatic.

2.3 Data Description

Data used in this paper can be classified in two categories: Census and household registration data. These data both show the population status, but in different ways.

Census data are collected from the Department of Census, Directorate-General of Budget, Accounting and Statistics (DGBAS), Executive Yuan every 10 years. Census were done in Taiwan for more than 100 years. with the recent ones being in 1980, 1990, 2000, 2010 and 2020. Among them, 1980, 1990 and 2000 were conducted based on a complete enumeration of residents but 2010 and 2020 were conducted using sampling survey. Census contains detailed information and more accurate in "who is living in what place".

Household registration data are collected by the Department of Household Registration, Ministry of the Interior, Taiwan. There are a lot of population related data, for example gender and age distributions, educational attainments, marital statuses etc ..., which can be downloaded and used for understanding the population statuses of Taiwan. These data are updated and released every month. The household registration data are records of "who registered in what place" for regulations, which may not actually the place to live.

Although both data are not exactly the same, but the population of each age group looks similar, with a correlation coefficient of 0.997. We thus can consider approximating the population distribution using household registration data when the Census data is not available.

Table 1: General convention of this paper.

Symbol	Meaning
$A^p_y[r][i]$	general convention
A	name of the main 2D array
y	year
p	with p, it means a probability distribution without p, its a number
r	region index
i	group index
C_A_y	Array A generated using Census data
R_A_y	Array A generated using Household Registration data
M_A_y	Array A generated using PopuSet
H_A_y	Array A generated using an arithmetic method based on HND_y
A_A_y	Array A generated using an arithmetic method based on AGD_y

3 PROBLEM AND ALGORITHM

In this section, we first describe the notations and definition used in this paper. Then we describe our problem. Table 1 is the general convention used in this work. HSD is a 2D array

$$HSD_y = \{(H_y[1][1], H_y[1][2], \cdots, H_y[1][n_{HHP}]), \\ (H_y[2][1], H_y[2][2], \cdots, H_y[2][n_{HHP}]), \cdots, \\ (H_y[n_R][1], H_y[n_R][2], \cdots, H_y[n_R][n_{HHP}])\},$$

where n_{HHP} is the total number of different HHP's and n_R is the total number of regions. $H_y[r][i]$ is the number of households with the ith HHP in the region r. HHP is a 2D array

$$HHP_y = \{(T_y[1][1], T_y[1][2], \cdots, T_y[1][n_{AG}]), \\ (T_y[2][1], T_y[2][2], \cdots, T_y[2][n_{AG}]), \cdots, \\ (T_y[n_{HHP}][1], T_y[n_{HHP}][2], \cdots, T_y[n_{HHP}][n_{AG}])\},$$

where n_{AG} is the maximum number of age groups. $T_y[i]$ denote the ith row which is the ith HHP pattern. Each column represents an age group, and a number in that column is the number of members in the specific age group of that HHP pattern. Therefore, $T_y[i][j]$ is the number of members of household pattern i in age group j. AGD is a 2D array

$$AGD_y = \{(A_y[1][1], A_y[1][2], \cdots, A_y[1][n_{AG}]), \\ (A_y[2][1], A_y[2][2], \cdots, A_y[2][n_{AG}]), \cdots, \\ (A_y[n_R][1], A_y[n_R][2], \cdots, A_y[n_R][n_{AG}])\},$$

where $A_y[r][i]$ is the number of ith age group in the region r. HND is a 2D array

$$HND_y = \{(N_y[1][1], N_y[1][2], \cdots, N_y[1][8]), \\ (N_y[2][1], N_y[2][2], \cdots, N_y[2][8]), \cdots, \\ (N_y[n_R][1], N_y[n_R][2], \cdots, N_y[n_R][8])\},$$

where $N_y[r][i]$ is the number of households comprising of i people, $i \leq 7$, and $N_y[r][8]$ is the number of households with 8 people or more in region r. Let $P(HND_y[r])$ be the probability distribution representation of $HND_y[r]$ which is the array $(\frac{HND_y[r][1]}{|HND_y[r]|}, \frac{HND_y[r][2]}{|HND_y[r]|}, \cdots, \frac{HND_y[r][n_i]}{|HND_y[r]|})$ where $|HND_y[r]| = \sum_{\forall i} HND_y[r][i]$. $P(HSD_y[r])$ can be define in the same way. Thus $P(HND_y[r]) = N^p_y[r] = (N^p_y[r][1], N^p_y[r][2], \cdots, N^p_y[r][8])$ and $P(HSD_y[r]) = H^p_y[r] = (H^p_y[r][1], H^p_y[r][2], \cdots, H^p_y[r][n_{HHP}])$.

Assume that year y is not a census year, but we want to construct the household structure distribution for year y. All we have from year y are the population's age group distributions (denoted by AGD_y) and household number distribution (denoted by HND_y). And we can look back to find closet Census year x. For that year, not only C_AGD_x, C_HND_x and C_HSD_x are available. Using these available data, we build M_HSD_y. To validate, we can pick a census year as y. And construct M_HSD_y with our method by assigning x as the previous census year. Since C_HSD_y exists, we then compare M_HSD_y and C_HSD_y to get an idea of how good our algorithm is.

3.1 PopuSet

We have a detailed information published in Census every 10 years, but only some aggregated monthly updated information from other sources. The approach we will be using is to generate a population model every 10 years. Then an algorithm called PopuSet is used to update the model by using the updated data yearly. This section describes the algorithm PopuSet we used to generate M_HSD_y for year y.

The high level ideas of this algorithm is to revamp C_HSD_x to form M_HSD_y using aggregated information. First of all, we calculate the changes from year x to year y with respect to the number of people in each age group. We use δ_j to denote the ratio of proportion of age group j for different year. Using δ_j, we then calculate the estimated occurring probability of HHP_i among all household patterns in year y by multiplying the corresponding δ_j's. Hence the occurring probability for ith HHP, can be estimated as $H^p_y[r][i] = H^p_x[r][i] * \Pi_{\forall j} \delta_j^{T_y[i][j]}$. With the adjusted occurring probability of each household pattern, $H^p_y[r][i]$, we then adapt a Monte-Carol approach to generate each household of a particular size one by one using the occurring probability of H^p_y.

In this algorithm, we first need to covert all the data to fit the system format. After that we do a basic probability revamp based on the difference of the populations. This step is called "basic/advanced" because it may need an advance revamp if the quality is not good enough. Step 3 is the main part, we generate data iteratively until the constrains are met. The last step is to check whether the quality of the generated data good enough. If not, we go back to the probability revamp step to do some advance revamp then we repeat the above process until the quality is acceptable. The detail of each step is describe below.

Algorithm 1: PopuSet.

```
Input: $C\_HSD_x$, $C\_HND_x$, $C\_AGD_x$;
       $R\_HND_y$, $R\_AGD_y$.
Output: $M\_HSD_y$.
Initialization;
for all regions: do
    Data conversion; (Algorithm 2)
    repeat
        Basic/Advanced Probability Revamp; (Algorithm 3)
        Iterative generating; (Algorithms 4)
        Quality Checking; (Section 3.1.4)
    until quality is acceptable
```

3.1.1 Data Conversion

The pseudo-code of this step is shown in Algorithm 2. The purpose of this step is to convert existing data into the format that fit to the system. Denote $Pop[i]$ the number of population in ith age group from data. n_{AG} is the number of age groups we need, n_{PopD} is the number of age groups from data. We declare an array AGD that contain n_{AG} value, then go through the data for each age and then groups them as the specification given.

Algorithm 2: Data Conversion.

```
Input: $Pop[n_{PopD}]$.
Output: $AGD[n_{AG}]$.
Initial: $AGD[n_{AG}] = \{0\}$;
for $i = 1$ to $n_{PopD}$ do
    for $j = 1$ to $n_{AG}$ do
        if $i \in A[j]$ then
            $AGD[j]$ += $Pop[i]$;    ▷ grouping the population into its corresponding age group.
```

3.1.2 Basic/Advanced Probability Revamp

Algorithm 3 gives the detailed calculations needed to it. For the basic revamping part, we adjust the probability according to the differences in the two data. The revamped probability of each HHP ($H_x^p[i]$) is equal to the original probability times the difference in each age group. If the quality of the generated data only by the basic revamp is not good enough, then we use an advanced revamp. The advanced revamp only adjusts few group types that not good enough. For example we always lack of population in age preschool children, it causes by the restrict of there is no household containing only preschool children. Thus it is harder to add a new household containing multiple members when each of the population in other groups are fully allocated. We can do an advanced revamp by adding an extra priority to the household containing preschool children. When we raised the probabilities of all household containing preschool children, the results get better.

Algorithm 3: Basic/Advanced Probability Revamp.

```
Input: $C\_HSD_x[n_{HHP}], C\_HHP_x[n_{HHP}][n_{AG}]$;
       $C\_AGD_x[n_{AG}], R\_AGD_y[n_{AG}]$.
Output: revamped $C\_HSD_x[n_{HHP}]$.
for $j = 1$ to $n_{AG}$ do
    $A_x^p[j] = \frac{A_x[j]}{|A_x|}$; $A_y^p[j] = \frac{A_y[j]}{|A_y|}$;
    $\delta_j = \frac{A_y^p[j]}{A_x^p[j]}$;    ▷ calculate the change of age group $j$
for each possible $HHP_i$, $i$ from 1 to $n_{HHP}$ do
    $H_x^p[i] *= \prod_{j=1}^{n_{AG}} (\delta_j)^{T_x[i][j]}$;    ▷ revamp the probability
```

3.1.3 Iterative Generating

The detail of the iterative generating process is shown in Algorithm 4 There are multiple stages in this step. Denote $\alpha_i = (\alpha_i[1], \alpha_i[2], \cdots, \alpha_i[8])$ the weight for refining the priority of $R\_HND_y^p$ in stage i, $\beta_i = (\beta_i[1], \beta_i[2], \cdots, \beta_i[8])$ the target completion ratio of R_HND_y in stage i. We add a set of weight (α_i) on $R\_HND_y^p$ in every stage to refine the priority of reading which group first. We switch to the next stage until a given conditions $\beta_i \cdot R\_HND_y$ arrives. For example the output result of the naive algorithm has a low fitting rate on $N_y[6]$ to $N_y[8]$. Then we use a two-stages approach by picking HHP containing at least 6 members in the first stage and then the rest in the second stage.

We start to generate M_HSD_y with revamped C_HSD_x iteratively. Array $AGD_y^{'}$ is used to record the allocated population in each age group. First, pick a household size n based on $R\_HND_y^p$. A random HHP containing n members is picked according to the revamped $C\_HSD_x^p$. We then check if R_AGD_y has enough quota to add. If yes, we add this HHP into M_HSD_y and reset the failure counter. Otherwise, we increase the failure counter by 1 and then try picking a new HHP. We set an upper bound n_{try} to prevent our program running forever.

Algorithm 4: Iterative Generating.

```
Input: revamped $C\_HSD_x[n_{HHP}], R\_AGD_y[n_{AG}]$;
       $C\_HHP_x[n_{HHP}][n_{AG}], R\_HND_y[8]$.
Output: $M\_HSD_y[n_{HHP}]$.
Initial: $AGD'_y[n_{AG}] = \{0\}$, $HND'_y[8] = \{0\}$, $stage = 1$, $error = 0$;
for $stage = 1$ to $n_{Stage}$ do
    while $error \le n_{try}$ do    ▷ try until fail to add any new $HHP$ for $n_{try}$ times.
        Random pick a number $n$ based on $(\alpha_{stage} \cdot R\_HND^p_y)$.
        Random pick a $HHP$ with the index $h$ according to revamped $C\_HSD^p_x$;
        if $\forall i, AGD'_y[i] \le R\_AGD_y[i]$ then
            Add $HHP_h$ into $M\_HSD_y$.
            for $i = 1$ to $n_{AG}$ do
                $AGD'_y[i]$ += $T_x[h][i]$;
                $HND'_y[n]$ ++;
            $error = 0$;  ▷ reset $error$ if successful.
        else
            $error$++;
    if $\forall j, HND'_y[j] \ge (\beta_{stage} \cdot R\_HND_y[j])$ then
        $stage$++;
```

3.1.4 Quality Checking

In the quality checking part, we calculate the population and household composition's weight root mean square error (RMSE) between the generated and household registration data to evaluate whether the result is good. The smaller the value is, the better the result is. Define $\mathrm{R}(A,B)$ to be the RMSE of A over B. As shown in Equation 1, we calculate RMSE of all age groups in all regions using the formula below.

$$\mathrm{R}(A,B)=\sqrt{\sum_{i=1}^{n_R}\sum_{j=1}^{n_i}\frac{A[i][j]}{|A|}\left(\frac{A[i][j]-B[i][j]}{A[i][j]}\right)^2} \quad (1)$$

4 EXPERIMENTAL DESIGN

We have raw data from Census years 1990, 2000, and 2010. Thus we can use the household distribution from previous Census to construct a household distribution for next Census. Then compare the true household structure distribution of the recent Census year with our construction to validate our process. We have two validations for M_HSD_y, which are building year 2000 from year 1990, and building year 2010 from year 2000 respectively. We also compare our results with the two published arithmetic based methods (UN DESA, 1952). The first one is to do an arithmetic adjustment based on age group distributions, and the second one is based on household number distributions. A_HSD adjusted based on age group distribution is carried out in a way that is the same as the basic revamp in Algorithm 3. H_HSD adjusted based on household number distribution is calculated by Equation 2.

$$H^p_y[r][i] = H^p_x[r][i] * \frac{N^p_y[r][i]}{N^p_x[r][i]} \quad (2)$$

Another evaluation approach is to compare the simulated epidemic results. To catering to the simulation system SimTW, we construct the household structure distribution for each region. We do not make it explicit in the descriptions of the algorithms to make the presentation clearer. Below is a recap of the relevant parameters used in the simulation system. The parameters that we use are as follows: The system has a total of 5 age groups ($n_{AG} = 5$). Households containing 8 members is the largest household in the system. The registration data have the population age distribution from 0-year-old to above-100-year-old ($n_{PopD} = 101$). We set the maximum failure limit $n_{try} = 50,000$.

We evaluate our results with two procedures. The first is the detailed distribution of the mock population generated by SimTW using those generated HSD_y. We show the average age, average household size and the population distribution in the mock populations. Then we compare with RMSE's of C_AGD_y and C_HND_y respectively. The second part is to compare the simulation results with C_HSD_y's and from generated HSD_y's. The simulation experiments include the two types of influenza virus. We choose $P_{trans} = \{0.08, 0.20\}$ for those virus (denote as FLU_{08} and FLU_{20} respectively). The FLU_{08} can be seen as the A/H1N1 virus that first occurred at year 2009 in Mexico (Bautista et al., 2010). FLU_{20} roughly corresponds to the SARS virus in year 2005 (Bauch et al., 2005). The R_0 at years 2000, 2010 and 2020 all shown in Table 2. The A/H1N1 virus occurred at years 2009 to 2010, with R_0 being 1.2 ∼ 1.4 according to the (Dorigatti et al., 2012) research. The virus in others year using the same P_{trans} as the occurrence year but having difference R_0's due to the difference in social network and population compositions.

Table 2: R_0 of FLU_{08} and FLU_{20} from year 2000 to 2020.

Year	FLU_{08}	FLU_{20}
2000	1.369	3.227
2010	1.306	3.047
2020	1.229	2.865

After validation, we then build M_HSD_{2020} from C_HSD_{2010} which we aim for. We run SimTW using

Table 3: Statistics of the mock population compare to with C_HSD_y.

X_HSD_y	age_{avg}	$size_{avg}$	G_1	G_2	G_3	G_4	G_5
M_HSD_{2000}	1.002	0.973	0.997	1.000	1.000	1.000	1.001
H_HSD_{2000}	0.934	1.009	1.088	1.155	1.112	0.905	0.851
A_HSD_{2000}	0.884	1.195	1.134	1.309	1.104	0.866	0.694
M_HSD_{2010}	1.000	0.993	0.997	1.000	1.000	1.000	1.000
H_HSD_{2010}	0.914	1.005	1.420	1.163	1.187	0.898	0.809
A_HSD_{2010}	0.985	1.038	1.013	1.106	1.072	0.935	1.057

M_HSD_{2020} and check whether the result is reasonable.

5 VALIDATION

This section shows the validation processes. All simulation experiments have been performed 100 times with the average result reported.

5.1 Statistics

Some of the basic statistics include average age (age_{avg}), average household size ($size_{avg}$) and age group distribution ($G_1 \sim G_5$) using different models are shown in Table 3.

From Table 3, we can see that M_HSD has good results in both years 2000 and 2010. H_HSD and A_HSD generated by arithmetic methods have some significant differences. For example, the ratios of school-age children are too high and those of elders are too low for A_HSD_{2000}. Furthermore, the ratios for preschooler children are too high for H_HSD_{2010}. However, M_HSD fits the population distribution well.

5.2 RMSE Comparison

In this section, we compare RMSE over C_HSD between M_HSD, H_HSD and A_HSD. As shown in Table 4, M_HSD has the lowest RMSE over C_AGD_y. RMSE over C_HND_y also has the lowest value in year 2010.

Table 4: RMSE of mock population compare with C_HSD_y.

X_HSD_y	R(C_AGD, X_AGD)	R(C_HND, X_HND)
M_HSD_{2000}	0.015	0.082
H_HSD_{2000}	0.146	0.072
A_HSD_{2000}	0.216	0.502
M_HSD_{2010}	0.013	0.038
H_HSD_{2010}	0.190	0.081
A_HSD_{2010}	0.136	0.219

5.3 Simulation Result Comparison

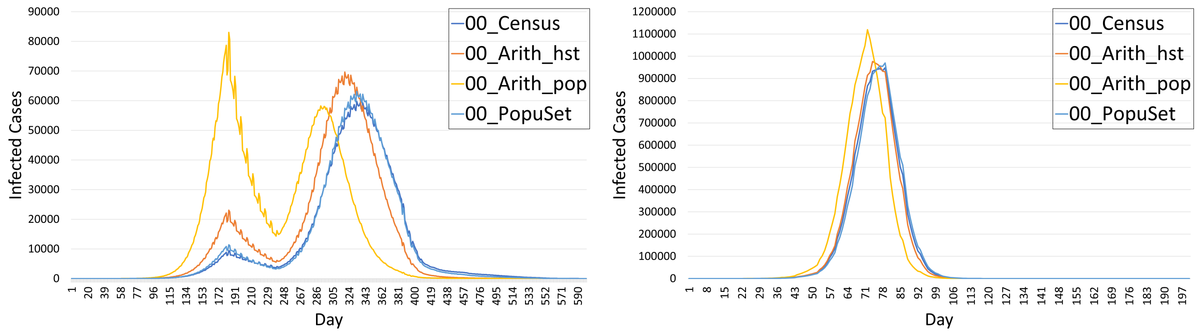
In this section we further run the simulations with all HSD's generated using different approaches. We compare all of the results by calculating the correlation coefficient (CC) of the daily infected cases group by group from G_1 to G_5 over C_HSD_y. There are a total of 16 simulation's configurations, which are the combinations of 2 diseases, 2 different years and 4 HSD's generation approaches. The configuration of a disease in year 20YY is denote as YY_DISEASE, for example FLU_{08} in year 2000 is denote as 00_FLU_{08}. We randomly add one index case every five days and the duration of a simulation run is set at 930 days. Note that in the rest of the paper, we may only show data for a specific number of days and not all 930 days for sake of simplicity.

The results with the configuration 00_FLU_{08} are shown in Table 5 and Figure 2(a). We can see that the simulation using M_HSD_{2000} has the highest CC results in all fields. Although the CC value of H_HSD_{2000} also has nice result, but there still some significant differences when we compare the daily infected cases. A_HSD_{2000} shows a huge difference comparing to others because of a larger average household size and a high ratio of school-age children. H_HSD_{2000} shows a better result comparing with A_HSD_{2000}, but also have a significant higher front peak and an earlier second peak. M_HSD_{2000} looks almost the same with C_HSD_{2000}. Figure 2(a) shows the daily infected cases.

Table 5: Correlation coefficient of all age groups based on C_HSD_{2000} using the configuration 00_FLU_{08}.

00_FLU_{08}	G_1	G_2	G_3	G_4	G_5
M_HSD_{2000}	1.00	1.00	1.00	1.00	1.00
H_HSD_{2000}	0.94	0.95	0.96	0.94	0.93
A_HSD_{2000}	0.41	0.46	0.47	0.40	0.40

CC's of other settings compared with C_HSD_{2000} are shown in Table 6. M_HSD_{2000} has value above 0.99 in all experiments at all fields. H_HSD_{2000} and A_HSD_{2000} also have good CC results, especially for FLU_{20}. As shown in Table 2, all of the diseases hav-



(a) FLU_{08} (b) FLU_{20}

Figure 2: The daily infected cases of FLU_{08} and FLU_{20} at year 2000.

ing large R_0's lead to faster pandemics. That is, most of the individuals are infected at early days which shown in Figure 2(b). Even CC values are high, we can still find that there are significant differences in Figure 2(b). A_HSD_{2000} always get a higher and quicker pandemic at all experiments. *PopuSet* method also has the best simulation result in the year 2010 as seen in Table 7.

Table 6: Correlation coefficients of all age groups.

00_FLU_{20}	G_1	G_2	G_3	G_4	G_5
M_HSD_{2000}	1.00	1.00	1.00	1.00	1.00
H_HSD_{2000}	1.00	1.00	1.00	1.00	1.00
A_HSD_{2000}	0.93	0.93	0.94	0.93	0.92

Table 7: Correlation coefficients of all age groups in year 2010.

10_FLU_{08}	G_1	G_2	G_3	G_4	G_5
M_HSD_{2010}	0.99	0.99	0.99	0.99	0.99
H_HSD_{2010}	0.94	0.94	0.97	0.94	0.94
A_HSD_{2010}	0.75	0.76	0.84	0.76	0.74
10_FLU_{20}	G_1	G_2	G_3	G_4	G_5
M_HSD_{2010}	1.00	1.00	1.00	1.00	1.00
H_HSD_{2010}	1.00	1.00	1.00	1.00	1.00
A_HSD_{2010}	0.99	0.99	1.00	0.99	0.99

6 RESULT AND DISCUSSION

We demonstrate in Section 5 that *PopuSet* generates a HSD_y that is suitable for the simulation system when R_AGD_y and R_HND_y are given. The raw data of Census 2020 are not released, but the household registration data are available.

In this section, some statistics and simulation results of M_HSD_{2020} are compared with R_AGD_{2020} and R_HND_{2020} as shown in Table 8. The ratio of each age group fits well. The average age and household size also fit well and both RMSE values look good. Every ratio of whole population's statistic fits well and both $\text{R}(R\_AGD_{2020}, M\_AGD_{2020})$ and $\text{R}(R\_HND_{2020}, M\_HND_{2020})$ look good, too.

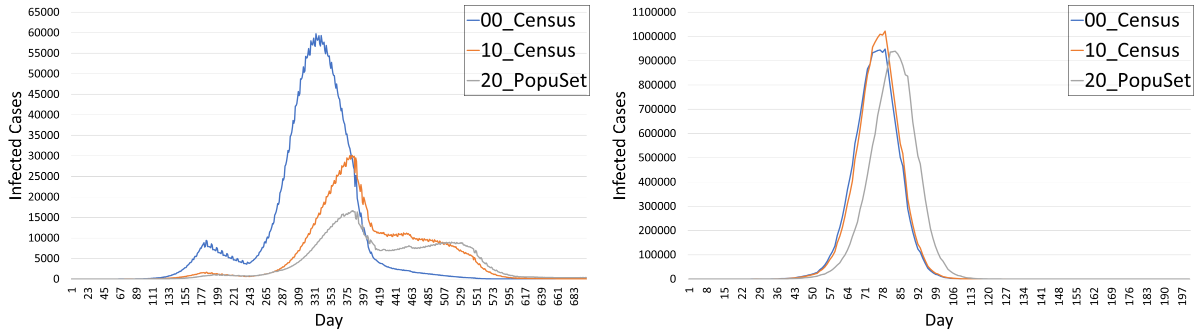
Table 8: Statistics of M_HSD_{2020} compare to with R_HND_{2020} and R_AGD_{2020}.

	Value
average age	1.000
average household size	0.995
preschooler children	0.996
school-age children	0.997
young adults	0.997
adults	0.997
elders	0.997
$\text{R}(R\_AGD_{2020}, M\_AGD_{2020})$	0.030
$\text{R}(R\_HND_{2020}, M\_HND_{2020})$	0.043

There are no C_HSD_{2020} simulation's result to be compared with, but we can still compare with C_HSD_{2000} and C_HSD_{2010} to check if the trend looks reasonable. Figure 3 shows the simulation's result group by all diseases mentioned in Section 4. We can see that the pandemic become milder. The facts that a smaller household size and an aging society both lead to a smaller pandemic (Lin et al., 2021; Chang et al., 2015), we conclude that the trend of the simulation's results look reasonable.

7 CONCLUSIONS

We have shown a method called *PopuSet* to generate an approximated household structure based on the existing household structure of previous Census and yearly updated household registration data. This generated HSD_y has better properties such as better fitted population distributions and household sizes, comparing with those generated by the arithmetic methods.



(a) FLU_{08}

(b) FLU_{20}

Figure 3: The daily infected cases of FLU_{08} and FLU_{20} year 2000, 2010 and 2020.

Take SimTW as an example, the mock population has a great impact to the simulation result, but it can only be updated every ten years from a costly Census survey. *PopuSet* performs some kinds of "update" every year to C_HSD_y.

We note that *PopuSet* can use some further improvements, especially when SimTW is simulating diseases with $R_0 \approx 1$. The picking order of smaller or larger households, the revamping strategy of probability are some of the parts that can be improved and reasonable conjecture or heuristic may help. More related data and insightful information from data also an important way to improve. We currently do not have updates of information on worker and student flows in aggregated forms. Without those data, the changing in social network cannot be updated. Our current approach is to extrapolate linearly which may not be a good practice when the societal structure, such as rapid aging, and social interaction, such as the average household size, are changing in a very fast pace.

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