

Vertical kinship distribution at the population level: a Mamushka approximation

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Abstract

Understanding the population-level distribution of parents, grandparents, and great-grandparents is increasingly important as fertility declines and kin networks thin. However, standard kinship demography tools do not easily capture these distributions when vertical kin are shared across individuals. We introduce a simple approximation to estimate age-specific proportions of women who are childless, mothers, grandmothers, and great-grandmothers from period fertility and mortality schedules. The approach relies on conditional first-order fertility hazards combined with standard age-specific fertility and survival rates, assuming a time-invariant regime and an

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age-specific distribution of parity. We illustrate the method using Argentine census data and vital statistics, and assess its performance by comparison with a demographic microsimulation. Results show pronounced declines over time in the prevalence of higher-order generational roles, alongside strong subnational heterogeneity. These findings demonstrate how declining fertility reshapes vertical kin availability and provide a tractable tool for studying kinlessness and intergenerational support in population ageing contexts. A key Further development can formally account for heterogeneity across multiple dimensions.

Keywords: Kinship; Family; Kinlessness; Childless; Grandmotherhood

1 Introduction

Demographic changes shape both the size and structure of kinship networks, as well as the time individuals spend in each kin role (Alburez-Gutierrez et al., 2023a; Margolis, 2016; Chapman et al., 2018). In the context of the demographic transition, it is expected that the number of living biological kin for a 65-year-old person will decline by approximately 38% globally, with the steepest reductions projected for Latin America and the Caribbean. Kinship composition is also undergoing a structural transformation: from predominantly “horizontal” families, characterized by the presence of lateral kin (e.g., siblings and cousins), to increasingly “vertical” configurations, with a higher prevalence of ascendants and descendants, such as parents, children, and grandchildren (Bengston et al., 1990).

Declining fertility and increasing longevity result in fewer children, grandchildren, and great-grandchildren, and thus, a growing share of older individuals will not have

living descendants (Margolis and Verdery, 2017; Verdery and Margolis, 2017). For instance, in China, the average number of grandchildren per individual is projected to fall from 15 in 1950 to just 3 by 2100 (Alburez-Gutierrez et al., 2023b). This demographic shift exposes individuals to historically unprecedented levels of vulnerability in later life, particularly due to reduced availability of informal care and emotional support, and increased dependence on formal welfare systems. The term *kinlessness* refers to the condition of having no surviving close relatives—such as children, parents, siblings, or spouses—especially in old age (Margolis and Verdery, 2019; Ornstein et al., 2025). This phenomenon is gaining increasing attention in demographic and social research due to its implications for caregiving arrangements, social isolation, and support networks. As societies face rising dependency ratios and increasingly complex care dynamics, assessing the availability of kin becomes essential for informed public policy and long-term care planning (Taylor et al., 2023).

However, this shift also presents an opportunity to reconceptualize care provision at the population level. Although gains in healthy life expectancy do not clearly outpace those in overall lifespan (Su et al., 2023), a growing segment of older individuals in their 60s and 70s may experience relatively good health while lacking biological kin to provide informal support. This convergence of kinlessness and substantial available person-time raises questions of substantive and technical interest: How many individuals are (not) parents at each age within a given population? What proportion are (not) grandparents or (not) great-grandparents? Hünteler (2022) introduced the notion of “generational placement” to refer to an individual’s genealogical position in the family: a status determined by the absence or presence of direct ancestors and descendants. Understanding the population-level distributions of these generational

placements within populations is of increasing relevance for social policy given rapid population aging coupled with declining family sizes: How many older individuals lack descendants on whom they could potentially rely for informal support?

The increase in childlessness and the postponement of marriage and childbearing also impact the proportion of the population that ever becomes grandparents, as well as the age at which grandparenthood begins (Margolis, 2016). Being a grandparent is no longer a quasi-universal experience among the older population. In much of Latin America, the term *abuelos* is often used interchangeably with “older adults,” obscuring important demographic distinctions. Despite their demographic and social significance, grandparent roles are seldom captured in censuses or surveys—except indirectly through multigenerational household composition. Grandparents frequently provide financial, emotional, and caregiving support to younger generations. In England and Wales, for example, more than half of children in kinship care live with one or more grandparents (Office for National Statistics, 2023).

What are the actual demographic tools to measure this at the population level? Contemporary kinship demography techniques allow for the estimation of kinship networks from the perspective of Ego, a representative individual in the population (Caswell, 2019). In a stable population, the number of Egos is given by the expression $\int_0^\omega B e^{-ra} l(a) da$, where a denotes age, $l(a)$ is the survival function, r is the intrinsic growth rate, and B represents the total number of births at a given reference time. These Egos may share common kin, which introduces complexities when aggregating kinship measures at the population level. For example, instead of knowing how many grandchildren an average woman aged a has, we would like to know what proportion of woman aged a have a grandchildren.

In this paper, we introduce an analytical approach to approximate the proportion of women in a population who are childless (i.e., ‘not mothers’, or ‘only daughters’), mothers, grandmothers, and great-grandmothers, based on given demographic rates. Our focus is on identifying the share of the population with and without vertical kin—an issue closely related to the concept of “fading family lines”, which refers to the absence of biological descendants across successive generations, with both social and genetic implications at the population level (Kolk and Skirbekk, 2022). We develop a set of formal relationships to capture this generational placement and apply the model to the Argentine context, comparing two contrasting fertility regimes over the past two decades and examining internal heterogeneity at the subnational level. Finally we compare these results with a microsimulation based on same risks, and apply the method to another country with available registers of kinship availability, highlighting in both exercises the relevance of heterogeneity for age-specific accuracy.

2 Method

Egos sharing common kin are a challenge when studying the population distribution of kin. For instance, estimating the number of mothers by age requires a population-based approach that accounts for the fact that multiple Egos—such as siblings—may share the same mother. If not properly adjusted, this leads to overcounting, since shared kin (e.g., parents, grandparents) are effectively “reported” multiple times by different Egos. This distinction is crucial: while mathematical kinship models (Caswell, 2019) often compute average numbers of kin per Ego, demographic interest may lie in the distribution of kin roles across the population.

More generally, the issue arises when considering kin types that are shared among Egos, especially ancestors and collaterals. When aggregating across individuals without accounting for this overlap, the total number of kin can be substantially overestimated (akin to summing individual trees and losing sight of the wider forest). This methodological nuance is critical for producing valid estimates of generational placements and kinlessness in populations using mathematical models.

Our goal is to derive expressions to approximate the proportion of women in a population who are childless, mothers, grandmothers and great-grandmothers, given a prevailing set of demographic rates. We aim to group the population according to different generational placements, like the Russian nesting doll shown in figure 1. In Argentina and other countries of Latin America, these dolls are affectionately known as *Mamushkas*, a portmanteau of *madre* (mothers) and *Babushka* (an older woman or grandmother, in Russian). Here, we use Mamushkas as a metaphor for the (nested) generational placements that we are interested in.

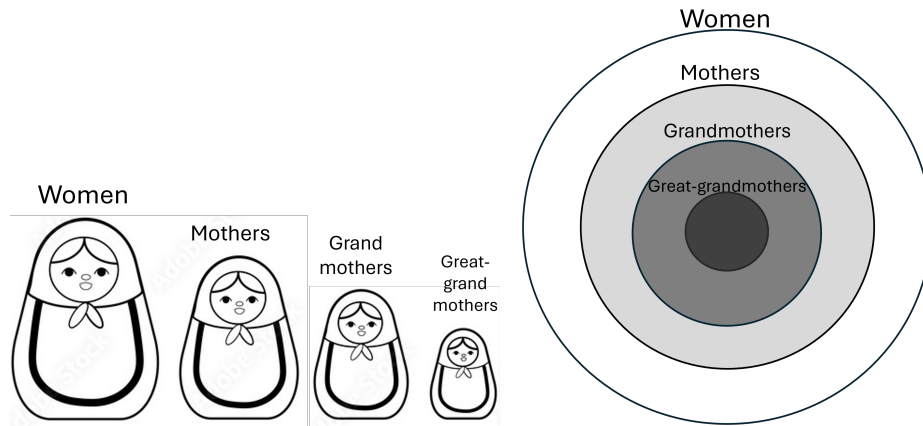


Figure 1: At a given age, a portion of living women are mothers, a portion of those are grandmothers, and a portion of those are great-grandmothers. The white area is childless (*only* daughters), the light-grey area is *only* mothers and the dark-grey area is *only* grandmothers.

2.1 Mothers

Let us estimate the percentage of women who have become mothers by a given age in a stable population model: each woman belongs to a synthetic cohort based in cross-sectional rates (we add flexibility on this assumption in a further section). Following a life course perspective (Krishnamoorthy, 1979), we define two key measures: the probability that a newborn eventually becomes a mother at age a , denoted $\alpha(a)$, and the cumulative proportion of mothers up to that same age, denoted $m(a)$:

$$\alpha(a) = e^{-\int_0^a \mu(x) + f_1(x) dx} f_1(a) \quad (1)$$

$$m(a) = \int_0^a \alpha(x) dx \quad (2)$$

$\mu(a)$ is the mortality hazard rate by age, and $f_1(a)$ the fertility hazard rate for a first birth, that is, the instantaneous risk of a parity-zero woman transitioning to motherhood at age a . This is similar to a survival function for the risk of becoming a mother where all women are exposed from birth. In this framework, the complement of the cumulative survival function corresponds to the proportion of women who have already transitioned to motherhood by a given age, whereas the survival curve itself captures the remaining childless fraction. While we focus here on the initial transition to motherhood, extending this to a multi-state parity synthetic population produces a fertility increment-decrement table (HFD, 2024).

From a population perspective, the proportion of living mothers aged a , $M(a)$, can be expressed as the proportion of women in a birth cohort (with initial size Be^{-ar} and actual population $N(a) = Be^{-ar}l(a)$ at age a) who become mothers and also survive

to age a :

$$\begin{aligned}
M(a) &= \frac{1}{N(a)} B e^{-ar} \int_0^a e^{-\int_0^x \mu(s) + f_1(s)} f_1(x) \frac{l(a)}{l(x)} dx \\
&= \frac{1}{N(a)} B e^{-ar} l(a) \int_0^a e^{-\int_0^x \mu(s)} e^{-\int_0^x f_1(s)} f_1(x) \frac{1}{l(x)} dx \\
&= \frac{1}{N(a)} B e^{-ar} l(a) \int_0^a l(x) e^{-\int_0^x f_1(s)} f_1(x) \frac{1}{l(x)} dx \\
&= \int_0^a e^{-\int_0^x f_1(s)} f_1(x) dx
\end{aligned} \tag{3}$$

As a result, the age-specific first-birth hazard $f_1(x)$ allows us to estimate the proportion of women who have become mothers at each age. We have thus identified the second doll in figure 1 (the first doll was all women); we refer to these as being ‘at least mothers,’ meaning that some proportion of them will go on to become grandmothers.

The overall proportion of mothers within the total female population can be obtained as a weighted average across the female age distribution. Specifically, if we denote the population share at age a as $c(a) = \frac{N(a)}{N}$, where $N(a)$ is the number of women at age a and N is the total number of women, then the aggregate proportion of mothers is given by:

$$M = \int_0^\omega c(a) M(a) da \tag{4}$$

An analogous analysis can be done for men, with their own fertility and mortality age schedule. Let us denote the probability of becoming a father by $p(a)$ and the percentage of fathers among all men, $P(a)$. Male fertility schedules typically exhibit

later onset and greater age dispersion compared to female fertility, particularly in populations where men continue fathering children well into older ages (Schoumaker, 2019; Caswell, 2022). Consequently, the age pattern of fatherhood $P(a)$ will reflect not only biological and behavioral aspects but also partnership dynamics, such as age gaps between partners and patterns of remarriage.

2.2 Grandmothers

Now let us estimate the proportion of grandmothers by age. The timing of first-time motherhood determines when individuals become at risk of entering a second-order kinship role, grandparenthood (Leopold and Skopek, 2015). In this context, becoming a grandmother depends on whether a woman's children become parents themselves. At age a , the number of daughters ever born to an individual (Ego) is given by $F(a) = \int_0^a f(x) dx$, where $f(x)$ is the age-specific fertility rate. For each age x (with $x < a$), the number of daughters born is $f(x) b_f$, where b_f is the proportion of female births. The probability that a daughter born at age x becomes a mother by the time Ego reaches age a (i.e., over a period of $a - x$ years) is given by $m(a - x)$. We define $m_d(a)$ as the probability that a daughter of a woman aged a eventually transitions into motherhood:

$$\begin{aligned} m_d(a) &= \frac{\int_0^a f(x) b_f [\int_0^{a-x} l(s) e^{-f_1(s)} f_1(s) ds] dx}{F(a) b_f} \\ &= \int_0^a \frac{f(x)}{F(a)} m(a - x) dx \end{aligned} \tag{5}$$

Similar to total number of living granddaughters in Keyfitz and Caswell (2005)

eq. 15.2.6

The same approach can be applied from the perspective of sons, using male-specific fertility rates. The proportion of sons who become fathers by the time Ego reaches age a can be expressed as: $p_s(a) = \int_0^a \frac{f(x)}{F(a)} p(a-x) dx$, where $p(a-x)$ is the probability that a son born when Ego was aged x becomes a father within the remaining $a-x$ years (analogous to $m(a-x)$). The mean age at which individuals enter grandparenthood plays an important role in determining the length of time spent in that role, with implications for intergenerational interaction and support dynamics (Shubat and Bagirova, 2022).

We can model this process using a continuous binomial distribution (Iliencko, 2013), where the probability of "success" in each "trial" is given by $m_d(a)$ (or $p_s(a)$ for sons), and the size parameter corresponds to the number of daughters (or sons) ever born by age a : $F(a) b_f$ (or $F(a) (1 - b_f)$). While the binomial distribution assumes homogeneous behavior across women (see Table C in Figure 5), it offers a tractable framework for presenting the core methodological idea (further considerations are discussed in Section 3.3). The probability that a mother aged a is a grandmother can be estimated as¹:

$$gm_m(a) = 1 - [1 - m_d(a)]^{[F(a) b_f]} [1 - p_s(a)]^{[F(a)(1 - b_f)]} \quad (6)$$

This formulation assumes that each child has an independent and identical probability of becoming a parent. However, we know that older daughters are more likely

¹The probability for two non-negative independent variables to be positive is $P(A > 0 \& B > 0) = 1 - P(A = 0 \& B = 0) = 1 - P(A = 0) P(B = 0)$.

to have had children than younger ones, due to longer exposure to childbearing risk. Our approach effectively estimates a representative probability by incorporating time exposure in Equation 5, weighting by the age-specific maternity function (if Ego had all her daughters during the last year, no matter how many, $m_d(a)$ will be negligible).

If sex-specific rates are quite similar, then we can simplify the expression to:

$$gm_m(a) = 1 - [1 - m_d(a)]^{F(a)} \quad (7)$$

The probability of having descendants increases both with higher parity and with a greater likelihood that each child becomes a parent—two perfectly linked factors in a stable population setting. As the number of children grows, so does the chance that at least one of them will go on to have children of their own. These dynamics jointly determine the probability of transitioning into the role of grandmother. Finally, the proportion of women who are at least grandmothers at age a is:

$$GM(a) = gm_m(a) M(a) \quad (8)$$

With this, we reveal the third layer of the Mamushka structure. The proportion of mothers at age a who have not yet become grandmothers is given by $M(a) - GM(a) = 1 - gm_m(a)$, corresponding to the light-grey area in Figure 1. The overall share of grandmothers in the total female population, denoted GM , can be calculated using the population-weighted approach described in Equation (4). The same method applies analogously to estimate the proportion of grandfathers in the male population.

2.3 Great-grandmothers (and older ancestry)

Note that each Ego can have up to four great-grandmothers, which means that in long-lived populations, initial intuition suggests that the number of great-grandparents (especially great-grandmothers because of their differential longevity) can be significant at the population level. To estimate their prevalence, and because the underlying demographic process spans three generational steps (Kolk and Skirbekk, 2022), we first calculate the proportion of granddaughters who become mothers out of the total number of granddaughters:

$$\begin{aligned} m_{gd}(a) &= \int_0^a \frac{f(x)}{F(a)} \left[\int_0^{a-x} \frac{f(s)}{F(a-x)} m(a-x-s) ds \right] dx \\ &= \int_0^a \frac{f(x)}{F(a)} m_d(a-x) dx \end{aligned} \tag{9}$$

As before, this probability serves as the parameter of a (continuous) binomial distribution, with a size parameter given by the total number of granddaughters ever had: $\int_0^a f(x)R(a-x) dx$. A similar approach can be applied for grandsons, where $p_{gs}(a)$ represents the probability that a grandson becomes a father. Then, the probability that a grandmother becomes a great-grandmother, denoted as $ggm_{gm}(a)$, can be derived analogously to equation 6, by adjusting the size and probability parameters accordingly. Finally, the proportion of women who are at least great-grandmothers at age a is given as a subset of the grandmothers:

$$GGM(a) = ggm_{gm}(a) GM(a) \tag{10}$$

The proportion of women who are only grandmothers (i.e., not yet great-grandmothers) at age a is given by $GM(a) - GGM(a) = 1 - ggm_{gm}(a)$, corresponding to the dark-grey area in Figure 1. The overall share of great-grandmothers in the total population, denoted GGM , can be calculated using the population-weighted approach in Equation 4. The same method applies to estimate the proportion of great-grandfathers. This logic can also be extended to higher kinship orders. For example, in the case of great-great-grandmothers, one must first estimate $m_{ggd}(a)$ (the probability that a great-granddaughter becomes a mother), determine the total number of great-granddaughters at age a (as the size parameter), define the transition probability $gggm_{ggm}$, and finally obtain the resulting proportion $GGM(a) = gggm_{ggm}(a) GGM(a)$.

2.4 Childless women

By definition, everyone in a population is a son or daughter. As a result, the entire population in Figure 1 is composed of individuals who are (at least) daughters (or sons). Childless individuals (the white area in Figure 1) are the complement of the individuals who are “at least mothers” (or “at least fathers”):

$$D(a) = 1 - M(a) \tag{11}$$

A related measure—closely tied to the Mamushka concept—is the proportion of individuals, by age, who are part of a siblinghood (i.e., those with at least one sibling). We address this question in the appendix 5.1 and show some results for Argentina.

In this section, we have shown that the Mamushka distribution in a theoretical

population can be derived using only age-specific mortality, fertility, and the first-birth hazard function $f_1(x)$. In the next section, we explore an indirect method for estimating $f_1(x)$ when full data are not available, with the goal of making the approach applicable to different real-world settings, and making it comparable across time and space.

3 Results

3.1 Indirect estimate of $f_1(x)$

Estimating $f_1(x)$ requires knowledge of the distribution of women by age and parity status, as well as birth order statistics. Developing a time series for this is challenging and only feasible in some countries. The Human Fertility Database protocol (HFD, 2024) differentiates between situations where long-term cohort data is available, allowing for the construction of fertility histories for each cohort (setting the parity-age distribution for each cohort by year), and those where population registers, censuses, or surveys provide partial counts of women by age and parity, which can be tracked through birth registration by age and order. When such data is available, this is the preferred method for calculating $f_i(x)$.

One simple approach for period estimates stems from the fact that $f_1(x)$ can be expressed as the product of the proportion of first-order births $b_1(x)$, the proportion of women who are not yet mothers $[1 - M(x)]$, and the fertility rate at that age $f(x)$. We can derive $f_1(x)$ by examining the ratio $\frac{f_1(x)}{f(x)}$ and then getting an expression for $f_1(x)$:

$$\begin{aligned}
\frac{f_1(x)}{f(x)} &= \frac{\frac{B_1(x)}{W_0(x)}}{\frac{B(x)}{W(x)}} = \frac{b_1(x)}{1 - M(x)} \\
f_1(x) &= \frac{b_1(x)}{1 - M(x)} f(x)
\end{aligned}
\tag{12}$$

Here $B_1(x)$ represents first-order births for women aged x , $W(x)$ represents the number of women aged x , and $W_0(x)$ represents the number of women who are not mothers at age x (so $1 - M(x) = \frac{W_0(x)}{W(x)}$), both in terms of exposures for the calendar year. The three components can be obtained relatively easily: census data on age distribution by parity provides the proportion of mothers, while $b_1(x)$ can be derived from administrative records or census data. In many countries, the fertility section of the census asks about the date or the mother's age at the birth of her last child (or simply whether a child was born in the last year). By cross-tabulating women with parity one among those who had a child in the last year, it is possible to estimate $b_1(x)$. Lastly, the fertility rate $f(x)$ can be sourced externally (for example from United Nations, Department of Economic and Social Affairs, Population Division (2022)), calculated using direct methods (vital statistics and exposures) or estimated using classical indirect methods (Moultrie TA and Zaba, 2013) ²

In addition to requiring an estimate of $f_1(x)$, a key advantage of our approach is that it only necessitates knowledge of $f_{2+}(x)$ (the fertility rate among women who are already mothers) rather than the full set of parity-specific rates ($f_2(x)$, $f_3(x)$, etc.).

²Another approach relies on the fact that many Latin American countries include a survey or census question regarding the age or date of first childbirth (Nathan, 2015).

Moreover, $f_{2+}(x)$ can be derived from available inputs using the following expression:

$$f_{2+}(x) = \frac{f(x) - [1 - M(x)]f_1(x)}{M(x)} \quad (13)$$

This equation is based on the fact that the observed fertility rate at age x is a weighted average of the rates for mothers and non-mothers: $f(x) = M(x)f_{2+}(x) + [1 - M(x)]f_1(x)$. This formulation allows us to compute parity-specific fertility rates efficiently, without requiring detailed parity histories.

3.2 Estimates for Argentina

Argentina underwent an early demographic transition within the Latin American context (Pantelides and Rofman, 1983): by the mid-20th century, its total fertility rate (TFR) had already declined to approximately 3.2 children per woman (United Nations, Department of Economic and Social Affairs, Population Division, 2024), but then experienced a slower pace of fertility decline, remaining relatively stable between 1980 and 2010. In recent years, Argentina has experienced an accelerated decline, with TFR dropping to 1.5 by 2020, a situation that was observed in other countries of the region (Pardo et al., 2025). During this period, the mean age at childbearing shifted from 27.9 to 29.2. In terms of female mortality, life expectancy at birth increased from 65.2 years in the mid-20th century to over 80 years today (United Nations, Department of Economic and Social Affairs, Population Division, 2024), and life expectancy at age 65 rose from 14.5 to 19.5 years over the past five decades. The former, heavily influenced by infant mortality, increases the survival of Ego's descendants, whereas the latter translates into greater longevity among Ego's

ascendants (Preston et al., 2000).

This shift offers a valuable opportunity to compare the Mamushka distribution under two distinct fertility regimes, corresponding to the years 2001 and 2022—both census years in Argentina. We apply the approximation described in Section 2 to estimate the Mamushka distribution for each year. To do so, we prepared estimates of $f_1(x)$ following Section 3.1, using census data to determine the proportion of mothers by age³, vital statistics to obtain values for $B_1(x)$, and external sources to estimate the overall fertility rate (United Nations, Department of Economic and Social Affairs, Population Division, 2024).

Some interesting patterns emerge in Figure 2: $f_1(x)$ declined by more than half for women under 30, while the overall fertility rate $f(x)$ decreased by about a third. For women aged 15-19, the fertility risk dropped to the same level as that of women aged 40-45, a group whose fertility rate did not change significantly.

³In the last three Argentinian censuses, the question on fertility asked whether the respondent had given birth in the previous year.

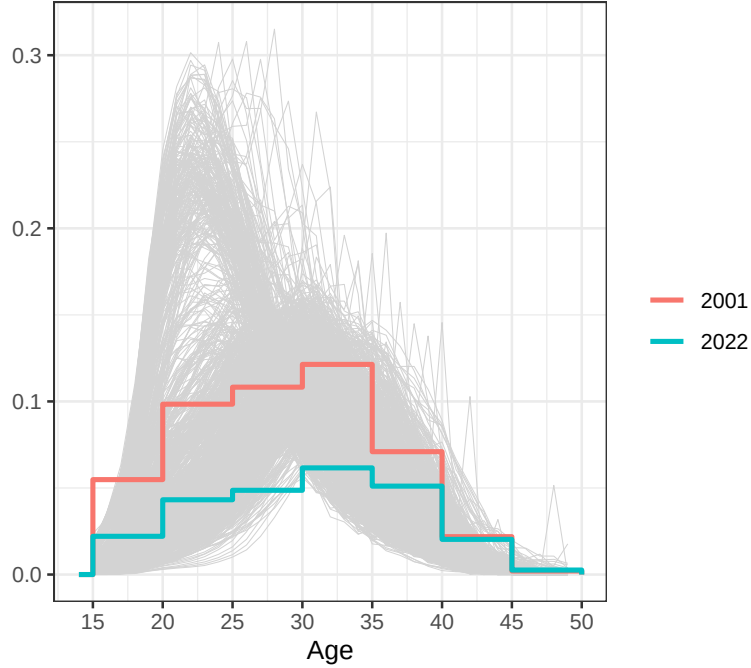


Figure 2: Conditional first-order rates in Argentina in 2001 (red) and 2022 (blue) (abridged age groups). Grey lines in the background show the same rates (single ages) for all available country-years in the Human Fertility Database since 1980.

Using single-year age rates for order-specific fertility (with quinquennial rates from Figure 2, uniformly disaggregated into single years of age) and mortality from United Nations, Department of Economic and Social Affairs, Population Division (2024), we apply a multi-stage kinship model (Caswell, 2020) using the DemoKin R package (Williams et al., 2023) to estimate the distribution of descendants by parity at each age of Ego, within a time-invariant framework. The results that we use are, following Caswell (2020) notation: $\phi^{parity}(a)$, $d^{parity}(a)$, $gd^{parity}(a)$ and $ggd^{parity}(a)$ (equation 18 in Caswell (2020)). Those are vectors of expected Focal, children, grandchildren and great-grandchildren by parity stage when Focal is a years old. We accumulate by parity all descendants, not only the living ones (as the original paper). A dead

children do not change her/his last parity status since death. Based on that, we compute the probabilities m , m_d , and m_{gd} , and subsequently derive gm_m and ggm_{gm} using the equations presented in the previous section. For simplicity, we assume that fertility and mortality rates do not differ by sex and use the female schedules for all calculations.

In a population with Argentinian fixed rates from 2001 and 2022, the Mamushka distribution by age would follow the pattern shown in Figure 3 (the more detailed distribution, with M , GM and GGM can be found in Figure 12 in the Appendix). In 2001, only about 10% of women aged 40 and above were not mothers, which aligns with the 2001 census observation, largely due to the relative stability of fertility in previous decades. However, by 2022, this figure would triple to around 30%.

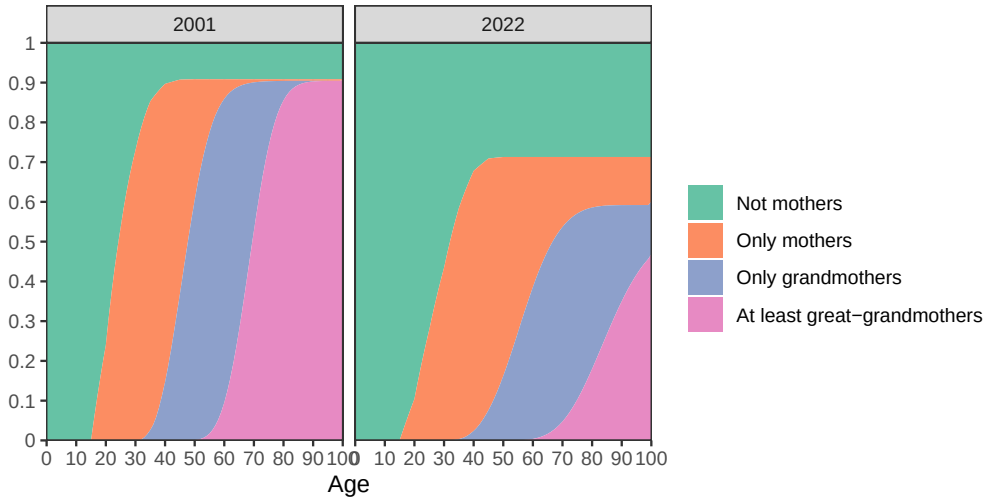


Figure 3: Distribution of Argentinian women by vertical kinship role based on 2001 and 2022 rates. The female population at each age can be split into four stages within the Mamushka: childless (not mothers, only daughters), only mothers (not grandmothers), only grandmothers (not great-grandmothers) and at least great-grandmothers. See Table 2 in the Appendix for full results.

What has been the empirical experience of real cohorts with comparable fertility

levels? Figure 4 presents a comparison between our synthetic Argentinian cohorts and observed cohort outcomes from Europe and Asia, offering a plausible reference scenario. In particular, childlessness has risen sharply in East Asia; for example, among Japanese women born in 1970, 27% remained childless (Sobotka, 2021)⁴. The relationship between childlessness and cohort fertility rate (CFR) is not linear, as illustrated in Figure 5, and the observed variation is likely driven by dispersion in parity distributions rather than average fertility levels alone—especially considering that all displayed cohorts exhibit CFRs above 1. For instance, the 1970 Swedish cohort, with a CFR of 2, still had a childlessness rate of 12% according to population register data (Kolk et al., 2021) (actually a dot in Figure 5).

⁴A permanently childless woman is defined as one who has not had any children by the end of her reproductive years, typically between ages 45 and 49 (OECD, 2021).

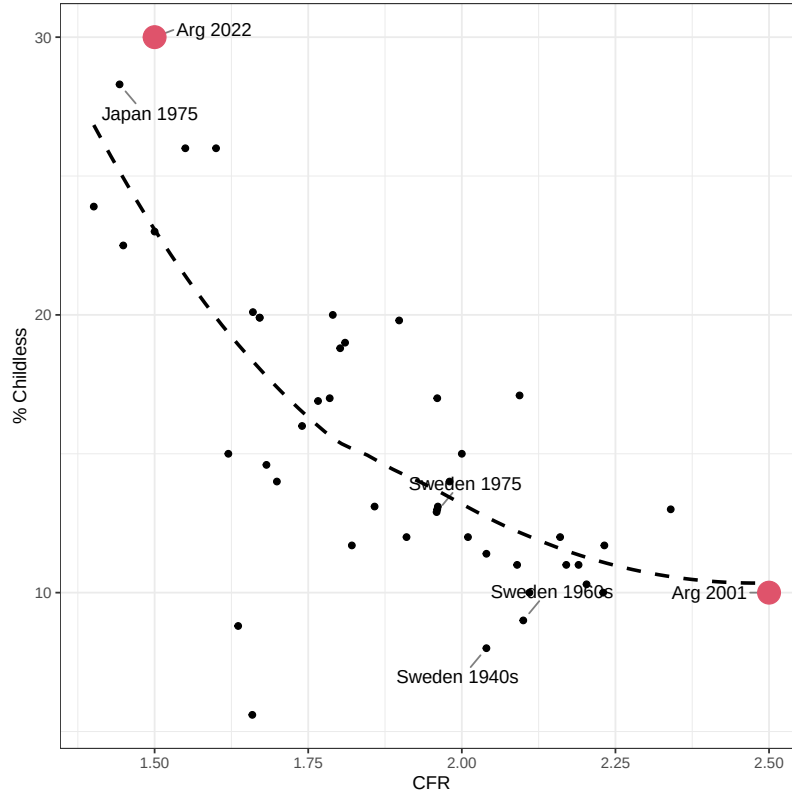


Figure 4: Cohort completed fertility rate and childless proportion. Argentina period estimates (red dots) in context. Countries: Austria, France, Great Britain, Italy, Netherlands, Norway, Poland, Sweden, Switzerland, United States, Canada, Denmark, Ireland, Finland, Estonia, Japan, Spain, Hungary, Czechia, Bulgaria, Iceland, Slovenia, Lithuania, Portugal, Hong Kong, Singapore, Germany. Selected cohorts from the 1940s to the 1970s. Based on Beaujouan et al. (2023), Sobotka (2021) and OECD (2021)

Continuing with the analysis over Figure 3, in 2001 nearly all women who became mothers eventually transitioned into grandmotherhood, and at older ages into great-grandmotherhood, as indicated by high values of gm_m and ggm_{gm} (see Table 2 in the Appendix). This pattern was largely driven by a higher TFR, which increased the likelihood that at least one child would go on to have children of their own. By 2022, however, this intergenerational continuity has weakened significantly: although

approximately 70% become mothers by age 80, 60% would be grandmothers.

If we apply the Mamushka distribution estimated from 2001 and 2022 rates to the 2022 census age structure, we observe a significant shift in the distribution of kinship roles. Depending on the reference year, 42% or 58% of the population would be childless (i.e., not mothers), while the remaining 58% or 42% would be mothers. Similarly, 29% or 13% would be grandmothers, and 9% or 2% great-grandmothers. By 2022, the probability of experiencing grandmotherhood (conditional on having become a mother) had declined, making grandmotherhood a less common life experience for mothers than motherhood itself.

3.3 Heterogeneity

It is known that $M(a) < 1$ for any $a > 0$: not everybody experiences the event of becoming a mother. Critically, the level of fertility, whether measured by period or cohort, does not fully determine the proportion of mothers. Rather, it is the distribution of fertility across the population that matters. A typical source of heterogeneity is education: there is a well established evidence that exists a negative relationship between women's education and fertility, and that it has varied across place and time (Nisén et al., 2020; Sobotka et al., 2017). For instance, if the variance in ultimate parity was zero and $TFR = 1$, then all women would have exactly one child, making the entire population of women mothers (as depicted in cases B and C in Figure 5). The dispersion across ages, however, is governed by the shape of $f_1(a)$. Given the same cumulative unconditional first-order fertility, expressed as $F_1(a) = \int \frac{B_1(x)}{N(x)} dx$, the proportion of mothers at each age can vary depending on the timing and spread of first births (compare case B and case C in Figure 5). This underscores the importance

of considering fertility dispersion patterns, not merely average levels, when analyzing the demographic composition of motherhood at the population level.

Age	Woman				Woman				Woman			
	A	1	2	3	B	1	2	3	C	1	2	3
	0				0				0			
	1				1				1			
2					2				2			

Figure 5: Each table implies the same cohort fertility rate ($CFR = 1$) but different levels of $f_1(a)$. Three women (columns) transition through three ages (rows). Shaded women have a child at the end of the year. Table A: 1/3 of all women eventually become mothers; first birth rates are 1/3 for the first age and zero elsewhere. Table B: 1/3, 2/3 and 1 of all women are mothers at each age; first birth rates are 1/3, 1/2 and 1. Table C: 0, 1 and 1 of all women are mothers at each age; first birth rates are 0, 1 and 0 (no exposures), by age.

We implement a simple individual-based microsimulation to examine the stable distribution of vertical kin types under fixed age-specific fertility and mortality rates of Argentina in 2001. The aim is to determine whether the estimates from our Mamushka approximation are consistent with the microsimulation. The model initializes with a population of women and men of 5,000 each, with random distribution by single age, and evolves in discrete annual time steps over a 300-year horizon. Female fertility follows age and parity risks, f_1 and f_{2+} . Each woman may experience at most one birth per year, with the probability determined by her age and whether the birth would be of first or higher order. Mortality is applied independently for every individual using age-specific death probabilities. Mortality and fertility inputs are those used in section 3.2.

To generate complete genealogies, every newborn is assigned both a mother (the reproducing woman) and a father of the same age (for the sake of comparison against assumption in section 2 and applied in section 3.2) and who has not yet been assigned a birth in the current simulation year. This approach tries to preserve the strictly female-determined nature of fertility while enabling the transmission of kinship links through both maternal and paternal lines, avoiding imposing a male fertility schedule, with the danger of having duplicated births.

After 300 years of simulation (with a mean age at first birth of 28 in 2001, more than 10 generational intervals), all women alive constitute the population used for analysis. Kin statuses are assigned by traversing genealogical links: a woman is classified as a mother if she has ever borne a child (no matter whether the child is alive); as a grandmother if at least one of her children (of either sex, and traced via maternal or paternal links) has reproduced (no matter if child or grandchild are alive); and as a great-grandmother if at least one of her children is themselves classified as a grandparent (no matter if child, grandchild and great-grandchild are alive). These definitions ensure that all feasible lineage pathways contribute to the formation of vertical kin types. See the Supplemental Materials section 4.0.3 to reproduce the results.

Microsimulation outputs closely replicate the input rates, demonstrating internal consistency (Figure 15). Based on this, the proportions of mothers, grandmothers, and great-grandmothers by age were estimated and compared with the Mamushka approximation. Results indicate a strong alignment in the case of mothers and grandmothers (Figure 6), successfully capturing the S-shape accumulation pattern in the transition to each kin role. For great-grandmothers, the microsimulation displays

a slightly flatter slope between ages 70 and 90 and increasing variability with age. When aggregated in decennial age groups weighted by the simulated population (Table 4), the total proportions reach 65% vs. 68% for mothers, 32% for grandmothers in both approaches, and 9% for great-grandmothers. Age-specific comparisons show a persistent slight underestimation by the Mamushka model for mothers, negligible differences for grandmothers, and an overestimation of around 10% (0.08/0.88) for great-grandmothers between ages 80 and 89. Overall, these findings suggest that the proposed formal approximation produces reasonably accurate results under a stable demographic regime.

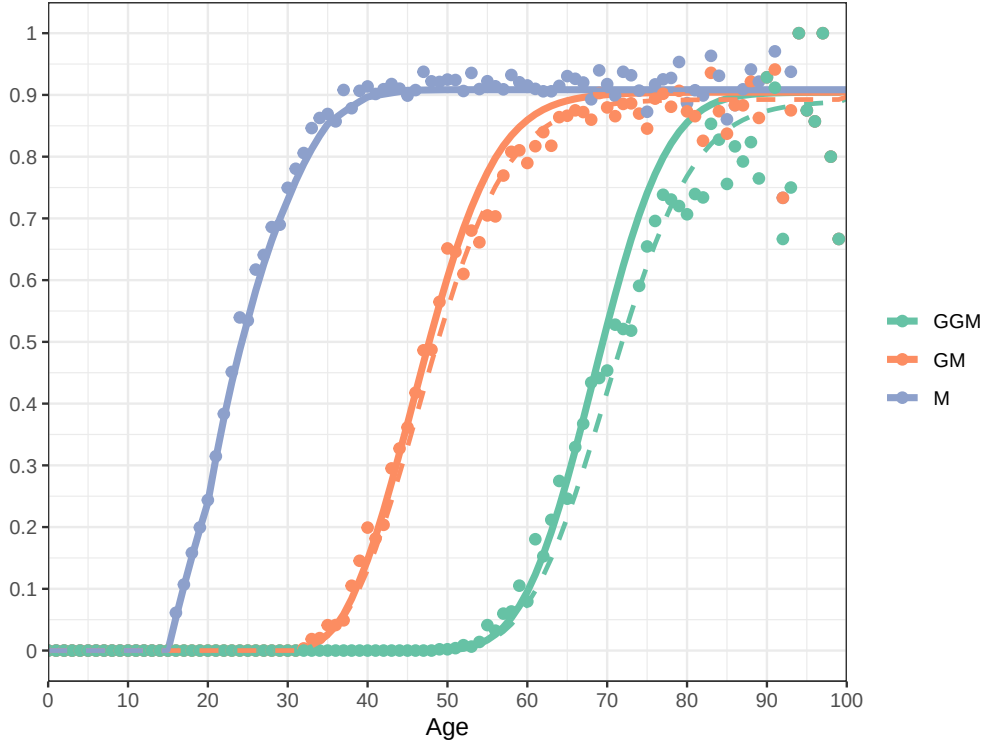


Figure 6: Proportion of female population by age that are mothers (M), grandmothers (GM) and great-grandmothers (GGM). Microsimulation (dots), Binomial Mamushka (lines) and Beta-Binomial Mamushka (dashed lines, over-dispersion parameter set to 5). Argentina 2001 rates.

A possible explanation for the observed overestimation of *GGM* at older ages relates to the conceptual discussion in Section 5. Fertility is a zero-inflated process Barakat (2017), meaning that births tend to cluster rather than distribute uniformly across the population. As a result, the number of women transitioning into motherhood—and thus into higher-order kin roles—may be lower than predicted by standard models. This overdispersion is not fully captured by the binomial assumptions used in estimating gm_m and ggm_{gm} in the Mamushka model. To better account for this phenomenon, we experimented with a beta-binomial specification, in which, for instance, the probability that a mother aged a becomes a grandmother is modelled with a beta-distributed parameter:

$$\begin{aligned} gm_m &\sim \text{Binomial}(m_d, F) \\ m_d &\sim \text{Beta}(\alpha, \beta) \end{aligned} \tag{14}$$

Rewriting as $\alpha = \kappa m_d$ and $\beta = \kappa(1 - m_d)$, we define κ as a dispersion parameter: when $\kappa \rightarrow \infty$, the model reduces to the binomial case, while lower values introduce heterogeneity. We applied $\kappa = 5$ across all ages (level dispersion), by trial and error, observing improved fit for *GM* and *GGM* at older ages (Figure 6, dashed lines). This suggests that overdispersion plays a non-trivial role, particularly for great-grandmothers, where estimation depends multiplicatively on grandmother heterogeneity. Makes sense: giving to all woman the same probability makes that all of them have some chance of having a children, when this is not the case, and this effect propagates over the vertical descendents line. Addressing this rigorously may require more complex modelling of m_d , which itself aggregates age-specific risks

across multiple childbearing events, resulting in a weighted mixture of cohorts' fertility. Empirical estimation of (κ) would require linked fertility histories across generations. For each woman, the data should include her date of birth, the number of biological daughters, each daughter's date of birth, and the timing of each daughter's transition to motherhood. Additional characteristics, such as educational attainment and place of residence, would help distinguish observed compositional differences from residual clustering within maternal lineages. The present approach captures only the marginal mean probability that a daughter becomes a mother; it does not identify the covariance in motherhood outcomes among daughters from the same family. These findings therefore provide a basis for further data exploration and for incorporating lineage-level fertility heterogeneity into future refinements of the model.

Given the importance of population heterogeneity for estimating the distribution of generational placements in the Mamushka model, we next disaggregate the analysis at the subnational level.

3.4 Subnational analysis

Demographic differences between provinces in Argentina have been declining in the context of the national fertility reduction and epidemiological transition. In 2022, Argentina provinces can be divided into three groups in terms of fertility and mortality levels (see Figure 13 in the Appendix). All provinces are below replacement rate but with a range from 1 to 2 child per woman in 2022, with a pattern by age of $f_1(x)$ that captures a delay in first child (see Figure 14 in the Appendix). For example, the Ciudad Autónoma de Buenos Aires (CABA), with a TFR close to 1, shows the highest first-birth rate in the 35–39 age group—a pattern also observed in Misiones,

where the TFR is closer to 2 (see Figure 7). However, Misiones exhibits significantly higher first-birth risks at younger ages, highlighting important subnational differences. Interestingly, the age pattern of second or higher-order births is quite similar between the two provinces from age 35 onward, suggesting that once a woman has had a first child, parity progression risks converge despite broader differences in younger fertility timing and level.

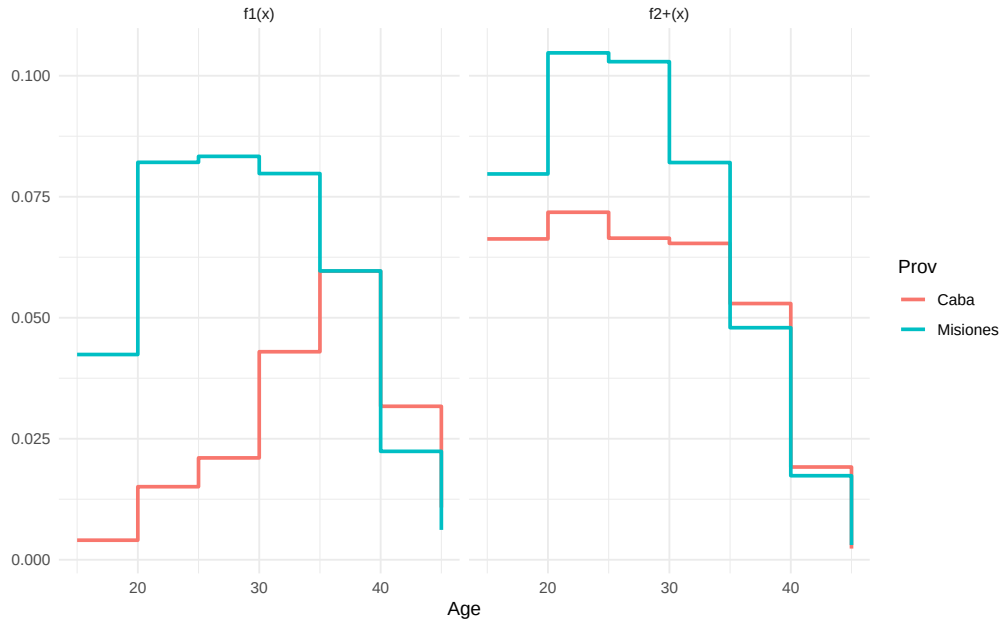


Figure 7: First and second (or higher) birth rates by age in 2022. Argentinian provinces: CABA and Misiones

As discussed in Section 2, heterogeneity plays a crucial role in shaping the Mamushka distribution. The demographic differences highlighted above are reflected in the implicit Mamushka profiles across provinces in 2022 (see Figure8). For instance, at age 50, the proportion of women who are at least mothers is approximately 60% in CABA, compared to 90% in Misiones. At age 90, the share of women who are at least

grandmothers reaches 35% in CABA and 85% in Misiones. These differences become even more pronounced for GGM: at age 90 less than 5% of women in CABA would be great-grandmothers, compared to 80% in Misiones. These contrasts underscore the importance of accounting for regional variation when assessing kinship roles and potential caregiving dynamics at the population level.

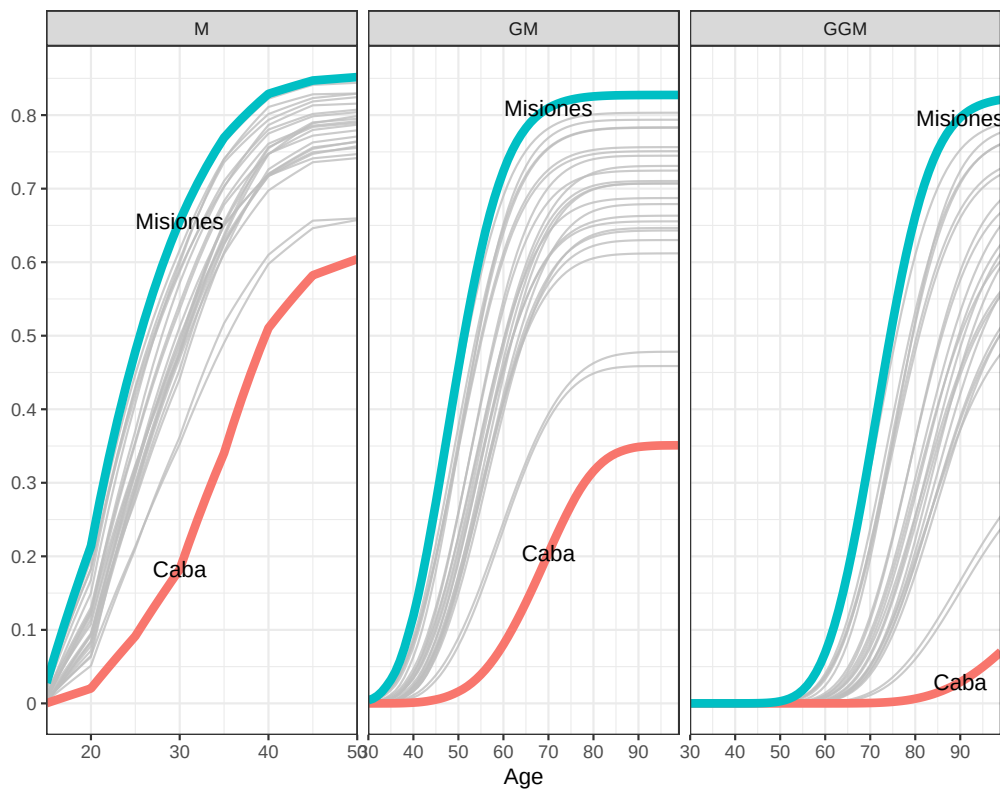


Figure 8: Mamushka distribution based on 2022 rates. Proportion of female population by age that are mothers (M), grandmothers (GM) and great-grandmothers (GGM). Argentinian provinces others than CABA and Misiones shown as grey lines in the background.

Using the standardized national age structure from the 2022 census, we estimate that 54%, 24%, and 7% of women in the province of Misiones are mothers (M), grandmothers (GM), and great-grandmothers (GGM), respectively. While in CABA those

proportions are 30.8%, 4.2% and 0.1%. The marked variation in these proportions across provinces highlights the importance of tailoring family policies, particularly those concerning reciprocal caregiving potential, to specific regional demographic contexts. A uniform policy approach would overlook the substantial heterogeneity in kinship structures and generational availability across subnational populations.

3.5 Time-Varying case: Sweden in 2017

The applications presented in the preceding sections assume a stationary demographic regime. This assumption makes it possible to characterize the implicit family structure associated with a given set of fertility and mortality schedules using relatively accessible demographic data. But this constant-risk scenario does not hold for populations undergoing rapid changes in fertility and mortality patterns. Jiang et al. (2025) found that differences in the number of living kin and its mean and variability age distribution, depends strongly on the speed of fertility decline. In particular, the rate $f_1(x)$ —representing the transition to first birth—is sensitive to the postponement of fertility, a hallmark of the Second Demographic Transition (Van de Kaa, 1994).

A dynamic approach would involve modelling time-varying rates, transforming $m_d(a)$ (motherhood) and $m_{gd}(a)$ (grandmotherhood) into cohort-based measures when longitudinal data or a time series of period rates by age are available. With this we can estimate total descendants (alive or not) by parity (zero or at least one), at each age of Ego, which is the intermediate results for computing final results. Such an extension is feasible because the necessary methodological tools and computational implementations are already available (Butterick et al., 2025; Williams et al., 2023). We evaluate this dynamic version by comparing its estimates with Swedish register-

based results for 2017 (Kolk et al., 2021). For this purpose, we use age-specific fertility schedules for Sweden from the Human Fertility Database (HFD, 2024) for the period 1970–2017, together with mortality schedules covering the same years. As in any dynamic implementation based on an observation window beginning at a finite date, assumptions are required for demographic conditions before 1970, the first year for which the input series are available (Caswell, 2022).

Results show that the Mamushka approach matches Kolk’s empirical data reasonably well at older ages (ultimate distribution in Fig. 9), but it moves both motherhood and grandmotherhood transitions too early. For motherhood, Mamushka strongly overestimates prevalence in young adult ages, reaching 79% at age 30 compared with 51% in the register; after age 40 the two series are much closer. Register shows that only 2% of females aged 20 years old are already mothers, where our estimates are round 10%, close to Argentina period estimate for 2022. For grandmotherhood the same pattern appears later: Mamushka estimates 50% grandmothers at age 50 versus 17% in the register, and 80% versus 57% at age 60, but convergence improves after about age 70. The main likely source of discrepancy is timing: Mamushka uses a period/parity-based approximation that smooths cohort histories and independence structure with data only starting in 1970, while Kolk et al. (2021) empirical estimates reflect actual Swedish cohort fertility timing and realized intergenerational age spacing for a century. This is all the dimensions of heterogeneity playing together in a century of demographic Swedish experience: level and age pattern dispersion (including migration effects), inter-generational dependence and mortality-fertility correlation, all changing in time. Even in that situation, our adapted approach to a time-varying framework shows a very good approximation to M in ages higher than

40, and *GM* after age 70. Future work can go in the direction of formalizing sources of heterogeneity and decompose its impact.

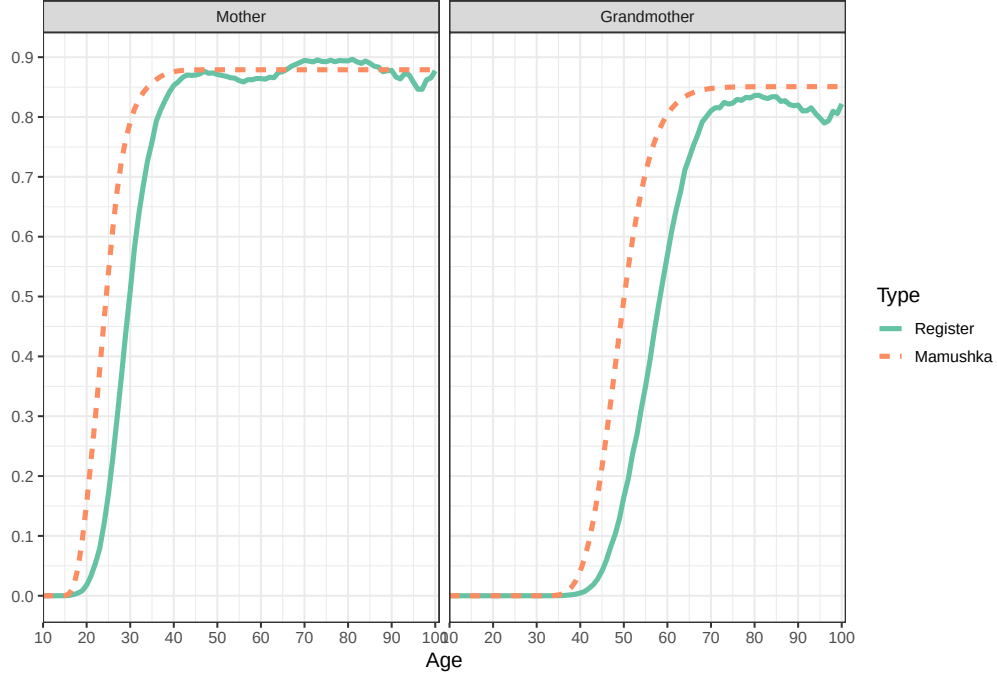


Figure 9: Proportion of Swedish females that are mother and grandmother in 2017. Swedish register (Kolk et al. (2021)) and Mamushka approximation with 1970-2017 data (HFD, 2024)

4 Discussion

There is growing interest in the study of kinlessness at older ages. The “fading of family lines,” whereby segments of the older population have no descendants, is of particular demographic and policy relevance (Margolis and Verdery, 2017; Verdery and Margolis, 2017; Kolk and Skirbekk, 2022). For these individuals, the absence of potential informal caregivers and sources of emotional support may increase reliance on formal welfare and long-term care systems. As fertility declines and family sizes

contract, a growing proportion of older adults may lack close kin, even while remaining in relatively good health and potentially able to provide care to others. In this context, understanding the population-level distribution of generational roles—such as motherhood, grandmotherhood, and great-grandmotherhood—becomes increasingly relevant in the context of population ageing and changing family structures.

This paper introduced a simple approach for computing the proportion of women in a population who are childless, mothers, grandmothers, and great-grandmothers (analogous analysis can be done for men following the described variation at each step in 2). Instead of focusing on the family tree of an average member of the population (as is common in actual kinship demography techniques), we looked at the whole population as made up of layers of generational placement, or “dolls” in a Mamushka model. Using basic demographic data (mortality, fertility, and the age pattern of first births) we were able to estimate the share of women in each of these kinship roles by age. One key strength of this method is that it can be useful even when detailed data are missing (detailed genealogical or longitudinal data), making it useful for countries or regions with limited information.

Our application to Argentina demonstrates how changes in fertility patterns influence the structure of kinship roles within the population. With 2001 demographic conditions, approximately 90% of women become mothers, and a large share of those become grandmothers or great-grandmothers at older ages. By 2022, however, this structure had shifted significantly: round 70% become mothers (30% are childless) and 60% grandmothers. We also found substantial subnational variation. For instance, at older ages the proportion of women who are at least grandmothers is 35% in the Ciudad Autónoma de Buenos Aires (CABA) compared to 85% in Misiones.

Differences are even larger for great-grandmotherhood. Such disparities highlight the importance of avoiding reliance on national averages when designing policies, as they may obscure critical regional differences in family structure and the availability of kin-based caregiving.

Several limitations of the approach should be acknowledged. First, we do not present an exact algebraic formulation of the Mamushka model, primarily because motherhood begins with the discrete event of a woman’s first birth. Grandmotherhood and great-grandmotherhood are also generated by discrete and interdependent fertility transitions occurring across several descendants. We therefore rely on population-level averages and probabilistic distributions that approximate the timing and accumulation of these events.

The main limitation is the treatment of heterogeneity. As shown in Figure 5, the standard binomial assumption may affect the estimated distribution of mothers, particularly at intermediate ages and near the end of the reproductive period. Parity distributions are often non-normal, zero-inflated, and highly skewed (Tuljapurkar et al., 2020), and may depart substantially from simple Poisson or binomial assumptions (Barakat, 2017). At the same time, some recent low-fertility settings display increasingly concentrated or underdispersed parity distributions (Hruschka and Burger, 2016). Heterogeneity may operate through fertility levels, the age pattern of births, parity progression, socioeconomic characteristics, place of residence, and correlations in reproductive behaviour among members of the same family. The microsimulation comparison for Argentina in 2001 showed strong agreement for mothers and grandmothers but a moderate overestimation of great-grandmothers at older ages. The exploratory beta-binomial specification improved the fit by allowing the probability

of descendant reproduction to vary across family lineages. This result is substantively plausible: assigning the same probability of parenthood to all descendants distributes births too evenly across families, whereas in actual populations some lineages contain several individuals who become parents and others contain none. Because great-grandmotherhood depends on reproductive transitions across successive generations, this heterogeneity may accumulate along the descendant line. Nevertheless, the dispersion parameter used in this exercise was selected by trial and error and should be interpreted as a sensitivity parameter rather than an empirical estimate. Estimating this heterogeneity empirically would require linked fertility histories across generations.

The comparison with Swedish register data complements these stationary applications by evaluating the method under time-varying demographic conditions. The dynamic Mamushka implementation approximates the ultimate prevalence of motherhood after age 40 and grandmotherhood after age 70 reasonably well, but places both transitions too early in the life course relative to the empirical estimates reported by Kolk et al. (2021). This suggests that the method performs better in estimating the eventual proportion reaching each generational placement than in reproducing its precise age schedule when fertility timing and intergenerational spacing have changed substantially across cohorts.

We also do not consider whether a woman’s children, grandchildren, or great-grandchildren remain alive. A woman is classified as a grandmother once at least one of her children has reproduced, regardless of whether the child or grandchild survives to her current age. However, an exercise within the microsimulation framework showed that requiring at least one living descendant has only a limited effect under

the Argentine 2001 mortality regime. Counting only women with one or more living descendants reduces the proportion of mothers by approximately 1 percentage point at age 60, 2 percentage points at age 70, and 2.5 percentage points at age 80, with negligible effects on the estimated proportions of grandmothers and great-grandmothers. These differences are based on a life expectancy at birth of approximately 74 years in 2001 and would be expected to be smaller in populations with lower mortality.

Overall, the Mamushka framework provides a bridge between formal kinship demography and the population-level study of generational placement. Its contribution is not to replace longitudinal registers or microsimulation, but to produce comparable indicators in settings where those resources are unavailable. The applications show that it can identify substantial temporal and regional differences in the prevalence of vertical kin roles, while the validation exercises reveal greater accuracy for lower-order roles, older ages, and relatively stable demographic regimes. Future developments should incorporate empirically estimated family-level heterogeneity, longer cohort histories, and explicit measures of descendant survival, allowing the framework to be used for projections of generational placement as kinlessness becomes more prevalent.

4.0.1 Acknowledgements

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4.0.2 Funding

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4.0.3 Supplemental online material

Reproducible workflow can be found in https://github.com/IvanWilli/Mamushka_Kinship.

5 Appendix

5.1 Individuals who have siblings

Kinlessness also implies the absence of close horizontal kin, such as siblings. Average sibship sizes have declined in nearly all countries (Präg et al., 2020), and family size is a key determinant of children’s educational outcomes and broader life chances (Björklund and Salvanes, 2010). Closely related to the Mamushka framework is the question: what proportion of the population, at each age, has no siblings?

Preston (1976) highlighted the distinction between mean parity from the perspective of women and average sibship size, with the latter generally having lower variance because it excludes parity-zero cases. Because the availability of siblings depends on mother’s fertility, here we change the point of view from the Mamushka framework, focusing on the probability that an individual aged a has at least one sibling. This probability depends on whether the individual’s mother reached a parity of two or more. Let $W(a)$ represent the maternity age distribution and $R(a)$ the net reproductive rate (i.e., the expected number of children a woman has by age a , adjusted for survival). Then, under fixed rates on time, the probability that an individual aged a has siblings can be expressed as:

$$S(a) = \int_0^\omega W(x) p[R(x+a) > 1] dx \quad (15)$$

Where $p[R(x+a) > 1]$ represents the probability of having more than one children at age $x + a$. In this context, $W(x)$ reflects the implicit female age distribution, weighted by the fertility schedule (Caswell, 2019). To evaluate $R(x)$, a statistical distribution for fertility outcome is required. If we assume first that survival is close to 1 during childbearing ages, we can model a Poisson distribution on parity $\Pi(a)$, which is a common approach in demographic modeling, with parameter $F(x)$ (the cumulative fertility up to age x) (Caswell, 2024). Under this scenario, the probability that a woman has more than one child is:

$$\begin{aligned} p[\Pi(a) > 1] &= 1 - P[\Pi(a) = 0] - P[\Pi(a) = 1] \\ &= 1 - e^{-F(a)} - F(a)e^{-F(a)} \\ &= 1 - e^{-F(a)}[1 + F(a)] \end{aligned} \quad (16)$$

This allows us to compute the probability that an individual aged a has at least one sibling. Under 2001 fertility conditions in Argentina, a newborn had an estimated 35% chance of having siblings, increasing to around 70% by age 20. In contrast, under 2022 fertility conditions, the probability begins at approximately 16% and reaches less than 45% by age 20. Under 2022 conditions, 30% of woman would be childless (3), and more than half of them (assuming no generational correlation on fertility risk) would not have siblings (and consequently nieces and nephews).

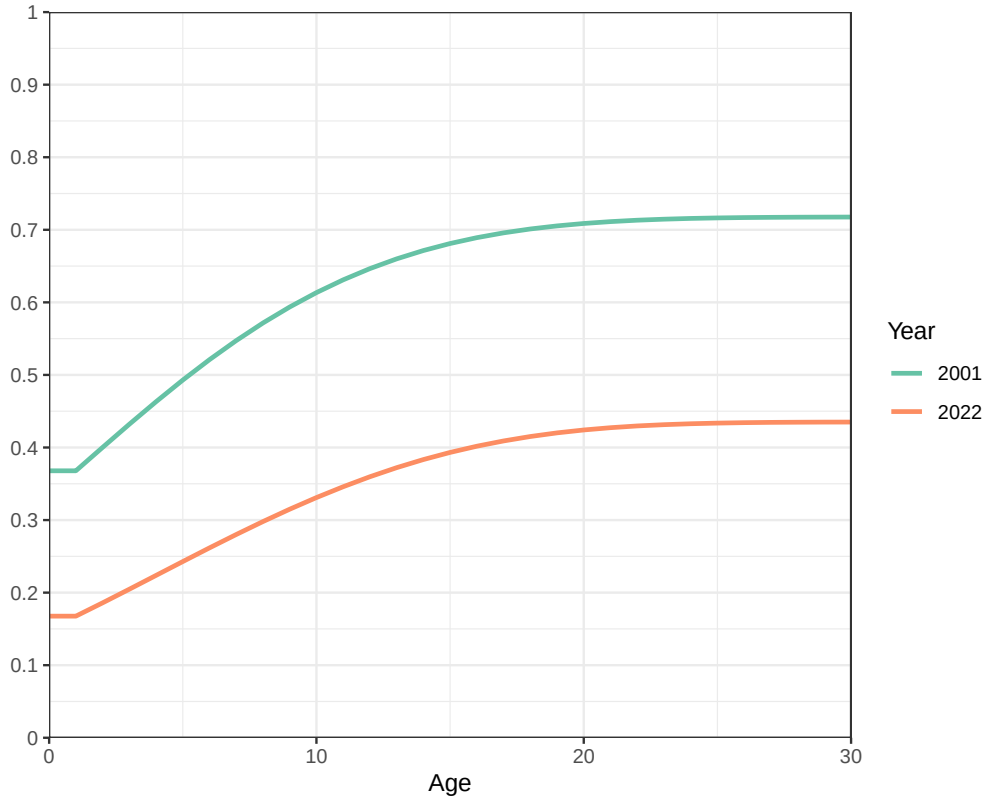


Figure 10: Population proportion who had siblings by age, under 2001 and 2022 fertility conditions in Argentina

5.2 Poisson approximation

Caswell (2024) showed that the expected mean and variance in the number of living kin are quite similar for certain types—especially descendants—which makes the Poisson distribution a reasonable approximation for calculating summary statistics such as quartiles. However, for ascendants, a binomial distribution is generally more appropriate, aligning with our approach, particularly when viewed from the perspective of living kin counts.

In our case, we chose to model the probabilities of becoming a grandmother, for

instance, using a binomial distribution. It is helpful to clarify what each assumption implies. Let $F_d(a)$, $F_{gd}(a)$, and $F_{ggd}(a)$ denote the number of children, grandchildren, and great-grandchildren ever born to Ego by age a . Under a Poisson framework, the probabilities of being a mother, grandmother, and great-grandmother are respectively given by: $M(a) = 1 - \exp^{-F_d(a)}$, $GM(a) = 1 - \exp^{-F_{gd}(a)}$ and $GGM(a) = 1 - \exp^{-F_{ggd}(a)}$.

As shown in the results for Argentina (Figure 11), the Poisson assumption implies that nearly every woman under 2001 fertility conditions would become a mother, grandmother, and great-grandmother. However, the differences become more pronounced under 2022 conditions, where changes in age distribution and fertility levels are more substantial. The key limitation of the Poisson model lies in its disregard for the timing of fertility: it assumes that all births could occur immediately before age a , thus ignoring time exposure needed for descendants to transition into parenthood themselves. More broadly, the Poisson distribution is a limiting case of the binomial distribution, valid when the number of trials is large and the probability of success is small—conditions that do not hold in our context.

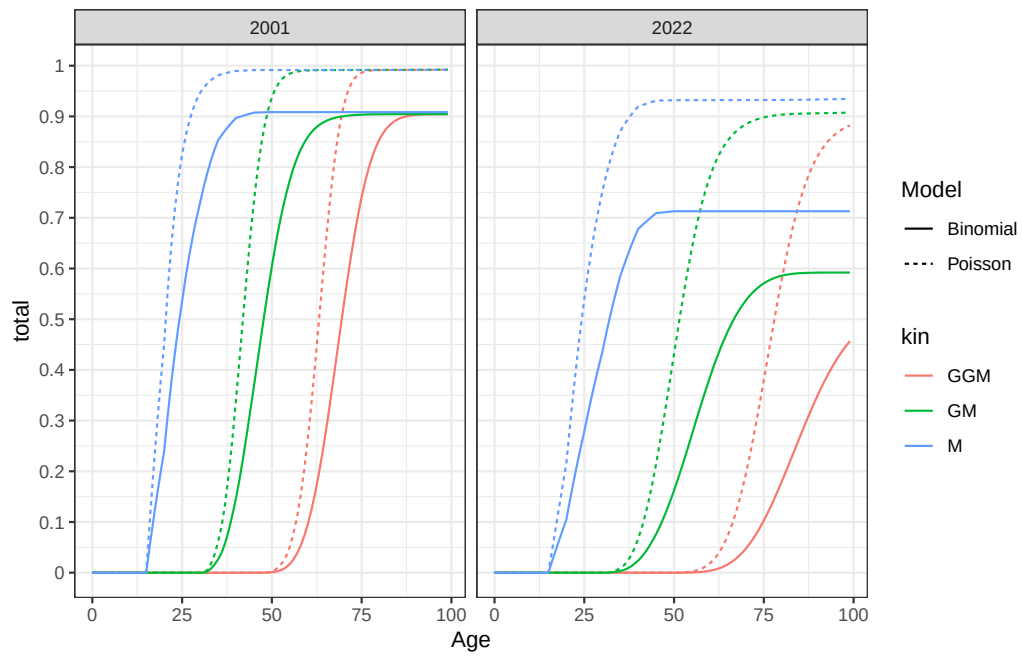


Figure 11: Poisson approximation and current binomial results. Argentina 2001 and 2022.

Year	Age	M(x)	%B ₁ (x)	f(x)	f ₁ (x)	f ₂₊ (x)
2001	15	12%	76%	0.06	0.05	0.12
2001	20	41%	47%	0.12	0.10	0.16
2001	25	63%	31%	0.13	0.11	0.14
2001	30	80%	22%	0.11	0.12	0.11
2001	35	88%	14%	0.06	0.07	0.06
2001	40	90%	11%	0.02	0.02	0.02
2001	45	91%	12%	0.00	0.00	0.00
2022	15	6%	80%	0.03	0.02	0.08
2022	20	31%	46%	0.06	0.04	0.11
2022	25	55%	30%	0.07	0.05	0.09
2022	30	70%	26%	0.07	0.06	0.07
2022	35	82%	20%	0.05	0.05	0.05
2022	40	87%	18%	0.01	0.02	0.01
2022	45	89%	30%	0.00	0.00	0.00

Table 1: Estimates of $f_1(x)$ and $f_{2+}(x)$ based proportion of mothers, percentage of newborn of order 1 and fertility rate. Argentina, 2001 and 2022

5.3 Additional tables and figures

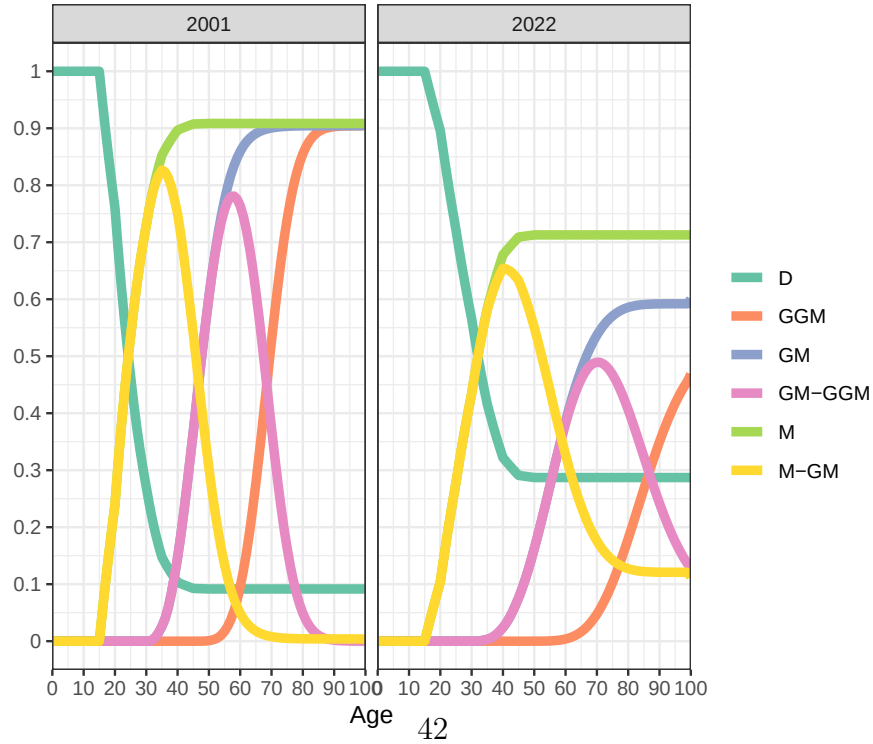


Figure 12: Distribution of only daughters (D, no-mothers), only mothers (M-GM), only grandmothers (GM-GGM) and greatgrandmothers (GGM). Argentina, based on 2001 and 2022 rates. See table 2

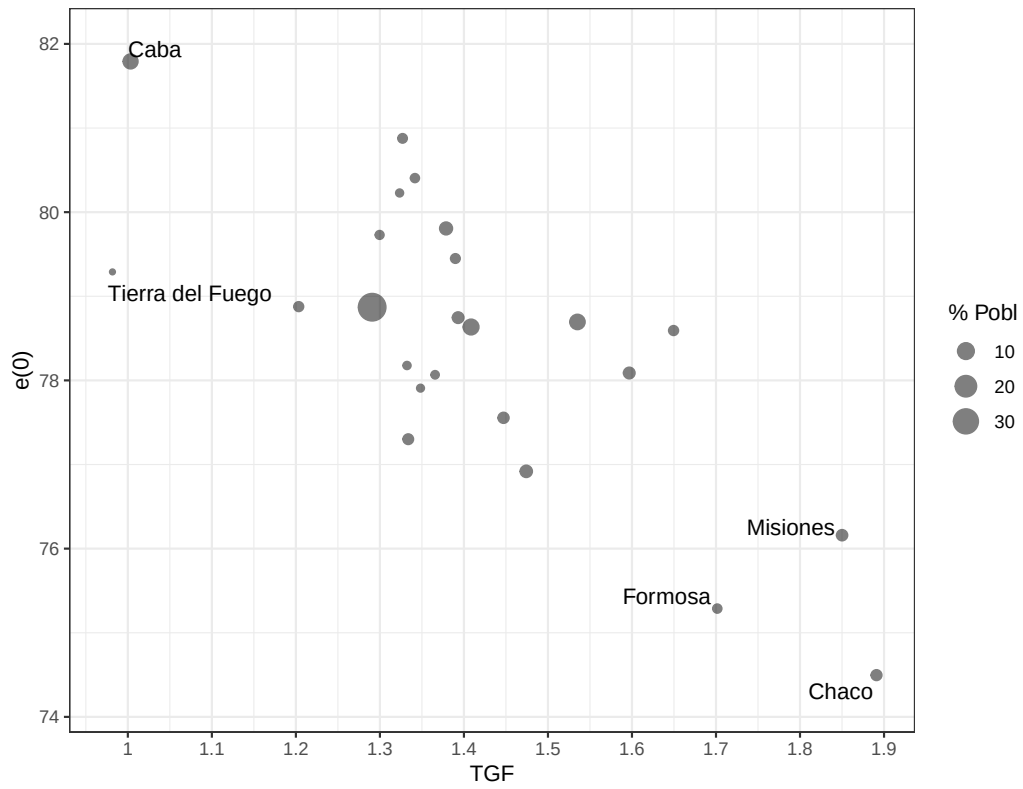


Figure 13: Life expectancy at birth and total fertility rate in 2022. Argentina provinces. Population comes from 2022 census and events comes from 2022 VR. Adjusted mid-year population is not published yet.

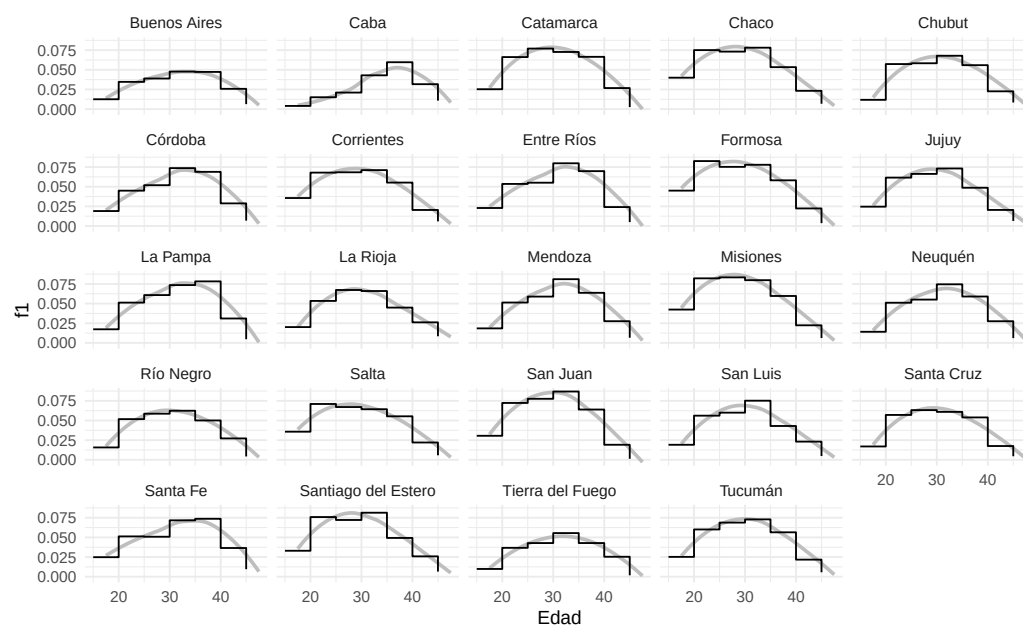


Figure 14: Rate of first child in 2022. Argentina provinces

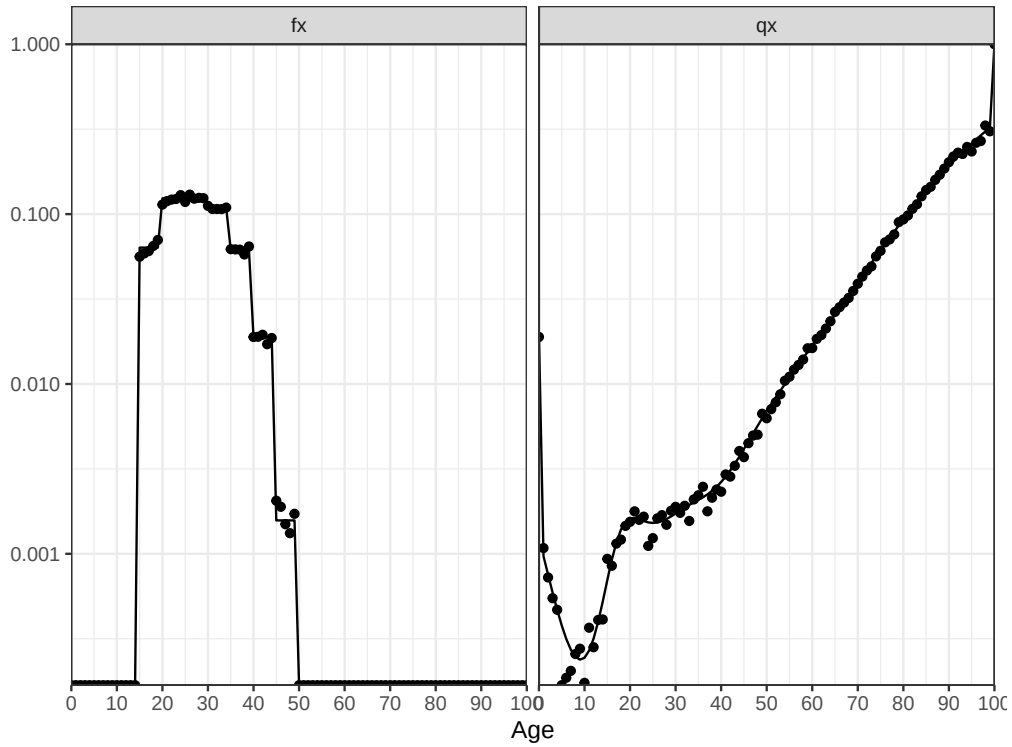


Figure 15: Fertility rates ($f(x)$) and death probabilities ($q(x)$) in microsimulation (dots) and input data (lines). Argentina 2001. Microsimulation results was produced using the last 50 year-iterations

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Table 2: Distribution of Mamushka (capital letters), and others proportions. Argentina, based on 2001 and 2022 rates

Year	Age	D	M	GM	m_d	m_{gd}	gm_m	GGM	ggm_{gm}
2001	15	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2001	20	0.76	0.24	0.00	0.00	0.00	0.00	0.00	0.00
2001	25	0.46	0.54	0.00	0.00	0.00	0.00	0.00	0.00
2001	30	0.27	0.73	0.00	0.00	0.00	0.00	0.00	0.00
2001	35	0.15	0.85	0.03	0.01	0.00	0.03	0.00	0.00
2001	40	0.10	0.90	0.15	0.07	0.00	0.16	0.00	0.00
2001	45	0.09	0.91	0.37	0.19	0.00	0.40	0.00	0.00
2001	50	0.09	0.91	0.60	0.35	0.00	0.67	0.00	0.00
2001	55	0.09	0.91	0.77	0.53	0.01	0.85	0.02	0.02
2001	60	0.09	0.91	0.86	0.69	0.03	0.95	0.10	0.11
2001	65	0.09	0.91	0.89	0.79	0.08	0.98	0.28	0.31
2001	70	0.09	0.91	0.90	0.85	0.16	0.99	0.53	0.59
2001	75	0.09	0.91	0.90	0.87	0.28	0.99	0.74	0.82
2001	80	0.09	0.91	0.90	0.88	0.41	1.00	0.86	0.95
2001	85	0.09	0.91	0.90	0.88	0.56	1.00	0.89	0.99
2001	90	0.09	0.91	0.90	0.88	0.68	1.00	0.90	1.00
2001	95	0.09	0.91	0.90	0.88	0.77	1.00	0.90	1.00
2001	100	0.09	0.91	0.91	0.91	0.85	1.00	0.91	1.00
2022	15	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2022	20	0.90	0.10	0.00	0.00	0.00	0.00	0.00	0.00
2022	25	0.72	0.28	0.00	0.00	0.00	0.00	0.00	0.00
2022	30	0.57	0.43	0.00	0.00	0.00	0.00	0.00	0.00
2022	35	0.42	0.58	0.00	0.00	0.01	0.00	0.00	0.00
2022	40	0.32	0.68	0.02	0.03	0.00	0.04	0.00	0.00
2022	45	0.29	0.71	0.08	0.07	0.00	0.11	0.00	0.00
2022	50	0.29	0.71	0.16	0.16	0.00	0.23	0.00	0.00
2022	55	0.29	0.71	0.27	0.28	0.00	0.38	0.00	0.00
2022	60	0.29	0.71	0.39	0.41	0.01	0.54	0.00	0.01
2022	65	0.29	0.71	0.48	0.53	0.03	0.67	0.02	0.03
2022	70	0.29	0.71	0.54	0.61	0.06	0.75	0.05	0.09
2022	75	0.29	0.71	0.57	0.66	0.11	0.80	0.10	0.18
2022	80	0.29	0.71	0.59	0.69	0.19	0.82	0.18	0.31
2022	85	0.29	0.71	0.59	0.70	0.29	0.83	0.27	0.45
2022	90	0.29	0.71	0.59	0.70	0.40	0.83	0.35	0.59
2022	95	0.29	0.71	0.59	0.70	0.50	0.83	0.42	0.70
2022	100	0.29	0.71	0.60	0.71	0.59	0.84	0.47	0.78

Table 3: Proportion of mothers, grandmothers and great-grandmothers over entire population, under 2022 rates and 2022 census age-structure. Argentina provinces

Province	M	GM	GGM
Misiones	53.9	24.1	6.9
Formosa	53.7	23.3	6.5
Chaco	51.9	21.4	5.3
Santiago del Estero	51.2	20.9	5.0
San Juan	51.1	20.9	4.8
Corrientes	50.2	20.4	4.8
Salta	50.1	20.1	4.7
Catamarca	49.4	17.8	3.2
Tucumán	48.0	17.6	3.2
Jujuy	47.1	16.1	2.6
Santa Fe	46.9	16.6	2.8
Entre Ríos	46.8	16.0	2.5
La Pampa	46.2	14.8	1.9
Mendoza	46.2	15.5	2.2
La Rioja	45.7	15.1	2.3
San Luis	45.0	14.7	2.1
Córdoba	44.7	14.2	1.8
Santa Cruz	44.5	13.5	1.7
Chubut	44.4	13.6	1.7
Neuquén	44.4	13.3	1.5
Río Negro	43.5	13.5	1.7
Tierra del Fuego ⁵	37.5	8.5	0.5
Buenos Aires	37.2	8.9	0.6
CABA	30.8	4.2	0.1

Table 4: Mamushka (binomial distribution) and Microsimulation proportions (mothers, grandmothers and great-grandmothers) by total and decennial age groups

Age	Mamushka			Microsimulation			Difference (Mam – Micr)		
	M	GM	GGM	M	GM	GGM	M	GM	GGM
10–19	0.05	0.00	0.00	0.07	0.00	0.00	-0.02	0.00	0.00
20–29	0.49	0.00	0.00	0.56	0.00	0.00	-0.07	0.00	0.00
30–39	0.83	0.03	0.00	0.85	0.05	0.00	-0.03	-0.02	0.00
40–49	0.90	0.34	0.00	0.92	0.38	0.00	-0.02	-0.05	0.00
50–59	0.91	0.74	0.02	0.92	0.74	0.04	-0.02	0.00	-0.02
60–69	0.91	0.88	0.26	0.91	0.86	0.28	0.00	0.02	-0.03
70–79	0.91	0.90	0.69	0.93	0.90	0.63	-0.02	0.00	0.05
80–89	0.91	0.90	0.88	0.92	0.90	0.80	-0.01	0.01	0.08
90–99	0.91	0.90	0.90	0.94	0.90	0.87	-0.03	0.01	0.04
Total	0.65	0.32	0.09	0.68	0.32	0.09	-0.03	-0.01	0.00