

# The Impact of Household Structures on Pandemic Influenza Vaccination Priority

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**Abstract:** The household structure is an important aspect of population based simulation. How to generate a mock population with specific household structure characteristics is thus an important question. The network structure is one of the dominant factors for contact-based disease transmission. And household structure is the most important source of close contact among small groups. We identify the percentage of elderly-children households as an important character and study the process to generate mock population with specified percentage of elderly-children households. The generated mock populations are fed into the agent-based simulation module to study the impact of household structure on vaccination policy.

## 1 INTRODUCTION

Household structures are important for many application domains. Household structures change over time and vary geographically and culturally (OECD, 2011). Network structures affect the disease spreading patterns. Household structure is an important component of the transmission network of infectious disease. Because of the strong interactions present, households are one of the most important heterogeneities to consider, both in terms of predicting epidemic severity and as a target for intervention (House and Keeling, 2009).

Family are different in different area. Among the Asian countries, at least 80 percent of children are raised by two-parent families, and at least 40 percent are also living with extended family members (Trends, 2013), while in Europe at least 15 percent are living with extended family members. For example, the percentage of households where grandparents live with grandchildren is reported to be ranged from 9.2 percentage to 20.5 percent in Asia and from 0.1 percent to 3.9 percent in western and northern Europe, Table 1.

Taiwan is approaching an aging society at an

Table 1: The household structure in Europe and Asia(<http://ec.europa.eu/>).

country		m<15 & M≥65(%)
Asia	Indonesia	9.2
	Taiwan	15.0
	Thailand	16.5
	Vietnam	20.5
Europe	Belgium	0.1
	Finland	0.9
	Germany	1.1
	Italy	3.1
	Luxembourg	0.7
	Netherlands	< 0.1
	Poland	3.9
United Kingdom	0.9	

M: the oldest person's age in a family.

m: the youngest person's age in a family.

alarming rate, due to the rapid decline of birthrate as well as longer life expectancy. As shown in Figure 1, from 2000 to 2012, the youth population (less than 15 years old) dropped from 21 percent to 15 percent, while senior population (age 65 and up) increased from 8 percent to 11 percent. The average household size is also declining for decades, from 5.9 in 1966 to 3.0 in the 2010, Fig 2. It is conceivable that the

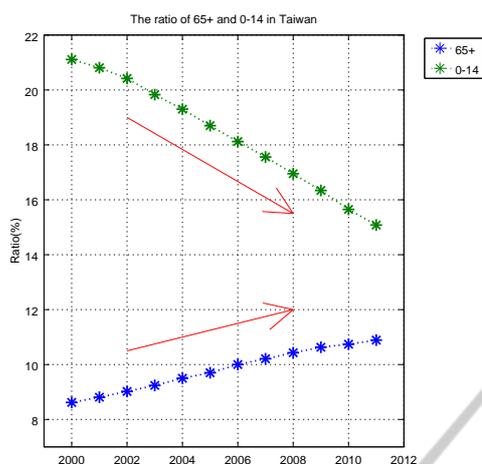


Figure 1: The ratio of over 65 years old and 0-14 in Taiwan(2000–2011).

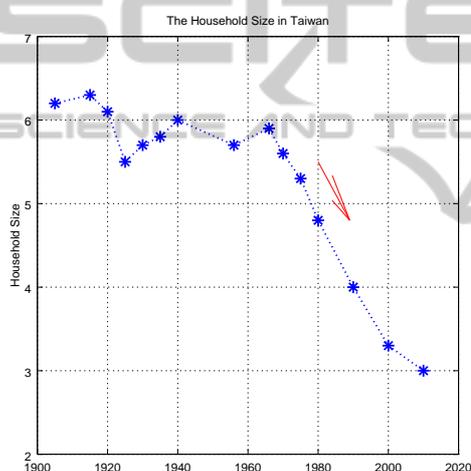


Figure 2: The household size in Taiwan(1900–2010).

living or parenting arrangements in Asia may differ from those in the West. It is not uncommon in Taiwan that grandparents live with grandchildren, or for grandparents to help taking care of their young grandchildren on a daily basis. In such a circumstance, both care givers (seniors) and care takers (toddlers or young children) may have much more contact than their counter parts in countries where seniors do not live with young children. And the fact that these two age groups are also most susceptible to influenza infections makes this pattern even more interesting from disease prevention perspective. "Does this special feature of age composition within the household contribute to any divergent cross-cultural patterns of disease infections? When contact patterns in everyday life are subject to such cultural norms, policy makers should make the best use of diary-generated empirical data and design intervention strategies accordingly" (Fu et al., 2012).

We study the household structure of two census data from Census 2000 and Census 2010 in Taiwan. In order to study the impact of household structure on epidemiology, we have to find a method to generate mock population with specific household structure characteristics. A simulation approach to generate household structure is proposed by Geard et al. (Geard et al., 2013). In this paper we proposed to formulate it as a mathematical programming. The specific household characteristics are the primary constraints and other "desired properties" are secondary constraints. The generated mock populations are applied to explore the impact of household structure on vaccination priority for influenza. We use the agent-based disease spreading simulation software to carry out our studies (Tsai et al., 2010). The concepts of the simulation software is similar to Germann's work. (Germann et al., 2006). And based on the census data from 2000 and 2010 to generate our initial sample population. Given a specified ratio of elderly-children households, a transformation process is developed to generate the sample population with the given ratio from the initial population. Two vaccination policies are compared, namely, school children only and elderly only. The rationales to vaccinate school children only are two folds. First, students have close contact with each other, vaccinating students can reduce the number of students infected by other students. So that the chance of a school age kid brings virus home is reduced. Second, it is more cost effective to vaccinate students because they are at a centralized location - the school. The rationale to vaccinate elderly only is mainly to reduce the number of severe cases and fatal cases.

We note that the selected vaccination policies are only for demonstration the effect of household structure on disease spreading.

## 2 MATERIAL AND METHOD

The household structure for the generation of a mock population is a probability distribution over household patterns.

The specific of the possible patterns depends on the applications. In this paper, the entire population is classified into five age groups: preschoolers (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). And a household pattern is a ten dimensional tuple, for 5 age groups and genders, that is we keep track on the number of males and females in each age group of a household. We set seven to be the upper bound of each

entry. Therefore, there are  $8^{10}$  possible patterns and each pattern can be encoded in 4 bytes. Let  $H$  denote the set of patterns, a *household structure distribution* (HSD) is a probability space,  $(H, p)$  where function  $p$  maps an element in  $H$  to a probability. A characteristic of household structure is a measurement of the HSD. For example, the percentage of elders (over 65), or the percentage of households with preschoolers and elders. However, it would be difficult to know the percentage of household in which children live with both parents because we do not capture that relation in our setting. Usually, we have some other data related to or constraint on household structure distribution such as the age distribution of the population. In general, we can treat any statistical measurements of a population as soft constraints and the goal is to generate a mock population that "satisfies" them.

Since all the surveys and measurements are snapshots and subjected to noises, it is usually impossible to satisfy all the constraints. For our study, the important characteristic of a HSD is the elder-children ratio (EC ratio), which is the percentage of households with elderly and a young person under 15. Since the HSD does not capture enough information to determine if a school-age child is under or over 15 years old, we have to utilize the age distribution data from the census to decide stochastically the age of a school-age child.

The mock population is constructed according to national demographics and daily commuter (worker flow) statistics from Taiwan Census 2010 Data (<http://www.stat.gov.tw/>) in order to retain some population characteristics.

The generated mock population with desired HSD is fed into the simulation software developed by Tsai et al. (Tsai et al., 2010). Below is a brief description of the simulation module.

The connection between any two individuals indicates the possibility of regular (daily) and relatively close contact that could result in the successful transmission of the flu virus. An important parameter is the disease depends on transmission probability denoted  $P_{trans}$ . It is the probability that an effective contact results in an infection.

A contact group is a close association of individuals, where every member is connected to all other members in the group. We designate ten classes of such contact groups in our model: community, neighborhood, household cluster, household, work group, high school, middle school, elementary school, daycare center, and playgroup. It is important to note that these contact groups do not represent all people at any physical location such as a workplace or school, but rather the groups of people who share the same sur-

rounding activities and sustain regular close contact for potential viral infection.

Each individual is a member of one of the five age groups throughout the simulation can belong to several contact groups simultaneously at any time. The probability of any two individuals staying in contact that could result in the successful transmission of the flu virus is called the contact probability, and an empiric value is assigned depending on the group where contact occurs and the ages of both individuals.

Age not only affects the probability of an individual being infected, it also determines the individual's daytime contact groups: preschoolers stay either in daycare centers or in playgroups; school-age children stay either in schools or in households as dropouts; young adults and adults stay either in work groups or in households if unemployed.

Each simulation runs in cycles of two 12-hour periods, daytime and nighttime, with each cycle representing a day in the simulation. The simulation can cover any specified duration of days; we usually operate in 180 days for typical influenza season, but there are times when 365 days duration is imperative for a slow progressing epidemic. Contact occurs between individuals in each contact group every day, there are no exceptions for weekends or holidays until we can properly ascertain their effects.

During nighttime, contact occurs only in communities, neighborhoods, household clusters, and households; whereas in the daytime, contact occurs in all contact groups. Children do not go outside of their residential community for daytime activities because the probabilities for such occasional contacts are too low to be captured by any contact group. The only inter-community transmission occurs when working adults commute between household and work group as specified by worker flow data as well as school children commute between household and school as specified by school flow (Tsai et al., 2010).

To derive a series of household structure with specified EC ratio, we designed a simple *household structure evolution* process to transform the set of parameters so that the percentage of EC household in the mock population generated by the modified parameters is sufficiently close to the designated number. We formulate the process as a linear programming problem, the objective function is designed to avoid introducing dramatic "changes" to other important aspects of the household structures. The detail is described in Figure 3.

A simulation setting is a set of parameters, which include  $P_{trans}$  and household structure. To study the effect of vaccine policies, we fix a simulation setting and simulate each vaccination policy. For each policy,

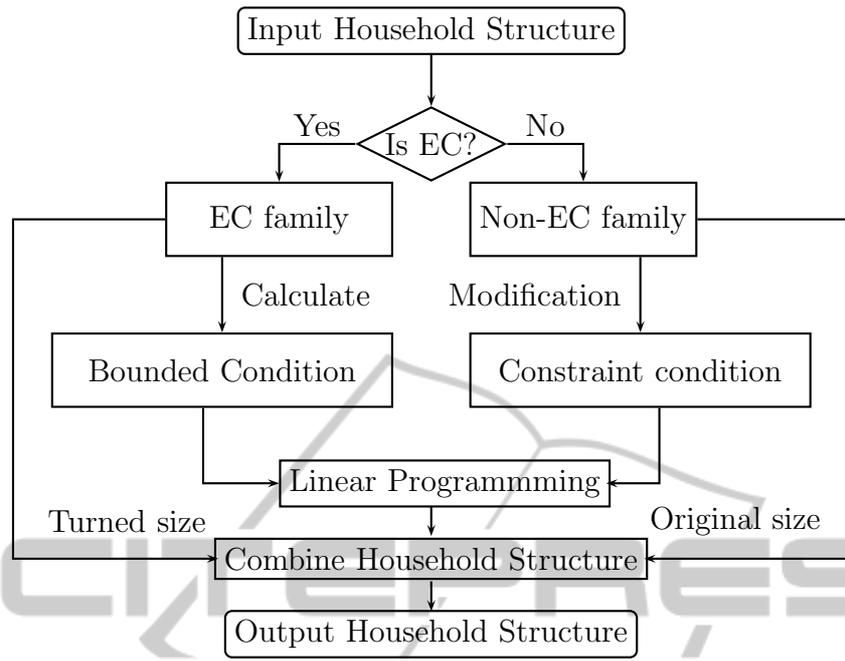


Figure 3: Flow Chart of Using Linear Programming.

Table 2: The household size in each EC ratio(mock population).

EC ratio	#population	#0-4	#5-18	#19-29	#30-64	#65+	household size
30%	23,088,322	972,361	4,265,569	3,079,993	11,588,807	3,181,592	3.09
20%	23,087,718	938,074	4,217,799	3,124,340	11,686,059	3,121,446	3.05
10%	23,086,465	897,650	4,156,653	3,182,322	11,791,448	3,058,392	3.01
0.0%	23,079,732	970,817	4,262,075	3,078,738	11,590,107	3,177,995	2.78

'#': the number of

we first carry out the baseline simulation which is the simulation without any intervention. Then the simulation with intervention policies are carried out with the same setting. We start the vaccination at the 70<sup>th</sup> days and the number of available vaccine is 1.8 million doses, the vaccine efficacy is set at 36% – 90%.

For each simulation run, we record the number of infected cases for each group. We then take the average of simulation runs with the same setting and intervention policy to be the outcome of that specific policy.

The difference between the baseline and a intervention policy is the effect of the intervention, and in our case it is the difference of the number of infected cases of each age group.

Note that we compare different policies with the same setting and only focus on the number of infected cases for each age group. If the numbers of reduced infected cases for one policy, A, is always better than the other policy, B, we can safely conclude that policy A is superior than policy B. However, if a vaccination policy is to set the priority of receiving vaccination

among age groups, it will be difficult to find a superior policy because a policy targeted at a specific age group always results in the fewest infected cases for that group.

We introduce a cost function,  $C$  which maps a five dimensional point (the numbers of infected cases for each age group) to a real number. Given a policy A, the cost saved by A is  $C(base) - C(A)$ , that is the cost difference between baseline and policy A. We say that policy A is better than policy B with respect to cost function  $C$ , if and only if the cost saved by A is greater than B. For example, if we define  $C(n_1, n_2, n_3, n_4, n_5)$  to be the summation of the five numbers, we are comparing the number of infected cases reduced. The costs of infected cases among different age groups can be different (Meltzer et al., 1999). Here we adopt a cost function which highlight the different between elderly and others. Let  $C$  be a cost function with parameter  $\alpha$  be:

$$C_{\alpha}(n_1, n_2, n_3, n_4, n_5) = n_1 + n_2 + n_3 + n_4 + \alpha * n_5$$

Function above captures the idea that the cost of an elderly case is  $\alpha$  times of the other age groups and

the costs of all the other age groups are the same. We define an equilibrium point for policy A and B to be  $\alpha^*$  such that  $C_{\alpha^*}(A) = C_{\alpha^*}(B)$ . Since  $C_{\alpha}$  is a linear function, there is a unique equilibrium point between two policies.

### 3 RESULTS

From the HSD perspective, the census data from 2000(C2000) and 2010(C2010) can be described as following: there are 11283 household patterns in C2000, 7072 in C2010 and a total of 11543 patterns ever appeared in C2000 or C2010. There are 6813 patterns appeared in both C2000 and C2010. The summation of the probability of the common patterns is greater than 0.99 for both C2000 and C2010. The Pearson correlation between these two HSDs is around 0.95. There are 4470 patterns only appeared in C2000 while 259 only in C2010. The apparent discrepancy is due to the fact that C2010 only survey 16 percent of the household while C2000 surveyed every household.

Based on processes described above, we successfully generated populations with specified characteristics. In Table 2, the generated mock populations have specified EC ratio, and the population is highly correlated with original population, the Pearson correlation ranging from 0.998 to 0.999.

The  $R_0$  for the baseline case of each mock population is calculated and summarized in Table 3. We note that with the same transmission probability, the lower the EC ratio the smaller the  $R_0$ . And this can be explained by the fact that average household size decreases as EC ratio decreases. That is the difference of the network structure is the main reason for the variation in the table.

We compare two vaccination policies, student only and elder only. The results are summarized in Table 4.

From the summary, we note that the student only policy outperforms elder only for all age group except seniors. That is the student only policy reduced the number of infected cases more than elder only policy in all four age groups excluding seniors. The can be

Table 3:  $R_0$ .

EC ratio	transmission probability			
	0.08	0.09	0.10	0.11
30%	1.055	1.194	1.308	1.442
20%	1.053	1.182	1.302	1.432
10%	1.041	1.169	1.294	1.428
0.0%	0.910	1.122	1.247	1.352

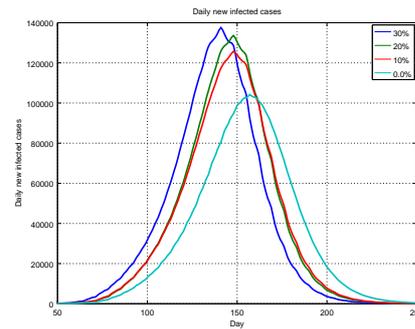


Figure 4: Daily new infected cases in different EC-family ratio. ( $P_{trans}$  is 0.09).

explained by the fact that compared with seniors the students have more contacts. Therefore, vaccinating students not only protect the vaccinated students also limits the spreading more than vaccinating seniors.

Two cost functions are applied to compare the cost benefit of different policies, one is the cost matrix from Melzer (Meltzer et al., 1999) and the other is the cost function with parameter  $\alpha$ , which is cost ratio between the elderly and other age groups. The results applying Melzer cost matrix is summarized in Table 5. We again observe that student only policy outperforms elder only. The results of applying  $C_{\alpha}$  are summarized the value of the equilibrium points in Table 6. We note that the value of the equilibrium point increases when EC ratio lowered, this is a curious phenomena needs further investigation.

### 4 CONCLUSIONS AND DISCUSSION

We designed a simple method to generate household structure distribution with specified characteristics. The method can ensure that the resulting distributions are "similar" to the original distribution. A more thorough study maybe needed to give the method a more solid theoretical foundation. The household structure distribution can have impact on the vaccination priority. However, to apply the method to real situation at least following issues have to be explored.

First, instead of using point estimation, that is the average outcome of simulation runs, interval estimations are necessary for policy makers to have more information about the difference among different options. Instead of taking the average of simulation runs, we can observe important outcome variables as sampled by simulation runs. Based on our past experiences, most of the observed quantities fit normal

Table 4: Basic data( $P_{trans}$  is 0.09).

	infected cases					
	0-4	5-18	19-29	30-64	65+	total
30% (baseline)	239,745	1,706,801	956,525	3,441,096	954,530	7,298,697
30% (p1)	220,505	1,630,385	882,697	3,165,843	673,903	6,573,333
30% (p2)	194,734	1,093,766	811,178	2,877,378	793,026	5,770,082
20% (baseline)	225,593	1,669,545	955,546	3,410,050	915,534	7,176,268
20% (p1)	206,630	1,587,315	875,068	3,113,949	620,845	6,403,807
20% (p2)	177,356	1,005,881	789,590	2,773,512	739,373	5,485,712
10% (baseline)	208,842	1,622,788	955,966	3,371,757	873,679	7,033,032
10% (p1)	191,289	1,542,433	873,912	3,072,764	584,062	6,264,460
10% (p2)	161,939	958,344	781,978	2,712,316	698,209	5,312,786
0% (baseline)	199,815	1,567,902	847,755	3,034,015	717,711	6,367,198
0% (p1)	187,902	1,506,673	783,991	2,801,450	462,770	5,742,786
0% (p2)	141,077	832,923	640,380	2,246,715	525,263	4,386,358

p1 is elder only.

p2 is student only.

Table 5: Cost in Meltzer's work( $P_{trans}$  is 0.09).

EC ratio	baseline(x10 <sup>9</sup> \$)	p1(x10 <sup>9</sup> \$)	p2(x10 <sup>9</sup> \$)	baseline-p1(x10 <sup>9</sup> \$)	baseline-p2(x10 <sup>9</sup> \$)
30%	54.03	48.18	44.16	5.85	9.87
20%	53.24	47.01	42.23	6.23	11.01
10%	52.34	46.12	41.06	6.22	11.28
0.0%	46.78	41.70	33.63	5.08	13.15

p1 is elder only.

p2 is student only.

Table 6: The equilibrium point under different transmission probability and EC ratio.

		$P_{trans}0.09$	$P_{trans}0.10$	$P_{trans}0.11$
EC ratio	30%	7.74	3.99	2.85
	20%	8.74	4.16	2.93
	10%	9.34	4.40	3.03
	0.0%	22.71	7.15	4.39

distribution well. Interval estimations of normal distribution can then be applied.

Second, it is observed that policy options depends on the transmissibility of the virus which is not observable before the pandemic starts. Therefore, a carefully designed early estimation process is very important. The process will utilize the early data about the epidemic to predict important parameters which are important for decision makers. We believe that early data, say for the first 2 months, can be applied to get good estimations. But more experiments are necessary to ensure it.

Third, more policy options should be evaluated. In this study, we only consider two options. To make real life recommendations, more options should be evaluated. Forth, it is beneficial to design good visualization methods to facilitate decision process.

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