Building a large synthetic population from Australian census data

Bhagya N. Wickramasinghe¹, Dhirendra Singh¹, and Lin Padgham¹
RMIT University, Melbourne, Australia
first.last@rmit.edu.au

Abstract. We present work on creating a synthetic population from census data for Australia, applied to the greater Melbourne region. We use a sample-free approach to population synthesis that does not rely on a disaggregate sample from the original population. The inputs for our algorithm are joint marginal distributions from census of desired person-level and household-level attributes, and outputs are a set of comma-separated-value (.csv) files containing the full synthetic population of unique individuals in households; with age, gender, relationship status, household type, and size, matched to census data. Our algorithm is efficient in that it can create the synthetic population for Melbourne comprising 4.5 million persons in 1.8 million households within three minutes on a modern computer. Code for the algorithm is hosted on GitHub.

Keywords: Population Synthesis · Algorithm · Agent-Based Simulation

1 Introduction

A synthetic population is an algorithmically generated virtual population that matches some known views, such as those given by census tables, of a real population. The aim of population synthesis is to construct instances of persons and households and assign to them attributes of the real population, such as age, sex, and relationships, in such a way that the virtual population is a good match, statistically, to the real population, with respect to those attributes. Synthetic populations are often used in agent-based simulations so real-life phenomena can be replicated and “what-if” scenarios explored. Our own effort is driven by ongoing work with emergency services in modelling community evacuations to improve preparedness for bushfires and floods in Australia. This work also fits in a larger project with social science researchers looking at developing an understanding of how households make housing decisions, to answer questions around what kind of housing stock we should build to get the kinds of communities we aspire to in Plan Melbourne 2050¹.

We use a sample-free approach to population synthesis that does not rely on a disaggregate sample from the original population to seed the algorithm, as is required by established methods like Iterative Proportional Updating (IPU) [18]. This is particularly useful in the Australian context where samples are not freely

¹ http://www.planmelbourne.vic.gov.au/
available and come with substantial restrictions on use. Joint marginal distributions for exactly the desired attributes of the population can readily be downloaded from the Australian Bureau of Statistics (ABS) website\(^2\) making it unnecessary to use techniques like Iterative Proportional Fitting (IPF) \(^4\)\(^6\) for deriving such. Our work is more closely related to that of Huynh et. al \(^10\) that also employs a sample-free approach for Australia, but uses a different mechanism for assigning individuals to households. We also use the more recent census data from 2016 (catering to any changes in data format) and report better accuracy on the match to census data.

Our approach can be used to build a synthetic population for any area of Australia covered by the census. The program outputs the population at the granularity of Statistical Area Level 2 (SA2) that represents a community with about 10,000 residents, and typically corresponds to officially gazetted state suburbs and localities\(^3\) We demonstrate the approach using 2016 census data\(^4\) for all 309 SA2s of Greater Melbourne consisting of 4,485,211 persons in 1,832,043 households\(^5\) The program takes about 3 minutes to perform the data cleaning routines and generate the population on a 64-bit computer with 8 \(\times\) 3.40GHz cores and 8 GB RAM (Intel\(^\text{®}\) Core\(^\text{TM}\) i7-4770 CPU). The full source code for the algorithm, all supporting scripts, instructions for running the program, as well as the final generated population files for Melbourne are available from the GitHub repository\(^6\).

The remainder of the paper is laid out as follows. Similarities and differences to other related works are first covered in Section 2. We then describe our algorithm in Section 3 and compare the quality of the produced synthetic population to the original census data in Section 4. We further compare our approach in detail to relevant existing techniques in Section 5 and conclude with a discussion on nuances in Section 6.

2 Related Work

There is substantial work on population synthesis for agent based models \(^8\). Much of this focuses on creating individuals within households based on census data, as we do here. In many countries the required joint distributions are not directly available from census data, and techniques like Iterative Proportional Fitting (IPF) \(^4\)\(^6\) are used to construct the desired joint aggregated (marginal) distributions using a set of available marginals and a disaggregate data sample (microdata). Other sampling techniques that have been proposed include the Gibbs sampler with Markov Chain Monte Carlo simulation \(^5\) and Quasi-random integer sampling \(^14\).
Of the sample-based approaches, IPF is a widely used deterministic re-weighting technique to merge data distributions at the same aggregation level. It takes a set of marginal distributions and a disaggregate data sample from the underlying population (the seed) and iteratively adjusts (reweights) the seed to match the marginal distributions [3]. GREGWT (Generalised Regression and Weighting) is also an iterative re-weighting algorithm used by the Australian Bureau of Statistics [15]. Iterative Proportional Update (IPU) [18] and Hierarchical IPF [11] are two deterministic re-weighting techniques similar to IPF but designed to merge data distributions of different aggregation levels, e.g., person and household level distributions. The sample data used in these works represent the population at both aggregation levels.

Combinatorial optimisation techniques [8] use two marginal distributions at person and household levels and a sample from the underlying population containing household structures as inputs. The process starts by generating an initial estimate of the whole population by cloning households with persons from the data sample. This approach ensures realistic household structures and accurate relationships within the household. The goodness of fit of the estimate is then optimised against an objective function using a combinatorial optimisation method like hill climbing, simulated annealing or genetic algorithms [1, 12, 16]. The main drawback of these approaches is possible loss of heterogeneity due to repeated cloning from a small subset of households [5].

The above methods assume availability of a disaggregate data sample, which is not always available or if available may be undesirable due to restrictions on use. Alternative sample-free methods instead employ heuristics to infer household structures [10]. Additionally, [17] show that populations of the same aggregation level (person or household level) can be constructed without a sample when joint marginal distributions with sufficiently overlapping attributes are available.

Yet another approach is to generate household templates by taking all combinations of person and household types, and using them to perform Monte Carlo sampling considering known person and household level distributions. However, the number of combinations grows exponentially in the number of person and household types, as shown by [7] for a region in France. We evaluated this approach also for Melbourne with 2 household attributes with 8 and 14 values respectively giving 112 categories, and 3 person attributes with 2, 8 and 8 values, giving 172 categories. On a 14 core (2.6 GHz) supercomputer with 1TB RAM however, the process failed to complete after 48 hours.

Due to the computational complexity of the above approach heuristics are typically used to place individuals into households. In this approach household instances are formed by selecting a household and suitable persons from corresponding pools, without replacement, according to population heuristics [2,10]. This is the general approach we have used. We compare our approach to that of [10] as well as to the well-known IPU technique [18] further in Section 5.
3 Population Synthesis Approach

The complete population synthesis process involves downloading the input person-level and household-level marginal distributions from the ABS website using the TableBuilder software tool; running the pre-processing script that performs some data cleaning steps and generates the required counts for the different person and household categories according to the downloaded marginal distributions; and running the population synthesis algorithm (Section 3.3).

The output of the program is the population of each SA2 in three comma-separated-values (.csv) files containing person, families (of persons), and households (of families). Each record (row) in the household file primarily contains a unique ID for the household, the household size, the family household composition of the primary family and an ID representing the primary family. A record in the families file represents each family with a unique ID, the family household composition category of the family and the household ID it belongs to. A record in the persons file represents persons with unique IDs, their age, sex, relationship status, family ID, household ID and the IDs of their partner, father, mother, children and relatives. Together the columns in the output files constitute a valid database schema that could easily be loaded and manipulated in any database management system.

3.1 Person-level Categories Input

Person-level attributes that we chose to include in the synthetic population consist of eight age categories (0-14, 15-24, 25-39, 40-54, 55-69, 70-84, 85-99, and 100 and over), two gender categories (Male and Female) and eight family/household relationship categories that we obtained by aggregating the census categories as per Table 1. This gave us 128 customised person categories (2×8×8). Note that not every custom person category is valid, for instance an individual in the 0-14 age bracket cannot have the Married relationship status. The total number of legal person-level categories are actually 90.

Married is assumed to imply a heterosexual relationship for simplicity, even though census data includes also homosexual marital partnerships. Children are categorised as Dependent under 15 child (aged 0-14), Dependent student (aged 15-24, studying full-time, living with parents), or Non-dependent over 15 child (aged 15 or over, not studying full-time, living with parents). The age bins above age 24, e.g., 25-39 are arbitrarily chosen. Relative is a related individual who lives in a family household but is not part of the family nucleus, or forms a family nucleus from a non-marital/non-parental relationship, e.g., siblings living in the same household. Group household includes individuals living together with other non-related individuals, e.g., tenants in a shared house, while a Lone person lives alone.

In the input data, where a person could be assigned one of several relationship types, the ABS uses certain rules to determine the relationship status, such as in order of priority: marital, then parental/child relationship, then relative. In
Table 1: Custom relationship status categories based on classifications used by Australian Bureau of Statistics

| Custom category          | Original categories                                                                 |
|--------------------------|--------------------------------------------------------------------------------------|
| Married                  | Husband, Wife or Partner in de facto marriage, female same-sex couple                |
|                          | Husband, Wife or Partner in de facto marriage, male same-sex couple                  |
|                          | Husband, Wife or Partner in de facto marriage, opposite-sex couple                   |
|                          | Husband, Wife or Partner in a registered marriage                                    |
| Lone parent              | Lone parent                                                                          |
| Dependent under 15 child | Foster child under 15                                                                  |
|                          | Grandchild under 15                                                                   |
|                          | Natural or adopted child under 15                                                    |
|                          | Otherwise related child under 15                                                     |
|                          | Step child under 15                                                                   |
|                          | Unrelated child under 15                                                              |
| Dependent student        | Natural or adopted dependent student                                                  |
|                          | Dependent student step child                                                          |
|                          | Dependent student foster child                                                       |
| Non-dependent over 15 child | Non-dependent foster child                          |
|                          | Non-dependent step child                                                              |
|                          | Non-dependent natural, or adopted child                                               |
| Relative                 | Brother/Sister                                                                        |
|                          | Cousin                                                                               |
|                          | Father/mother                                                                         |
|                          | Grandfather/grandmother                                                               |
|                          | Nephew/niece                                                                          |
|                          | Non-dependent grandchild                                                              |
|                          | Other related individual (nec)                                                        |
|                          | Uncle/aunt                                                                           |
|                          | Unrelated individual living in family household                                       |
| Group household          | Group household member                                                                |
| Lone person              | Lone person                                                                          |
| Ignored                  | Visitor(from within Australia)                                                         |
|                          | Not applicable                                                                        |
|                          | Other non-classifiable relationship                                                   |
for instance, a household with two persons cannot be a 3-Family household, and the total number of valid categories here is 65.

The ABS uses rules to assign family types in the data when one of several below types apply, such as: marital only as Couple only, marital and parent/child as Couple family with children, parent/child only as One parent family and relative relationships only as Other family. Except for Other family, relative relationships are ignored when deciding the family type. In multi-family households, the primary family is selected in the prioritised order of Couple family with children, then One parent family and finally Couple only or Other family with equal priority.

3.3 Population Synthesis Algorithm

We construct the population in five stages. The first is to instantiate all the persons instances with their attributes. Next is to form the basic structures for all the inferable families with the minimum persons required as per the family type. We can infer that all the Lone parents must form basic one parent families with a child because Lone parents cannot be in any other family type, and all the Married Males and Females must form couples. Further based on the households data distribution we can form basic structures needed for primary Couple Family with Children families by pairing a previously formed couple with a child and primary Other Family units by pairing two Relatives.

The third stage is instantiating all the family households with the correct primary family using the basic family instances, Group Households with Group household persons and Lone Person households with Lone person instances. The fourth stage is heuristically adding non-primary families to the incomplete family households. After this step all the family households have required families and some may even have all the required members. Finally, the remaining incomplete households are completed by adding remaining Children and Relatives.

As an optional last step, we can assign households in a SA2 to known street addresses in that SA2 (assigned arbitrarily) which can be useful for geography-based applications. We describe the full algorithm in steps below.

Stage 1 — Create All Persons

S1—Clean the input distributions obtained from TableBuilder. Discrepancies exist between the household and individual data obtained either due to limitations in the data collection process or random errors deliberately introduced by ABS in the census data to protect privacy. We make adjustments to remove these discrepancies to the extent possible including ensuring the number of individuals in each set are the same, ensuring there are enough married males and females to create the couple families and so on. We treat the household-level data as the most correct, and adjust the individual-level data to match this.

S2—Create the required number of person instances and assign their attributes as per the input person-level categories distribution. At this stage a person is
assigned only an age bin. Once the algorithm has run to completion, we convert these to an age by stochastically selecting an age from the age distributions of persons in the SA2. This also considers *population heuristics* when selecting potential age values for a person to avoid any unrealistic relationships between persons. For example we require the parent-child age gap to be at least 15 years but not more than 45 years. The formed instances are added to separate pools as: *married-males, married-females, lone parents, children, relatives, group-households and lone persons*.

**S3**—If there are more persons represented in household-level compared to the individual-level distribution, they are instantiated without any attributes and added to the *extras* pool. These extras are used later in population construction if any person type does not have enough instances to form the required households.

### Stage 2 — Form All Known Basic Family Structures

**S4**—Form basic structures of *one parent* families by pairing each person in the *lone parents* pool with a person from the *children* pool in age descending order, adhering to the parent-child age gap constraint. The constructed family structures are put in the *basic one parent* family units pool.

**S5**—Form all the possible married *basic couples* by pairing two persons, each taken from the *married-males* and the *married-females* in the age descending order, until one or both pools is depleted. Any remaining persons will be used in later stages. All marital relationships are assumed to be heterosexual.

**S6**—Form the pool of *basic couple with child* family units by grouping a randomly selected unit from the *couples* pool and a child from the *children* pool, to match the number of households in the input household distribution where the primary family is of type *Couple Family with Child*. The parent-child age gap constraint applies here as before.

**S7**—Form *basic other family* units by grouping two randomly selected *Relative* persons to match the number of households where the primary family is of type *Other Family* according to the input household distribution.

### Stage 3 — Create All Households

**S8**—Create all households and assign the desired attributes: household size, primary family type, and number of family units, as per the household-level distribution and add them to the *incomplete-households* pool.

**S9**—Add each individual in the *lone-persons* pool to each *Lone person* households in the input households distribution and add the households to the *completed-households*.

**S10**—Complete the *Group households* by adding all the required person instances from the *group-households* pool and add the constructed households to the *completed-households* pool.

**S11**—Assign the primary family to each household in *incomplete-households* by selecting a family unit that matches the household’s primary family type from one of the basic family unit pools created in steps 4, 5, 6 and 7. This step utilises
all the units in the basic other family and the basic couple with child pools, as these pools only have families sufficient for primary families.

**Stage 4 — Assign Non-primary Families**

The following criteria applies to the selection of non-primary families: (a) to add any family type there must be at least one free slot for a new non-primary family; (b) to add a Couple family with no children or a Other family units there must be room for at least two more persons; (c) to add a One Parent family there must be room for at least two persons and the primary family must be either Couple Family with Children or One Parent family; and (d) to add a Couple Family with Children unit there must be room for at least three persons and the primary family type must also be Couple Family with Children.

**S12**—Assign remaining units in the basic one parent pool to randomly selected eligible households in incomplete-households pool that meet criteria (a) and (c) above until depleted or no eligible households remain. The same household may be selected more than once as long as it meets the eligibility criteria. Any completed households as a result are added to completed-households.

**S13**—Disassemble any remaining units in the basic one parent pool and add the persons to the children and the lone parent pools accordingly.

**S14**—Add remaining units in basic couples pool to randomly selected households in the incomplete-households that meet conditions (a), (b) and (d). If a household only meets conditions (a) and (b) the new family is added as a Couple family with no children unit. If the household meets conditions (b) and (d) the new family is either assigned as a Couple Family with Children, by adding a new child to it, or a Couple Family with no Children unit based on a user defined probability. Fully formed households are added to completed-households as before.

**S15**—Disassemble any unassigned families in basic couples and re-add those persons to the married-males and the married-females pools accordingly.

**S16**—Calculate the probability distribution \( \rho \) of the primary family unit having marital, parental or other as the main relationship.

**S17**—For every household in the incomplete-households that meets condition (a) stochastically select the relationship between the main two persons in the new family using \( \rho \). The new family type is then given by the following table:

| Selected relationship | Criteria met | New family type |
|-----------------------|-------------|----------------|
| parental              | (c)         | One Parent     |
| other                 | (b)         | Other Family   |
| marital               | (b)         | Couple with no Children |
| marital               | (d)         | Couple Family with Children or Couple Family with no Children chosen using user defined probability |

**S18**—Form a family with the basic structure for the determined family type according to steps 4–7. If there are insufficient persons of any required relationship status, new persons are drawn from the extras pool. The age and sex
properties of the new persons are set probabilistically based on the input persons
distribution considering population heuristics.

S19—Assign the new family to the household. If the household becomes complete add it to completed-households.

S20—Repeat steps S17–19 until all non-primary families are assigned.

Stage 5 — Complete Households with Children and Relatives

S21—Randomly select the households in the incomplete-households where the primary family type is One Parent family or Couple Family with Children and assign them persons from the children pool, while adhering to the parent-child age gap constraint. Children are only added to the primary family to ensure it has more children than the others. Completed households as a result are added to completed-households.

S22—If persons remain in the children pool for not having a suitable primary family add them to Couple Family with Children and One Parent secondary and tertiary families considering the parent-child age gap constraint and ensuring that the updated family stays smaller than the preceding families. Completed households are added to completed-households.

S23—Convert all the remaining persons in married males, married-females, lone parents and children to the extras pool by nullifying their relationship status but not age and sex categories.

S24—Add persons in the extras pool to the primary family of households in incomplete-households until the household reaches its expected size. The properties of the new person is determined probabilistically based on the distribution of Dependent under 15 child, Dependent student, Non-dependent over 15 child and Relative persons in the person-level distribution and considering the population heuristics. If there are persons in extras that match the decided age and sex categories use them by setting the correct relationship status, otherwise, all the properties are set to the expected values. Add the completed households to completed-households.

S25—Complete the population by assigning Relative to the remainder of incomplete-households until each household reaches its expected household size. Relatives are only added to the primary family of the household.

Steps 1–25 generate the population of persons, families, and households, for one SA2 area. The process is repeated for every SA2 in Greater Melbourne at which point the population synthesis is complete.

Stage 6 (Optional) — Assign households to dwellings

The population we have constructed is accurate at the granularity of a suburb (SA2). To assign households to street addresses, one simple approach could be to arbitrarily allocate households to known street addresses in the given SA2. Our approach however is to do slightly better, and get the distribution of households
correct to the more finer granularity of SA1—roughly the size of one block with about 400 persons.\(^9\)

We do this in two stages. First, for a given household, we figure out the most suitable SA1 within the given SA2 to assign the household to. To do this we download the distribution of household counts by household type and SA1 for each SA2 from ABS TableBuilder (and perform a preprocessing step to ensure that the SA1 household counts correctly match the SA2 household counts), and using this, randomly distribute the household instances in the synthesised population among the SA1s considering their household type. Then in the second stage we assign the household to a known street address in the allocated SA1.

The process of constructing the list of street addresses for each SA1 is the most expensive step in the entire process, since it requires a geometric calculation to determine whether a point (the coordinates of a street address) lies within a polygon shape (the SA1 boundary), and given that there are several hundred thousand street addresses in Melbourne, and several thousand SA1s. Note that this process need only be performed once, or whenever new street addresses need to be incorporated, which is not very often.\(^10\) Nevertheless, a naive combinatorial calculation is still very expensive and the computation takes several days on our test machine. To overcome this issue, we devise a two-pass process that is extremely fast. In the first pass, we do a quick calculation of whether an address point possibly lies within a given SA1 polygon by computing whether the point lies within the bounding box for the polygon. If the point does not lie inside the bounding box then we can be sure that it does not belong to that SA1. Only if it does do we perform the more expensive calculation of computing whether it actually lies within the SA1 polygon. This tremendously reduces the computation required, since a first-pass check for each address against each SA1 bounding box yields 2–4 possibilities that have to be checked in the second pass, compared to every SA1 being checked in the naive method. The two-pass method computes the full map of street addresses to SA1s in around 24 minutes on our test machine.\(^11\)

\section{Similarity to census data}

We evaluate the quality of the resulting synthetic population using cosine similarity which is a measure of similarity between two non-zero vectors.\(^13\) It is widely used in the information retrieval domain to measure the similarity between documents. For example, to measure the similarity of two documents, one would obtain a vector of unique word counts from each document and apply cosine similarity to obtain a value between 1 (high correlation) and 0 (no correlation). In a similar way, in our context we measure the similarity between the

\(^9\) www.abs.gov.au/websitedbs/D3310114.nsf/home/Australian+Statistical+Geography+Standard+
\(^10\) The street addresses data we use is obtained from Vicmap (www.land.vic.gov.au) in ESRI Shapefile format and does not change frequently.
\(^11\) Specifications of the machine are provided in Section 1
expected and the observed marginal distributions, which are discrete categorical distributions similar to the document comparison case. Cosine similarity is calculated as:

\[
\text{Cosine similarity} = \frac{\sum O_i E_i}{\sqrt{\sum O_i^2} \sqrt{\sum E_i^2}}
\]

where \(O\) is the observed distribution (vector) and \(E\) is the expected distribution.

Cosine similarity measures the angle between the two vectors on a Cartesian plane. If the two vectors coincide the angle is 0° and the corresponding cosine value is 1. It is also important to note that cosine does not take into account the magnitude of the two vectors, that means if the two populations are different in size but has the same distribution cosine similarity would report values close to 1. This behaviour has two main implications on population synthesis applications: (a) when using cosine similarity the size of the expected and observed populations need to reported to prove that there is no significant difference in population size and (b) cosine similarity is robust at the presence of unavoidable size differences between the expected and the observed, as long as differences are reasonable.

**Results** For each of the 306 SA2s, we measured cosine similarity for person-level and household-level distributions. As well, we evaluate the age assignment from age bins (Section 3.3 Step 2) by also calculating the cosine similarity for the distribution of ages achieved. Table 2 shows the cosine similarity results for the three distributions we tested. The number of SA2s that had cosine values greater than 0.99 were: 301/306 (or 98.4%) for person-level distribution, 306/306 (or 100%) for household-level distribution, and 18/306 (or 5.9%) for age distribution (98.4% were however greater than 0.9 for age distribution - still quite strong similarity). In all SA2s the total number of households were similar in both synthesised and census distributions, while total number of persons only exhibited about 2% difference on average.

| Distribution tested | SA2s with CS > 0.90 | SA2s with CS > 0.99 |
|---------------------|---------------------|---------------------|
| Person (90 categories) | 303 (99%) | 301 (98.4%) |
| Household (65 categories) | 306 (100%) | 306 (100%) |
| Age (101 categories) | 301 (98.4%) | 18 (5.88%) |

**Table 2: Cosine similarity (CS) results for 306 SA2s in Melbourne**

**Table 3: Census 2016 population for SA2s with cosine < 0.9**

| SA2                   | Total Persons | Total Households |
|-----------------------|---------------|-----------------|
| Braeside              | 12            | 9               |
| Melbourne Airport     | 60            | 17              |
| Port Melbourne Industrial | 3           | 5               |
A visualisation of the similarity achieved in an example SA2 of Yarraville that has a synthetic population of 13,926 persons in 5,533 households in the 2016 census, is given in figure 1. The diagonal line in these figures represents a perfect match, while the blue dots plot actual numbers for each category in the synthesized population. Figure 1a shows the 90 person categories, figure 1b shows the 65 household categories, while figure 1c shows the 7 age categories. As can be seen, all points are close to the diagonal, indicating strong similarity, as also indicated by the cosine similarity scores of 1 for households, 0.99 for person categories and 0.97 for persons by age, for this SA2.

Fig. 1: Similarity of Yarraville SA2 synthesized population to cleaned census data with respect to persons-level, household-level, and age categories; blue dots indicate numbers of the synthesized population for each category, with the diagonal line showing what would be a perfect match.

Three SA2s that performed poorly (cosine < 0.9) were Braeside, Melbourne Airport, and Port Melbourne Industrial that had very small resident populations of less than 1% of the average SA2 population of 10,000 (Table 3), and had more pronounced inconsistencies between person and household distributions. Performance is poor for these SA2s because with low counts there are limited options in each pool making it difficult to find a good match.

5 Comparison to other techniques

To further evaluate our approach, we compare it to two techniques: the well-known sample-based Iterative Proportional Updating (IPU) based synthesis method, and the sample-free approach of [10] to which our work is more closely aligned.

5.1 Evaluation against IPU based approach

We created the synthetic population for Melbourne using Iterative Proportional Updating (IPU) based method proposed in [18] that synthesises a population

\[\text{Some dots are on top of each other and can’t therefore be individually distinguished.}\]
with both person-level and household-level attributes like our algorithm in Section 3.3, but instead uses a disaggregated sample. Our intent here was to understand how our sample-free algorithm compares to a state-of-the-art sample-based technique. For this exercise, we used the IPU implementation published in the Urban Data Science Toolkit\textsuperscript{13}.

Since a disaggregated sample was unavailable for the 2016 census, we use the previous 2011 Australian census data for which this data could be accessed. The sample available to us represented 1% of each SA4 area in Greater Melbourne, where a SA4 typically contains over 100,000 persons as per the ABS hierarchy. To generate the population using IPU for each SA2 for Melbourne, we used the SA4 data corresponding to the SA2s we wanted to include.

The 2011 census data differed to the 2016 data described in Section 3.1 and 3.2. For 2011 at person level we only used 84 categories, being 6 relationship status categories (Married, Lone parent, Children, Relative, Group household, Lone person) \times 2 gender types \times 7 age categories with 85 or over as the oldest age category. For household level we only had 60 categories, being 6 size categories \([1,2,\ldots,6]\) \times 10 household unit types (Lone person + Group household + [1/2-Family \times 4 primary family types]).

We ran IPU as per \textsuperscript{18} with 84-category person-level and 60-category household-level input distributions for 278 SA2s in Melbourne\textsuperscript{14} for 20,000 IPU iterations to allow it to converge to 0.0001 quality of fit. For each SA2, the program generated 20 populations instances and output the one with highest goodness of fit. We then ran the Cosine similarity test on the IPU generated population and our population.

| Distribution       | SA2s with CS > 0.99 |
|--------------------|---------------------|
| Person-level       | IPU                 |
|                    | 274 (98.6%)         |
|                    | Ours                |
|                    | 274 (98.6%)         |
| Household-level    | IPU                 |
|                    | 277 (99.6%)         |
|                    | Ours                |
|                    | 278 (100%)          |
| Age                | IPU                 |
|                    | 275 (98.9%)         |
|                    | Ours                |
|                    | 275 (98.9%)         |

Table \textsuperscript{4} shows the quality of output of our algorithm compared to IPU on the 2011 census data. Both algorithms produce a very good match (>98.6%) on all three kinds of distributions tested. We note that run times for both algorithm were comparable with IPU taking 107s and our algorithm 150s to complete.

5.2 Comparison to Huynh et. al \textsuperscript{10}

Our work is influenced by \textsuperscript{10} that also uses a sample-free approach, uses a population heuristic as we do, and also applies to Australia, albeit to the Sydney region. Importantly, we note that in starting out we had discussions with the authors (prior to their work being published), were given access to their algorithm code, and had intended to use their approach adapted for Melbourne. We

\textsuperscript{13} https://github.com/UDST/synthpop
\textsuperscript{14} The 2011 census data lists 278 SA2s for Melbourne, as compared to 309 in 2016.
clarify here the reasons why we developed an alternative approach. First, the algorithm in [10] was designed for 2006 census data, whereas we wanted to work with the more recent 2011 data and the upcoming 2016 data that included some structural changes. Second, at that stage their existing work [9,12] used IPFP to construct the input joint distributions, which was no longer necessary given these could now be directly obtained using ABS TableBuilder. Third, their code at that stage was closed, and an open implementation that we could contribute to was some way away. We therefore decided to continue developing the work we had started, in parallel to work reported in [10]. We completed the work in 2016, and have spent significant effort since in making it usable Australia-wide.

Our approach differs from [10] as follows: (a) we use new SA2 areas introduced in the 2011 census, whereas they use CCD areas which were discontinued after 2006; (b) we generate multi-family households as per census data, while they assume households to have only one family and add members to it to fit household size; (c) we use exact age distributions from census, whereas they assign ages uniformly within each age bin which is less accurate; (d) we determine age gaps between couples using a configurable heuristic while they use a Gaussian distribution (in both cases actual data is unknown).

A direct comparison to [10] is not possible due to different census years used. For 2006 data [10] show that the distribution of number of households by family composition types matches perfectly for all CCDs. For the number of households by size, about 10% of CCDs are different. For person-level, the number of males/females by age and relationship status are different for 10% of CCDs. Our algorithm, for 2011 data, matches households by number and size perfectly, while person-level differences are less than 2% (Table 4).

6 Conclusion

We presented a sample-free approach to population synthesis in the Australian context, that uses heuristics for building the population of individuals and assigning them to households in dwellings. The algorithm is fast in that it can generate the full population of Melbourne with 4.5 million persons in 1.8 million households in less than three minutes on a recent-day computer. The algorithm produces a perfect match for all 65 household-level distributions for the 2016 and 2011 census data. For person-level categories, we find greater than 98% similarity for 2016 and 2011 census data when using the Cosine Similarity (CS) test.

The reason why our algorithm matches households perfectly is because our heuristic treats household distributions as the reference and adjusts person-level attributes to fit. The reason we did this was that our applications were focused on households rather than individuals. It would be straightforward to adjust this bias to spread it between the two data sets, or to regard the person level data as the reference, by slightly modifying the cleaning process which ensures consistency between the two data sets. This decision should be made based on the application for which the population is being constructed.

Household and family are interchangeable in [10].
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