DEMOGRAPHIC RESEARCH
A peer-reviewed, open-access journal of population sciences

DEMOGRAPHIC RESEARCH

VOLUME 54, ARTICLE 9, PAGES 263–308
PUBLISHED 11 FEBRUARY 2026
http://www.demographic-research.org/Volumes/Vol54/9/
DOI: 10.4054/DemRes.2026.54.9

Research Article

Probabilistic projections of distributions of kin over the life course

Joe Butterick

Jason Hilton

Jakub Bijak

Peter W. F. Smith

Erengul Dodd

Contents

Demographic Research: Volume 54, Article 9
Research Article

Probabilistic projections of distributions of kin over the life course

Joe Butterick[1]
Jason Hilton[2]
Jakub Bijak[3]
Peter W. F. Smith[4]
Erengul Dodd[5]

Abstract

BACKGROUND
Mathematical kinship demography is an expanding area of research. Recent papers have explored the expected number of kin a typical individual should experience. Despite the uncertainty of the future number and distributions of kin, just one paper investigates it.

OBJECTIVE
We aim to develop a new method for obtaining the probability that a typical population member experiences one or more of some kin at any age through the life course.

METHODS
Combinatorics, matrix algebra, and convolution theory are combined to find discrete probability distributions of kin number. We propose closed form expressions, illustrating the recursive nature of kin replenishment, using composition of matrix operations. Our model requires as inputs age-specific mortality and fertility.

CONCLUSIONS
We derive probabilities of kin number for fixed age of kin and over all possible ages of kin. From these the expectation, variance, and other moments of kin number can be found. We demonstrate how kinship structures are conditional on familial events.

---

[1] Corresponding author. Centre for Population Change, University of Southampton, UK.
Email: jb4u23@soton.ac.uk.
[2] Centre for Population Change, University of Southampton, Southampton, SO17 1BJ, UK.
[3] Department of Social Statistics and Demography, University of Southampton, UK.
[4] Department of Social Statistics and Demography, University of Southampton, UK.
[5] Department of Mathematics, University of Southampton, UK.

CONTRIBUTION

The paper presents the first analytic approach allowing the projection of a full probability distribution of the number of kin of arbitrary type that a population member has over the life course.

1. Introduction

Family relationships are a fundamental part of the social structures of human societies (Alburez-Gutierrez et al. 2022). Kinship ties have impacts on physical and mental well-being (Vlachantoni et al. 2024), social and economic inequalities between and within generations (Verdery and Margolis 2017; Margolis et al. 2024), and social and fiscal policy (Pittavino, Arpino, and Pirani 2025). However, direct data on kinship relationships are rarely collected, and generally only available for limited samples or in countries with high quality demographic registers (Kolk 2017). Studies that quantify the temporal changes in kinship networks are therefore extremely valuable.

In particular, understanding inequalities resulting from kinship relationships requires quantification of the diversity of kinship structures within the population. In addition, the future numbers and structures of kin remain uncertain. Microsimulation facilitates the study of these kinds of structures, offering rich and detailed output about family composition both inside and outside the household (e.g., Wachter, Hammel, and Laslett 1978; Hammel 2005; Margolis and Verdery 2019). However, microsimulation is computationally expensive and technically challenging to set up. This can be a barrier to its deployment (notwithstanding creditable recent work in opening up access to these tools, such as Thiele et al. 2023). As such, analytical models of kinship relationships are highly desirable for their much greater computational efficiency.

Recent years have witnessed a resurgence in mathematical modelling of kinship (Caswell 2019, 2020, 2022, 2024; Caswell and Song 2021; Williams et al. 2021; Coste et al. 2021), providing, for example, richer insight into the future structures of kinship (Alburez-Gutierrez, Williams, and Caswell 2023). Models of kinship have been applied to produce expected numbers of kin distributed by age or stage (or state) and sex for a representative population member, both within static and time-varying demographies. The term ’stage’ refers to any population characteristic for which individuals can transition in and out of – a dimension out of scope for the present study. Despite the expanding interest in the estimation of kinship, only one model developed since 2019 has explored estimating quantities beyond the mean number of kin (see Caswell 2024).

Population dynamics in the demographic context are driven by stochastic birth and death processes. That is, each (female) population member gives birth to a non-negative number of offspring (possibly zero), with variation between individuals’ reproductive profiles. Each population member either survives to the next age class or dies, giving rise to variation in age-specific mortalities. Demographers usually refer to these probabilistic events as “demographic stochasticity” (Keyfitz and Caswell 1997). Because population dynamics are governed by stochastic processes, and kinship dynamics are an emergent property of the population, an individual’s network of kin unfolds probabilistically.

This research complements and extends mathematical kinship demography by presenting a method to account for demographic stochasticity within the kinship network. Our paper is structured as follows: Section 1.1 provides a brief review of the relevant literature and existing mathematical frameworks for analysing kinship, while clarifying what sets this work apart. Section 1.2 outlines notation used. In Section 2 we introduce our assumptions and prerequisites for formally constructing the model: Section 2.1 outlines the general demographic assumptions and Sections 2.2–2.6 lay the mathematical foundations. Section 3 provides our novel derivations, organised into analytically distinct regimes. In Section 4 we apply the framework using UK age-specific mortality and fertility data, sourced from the Human Mortality Database (2024) and Human Fertility Collection (2024). We illustrate the analysis by showing selected model output and explore its implications. We conclude in Section 5 by considering the contribution, prospects, and limitations of this theoretical development with respect to the leading frameworks on kinship.

1.1 Relevant mathematical frameworks

There is a rich history of mathematical modelling of kinship which have considered demographic stochasticity. Already in the 1980s, research by Waugh (1981) and Joffe and Waugh (1982) apply branching processes with non-overlapping generations, namely the so-called Galton-Watson process, primarily focusing on biology and population ecology. Advancing on such methods Jagers (1982) and Jagers and Nerman (1984) include age structures (thereby accounting for overlapping generations) by utilising so-called Crump-Mode-Jagers (CMJ) branching process (Crump and Mode 1968). Although very relevant to the field of kinship research, due to their complexity, these papers proved for the most part too technically complicated to allow their wider adoption.

In a recent remarkable paper, Caswell (2024) treats an individual’s kin as a population of their own, and subject to the same variability in births and deaths as any other population. The author’s proposed model accounts for demographic stochasticity through projecting the mean and variance of an unknown kin-number distribution. The matrix projection model proposed by Pollard (1966), emulating a multitype Galton-Watson process, is applied to do so. Using the mean and variance in kin number, Caswell (2024) subsequently assumes appropriate statistical distributions to represent kin, fits prediction intervals, and thereby estimates uncertainty associated with kin-number distributions.

While the proposed framework is more accessible to demographers, ecologists, mathematicians, and perhaps the occasional physicist, the technical modelling approach can be challenged on theoretical grounds. For instance, although the distribution of kin will always be discrete with a non-zero support on the non-negative integers, an appropriate choice might require specific knowledge. Caswell (2024) states that Poisson distributions should apply when the mean is close to the variance and cites previous work which adheres to this assumption (Caswell, Margolis, and Verdery 2023).

An alternative approach would be to calculate the exact probability distribution of kin number. To do so, one could apply similar methods as Tuljapurkar et al. (2020), who directly calculate the so-called lifetime reproductive success (i.e., a distribution for the number of offspring an individual has over their life course). The benefit of this method, emphasised by Tuljapurkar et al. (2020), is that by constructing a probability distribution for the number of offspring, one can account for variability in reproduction between individuals. Another obvious benefit is that higher-order moments become readily available.

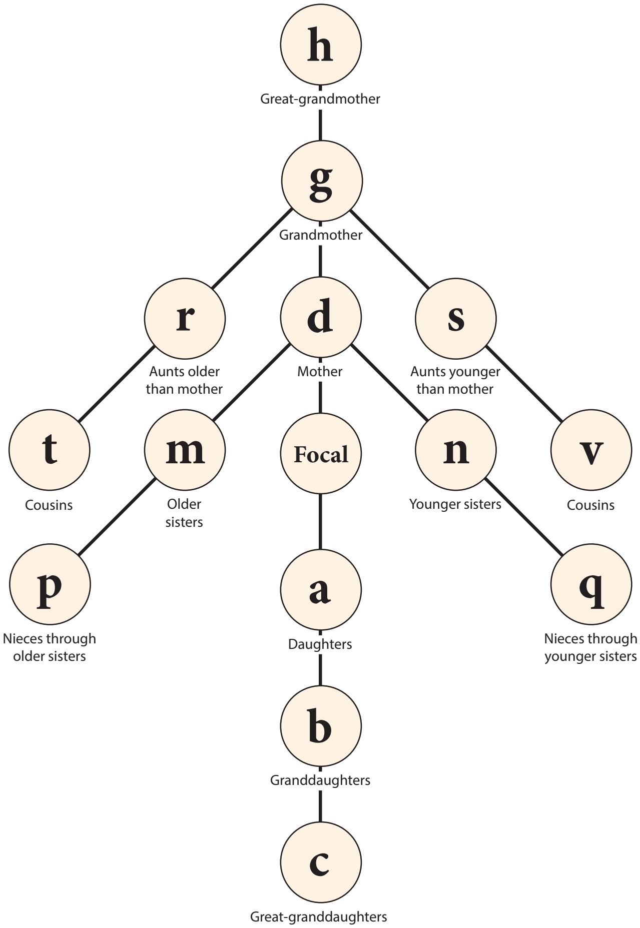
In this research, we develop a methodology for projecting the kin number of a typical female population member in a one-sex time-invariant age-structured demography (see the illustration in Figure 1 for kin types). Following the convention of the leading kinship models (Caswell 2019, 2020; Caswell and Song 2021; Caswell 2022) we refer to this individual as 'Focal.' We want to know Focal's kin network at each age of Focal's life. In the same vein as Caswell (2024), we seek to account for demographic stochasticity in the kinship network. Yet instead of projecting the mean and variance in kin number, we take inspiration from the methods of Tuljapurkar et al. (2020) and seek a discrete probability distribution to reflect kin number. In more detail, we would like to derive the probabilities that Focal experiences a certain integer number of kin by age of kin and age of Focal. For example in relation to Figure 1, consider Focal's older sisters (i.e., **m**). Suppose that Focal is aged y. With a set of probabilities, Focal will experience exactly zero, one, two, or more older sisters who are of exact age s (where obviously $s > y$).

For any generic of kin pictured in Figure 1, we write the probability mass function (pmf)

$$\mathbf{k}_s(y) = \begin{pmatrix} k_s^{(y)}(0) \\ k_s^{(y)}(1) \\ k_s^{(y)}(2) \\ \vdots \\ k_s^{(y)}(Q) \end{pmatrix} \tag{1}$$

to represent the number distribution of Focal's kin of type k who are of age s when Focal is of age y. The entries of Equation (1) give the probabilities that Focal experiences some number of that kin: The first, $k_s^y(0)$, provides the probability that Focal does not have any of the particular kin, the second, $k_s^y(1)$, provides the probability that Focal has exactly one of such kin, and the third, $k_s^y(2)$, provides the probability that Focal has exactly two of this kin. We impose a biologically reasonable upper bound Q, which acts to limit the maximum lifetime number of the particular kin type. To be explicit, Q is chosen such that Focal will experience considerably less than this value of any particular kin type during her life course. As illustrated through Equation (1), the last, or $(Q+1)$-th entry $k_s^{(y)}(Q)$, gives the probability that Focal has Q kin of type k, who are of age s when Focal is aged y.

Figure 1: The diagram and notation of kin used in the formal models of Caswell



Source: See e.g., Caswell 2019: passim.

1.2 Algebraic notation

The framework presented in this article includes mathematical derivations, some of which may not be obvious. Here we define the main algebraic objects of interest and summarise the notation used throughout this paper. Thus, stochastic matrices are denoted using blackboard bold – ($\mathbb{A}$), other matrices are denoted uppercase boldface ($\mathbf{A}$), vectors lowercase boldface ($\mathbf{a}$). Discrete probability distribution functions are denoted by boldface Greek symbols, (e.g., $\boldsymbol{\psi}$). When possible matrix entries will be given by lowercase letters, (e.g., $a_{i,j}$ the i, j entry of $\mathbf{A}$), but when notation is a pain – for instance when the matrix is a function of parameters $\mathbf{A}(x)$ – we may use $[\mathbf{A}(x)]_{i,j}$. The transpose of a matrix is denoted by †. The l_1 norm (on $\mathbb{R}^n$) is represented by $||\mathbf{x}||_1 = \sum_i^n |x_i|$; the l_2 norm (on $\mathbb{R}^n$) is represented by $||\mathbf{x}||_2 = \sqrt{\sum_i^n |x_i|}$. We denote the unit vector (a vector $\mathbf{e}$ with $||\mathbf{e}||_2 = 1$) with i-th entry one by $\mathbf{e}_i$.

A discrete convolution of two functions f and g defined on the integers is given by $(f \star g)[n] = \sum_{i=-\infty}^{\infty} f[i]g[n-i]$. For two distributions $\boldsymbol{\psi}_1 \in \mathbb{Z}^n$ and $\boldsymbol{\psi}_2 \in \mathbb{Z}^n$ we write the discrete convolution as $\boldsymbol{\psi}_1 \star \boldsymbol{\psi}_2$ with m-th entry defined through $(\psi_1 \star \psi_2)[m] = \sum_i \psi_1(i)\psi_2(m-i)$. Over a set of independent distributions $\{\boldsymbol{\psi}_{i_1}, \ldots, \boldsymbol{\psi}_{i_n}\}$ we write

$$\overset{n}{\underset{s=1}{\circledast}} \boldsymbol{\psi}_{i_s} = \boldsymbol{\psi}_{i_1} \star \boldsymbol{\psi}_{i_2} \star \cdots \star \boldsymbol{\psi}_{i_{n-1}} \star \boldsymbol{\psi}_{i_n} \tag{2}$$

and to represent the n-th convolution power of a distribution, we write

$$\boldsymbol{\psi}^{\star n} = \overbrace{\boldsymbol{\psi} \star \cdots \star \boldsymbol{\psi}}^{n}. \tag{3}$$

We provide a refresher (with an application to kinship) on the operation of discrete convolution in Appendix C . Lastly, we denote function composition by $(f \circ g)(x) = f(g(x))$, and moreover, $f^{[n]}(x) = (f \circ \cdots \circ f)(x)$ as the n-times composition of f. The ordered composition of functions $\{f_i, i = 1, \ldots, n\}$ is denoted by

$$\overset{n}{\underset{i=1}{\bigcirc}} f_i(x) = (f_n \circ \cdots \circ f_1)(x). \tag{4}$$

2. Model ingredients and assumptions

Here, we outline our assumptions and formally construct a model. Recall that we write $\mathbf{k}_s(y)$ to represent a $(Q+1)$-dimensional kin-number pmf with $(j+1)$-th entry giving the probability that Focal has exactly $j = 0, 1, \dots, Q$ kin of age s when she is age y. For consistency henceforth, we refer to the random variable j as "kin-number class".

2.1 Demographic dynamics

Our methods are applicable to large age-structured populations comprising one sex, and which are at demographic steady state – that is, those described by a time-invariant projection matrix. Consider a female population structured by age classes $i = 1, 2, \dots, n$. Within each age class i, let the number of births to an individual be described by a random variable $F_i \in \{0, 1, \dots\}$ with probabilities $\{\psi_i(0), \psi_i(1), \dots\}$. Define the vector $\boldsymbol{\psi}_i = (\psi_i(0), \psi_i(1), \dots)^\dagger$. Within each age class i, individuals' survival to age $i+1$ are defined through Bernoulli random variables, $U_i \in \{1, 0\}$ (where 1 represents survival and 0 death) with respective probabilities $\{u_i, 1-u_i\}$ where $u_i = \mathbb{E}[U_i]$.

Using $f_i = \mathbb{E}[F_i] = \sum_j j\psi_i(j)$ and u_i, we obtain the standard Leslie matrix (Allen 2010):

$$\mathbf{A} = \begin{pmatrix} f_1 & f_2 & f_3 & \dots & f_n \\ u_1 & 0 & 0 & \dots & 0 \\ \vdots & \ddots & \ddots & \ddots & \\ 0 & \dots & \dots & u_{n-1} & 0 \end{pmatrix}. \tag{5}$$

A population vector $\mathbf{x} = (x_1, x_2, \dots, x_n)^\dagger$ with x_i representing the number of individuals in age class i is projected from one time to the next through $\mathbf{x}_{t+1} = \mathbf{A}\mathbf{x}_t$. Given some initial population structure and large population, $\mathbf{x}_0$, we see $\mathbf{x}_t = \mathbf{A}^t\mathbf{x}_0$ with large-time behaviour ($t >> 0$) resulting in demographic stability: The relative sizes of each age class become constant and proportional to the stable age distribution, $\mathbf{w} = (w_1, w_2, \dots, w_n)^\dagger$, where $\mathbf{A}\mathbf{w} = \lambda\mathbf{w}$ (with $||\mathbf{w}||_1 = 1$). Here, λ, the spectral radius of $\mathbf{A}$, is within the demographic literature called the asymptotic population growth rate. The stable reproductive values in the population are given by $\mathbf{v}$ where $\mathbf{A}^\dagger\mathbf{v} = \lambda\mathbf{v}$ (we appropriately normalise $||\mathbf{v}^\dagger\mathbf{w}||_1 = 1$).

2.2 Defining kin of Focal: Her q-th ancestor and their g-th descendant

We adopt the characterisation that Focal and kin are defined through a common ancestor (Pullum 1982; Coste et al. 2021). Let q be the number of generations that separate Focal from her ancestor. Let g be the number of generations that separate Focal's kin from the ancestor. Define b_i as the age at which Focal's (direct) i-th generation ancestor gives birth to Focal's $(i-1)$-th generation ancestor (e.g., b_2 is the age at which Focal's grandmother gave birth to Focal's mother), and $\beta_q = y + \sum_{i=1}^{q} b_i$ to represent the age of Focal's q-th ancestor when Focal is aged y. Note that β_q may be biologically unrealistic, but this is not of importance within our framework. As we see below, we use an ancestor's present-time age as a means to establish their age when reproducing a collateral kin of Focal.

We define s_i as the current age of Focal's kin, related to Focal as the i-th generation descendant of Focal's q-th ancestor. For instance if $q = 2$, then s_2 is age of Focal's cousin when Focal is age y. Note that s_i may be biologically unrealistic. These quantities are used to derive the ages at which descendants of Focal's q-th ancestor reproduce. For instance, $s_{i-1} - s_i$ gives the age at which the $(i-1)$-th generation descendant produces the i-th generation descendant. As mentioned above, we also use s_{i-1} to derive the ages of ancestral reproduction. For instance, $\beta_q - s_1$ gives the age at which Focal's q-th ancestor produced a first-generation descendant that is not a direct ancestor of Focal.

We denote the probability mass function for Focal's $[g, q]$ kin which are of age s_g when Focal is age y by $\mathbf{k}_{s_g}^{g,q}(y)$, and term this an 'age-specific' pmf. We denote the kin-number probability mass function for kin who can be of age in some range Σ when Focal is y, by $\mathbf{k}_{\Sigma}^{g,q}(y)$.

2.3 The maternal age distribution

Here we probabilistically predict the age of Focal's q-th ancestor when she gives birth to Focal's $(q-1)$-th ancestor. Let ρ_x be the probability that if we randomly sample a newborn from the population, her mother is of age x. In a stable demography, the stable population age structure is proportional to $\lambda^{-i} u_1 \dots u_{i-1}$ (Goldman 1978). Hence, $\rho_x = u_1 \dots u_{x-1} f_x \lambda^{-x} / \mathcal{N}$ where $\mathcal{N}$ is a normalisation constant, which is from the Euler-Lotka equation $\mathcal{N} = \sum_{i=1}^{n} \big(\prod_{j=0}^{i-1} u_j\big) f_i \lambda^{-i} = 1$. As such, we see $w_1 u_1 \dots u_{x-1} = \lambda^{x-1} w_x$ and thus $\rho_x = f_x w_x / (\lambda w_1)$. Note that ρ_x recovers the $(1, x)$-th entry of the transition matrix of the so-called genealogical Markov chain associated with the population (Demetrius 1975; Tuljapurkar 1993). In a stable demography, we observe independence in the ages of ancestors' reproduction b_i, for $i = 1, \dots, q$.

2.4 How mortality affects the probabilities of experiencing j kin: The matrix U

Consider a distribution of numbers for offspring born to an arbitrary age mother, $\boldsymbol{\psi}$. Within the context of kinship, these newborns constitute a kin type of Focal: $\boldsymbol{\psi}$ could represent the probable offspring number of Focal's mother at some age after she had Focal, (i.e., a pmf for Focal's newborn younger sisters). Suppose that Focal is now 10 years old.

Suppose that her mother produced j younger sisters (with probability $\psi(j)$) 5 years ago. To understand how many younger sisters aged 4 Focal has at present (when she is 10), we need to calculate the probabilities that out of the possible numbers of newborn younger sisters, so many survive from age 0 to 4. In general, suppose that, with probabilities $k_{s'}(j)$, Focal has exactly $j = 0, 1, \dots, Q$ of some kin-type k who are aged s'. Then with another set of probabilities, $k_s(j)$, Focal will have j of the kin type when they are older (of age $s > s'$).

Here we show how these probabilities of survival from one age to another change the probability mass functions describing kin number. Our method is to construct a matrix $\mathbb{U}(s', s) \in \mathbb{R}^{(Q+1)\times(Q+1)}$, which, independent of Focal's age, acts on the probabilities $k_{s'}(j)$ that Focal has $j = 0, 1, \dots, Q$ kin of age s' to procure the probabilities that Focal has $k_s(j)$ kin of age s. Pre-multiplying this matrix through a pmf representing the number of kin of Focal aged s' produces a pmf representing the number of kin, conditional on survival, aged s. We construct $\mathbb{U}(s', s)$ as follows. First, note that each kin independently experiences the same probability $1 - u_{s'} \dots u_s$ of death between age s' and age s. Introducing the probability $\mathcal{U}(j, l, s', s)$ that out of j kin, some l survive from age s' to age s,

$$\mathcal{U}(j, l, s', s) = \binom{j}{l} (u_{s'} \cdots u_{s-1})^l (1 - u_{s'} \cdots u_{s-1})^{j-l}, \tag{6}$$

the (i, j) entries of $\mathbb{U}$ are defined through

$$\big[\mathbb{U}(s', s)\big]_{i,j} = \mathcal{U}(j-1, i-1, s', s), \tag{7}$$

and represent the probabilities that out of $j-1$ kin, $i-1$ survive from age s' to age s. The $(1, 1)$ entry of $\mathbb{U}(s', s)$ is 1, and acts on the $j = 0$ kin-number class: The probability that there are no kin aged s' will contribute to the probability that there are no kin aged s. As such, the probability that there are zero kin aged s' is simply added to the probability that there are zero kin aged s. The diagonal of $\mathbb{U}(s', s)$ represents the probabilities that all kin survive, while the top row (excluding the $(1, 1)$ entry) defines the probabilities that all of the $j = 1, 2, \dots, Q$ kin die (resulting in Focal having zero of such kin of age s).

To summarise, the matrix $\mathbb{U}$ projects kin-number pmfs of age s' to age s. The matrix is both upper-triangular (since survival cannot act to increase kin number) and column-stochastic (see Appendix B). The latter property distributes probabilities that from j kin, $i = 0, 1, \dots, j$ survive. We adopt the convention that $\mathbb{U}(s_1, s_2) = \mathbf{I}, \ \forall s_2 < s_1$.

2.5 The probabilities that out of j kin, l offspring are produced: The matrix F

Here we seek to find pmfs which describe the number of newborns created through the age-specific reproduction of one of Focal's kin. Let $\underline{n}$ be the minimum fertile age and $\bar{n}$ the maximum. While we are dealing with the reproduction of a direct ancestor of Focal, either $j = 0$ or $j = 1$ (Focal can only have one of these kin who is dead or alive). Assume that this ancestor is of age b_i. Then we know that its reproduction pmf is simply given through $\boldsymbol{\psi}_{b_i}$. Notice that if $b_i \notin [\underline{n}, \bar{n}]$, then $\boldsymbol{\psi}_{b_i}$ is the unit vector $\mathbf{e}_1$: All mass is in the probability that no offspring are born.

Regarding the reproduction of any other kin type of Focal (i.e., not ancestors) for which there may be $j = 0, 1 \ldots, Q$ many, we have to consider that each of the j reproducing kin has a probable number of offspring. For instance, Focal might have $j = 2$ sisters of age s, and each sister's reproduction is defined by their own offspring-number distribution. To account for this we create a matrix function $\mathbb{F}(s)$ (a function of the kin's age s) which projects the pmf of producer kin onto a pmf of their offspring. Because reproduction is independent between individuals, the probability that j kin produce l offspring is the l-th entry of the j-th power convolution of ψ_s (see Appendix C):

$$\begin{aligned}\text{Prob}\big\{ j \text{ kin of age } s \text{ produce } l \text{ offspring } \big\} &= \sum_{l_1} \psi_s(l_1) \sum_{l_2} \psi_s(l_2) \times \cdots \times \\ &\quad \sum_{l_j} \psi_s(l_j) \psi_s(l - l_1 - \cdots - l_{j-1} - l_j) \\ &= \psi_s^{\star j}(l). \end{aligned} \tag{8}$$

Using this information, one can create a column-stochastic matrix which projects the kin-number distribution of producer kin of age s onto a kin-number distribution of offspring kin:

$$\mathbb{F}(s) = \begin{pmatrix} 1 & \psi_s(0) & \psi_s^{\star 2}[0] & \ldots & \psi_s^{\star Q}[0] \\ 0 & \psi_s(1) & \psi_s^{\star 2}[1] & \ldots & \psi_s^{\star Q}[1] \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & \psi_s(Q) & \psi_s^{\star 2}[Q] & \ldots & \psi_s^{\star Q}[Q] \end{pmatrix} \in \mathbb{R}^{(Q+1)\times(Q+1)}. \tag{9}$$

Through $\mathbb{F}(s)\mathbf{k}_s$ we produce a pmf of offspring number encapsulating the reproduction of an arbitrary kin-type $\mathbf{k}_s$ of age s. The first entry of $\mathbb{F}(s)\mathbf{k}_s$ reads $k_s(0) + \psi_s(0)k_s(1) + \psi_s^{\star 2}[0]k_s(2) + \cdots + \psi_s^{\star Q}[0]k_s(Q)$, which one interprets as the probability that there are no producer kin (who do not reproduce), plus the probability that there is one kin who does not have offspring, plus the probability that there are two kin and neither have offspring, ..., plus the probability that there are Q kin and none of them have offspring. The second entry is $\psi_s(1)k_s(1) + \psi_s^{\star 2}[1]k_s(2) + \cdots + \psi_s^{\star Q}[1]k_s(Q)$, which reads the probability that there is one kin who has one offspring, plus the probability that there are two kin and between them produce one offspring (irrespective of ordering), ..., plus the probability that there are Q kin and between them all one offspring is produced. The last entry is $\psi_s(Q)k_s(1) + \psi_s^{\star 2}[Q]k_s(2) + \cdots + \psi_s^{\star Q}[Q]k_s(Q)$ and reads the probability that there is one kin who has Q offspring, plus the probability that there are two kin and between them Q offspring are produced, ..., plus the probability that there are Q kin and between them all Q offspring are produced. For all $s \notin [\underline{n}, \bar{n}]$ the matrix has a top row of ones and zeros everywhere else since there are no offspring born to infertile individuals.

2.6 Total kin versus age-distributed kin

Recall from Section 2.2 that $\mathbf{k}_s(y)$ represents an age-specific kin-number pmf for Focal's kin of age s when Focal is of age y, whereas $\mathbf{k}_\Sigma(y)$ yields a pmf for total kin (over all their possible ages) when she is y years old. The $(\bar{Q}+1)$-th entry of the latter distribution gives the full probability that Focal has $\bar{Q} \leq Q$ kin.

If the age-specific pmfs of Focal's kin are independent, then the following theorem (a proof of which is given in Appendix C) provides the pmf for $\mathbf{k}_\Sigma(y)$:

Theorem 1. The probability that Focal of age y has exactly $\bar{j}$ kin whose ages can range in $\Sigma = [z_1, z_n]$ is given by the $(\bar{j}+1)$-th entry of $\boldsymbol{k}_{z_1}(y) \star \cdots \star \boldsymbol{k}_{z_n}(y)$. Moreover, $\boldsymbol{k}_\Sigma(y) = \boldsymbol{k}_{z_1}(y) \star \cdots \star \boldsymbol{k}_{z_n}(y)$.

In the case of collateral kin which all descend from Focal's q-th ancestor, the age-specific pmfs of kin are conditionally dependent (on ages of ancestral reproduction) and we cannot apply Theorem (1). We explicitly consider the probabilities that Focal has some number of such kin between a given age range in Section 3.1 and Section 3.2, respectively.

In the case of ancestors – that is, if Focal can have at most one kin at any point in her life – we have the following lemma which describes the pmf for $\mathbf{k}_\Sigma(y)$:

Lemma 1. The probability that when Focal is aged y, she has an ancestor alive and of some age within the interval Σ is given by $p = \sum_{s\in\Sigma}[\boldsymbol{k}_s(y)]_2$ (where $[.]_j$ represents the j-th entry), resulting in $\boldsymbol{k}_\Sigma(y) = (1-p, p, 0, \ldots, 0)^\dagger$.

Lemma (1) is intuitive since Focal has, with probability $k_s^{(y)}(1)$ (the second entry of $\mathbf{k}_s(y)$), one living ancestor of age s. The probability that the ancestor is alive and within the age interval is then given by the sum over all ages s in the interval that the ancestor may be.

3. Towards the kin formulae

Using the above ingredients and observations, we now provide the explicit formulae for kin. We break down the formula into four theoretically distinct regimes. These regimes correspond to the branches of the tree in Figure 1. First, branches which extend right (older lineages) reflect kin which descend through older sisters of Focal's $(q-1)$-th ancestor. Second, branches which extend left (younger lineages) reflect kin which descend through younger sisters of Focal's $(q-1)$-th ancestor. Third, branches extending down reflect Focal's descendants. Lastly, branches extending up reflect direct ancestors of Focal. In the next sections we respectively deal with these cases in turn, while the particular case whereby kin descend through same-age-class sisters of Focal's $(q-1)$-th ancestor is dealt with in Appendix D. A more detailed break down of the formulae and how they relate to the established kinship model of Caswell (2024) is given in Appendix E. We provide an illustrative application of our framework in Section 4.

In order to simplify the exposition moving forwards, we introduce the operator

$$\boldsymbol{\mathcal{F}}^{i}_{[a,b]} := \underset{s_{i-1}=a}{\overset{b}{\circledast}} \mathbb{F}(s_{i-1}-s_i)\mathbb{U}(0, s_{i-1}-s_i), \tag{10}$$

which acts on the probability mass function of a kin-number distribution of newborn kin for an arbitrary $(i-1)$-th generation descendant of Focal's q-th ancestor. The operator, conditional on survival, takes the convolution over the reproduction of these kin between the age $a-s_i$ and $b-s_i$.

3.1 Kin which descend through older sisters of Focal's $(q-1)$-th ancestor

Here, we condition on each possible independent sequence of ancestral ages of reproduction $b_1, b_2, \dots, b_q$, to derive a conditional pmf for the offspring number of Focal's q-th ancestor at age $\beta_q - s_1$:

$$\mathcal{I}^{\mathcal{O}}_q = \boldsymbol{\psi}_{y+b_1+\cdots+b_q-s_1} = \boldsymbol{\psi}_{\beta_q-s_1}, \tag{11}$$

where the subtraction of s_1 arises since $\beta_q = y + b_1 + \cdots + b_q$ is the current age of Focal's q-th ancestor and s_1 that of their offspring. We update the operator defined in Equation (10) so that the first generation of Focal's q-th ancestor can only reproduce at age strictly older than Focal's $(q-1)$-th ancestor, while all subsequent descendants reproduce over the fertile bound:

$$\mathcal{F}^i_{\mathcal{O}} = \begin{cases} \mathbf{I}_{Q+1}, & \text{for } i = 1 \\ \mathcal{F}^i_{[\beta_{q-1}+1, \bar{n}+s_i]}, & \text{for } i = 2 \\ \mathcal{F}^i_{[\underline{n}+s_i, \bar{n}+s_i]}, & \text{for } i > 2. \end{cases} \tag{12}$$

Then the probability mass function describing the probabilities that Focal has a given number of these kin aged in Σ (if $\Sigma = [s_g]$ we recover the age-specific pmf) can be written as a composition of operators:

$${}^{\mathcal{O}}\mathbf{k}^{g,q}_{\Sigma}(y) = \sum_{b_1} \cdots \sum_{b_q} \rho_{b_1} \ldots \rho_{b_q} \underset{s_g \in \Sigma}{\circledast} \mathbb{U}(0, s_g) \bigcirc_{i=1}^{g} \mathcal{F}^i_{\mathcal{O}}\big(\mathcal{I}^{\mathcal{O}}_q\big). \tag{13}$$

In Equation (13) we conditionally sum over possible sequences $(b_i)_{i=1}^q$, each with probability measure $\prod_{i=1}^q \rho_{b_i}$. Conditional on each ancestral sequence, the kin-number random variables for distinct ages s_g are independent. The distribution for the sum of independent random variables is the convolution of the measures. Hence the pmf for the number of kin in age range $s_g \in \Sigma$, conditional on ancestral sequence, is the convolution of the age-specific pmfs. By the law of total probability, the weighted summation over all ancestral sequence results in the unconditional pmf. Simple examples of Equation (13) and how we ensure independence between the age-specific kin-number random variables in this method are shown in Appendix E-1 and Appendix E-2.

Consider in Equation (13) that $g = 1$. For each conditional sequence of ancestral reproduction, $\mathcal{I}^{\mathcal{O}}_q$ recovers a conditional pmf for the number of newborn kin, born to Focal's q-th ancestor before the birth of Focal's $(q-1)$-th ancestor. Focal's q-th ancestor produced Focal's $(q-1)$-th ancestor at age b_q, and at age $\beta_q - s_1$ she had $j = 0, 1, \ldots, Q$ many newborns with probabilities $\psi_{\beta_q - s_1}$. Pre-multiplication the pmf of newborns through $\mathbb{U}(0, s_1)$ procures a pmf of these kin at age s_1 (when Focal is age y). Otherwise, if $g > 1$ then the limits of s_1 (i.e., when $i = 2$) over which the convolution of reproductive ages are taken, defined through Equation (12), ensure that kin descend through older sisters of Focal's $(q-1)$-th ancestor. For $i > 2$ convolutions over reproductive ages have no constraints.

3.2 Kin which descend through younger sisters of Focal's $(q-1)$-th ancestor

We introduce the conditional pmf for the offspring number of Focal's q-th ancestor at age $\beta_q - s_1$ when they give birth to a first descendent younger than Focal's $(q-1)$-th ancestor:

$$\mathcal{I}^{\mathcal{Y}}_q = \mathbb{F}(y + b_1 + \cdots + b_q - s_1)\mathbb{U}(b_q, \beta_q - s_1)\mathbf{e}_2 = \mathbb{F}(\beta_q - s_1)\mathbb{U}(b_q, \beta_q - s_1)\mathbf{e}_2. \tag{14}$$

We apply the operator defined in Equation (10) so that the first generation of Focal's q-th ancestor is strictly younger than Focal's $(q-1)$-th ancestor, while all subsequent descendants reproduce over the fertile bound:

$$\boldsymbol{\mathcal{F}}^i_{\mathcal{Y}} = \begin{cases} \mathbf{I}_{Q+1}, & \text{for } i=1 \\ \boldsymbol{\mathcal{F}}^i_{[\underline{n}+s_i,\beta_{q-1}-1]}, & \text{for } i=2 \\ \boldsymbol{\mathcal{F}}^i_{[\underline{n}+s_i,\bar{n}+s_i]}, & \text{for } i>2. \end{cases} \tag{15}$$

The overall pmf for these kin who can be of any age within Σ (again $\Sigma = [s_g]$ recovers an age-specific pmf) is given by the composition

$$ {}^{\mathcal{Y}}\mathbf{k}^{g,q}_{\Sigma}(y) = \sum_{b_1}\cdots\sum_{b_q}\rho_{b_1}\dots\rho_{b_q} \mathop{\bigcirc\mkern-15mu\star}\limits_{s_g\in\Sigma} \mathbb{U}(0,s_g) \bigcirc_{i=1}^{g} \boldsymbol{\mathcal{F}}^i_{\mathcal{Y}}\big(\mathcal{I}^{\mathcal{Y}}_q\big). \tag{16}$$

In Equation (16), each summand term is conditioned on a specific sequence of ancestral reproductions: $(b_i)_{i=1}^{q}$. The conditional age-specific pmfs are therefore independent. As such, the sum of the random variables for age-specific kin number (with age in Σ) is given by the convolution of their distributions.

Given each conditioning sequence, the summand term is interpreted as follows: We first note that we know with certainty that Focal's q-th ancestor produces Focal's $(q-1)$-th ancestor at age b_q. Here the ancestor has a pmf defined through a unit vector with mass in the 1 kin-number class, $\mathbf{e}_2$. Consider the case of $g=1$. The composition reduces to $\mathbb{F}(\beta_q - s_1)\mathbb{U}(b_q, \beta_q - s_1)\mathbf{e}_2$: pre-multiplication of $\mathbf{e}_2$ by $\mathbb{U}(b_q, \beta_q - s_1)$ procures a conditional distribution representing the probabilities that Focal's q-th ancestor was alive at the age when she produced Focal's kin (at age $\beta_q - s_1$). Pre-multiplication then through $\mathbb{F}(\beta_q - s_1)$ procures a probability distribution representing their offspring, born after the birth of Focal's $(q-1)$-th ancestor. Pre-multiplication through $\mathbb{U}(0, s_1)$ then calculates the probabilities that between birth and age s_1 (when Focal is aged y) the kin survive.

While $g>1$, the case of $i=2$ is diametrically opposed to Section 3.1; the limits of s_1 over which the convolution of newborn-number probability distributions are taken are constrained such that $s_1 - s_2 \leq \beta_{q-1} - 1 - s_2$. This ensures that kin descend through younger sisters of Focal's $(q-1)$-th ancestor. For $i>2$ convolutions over reproductive ages have no constraints. Applications of Equation (16) used to derive Focal's younger sisters and cousins through aunts younger than Focal's mother are respectively given in Appendix E-3 and Appendix E-4.

3.3 Combining the older and younger lineages

When combining the kin of Focal, born to younger and older sisters of Focal's $(q-1)$-th ancestor, over some possible age range Σ, we must ensure the distributions are conditionally independent of the ages of ancestral reproduction. In other words, we can not simply convolve the terms in Equation (13) and Equation (16), but rather we must make specific calculations for total kin. This ensures that the convolution of the measures of the kin-number random variables gives the combined numbers of kin:

$$
\begin{aligned}
&{}^{\mathcal{O}\cup\mathcal{Y}}\mathbf{k}^{g,q}_{\Sigma}(y) = \\
&\sum_{b_1,\dots,b_q} \rho_{b_1}\dots\rho_{b_q}\Big[\mathop{\circledast}_{s_g\in\Sigma} \mathbb{U}(0,s_g) \mathop{\bigcirc}_{i=1}^{g} \boldsymbol{\mathcal{F}}^i_{\mathcal{O}}\big(\mathcal{I}^{\mathcal{O}}_q\big)\Big] \star \Big[\mathop{\circledast}_{s_g\in\Sigma} \mathbb{U}(0,s_g) \mathop{\bigcirc}_{i=1}^{g} \boldsymbol{\mathcal{F}}^i_{\mathcal{Y}}\big(\mathcal{I}^{\mathcal{Y}}_q\big)\Big]. \quad (17)
\end{aligned}
$$

3.4 Descendants of Focal

Descendants of Focal can be calculated through Equation (13) with $q := 0$. Recall s_i is the age of Focal's $i-$th direct descendant. By appealing to the operator in Equation (10) we define

$$
\boldsymbol{\mathcal{F}}^i_{\mathcal{D}} = \begin{cases} \mathbf{I}_{Q+1}, & \text{for } i = 1 \\ \boldsymbol{\mathcal{F}}^i_{[\underline{n}+s_i,\min\{y,\bar{n}+s_i\}]}, & \text{for } i > 1 \end{cases} \quad (18)
$$

and find the pmf of Focal's $g-$th descendant of age s_g when Focal is y, as

$$
{}^{\mathcal{D}}\mathbf{k}^{g,0}_{s_g}(y) = \mathbb{U}(0,s_g) \mathop{\bigcirc}_{i=1}^{g} \boldsymbol{\mathcal{F}}^i_{\mathcal{D}}\big(\boldsymbol{\psi}_{(y-s_1)}\big). \quad (19)
$$

Equation (19) tells us that Focal (who is assumed immortal) will have g-generation descendants of age s_g if she gives birth to offspring at age $y - s_1$, who in turn survive to $s_1 - s_2$ and reproduce at this age, continuing in this manner up to Focal's $(g-1)$-th generation descendant, who survives from birth to age $s_{g-1} - s_g$, at which point producing Focal's g-th descendant (who survives to age s_g). Because at each generation i of descent, Focal can have multiple descendants, the $(i+1)$-th generation descendants are given by the convolution of pmfs of the i-th generation over the fertile age range (recall Theorem (1)).

3.5 Ancestors of Focal

Ancestors of Focal correspond to the case whereby $g := 0$. Recall b_i is the age of Focal's i-th direct ancestor when producing the $(i-1)$-th. We obtain the closed form equation for the pmf of Focal's q-th ancestor of age s_0 when Focal is y through

$$ {}^{\mathcal{A}}\mathbf{k}_{s_0}^{0,q}(y) = (1-\mu)\mathbf{e}_1 + \mu \sum_{\beta_q = s_0} \mathbb{U}(b_q, s_0)\mathbf{e}_2, \;\; \mu = \sum_{\beta_q = s_0} \prod_{i=1}^{q} \rho_{b_i}. \tag{20} $$

The sum is taken over all possible arrangements of the ages b_i at which Focal's i-th ancestor produced Focal's $(i-1)$-th, such that the age of Focal's q-th ancestor when Focal is y, $\beta_q = b_1 + \ldots b_q + y$ is equal to s_0. The vector $\mu\mathbf{e}_2$ in Equation (20) assigns binomial probabilities that Focal's q-th ancestor is indeed defined through the genealogical sequence of b_i. We project the q-th ancestor to survive from age b_q – when last we knew it was in existence (producing $(q-1)$-th ancestor) to survival to her age $s_0 = b_1 + b_2 + \cdots + b_q + y$ when Focal is y. The vector $(1-\mu)\mathbf{e}_1$ re-normalises by adding to the pmf the probability that Focal's q-th ancestor was not defined by the sequence of b_i (i.e., is not of exact age s_0).

4. Application

Here, the model is applied. We source single year of age, period based (from 1974), UK fertility and mortality data from the Human Fertility Collection database and the Human Mortality Database (Human Fertility Collection 2024; Human Mortality Database 2024). We make the simplifying assumption that births follow a Poisson distribution. Thus, with an age-specific fertility rate f_i, the distribution ψ_i has entries giving the probabilities of having k offspring: $\{f_i^k e^{-f_i}/k!\}_{k=0}^{Q}$. Our assumption here in no way restricts the model but is simply used for progress. We could equally use, for example, empirical distributions of multiple births for a single year of age data. Deaths follow a Bernoulli distribution: We write $\{u_i, 1-u_i\}$ for the probabilities of survival from age i to $i+1$ (or not).

We set $Q = 6$ as an upper bound for the maximum lifetime kin number. Of course we could use a larger upper limit; however, it would be unlikely for an individual to experience more than six sisters, aunts, or cousins during their life.[6] In Appendix A we also explore the validity of the below results by comparing them to a microsimulation. All code and data used, as well as a comparison of the mean field results of this model to Caswell (2019), can be found at https://github.com/ButterickJoe/PMF_Kin.

---

[6] Based on the data we use here. In other demographies individuals may well experience such numbers of kin.

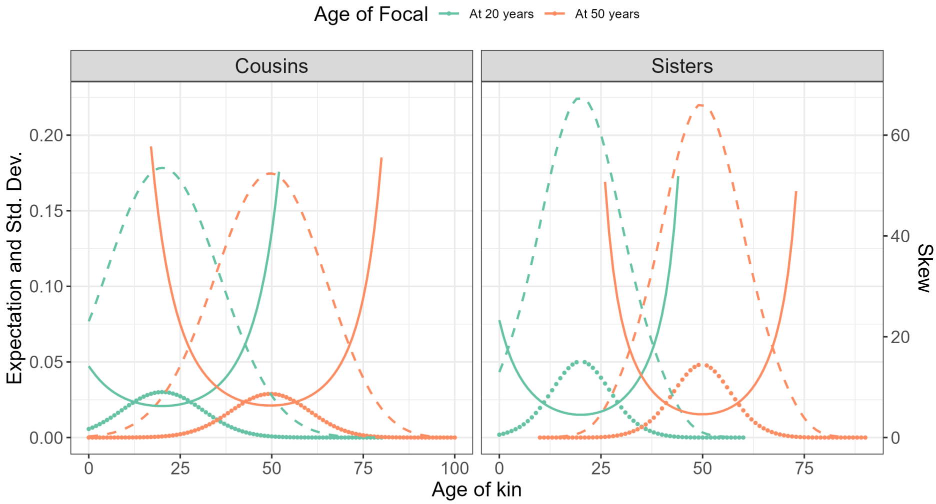
4.1 Unconditional distributions of kin

4.1.1 Sisters and cousins

Using Equation (13) and Equation (16) we are able to produce age-specific and total (over all kin ages) kin-number pmfs for Focal's younger and older sisters for each age y of Focal's life. Respectively, for each age s_1, or possible range of ages $s_1 \in \Sigma$, that Focal's sisters can be, the pmfs provide probabilities that Focal has exactly $j = 0, 1, \dots, Q$ of them. The complete pmf for the kin-number distribution of sisters Focal has is found by applying Equation (17). In the same manner, we use $g = q = 2$ to decompose Focal's cousins as descending from younger sisters of Focal's mother ${}^{\mathcal{Y}}\mathbf{k}_{\Sigma}^{2,2}(y)$ and older sisters of Focal's mother ${}^{\mathcal{O}}\mathbf{k}_{\Sigma}^{2,2}(y)$ with the combined kin-number pmfs for cousins found through Equation (17).

Figure 2 illustrates the age-specific pmfs describing the numbers of sisters and cousins of Focal, for two ages in Focal's life course: when she is aged 20 and aged 50. Plotted are expected kin numbers, the standard deviation in kin number, and the skewness in kin number. Because we consider probabilities that Focal experiences some number of kin of a specific age, nearly all the mass appears in the first (i.e., $k_s^{(y)}(0)$) entries of the pmfs: The distributions display a heavy (positive) skew.

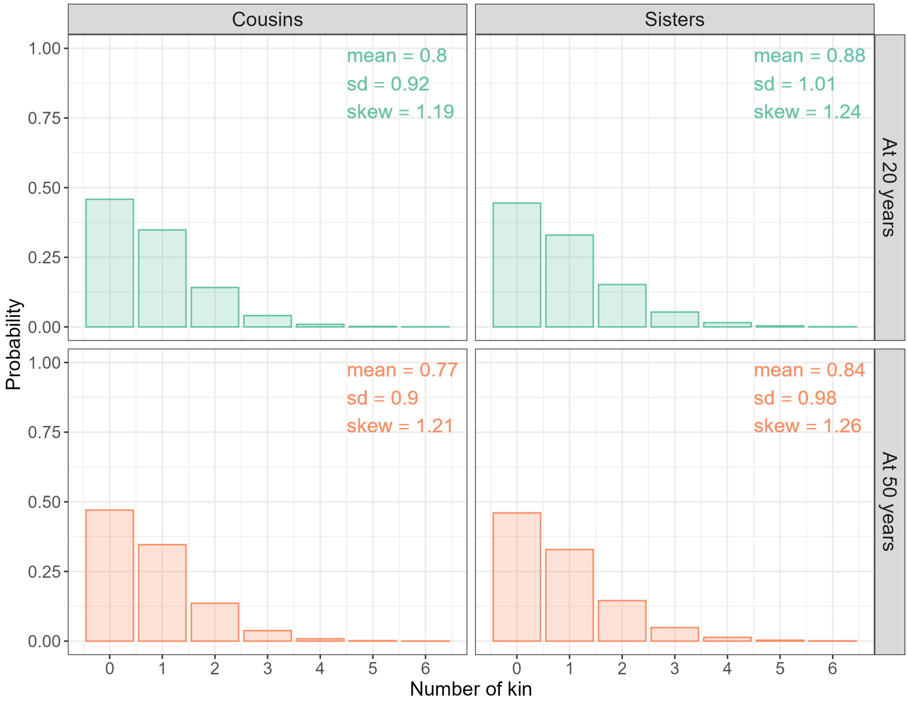
Figure 2: Theoretically predicted age-specific pmfs for Focal's sisters (right) and cousins (left) when Focal is aged 20 (turquoise) and 50 (orange)



Notes: Points show expectations, dashed lines show standard deviation, and solid lines show skew (separate y-axis). For ease of visualisation, we omit values ≥ 60 when plotting the skew.

Figure 3 illustrates our theoretically predicted pmfs for the total number sisters and cousins of Focal when she is aged 20 and 50. We predict that when Focal is aged 20 she has no sisters with a probability 0.45 and no cousins with a probability 0.46. When Focal is aged 50, we predict that she has no sisters with a probability 0.46 and no cousins with a probability 0.47. Also presented are statistics derived from the first, second, and third moments of the kin-number distributions.

Figure 3: Accumulated-kin pmfs for Focal's cousins (left) and sisters (right) when Focal is aged 20 (top row) and 50 (bottom row)

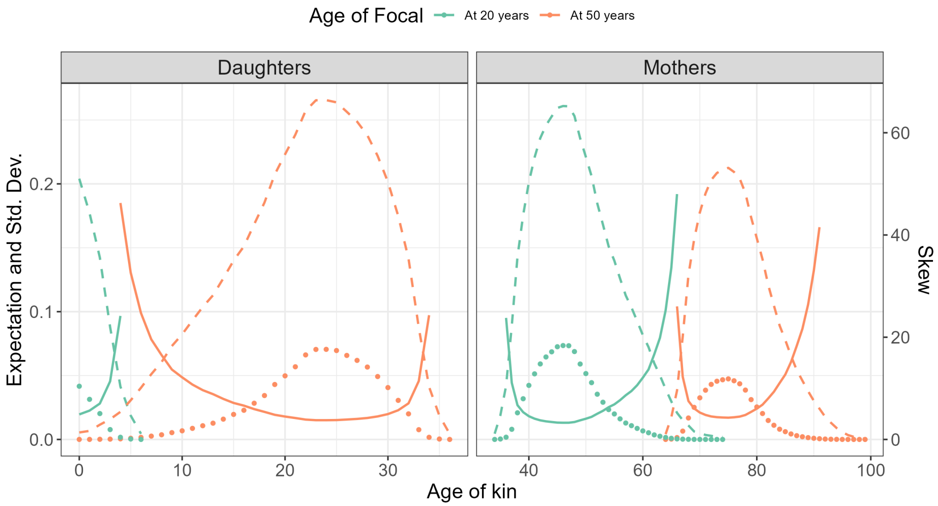


Note: Bars show the probability that Focal has a given number of kin.

4.1.2 Ancestors and descendants

Applying Equation (20) we obtain ${}^{\mathcal{A}}\mathbf{k}_{s_0}^{0,1}(y)$, the age-specific pmf for Focal's mother of age s_0 when Focal is y. Through Equation (19) we obtain ${}^{\mathcal{D}}\mathbf{k}_{s_1}^{1,0}(y)$, the age-specific pmf for Focal's daughters of age s_1 when Focal is age y. These distributions are visualised in Figure 4, where we plot the expected kin numbers, as well as the standard deviation and skewness in kin number. We focus on two different ages in Focal's life course: when she is aged 20 and 50. Notice that at age 20, the probability that Focal has a non-zero number of daughters only occurs for daughters up to age 6 (Focal begins reproduction at age 14), whereas, when Focal is 50 there is a non-zero probability that she has daughters aged up to 36. We again observe that the distributions are heavily skewed.

Figure 4: Theoretically predicted age-specific pmfs for Focal's daughters and mother when Focal is aged 20 (turquoise) and 50 (orange)



Notes: Left: daughters, right: mothers. Points show expectations, dashed lines show standard deviation, and solid lines show skew (separate y-axis). For ease of visualisation, we omit values ≥ 50 when plotting the skew.

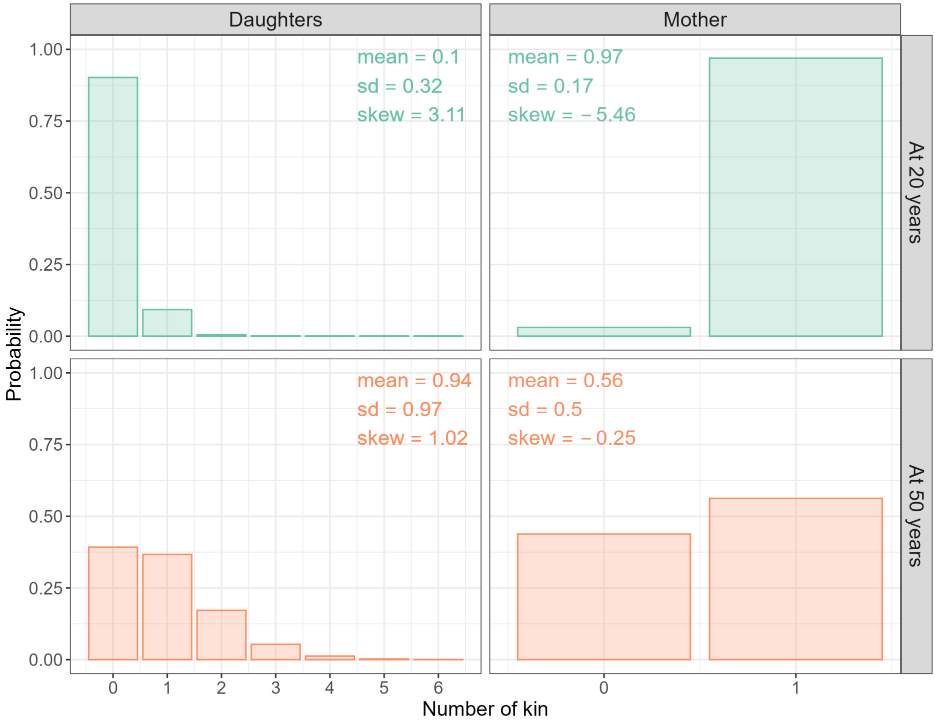
The pmf describing the probability that Focal's mother is alive is found using Lemma (1), and the total probable number of daughters of Focal using Theorem (1):

$$
{}^{\mathcal{A}}\mathbf{k}_{\Sigma}^{0,1}(y) = \Big[\sum_{s_0} {}^{\mathcal{A}}\mathbf{k}_{s_0}^{0,1}(y)\Big]_2 \quad \text{and} \quad {}^{\mathcal{D}}\mathbf{k}_{\Sigma}^{1,0}(y) = \mathop{\circledast}\limits_{s_1=0}^{y-\underline{n}} {}^{\mathcal{D}}\mathbf{k}_{s_1}^{1,0}(y). \tag{21}
$$

Figure 5 illustrates these pmfs. In each panel, the bars show the probabilities that Focal experiences a number of kin. The left column shows Focal's daughters, while the right Focal's mother. Rows show age of Focal. By comparing Focal at ages 20 and 50, we see how the probable numbers of kin change by age of Focal. Regarding daughters, when Focal is aged 20 and early in her reproductive cycle, we predict that she will experience one or more daughters with probability 0.098. Contrastingly, at age 50 when Focal has completed fertility, we predict that she will experience one or more daughters with probability 0.606.

Also illustrated are the three following topics, broken up over kin and age – the expected numbers of kin: daughters with 0.10 at age 20 and 0.93 at age 50, and mother with 0.97 at age 20 and 0.56 at age 50; the standard deviation in kin number: daughters with 0.32 at age 20 and 0.97 at age 50, and mother with 0.17 at age 20 and 0.50 at age 50; and the skewness in kin number: daughters with 3.11 when Focal is aged 20 and 1.02 when Focal is aged 50, and mother with –5.46 when Focal is 20 and –0.25 when Focal is 50.

Figure 5: Accumulated-kin pmfs for Focal's daughters and mother when Focal is aged 20 and 50



Notes: Rows show age of Focal. Left: daughters, right: mothers. Bars give the probability that Focal has a given number of kin; vertical lines show the expected numbers of kin; horizontal error bars show expected kin number ± standard deviation in kin number.

In Appendix A, we compare our above predictions of how the number of kin Focal changes over her life course to a direct stochastic simulation (see Figure A-3 and Figure A-4).

4.2 Conditional distributions of kin

Our method allows one to condition the probability that Focal experiences some number of one kin type on life-history events pertaining to other kin types. For example, consider Focal's sisters. To find the probability distributions for Focal's sisters, we apply a weighted average of the age-specific reproduction of Focal's mother over possible ages when she had Focal. Focal's mother, however, is one age when having Focal. It is thus of interest to remove the weighting and view the conditional pmfs of Focal's sisters, assuming certain (error-free) knowledge of Focal's mother's age when she had Focal.

Illustration – Focal's sibship conditioned on age of mother: Assuming that Focal's mother was aged b_1 when she had Focal, the respective conditional distributions representing the probability that Focal has $j = 0, 1, \dots, Q$ older or younger sisters of age s when she is aged y are

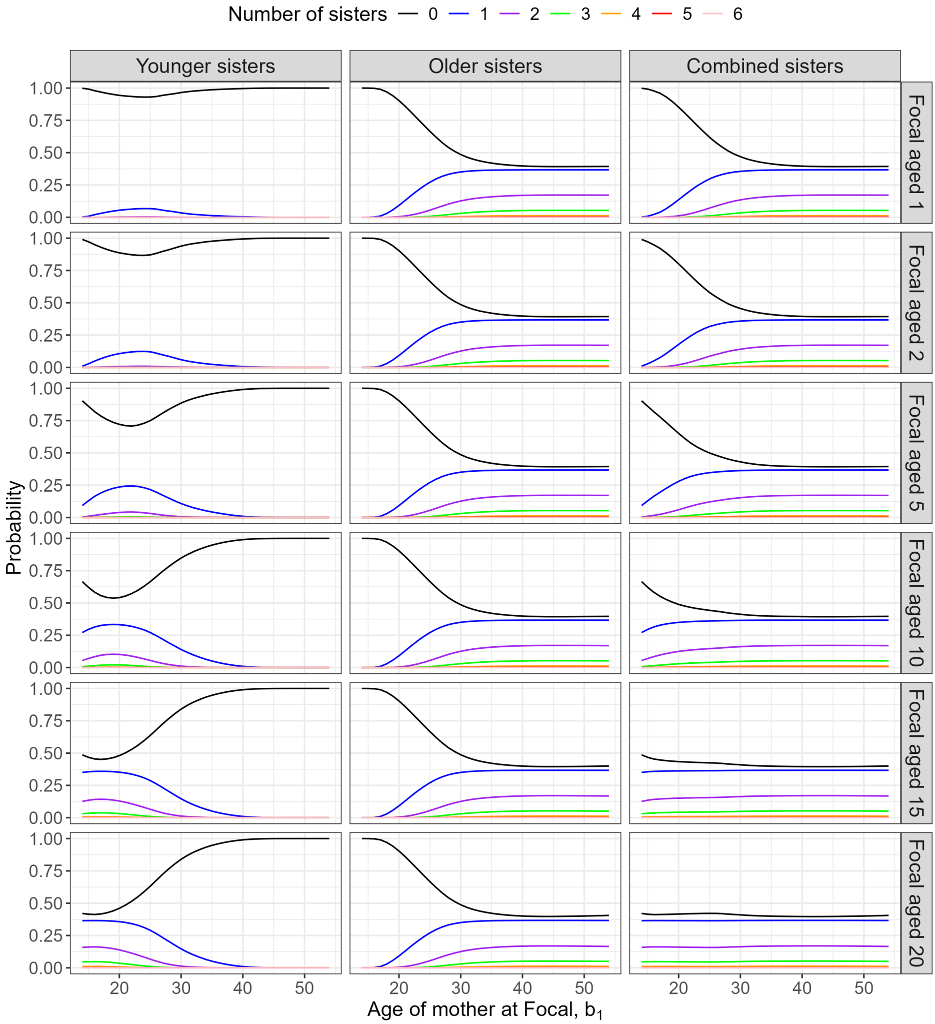
$$\begin{aligned} {}^{\mathcal{O}}\mathbf{k}^{1,1}_{s_1}(y; b_1) =& \mathbb{U}(0, s_1)\boldsymbol{\psi}_{b_1+y-s_1} \\ {}^{\mathcal{Y}}\mathbf{k}^{1,1}_{s_1}(y; b_1) =& \mathbb{U}(0, s_1)\mathbb{F}(b_1 + y - s_1)\mathbb{U}(b_1, b_1 + y - s_1)\mathbf{e}_2. \end{aligned}$$

The conditional pmfs of total older and younger sisters (over all possible ages) are

$$ {}^{\mathcal{O}}\mathbf{k}^{1,1}_{\Sigma}(y; b_1) = \underset{s_1=y+1}{\overset{n}{\circledast}} {}^{\mathcal{O}}\mathbf{k}^{1,1}_{s_1}(y; b_1), \;\; {}^{\mathcal{Y}}\mathbf{k}^{1,1}_{\Sigma}(y; b_1) = \underset{s_1=0}{\overset{y-1}{\circledast}} {}^{\mathcal{Y}}\mathbf{k}^{1,1}_{s_1}(y; b_1) \qquad (22)$$

and the convolution of the distributions in Equation (22) gives the overall probabilities that Focal has a sister (younger or older than herself), conditional on her mother being aged b_1 when she was born. For each $b_1 = \underline{n}, \dots, \bar{n}$, the different probable number of sisters of Focal, as per Equation (22), is shown in Figure 6. The left-hand panel shows probabilities that Focal has some number of younger sisters. Here, the younger Focal is, the less time her mother has to produce her younger sisters, and the less likely Focal has such kin. At older ages of Focal, the presence of younger sisters is more likely but depends on whether Focal was born earlier or later in the reproductive ages of the mother. Contrastingly, the middle panel – reflecting probabilities that Focal experiences some number of older sisters – remains invariant with respect to Focal's age. Here, the probabilities only change with the age at which Focal's mother had Focal. This is because Focal has accumulated all of her older sisters before birth. The right-hand panel gives the probability that Focal has some given number of combined (i.e., younger or older) sisters of any age.

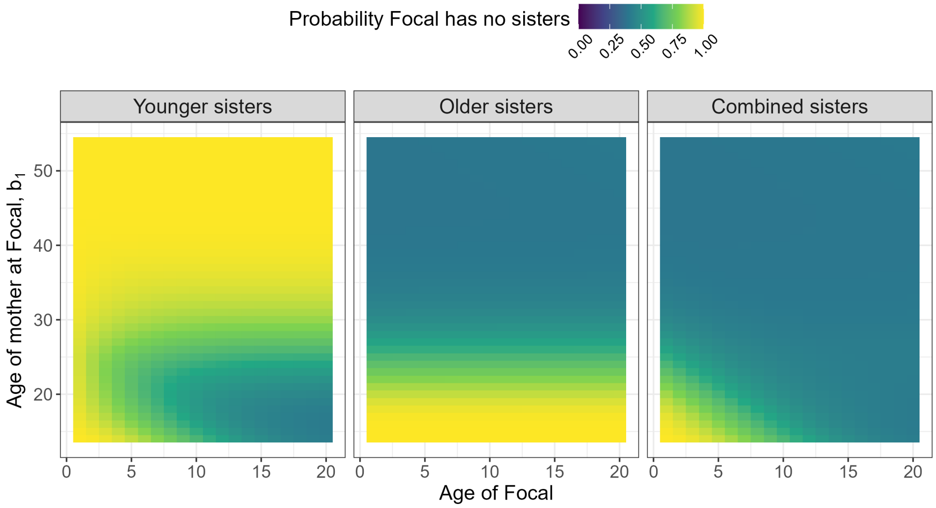
Figure 6: The probable number of sisters of Focal as a function of the age of Focal's mother, at different times in Focal's life



Notes: Rows give the age of Focal. Left: younger sisters; middle: older sisters; right: combined sisters.

We might also consider the probability that Focal has no sisters. These probabilities once again depend on the age of Focal's mother when Focal was born; see Figure 7. In the plot, the left panel, illustrating the probability that Focal has no younger sisters, demonstrates that the older Focal's mother is at birth of Focal, the less likely she experiences such kin. In this case, Focal simply doesn't accumulate younger sisters since mother is nearing the end of her reproductive interval. The more probable instances of Focal experiencing a younger sister occur when her mother is relatively young when having Focal, and when Focal is currently at an age whereby her mother will have completed reproduction. Interestingly, for Focal up to age 10, if her mother gave birth to her at a very young age (e.g., $b_1 = 15$) we find that it more probable for Focal to have no younger sisters compared to if Focal's mother gave birth to her at a mid-fertile age (e.g., $b_1 = 25$). Because age-specific fertility is unimodal in our example (1974; UK), if Focal's mother is young when mothering Focal she retains a low probability of reproduction in the immediate years after; thus Focal has to wait before accumulating younger sisters.

Figure 7: The probability that Focal has no sisters as a function of age, and conditional age of mother at Focal



Notes: Left: no younger sisters; middle: no older sisters; right: no younger or older sisters

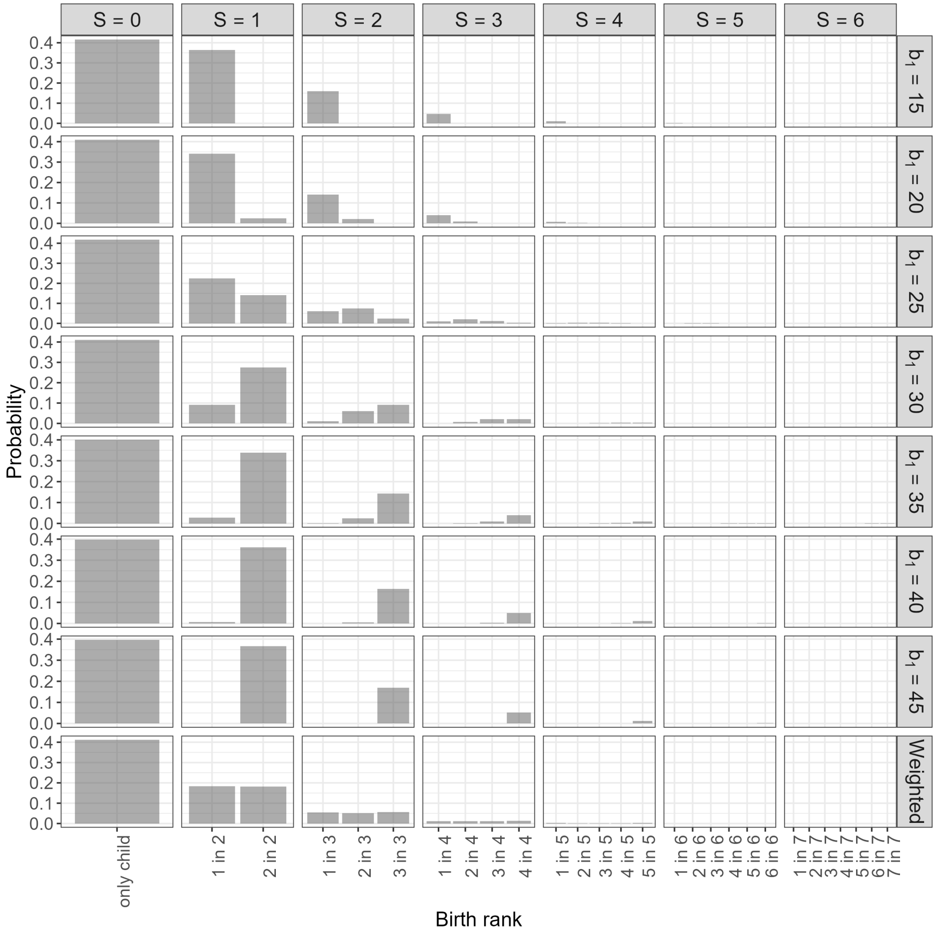
Note that in the present example we do not account for birth interval in the fertility modelling, or else we might expect to see more complex patterns in these heat maps, for example indicating that transition to gaining a first younger sister is less likely as Focal ages, separately from the fertility decline as mother ages.

Focal's sibship size S (excluding Focal) is a random variable, conditioned on the age of mother at birth of Focal, b_1. Let the variable $X_{i,j}$ indicate the probability that Focal has i older sisters and j younger sisters (i.e., $i + j = S$). Thus, for each possible sibship size, $j = S - i$, and as such

$$X_{i,S-i} = \left[{}^{\mathcal{O}}\mathbf{k}_{\Sigma}^{1,1}(y; b_1)\right]_i \left[{}^{\mathcal{Y}}\mathbf{k}_{\Sigma}^{1,1}(y; b_1)\right]_{S-i} \text{ where } \sum_{S\geq 0}\sum_{i=1}^{S+1} X_{i,S-i} = 1$$

with the right-hand side guaranteed by the conditioning on mother's age at birth of Focal. The variable $X_{i,S-1}$ allows us to calculate the probability of Focal's birth rank, as illustrated in Figure 8. Here we plot birth rank probabilities for Focal of age 20: (1) conditional on mother's age b_1 (by row) and (2) as a weighted mix over probable ages of mother (bottom row). Note that each of the rows sum to one because conditional on mother's age, they provide probabilities of Focal having $S = 0, 1, \ldots, 6$ sisters, and given that, Focal's birth order. We might also condition on sibship size, in which case we would simply re-normalise each panel.

Figure 8: Probability that when 20 years old, Focal experiences S sisters, and from them i are older; $S - i$ are younger



Notes: Conditioning on the age of Focal's mother at birth of Focal (b_1) is illustrated by rows (the bottom row shows the weighted average over all b_1). Columns give sizes of sibship (S).

5. Discussion

The research presented in this paper extends and enriches recent advances in modelling demographic stochasticity within kinship networks (Caswell 2024). Presently, the only published model to acknowledge the above-mentioned stochasticity accounts only for the mean and variance in kin number. Our proposed frameworks project a complete probability distribution of the number of kin, from which, higher-order moments or other quantities of interest (such as quantiles) can be readily obtained. Our framework thus provides a more comprehensive analysis of variability in kinship structures. The probabilistic nature of our framework allows conditioning kinship networks on particular life-history events (see Section 4.2). The approach presented here thus allows analytical results regarding demographic uncertainty that approach the richness of those obtained via microsimulation, providing population distributions of numbers of kin by age of both Focal and kin, for arbitrary kin types.

Our proposed framework treats probability distributions for age-specific mortality and fertility as model inputs. From these, the probability distributions of kin naturally emerge. This innovation allows one flexibility to choose from empirical distributions (e.g., single-year-of-age offspring probabilities) as well as parametric distributions. In contrast, fitting empirical distributions using the mean and variance in kin numbers – outputs of the state-of-the-art stochastic kinship model – would be challenging. Another innovation made here is that we reduce the dimensionality of the matrix projections. The size of the state space here is defined by life-time maximum kin number, Q. Although, as argued below, this does not necessarily offer a computational advance, this feature of our model alleviates the need for big state-space matrices.

In principle, our model utilises the theory of branching processes with incorporated age structure. We demonstrate the recursive nature of kin structures, quite similar to the seminal work of Goodman, Keyfitz, and Pullum (1974), however with convolutions of distributions implementing the next generation of kin rather than integrals over scalar expectations. Waugh (1981) provides a way to construct a joint probability generating function (pgf) for generation size over multiple generations in a Galton-Watson process, and then samples a typical “Ego” (rather than Focal) from a fixed generation (see, e.g., Section 7 in that paper). In this way, the author elegantly calculates what they refer to as Ego’s “sorority” (sibship) size. The addition of age structure in our framework builds on such work and allows one to calculate probabilities of birth order as well as overall sibship size. Moreover, in order to apply the methods proposed by Waugh (1981), one requires an analytic pgf (they use a fractional linear functional form). For progress here, we avoid such restrictions and maintain a discrete probability distribution, which is easier to extract from empirical data.

From a computational perspective, we cannot compete with the leading matrix-projection model Caswell (2024). The manner in which distributions of collateral relatives are calculated requires summations over ancestral reproductions and convolutions over their descendants. However, our equations are substantially faster to implement than an individual-based microsimulation model and, in the present context, are able to yield results of comparable complexity. Note that in higher-dimensional settings, for instance whereby additional stages reflect characteristics of kin, incorporating additional complexity into a microsimulation is likely to be easier than extending our analytical expressions.

When comparing the results presented in Section 4 to a direct stochastic simulation (available to explore at https://github.com/ButterickJoe/PMF_Kin) we find very good agreement in results. Comparisons for kin which form ancestors and descendants in Focal's family tree can be found in Figure A-3 and Figure A-4. Comparisons for sisters can be found in Figure A-1 and Figure A-2. Regarding sisters, we find what we consider to be very minor difference in the overall pmfs (see Figure A-2). One possible explanation for this discrepancy is Monte-Carlo error. Nonetheless, we cannot rule out the effects of demographic stochasticity. In finite populations, fluctuations in births and deaths will result in the realised proportions of individuals in each age class deviating from the stable distribution. Consider a population of size $N(t)$ at time t structured by age classes i so that $N(t) = \sum_i n_i(t)$. Recall from Section 2.1 that F_i is a random variable representing offspring number for an individual in age class i. Using $\bar{F}_i = (\sum_{j=1}^{n_i} F_i)/n_i$ to represent the average age-class reproductive value, the deviation in individual reproduction from the Leslie model is $f_i - \bar{F}_i = \epsilon_i$ and moreover, $\mathbb{E}[\epsilon_i^2] = \text{var}[\bar{F}_i|f_i] = \text{var}[F_i]/n_i$. Such demographic deviations mean that the proportions of mothers in each age class will fluctuate around some stationary distribution. That is, denoting $R_i(t) = \sum_{j=1}^{n_i} F_i$ as the total reproduction from age class i and $R(t)$ as the total reproduction over all age classes, the observed proportion of mothers of age i in the simulation, $R_i(t)/R(t)$, will not exactly correspond to ρ_i in the theoretical model. A comprehensive investigation of the effects of population size in simulated processes will provide an avenue for further research but is beyond the scope of the present article.

The present work is restricted by assuming a time-invariant, one-sex, age-structured population. Extending to time-dependent vital rates would reflect more realistic population dynamics. The main theoretical challenge here would be to probabilistically sample mothers from an unstable population (i.e., defining $\rho_{x,t}$). Methods in Butterick et al. (2025) pertaining to time-inhomogeneous genealogical Markov chains can readily achieve as much. The remainder of moving to time-varying demographics should be merely a case of careful indexing. Incorporating two sexes should also be relatively straightforward. Model ingredients requiring change would include projecting (1) survival independently by sex and (2) the numbers of newborns distributed by sex. Constructing block-structured matrices similar to those used in Caswell (2022), with $\mathbb{U}^{\text{f,m}}$, $\mathbb{F}^{\text{f,m}}$ in lieu of the projection matrices therein, would allow such progress. In this case, projecting older and younger lineages (Equation (13) and Equation (16)) would require little change, except for imposing a female dominance in direct ancestor reproduction and the output being a block-structured vector of female and male kin-number pmfs. Similarly, Focal's descendants would simply be represented by a block-structured vector of pmfs. One notable change would be that the probable ages at which ancestors reproduce would be sex-specific (i.e., $\rho^{\mathrm{f}}_{b_1}, \rho^{\mathrm{m}}_{b_1}$ respectively represent the probable ages of Focal's mother and father at her birth). As such, in order to project direct ancestors, Equation (20) would involve a double summation over both variables (both sexes). We are currently working on extending the present framework to accommodate both sexes and within a time-variant demography. Good progress has been made here; we hope this development will be the focus of a forthcoming paper.

An interesting but challenging prospect is to extend the present research to a multistate model. Such progress would require more in-depth consideration. For instance, construction of the matrices in Section 2.4 and Section 2.5 that form the core of this method would become complicated. As well as a function of age, the probability that $j = 1, 2, \dots$ kin die at some given time will also depend on their stages. Elements of the projection matrix $\mathbb{U}(s', s, g, f)$ under a multi-state model would have to provide the probabilities that so many kin survive from age s' to s, starting from stage g and ending in stage f. Progress in this direction would allow for a very rich investigation of kinship structures, perhaps paralleling the complexity of simulation. Including stage would allow for example, one to condition fertility profiles ($\boldsymbol{\psi}$) as dependent on elapsed time since last birth (as well as age). Not only would such an innovation provide a more accurate description for human kinship where it is known that time proximity between births can create a "sibling constellation" (Morosow and Kolk 2017), but would also be highly relevant in other species which experience postpartum infertility, such as toothed whales (suborder Odontoceti) (Ellis et al. 2024). Implementing stochastic age×stage structured kinship remains an open research problem.

In summary, the methodology proposed in this paper has, for the first time, enabled projecting a probability distribution of the (1) total number of kin and (2) age-specific distribution of kin of a typical population member. Having a complete distribution of kin allows for detailed analysis of probabilities of given numbers of relatives present at different parts of the life course, which is important from the point of view of studying the presence of support networks, availability of care, and more.

6. Acknowledgements

We would like to thank three anonymous reviewers for their rigorous and insightful comments on a first draft of the manuscript. In particular, we are extremely grateful to "Reviewer A" for noticing a minor error in our usage of the convolution of probability measures in a previous version of this work. We would like to thank Hal Caswell for valuable discussions and helpful comments on this project. All authors acknowledge that the research was supported by the Economic and Social Research Council (ESRC) CPC-Connecting Generations Centre (grant ES/W002116/1).

References

Alburez-Gutierrez, D., Barban, N., Caswell, H., Kolk, M., Margolis, R., Smith-Greenaway, E., Song, X., Verdery, A.M., and Zagheni, E. (2022). Kinship, demography, and inequality: Review and key areas for future development. SocArXiv. doi:10.31235/osf.io/fk7x9.

Alburez-Gutierrez, D., Williams, I., and Caswell, H. (2023). Projections of human kinship for all countries. *Proceedings of the National Academy of Sciences* 120(52): e2315722120. doi:10.1073/pnas.2315722120.

Allen, L.J.S. (2010). *An introduction to stochastic processes with applications to biology*. New York: Chapman and Hall/CRC.

Butterick, J., Hilton, J., Bijak, J., and Smith, P.W. (2025). A mathematical framework for time-variant multi-state kinship modelling [in press, pre-proof]. *Theoretical Population Biology* 163: 1–12. doi:10.1016/j.tpb.2025.02.002.

Caswell, H. (2019). The formal demography of kinship: A matrix formulation. *Demographic Research* 41(24): 679–712. doi:10.4054/DemRes.2019.41.24.

Caswell, H. (2020). The formal demography of kinship II: Multistate models, parity, and sibship. *Demographic Research* 42(38): 1097–1146. doi:10.4054/DemRes.2020.42.38.

Caswell, H. (2022). The formal demography of kinship IV: Two-sex models and their approximations. *Demographic Research* 47(13): 359–396. doi:10.4054/DemRes.2022.47.13.

Caswell, H., Margolis, R., and Verdery, A.M. (2023). The formal demography of kinship V: Kin loss, bereavement, and causes of death. *Demographic Research* 49(41): 1163–1200. doi:10.4054/DemRes.2023.49.41.

Caswell, H. and Song, X. (2021). The formal demography of kinship III: Kinship dynamics with time-varying demographic rates. *Demographic Research* 45(16): 517–546. doi:10.4054/DemRes.2021.45.16.

Caswell, H. (2024). The formal demography of kinship VI: Demographic stochasticity and variance in the kinship network. *Demographic Research* 51(39): 1201–1256. doi:10.4054/DemRes.2024.51.39.

Coste, C.F.D., Bienvenu, F., Ronget, V., Ramirez-Loza, J.P., Cubaynes, S., and Pavard, S. (2021). The kinship matrix: Inferring the kinship structure of a population from its demography. *Ecology Letters* 24(12): 2750–2762. doi:10.1111/ele.13854.

Crump, K.S. and Mode, C.J. (1968). A general age-dependent branching process. I. *Journal of Mathematical Analysis and Applications* 24(3): 494–508. doi:10.1016/0022-247X(68)90005-X.

Demetrius, L. (1975). Natural selection and age-structured populations. *Genetics* 79(3): 535–544. doi:10.1093/genetics/79.3.535.

Ellis, S., Franks, D.W., Nielsen, M.L.K., Weiss, M.N., and Croft, D.P. (2024). The evolution of menopause in toothed whales. *Nature* 627: 579–585. doi:10.1038/s41586-024-07159-9.

Goldman, N. (1978). Estimating the intrinsic rate of increase of population from the average numbers of younger and older sisters. *Demography* 15(4): 499–507. doi:10.2307/2061202.

Goodman, L.A., Keyfitz, N., and Pullum, T.W. (1974). Family formation and the frequency of various kinship relationships. *Theoretical Population Biology* 5(1): 1–27. doi:10.1016/0040-5809(74)90049-5.

Hammel, E.A. (2005). Demographic dynamics and kinship in anthropological populations. *Proceedings of the National Academy of Sciences* 102(6): 2248–2253. doi:10.1073/pnas.0409762102.

Human Fertility Collection (2024). Max Planck Institute for Demographic Research (Germany) and Vienna Institue of Demography (Austria). https://www.fertilitydata.org.

Human Mortality Database (2024). Max Planck Institute for Demographic Research (Germany), University of California, Berkeley (USA), and French Institute for Demographic Studies (France). http://www.mortality.org.

Jagers, P. (1982). How probable is it to be first born? And other branching-process applications to kinship problems. *Mathematical Biosciences* 59(1): 1–15. doi:10.1016/0025-5564(82)90105-5.

Jagers, P. and Nerman, O. (1984). The growth and composition of branching populations. *Advances in Applied Probability* 16(2): 221–259. doi:10.2307/1427068.

Joffe, A. and Waugh, W.A.O. (1982). Exact distributions of kin numbers in a Galton-Watson process. *Journal of Applied Probability* 19(4): 767–775. doi:10.2307/3213829.

Keyfitz, N. and Caswell, H. (1997). *Applied mathematical demography*. New York: Springer-Verlag.

Kolk, M. (2017). A life-course analysis of geographical distance to siblings, parents, and grandparents in Sweden. *Population, Space and Place* 23(3): e2020. doi:10.1002/psp.2020.

Margolis, R., Sheftel, M.G., Wang, H., Chandler, R.F., Newmyer, L., and Verdery, A.M. (2024). Older adults' descendants and family networks in the context of global educational expansion. *Population and Development Review* 51(1): 213–256. doi:10.1111/padr.12681.

Margolis, R. and Verdery, A.M. (2019). A cohort perspective on the demography of grandparenthood: Past, present, and future changes in race and sex disparities in the United States. *Demography* 56(4): 1495–1518. doi:10.1007/s13524-019-00795-1.

Morosow, K. and Kolk, M. (2017). How does birth order and number of siblings affect fertility? A within-family comparison using Swedish register data. *European Journal of Population* 36(2): 197–233. doi:10.1007/s10680-019-09525-0.

Pittavino, M., Arpino, B., and Pirani, E. (2025). Kinlessness at older ages: Prevalence and heterogeneity in 27 countries. *The Journals of Gerontology: Series B* 80(1): 180. doi:10.1093/geronb/gbae180.

Pollard, J.H. (1966). On the use of the direct matrix product in analysing certain stochastic population models. *Biometrika* 53(3-4): 397–415. doi:10.2307/2333647.

Pullum, T.W. (1982). The eventual frequencies of kin in a stable population. *Demography* 19(4): 549–565. doi:10.2307/2061018.

Thiele, T., Alburez-Gutierrez, D., Calderón-Bernal, L.P., Snyder, M., and Zagheni, E. (2023). Socsim microsimulation R package. https://github.com/MPIDR/rsocsim.

Tuljapurkar, S. (1993). Entropy and convergence in dynamics and demography. *Journal of Mathematical Biology* 31: 253–271. doi:10.1007/BF00166145.

Tuljapurkar, S., Zuo, W., Coulson, T., Horvitz, C., and Gaillard, J.M. (2020). Skewed distributions of lifetime reproductive success: Beyond mean and variance. *Ecology Letters* 23(4): 748–756. doi:10.1111/ele.13467.

Verdery, A.M. and Margolis, R. (2017). Projections of white and black older adults without living kin in the United States, 2015 to 2060. *Proceedings of the National Academy of Sciences* 114(42): 11109–11114. doi:10.1073/pnas.1710341114.

Vlachantoni, A., Evandrou, M., Falkingham, J., and Qin, M. (2024). Dynamics of unmet need for social care in England. *Ageing and Society* 44(6): 1247–1265. doi:10.1017/S0144686X22000745.

Wachter, K.W., Hammel, E.A., and Laslett, P. (eds.) (1978). *Statistical studies of historical social structure*. London and New York: Academic Press. doi:10.1016/B978-0-12-729150-5.50001-8.

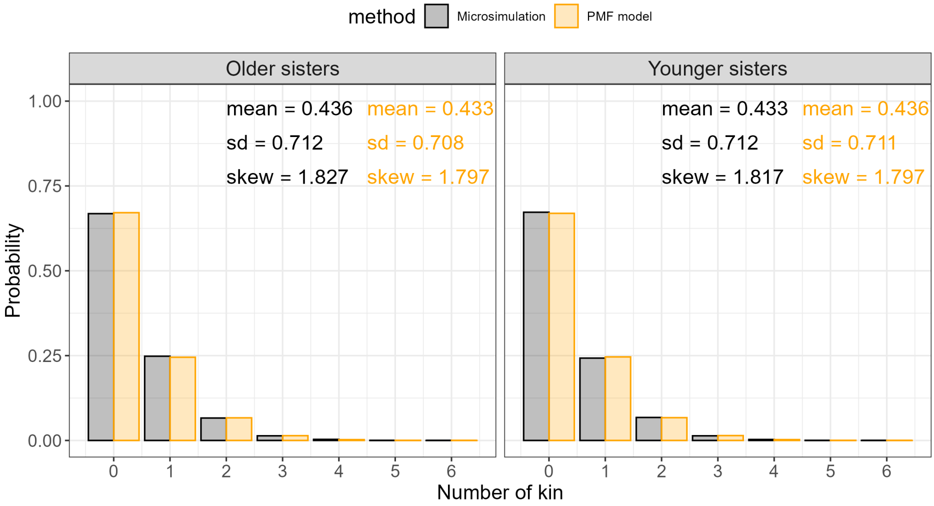
Waugh, W.A.O. (1981). Application of the Galton-Watson process to the kin number problem. *Advances in Applied Probability* 13(4): 631–649. doi:10.2307/1426964.

Williams, I., Alburez-Gutierrez, D., and the DemoKin team (2021). Demokin: An R package to implement demographic matrix kinship models. https://github.com/IvanWilli/DemoKin.

Appendix A: Supplementary figures

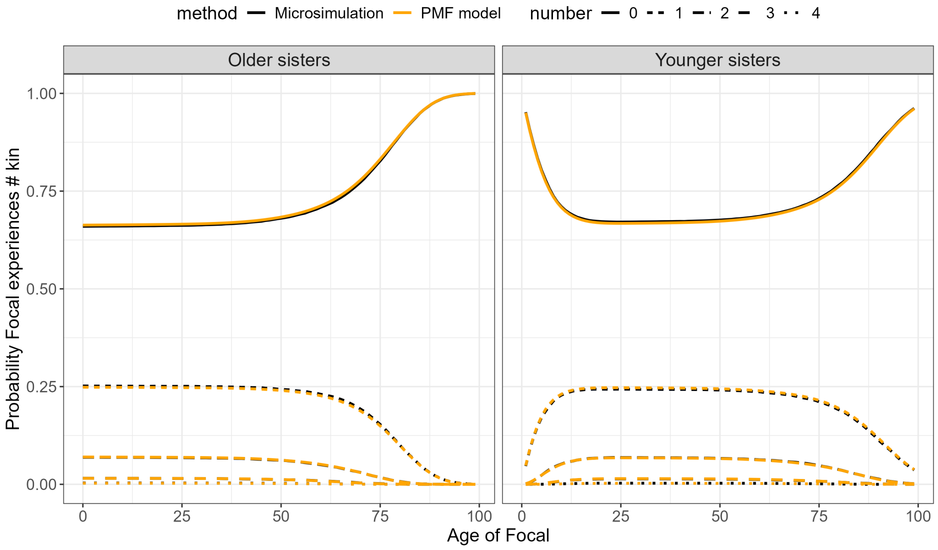
In Figure A-1 we compare the overall kin-number pmfs of total younger and older sisters of Focal predicted by our model (orange) to a stochastic simulation (black), when Focal is aged 40. In Figure A-2 we extend the comparison over all ages of Focal, and compare the probabilities that Focal experiences $j = 0, 1, 2, 3, 4$ sisters.

Figure A-1: Accumulated-kin pmfs for Focal's sisters when Focal is aged 40



Notes: Legend and colour compares the theoretical model to an agent-based simulation. Left: older sisters; right: younger sisters. Bars show the probability that Focal has a given number of sisters.

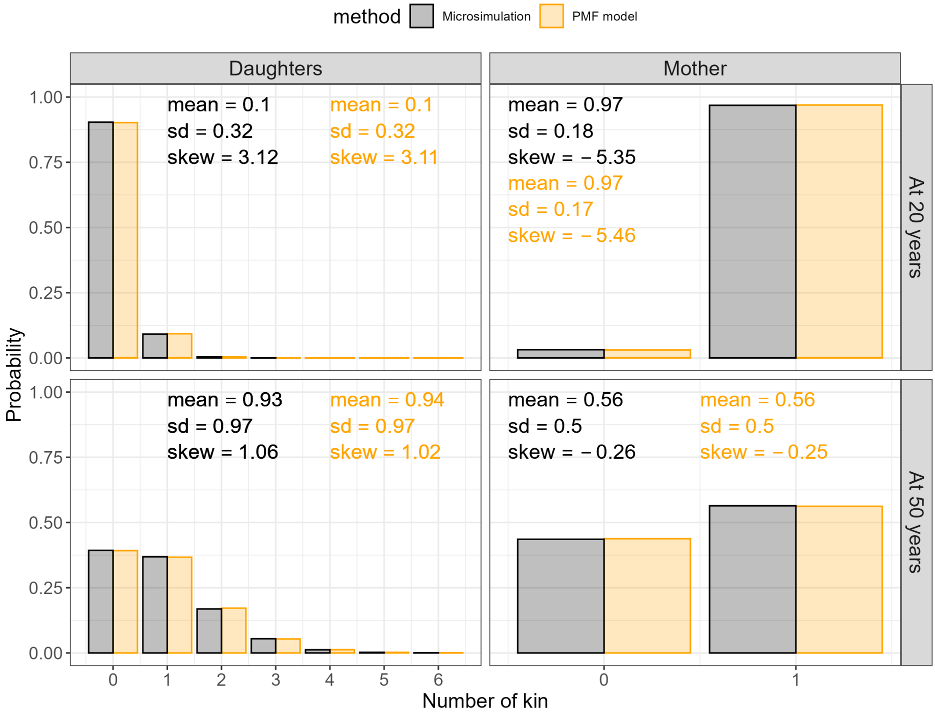
Figure A-2: Probable number of sisters over Focal's lifetime



Notes: Legend and colour compares the theoretical model to an agent-based simulation. Left: older sisters of Focal; right: younger sisters. Line type shows the probabilities that Focal has a given number of kin.

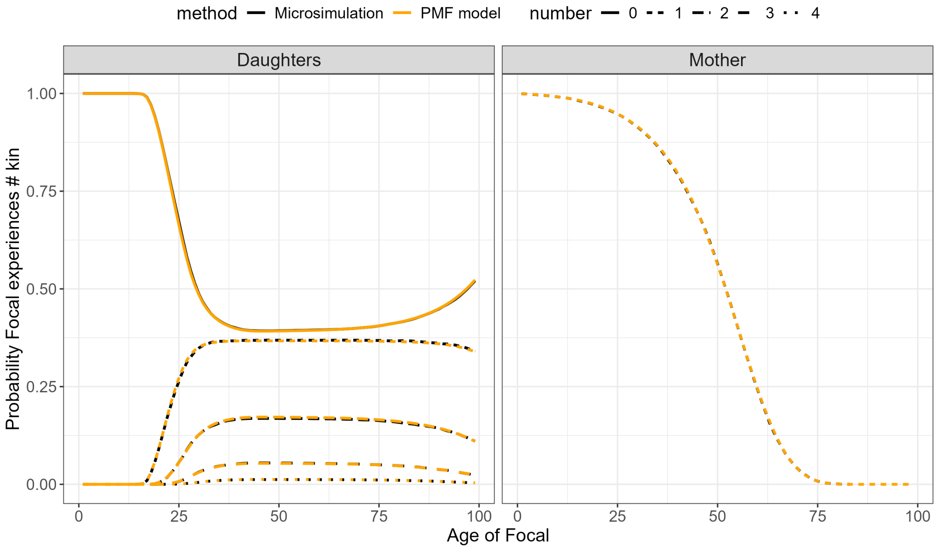
In Figure A-3 we compare our model's predicted kin-number pmf for Focal's mother and Focal's daughters (orange) to results obtained through a stochastic simulation (black). Shown are pmfs for two ages of Focal. In Figure A-4, we compare, for all ages of Focal the probability that Focal has $j = 0, 1, 2, 3, 4$ daughters and the probability that her mother is alive.

Figure A-3: Accumulated-kin pmfs for Focal’s daughters and mother when Focal is aged 20 and 50



Notes: Legend and colour compares the theoretical model to an agent-based simulation. Rows show age of Focal. Left: daughters; right: mother. Bars give the probability that Focal has a given number of kin.

Figure A-4: Probable parity of Focal (number of daughters) and the probability her mother is alive, by age of Focal



Notes: Legend and colour compares the theoretical model to an agent-based simulation. Left: Focal's daughters; right: Focal's mother. Line type compares the probabilities that Focal experiences a certain number of kin.

Appendix B: The matrix U

The matrix is column-stochastic as can be checked by observing that entries of the $j > 1$ columns obey the binomial expansion:

$$\begin{aligned} 1 &= \big[u_{s'} \dots u_s - (1 - u_{s'} \dots u_s)\big]^j = \sum_{i=0}^{j} \binom{j}{l} (1 - u_{s'} \dots u_s)^{j-l} (u_{s'} \dots u_s)^l \\ &= \underbrace{(1 - u_{s'} \dots u_s)^j}_{\left[\mathbb{U}(s's)\right]_{1,j}} + \underbrace{\binom{j}{1} (1 - u_{s'} \dots u_s)^{j-1} u_{s'} \dots u_s}_{\left[\mathbb{U}(s's)\right]_{2,j}} + \dots + \underbrace{u_{s'}^j \dots u_s^j}_{\left[\mathbb{U}(s's)\right]_{j,j}} \end{aligned} \tag{23}$$

Appendix C: Proof of Theorem 1 (and gentle reminder of convolutions)

Before providing the theorem proof we gently remind the reader how a discrete convolution operates on two distributions. The convolution measures how one distribution is augmented by another distribution. As the domain of one distribution is translated over the other, the overlap in the two distributions' domains is calculated. At each position in the translation, the sum of the element-wise products of the distribution ranges is calculated, producing the positional entry in a new distribution. In probability theory, if two independent random variables have given probability distributions, the distribution for the sum of the variables is the convolution of their distributions.

In the context of kinship, assume that there are two reproductive ages, 15 and 16. Suppose that the probability of having offspring at one age is independent of the probability of having offspring at the other age. Assume that at each age no more than two offspring can be born. Let $\boldsymbol{\psi}_{15} = (\psi_{15}(0), \psi_{15}(1), \psi_{15}(2))^{\dagger}$ and $\boldsymbol{\psi}_{16} = (\psi_{16}(0), \psi_{16}(1), \psi_{16}(2))^{\dagger}$. As $\boldsymbol{\psi_{16}}$ is translated over $\boldsymbol{\psi_{15}}$, we calculate the convolution schematically:

$$\begin{array}{ccccccc}
 & & \{\psi_{15}(0), & \psi_{15}(1), & \psi_{15}(2)\} & & \\
\{\psi_{16}(2), & \psi_{16}(1), & \textcolor{blue}{\psi_{16}(0)}\} & & & & \\
 & \{\psi_{16}(2), & \textcolor{blue}{\psi_{16}(1)}, & \textcolor{blue}{\psi_{16}(0)}\} & & & \\
 & & \{\textcolor{blue}{\psi_{16}(2)}, & \textcolor{blue}{\psi_{16}(1)}, & \textcolor{blue}{\psi_{16}(0)}\} & & \\
 & & & \{\textcolor{blue}{\psi_{16}(2)}, & \textcolor{blue}{\psi_{16}(1)}, & \psi_{16}(0)\} & \\
 & & & & \{\textcolor{blue}{\psi_{16}(2)}, & \psi_{16}(1), & \psi_{16}(0)\}.
\end{array} \tag{24}$$

Note that Equation (24) has $\boldsymbol{\psi_{15}}$ as the top row, and each subsequent row consists of $\boldsymbol{\psi_{16}}$ shifted rightwards by one element. The first entry of the resulting distribution consists of the blue entry in the second row of Equation (24) multiplied by the element of $\boldsymbol{\psi_{15}}$ that it is vertically aligned with. Similarly, the second entry consists of the sum of the product of the two blue elements in the third row of Equation (24) with the corresponding aligned elements of $\boldsymbol{\psi_{15}}$, and so on. The resulting distribution has first entry $\psi_{15}(0)\psi_{16}(0)$: the probability that no offspring are born. The second entry is $\psi_{15}(0)\psi_{16}(1) + \psi_{15}(1)\psi_{16}(0)$: the probability that exactly one offspring is born at 15 or 16. The third, fourth, and fifth entries respectively yield probabilities that there are exactly two, three, and four offspring born over the ages 15 and 16. Hence the convolution of the age-specific offspring-number distributions yields the overall offspring-number distribution over 'all possible' reproductive ages.

Proof of Theorem 1

Proof. Recall that the j-th entry of $\mathbf{k}_s(y)$ gives the probability that Focal has $j-1$ of these kin of age s when she is aged y, i.e., $k_s^{(y)}(j-1)$. Let $P_{\bar{Q}}^{a,b}$ be the probability that Focal has exactly $\bar{Q}$ kin at age y whereby kin can range between ages a and b. Suppose that the ages of kin can range only from $a = z_1$ and $b = z_2$ for example. Then

$$P_{\bar{Q}}^{1,2} = \sum_{q_1=0}^{\bar{Q}} k_{z_1}^{(y)}(q_1) k_{z_2}^{(y)}(\bar{Q}-q_1) = \big(k_{z_1}^{(y)} \star k_{z_2}^{(y)}\big)[\bar{Q}] = (\mathbf{k}_{z_1}(y) \star \mathbf{k}_{z_2}(y))_{\bar{Q}+1}. \tag{25}$$

Thus, $(\mathbf{k}_{z_1} \star \mathbf{k}_{z_2})$ is a discrete probability distribution with j-th entry the probability that Focal has exactly $j-1$ kin when aged y. If kin can be of ages z_1, z_2, z_3 then

$$\begin{aligned} P_{\bar{Q}}^{1,3} &= \sum_{q_1=0}^{Q} k_{z_1}^{(y)}(q_1) \sum_{q_2=0}^{Q} k_{z_2}^{(y)}(q_2) k_{z_3}^{(y)}(\bar{Q}-q_1-q_2) \\ &= \sum_{q_1=0}^{Q} k_{z_1}^{(y)}(q_1) \big(k_{z_2}^{(y)} \star k_{z_3}^{(y)}\big)[\bar{Q}-q_1] \\ &= \big(k_{z_1}^{(y)} \star k_{z_2}^{(y)} \star k_{z_3}^{(y)}\big)[\bar{Q}] \\ &= (\mathbf{k}_{z_1} \star \mathbf{k}_{z_2} \star \mathbf{k}_{z_3})_{\bar{Q}+1}. \end{aligned} \tag{26}$$

For any age y of Focal, the above reasoning leads us to believe that we can extend the convolutions of age-specific pmfs $\mathbf{k}_z(y)$ over all kin potential ages $z_i, i = 1, \ldots, n$ to obtain the number distribution. We use induction to show that if above holds for kin up to age z_{m-1}, then it holds for z_m (for notational ease we omit the superscript y). Suppose that the equality holds for z_1 to z_{m-1}, we see that by the induction hypothesis,

$$\begin{aligned} P_{\bar{Q}}^{1,m-1} &= \sum_{q_1=0}^{Q} k_{z_1}(q_1) \sum_{q_2=0}^{Q} k_{z_2}(q_2) \cdots \sum_{q_{m-2}=0}^{Q} k_{z_{m-2}}(q_{m-2}) k_{z_{m-1}}(\bar{Q} - \sum_{i=1}^{m-2} q_i) \\ &= \big(k_{z_1} \star k_{z_2} \star \cdots \star k_{z_{m-1}}\big)[\bar{Q}]. \end{aligned} \tag{27}$$

By shifting indices $i \to i+1$, by the induction hypothesis,

$$\begin{aligned} P_{\bar{Q}}^{2,m} &= \sum_{q_2=0}^{Q} k_{z_2}(q_2) \sum_{q_3=0}^{Q} k_{z_3}(q_3) \ \cdots \sum_{q_{m-1}=0}^{Q} k_{z_{m-1}}(q_{m-1}) k_{z_m}(\bar{Q} - \sum_{i=2}^{m-1} q_i) \\ &= \big(k_{z_2} \star k_{z_3} \star \cdots \star k_{z_m}\big)[\bar{Q}], \end{aligned} \tag{28}$$

i.e., the $\bar{Q}+1$-th entry of the distribution $\big(\mathbf{k}_{z_2} \star \cdots \star \mathbf{k}_{z_m}\big)$ gives the probability that there are $\bar{Q}$ kin over ages z_2 to z_m. The probability that there are $\bar{Q}$ kin over ages z_1 to z_m is therefore given by

$$\begin{aligned} P_{\bar{Q}}^{1,m} &= \sum_{q_1=0}^{Q} k_{z_1}(q_1) \sum_{q_2=0}^{Q} k_{z_2}(q_2) \sum_{q_3=0}^{Q} k_{z_3}(q_3) \ \ldots \\ &\quad \sum_{q_{m-1}=0}^{Q} k_{z_{m-1}}(q_{m-1}) k_{z_m}(\bar{Q} - \sum_{i=2}^{m-1} q_i - q_1) \\ &= \sum_{q_1=0}^{Q} k_{z_1}(q_1) \big(k_{z_2} \star k_{z_3} \star \cdots \star k_{z_m}\big)[\bar{Q} - q_1] \\ &= \big(k_{z_1} \star \cdots \star k_{z_m}\big)[\bar{Q}] = \big(\mathbf{k}_{z_1} \star \cdots \star \mathbf{k}_{z_m}\big)_{\bar{Q}+1}. \end{aligned}$$ □

Appendix D: Kin which descend through same-age sisters of Focal's $(q-1)$-th ancestor

Let the random variable S represent the total number of offspring of Focal's q-th ancestor at the age when she had Focal's $(q-1)$-th ancestor. Let S have distribution $\boldsymbol{\upsilon}_s$. Let the random variable representing the additional 'same-age' sisters of Focal's $(q-1)$-th ancestor be A. Then $A = S - 1$. Suppose that A has distribution $\boldsymbol{\phi}_s$.

By defining

$$\mathcal{I}_q^{\mathcal{S}} = \boldsymbol{\phi}_{b_q} \tag{29}$$

and using the operator

$$\boldsymbol{\mathcal{F}}^i_{\mathcal{S}} = \begin{cases} \mathbf{I}_{Q+1}, & \text{for } i = 1 \\ \boldsymbol{\mathcal{F}}^i_{[\beta_{q-1},\beta_{q-1}]}, & \text{for } i = 2 \\ \boldsymbol{\mathcal{F}}^i_{[\underline{n}+s_i,\bar{n}+s_i]}, & \text{for } i > 2, \end{cases} \tag{30}$$

the age-number probability distribution for kin which descend through same-age-class sisters of Focal's $(q-1)$-th ancestor and are of age $s_g \in \Sigma$ (we recover the age-specific pmf for $\Sigma = [s_g]$) can be written as

$${}^{\mathcal{S}}\mathbf{k}^{g,q}_{\Sigma}(y) = \sum_{b_1}\cdots\sum_{b_q}\rho_{b_1}\dots\rho_{b_q} \underset{s_g\in\Sigma}{\textcircled{$\star$}}\, \mathbb{U}(0,s_g) \bigcirc_{i=1}^{g} \boldsymbol{\mathcal{F}}^i_{\mathcal{S}}\big(\mathcal{I}^{\mathcal{S}}_q\big). \tag{31}$$

Notice that since $s_1 = \beta_{q-1}$, for $i = 2$, the convolution over s_1 reduces to one term,

$$\Big(\boldsymbol{\mathcal{F}}^2_{\mathcal{S}} \circ \boldsymbol{\mathcal{F}}^1_{\mathcal{S}}\Big)\big(\mathcal{I}^{\mathcal{S}}_q\big) = \sum_{b_1}\cdots\sum_{b_q}\rho_{b_1}\dots\rho_{b_q}\mathbb{F}(\beta_{q-1}-s_2)\mathbb{U}(0,\beta_{q-1}-s_2)\boldsymbol{\phi}_{b_q}, \tag{32}$$

only accounting for reproduction of Focal's q-th ancestor who belong to a group of children born at the same time as Focal's $(q-1)$-th ancestor. All subsequent convolutions over reproductive ages extend to the limits $\underline{n}$ and $\bar{n}$.

Within an age-structured demography all offspring are born into the first age class. Recall that Focal's q-th ancestor produces Focal's $(q-1)$-th ancestor at age b_q. This observed event means that the reproduction of Focal's q-th ancestor at this age, producing the additional same-age sisters of Focal's $(q-1)$-th ancestor, is not independent. We must condition on the given knowledge that one offspring is born: $v_{b_q}(S=j) = \psi_{b_q}(S=j|j>0) = (1-\delta(j))\phi_{b_q}(j)/\sum_{j\neq 0}\phi_s(j)$. Then using the fact that $S = A+1$, we have $\phi_{b_q}(A=j) = \phi_{b_q}(S-1=j) = \psi_{b_q}(S=j+1|j>0)$. Under the Poisson assumption in Section 4, we recover the so-called zero-truncated Poisson: $\phi_s(j) \to f_s^{j+1}/((\exp(-f_s)-1)(j+1)!)$.

Note that using Equation (31) we can combine the younger, older, and same-age-class lineages of Focal similar to Equation (17) in text:

$$
\begin{aligned}
&{}^{\mathcal{S}\cup\mathcal{O}\cup\mathcal{Y}}\mathbf{k}^{g,q}_{\Sigma}(y) = \\
&\sum_{b_1,\dots,b_q} \rho_{b_1}\dots\rho_{b_q} \times \Big[\underset{s_g\in\Sigma}{\circledast} \mathbb{U}(0,s_g) \overset{g}{\underset{i=1}{\bigcirc}} \boldsymbol{\mathcal{F}}^{i}_{\mathcal{S}}\big(\mathcal{I}^{\mathcal{S}}_{q}\big)\Big] \star \\
&\Big[\underset{s_g\in\Sigma}{\circledast} \mathbb{U}(0,s_g) \overset{g}{\underset{i=1}{\bigcirc}} \boldsymbol{\mathcal{F}}^{i}_{\mathcal{O}}\big(\mathcal{I}^{\mathcal{O}}_{q}\big)\Big] \star \Big[\underset{s_g\in\Sigma}{\circledast} \mathbb{U}(0,s_g) \overset{g}{\underset{i=1}{\bigcirc}} \boldsymbol{\mathcal{F}}^{i}_{\mathcal{Y}}\big(\mathcal{I}^{\mathcal{Y}}_{q}\big)\Big].
\end{aligned}
\tag{33}
$$

Appendix E: Illustration of the formulae in relation to Caswell's approach

In this section we illustrate our theoretical approach with annotation for ease of interpretation. We also relate our model to the established one of Caswell (2024) by referring to the notation used therein.

Older sisters (m) or $(g = 1, q = 1)$-kin

Using notation of the established kinship model (see Figure 1), through Equation (13) our model produces the following pmf for Focal's older sisters of age $s_1 \in \Sigma$ when Focal is aged y. Note that if $\Sigma = [s_1]$ we obtain the age-specific pmf, while if $\Sigma = [y+1, n]$ we obtain the pmf of total older sisters:

$$
\mathbf{k}^{1,1}_{\Sigma}(y) \equiv \mathbf{m}_{s_1}(y) = \sum_{b_1} \rho_{b_1} \underset{s_1\in\Sigma}{\circledast} \mathbb{U}(0,s_1)\boldsymbol{\psi}_{b_1+y-s_1}. \tag{34}
$$

Equation (34) is a function of Focal's age y and Focal's older sister's age s_1. We interpret the above by conditioning on the age of Focal's mother at each possible age at which she could have had Focal, b_1.

For each possible age we condition that mother had Focal, b_1, for Focal to experience an older sister of age s_1 when she is age y, mother must produce this kin at age $b_1 + y - s_1$. We calculate the pmf of newborns, $\boldsymbol{\psi}_{b_1+y-s_1}$. Pre-multiplication through $\mathbb{U}(0, s_1)$ calculates the pmf of the newborns who survive to be Focal's older sisters. We do this for each $s_1 \in \Sigma$, and convolve the resulting pmfs to obtain a pmf of older sisters, conditioned on b_1. Summing over b_1 with weights ρ_{b_1} yields the unconditional pmf for older sisters.

Illustration of independence

Consider the conditioning on the age of Focal's mother at birth of Focal, b_1. By fixing b_1, the random variables representing the numbers of newborn older sisters – for example, those who become ages $s_1' s_1'' \in \Sigma$ – are independent with measures uniquely defined by conditional pmfs $\boldsymbol{\psi}_{y-s_1'}, \boldsymbol{\psi}_{y-s_1''}$. As such, the sum of the age-specific kin-number random variables has distribution given by the convolution of the conditional pmfs. Applying this method for each b_1 with probability ρ_{b_1} yields the unconditional pmf for older sisters.

For example, consider $n = 1, 2, 3, 4$ age classes, that Focal is aged $y = 1$, and Focal's older sisters can be aged $s_1 = 2, 3, 4$. Suppose all age classes survive to the next with probability one. Equation (13) becomes

$$\sum_{b_1=1}^{4} \rho_{b_1} \mathop{\circledast}\limits_{s_1=2}^{4} \boldsymbol{\psi}_{b_1+y-s_1} = \\ \rho_1\big(\boldsymbol{\psi}_0 \star \boldsymbol{\psi}_{-1}\big) + \rho_2\big(\boldsymbol{\psi}_1 \star \boldsymbol{\psi}_0\big) + \rho_3\big(\boldsymbol{\psi}_2 \star \boldsymbol{\psi}_1\big) + \rho_4\big(\boldsymbol{\psi}_3 \star \boldsymbol{\psi}_2\big). \tag{35}$$

Here, the random variables for offspring number of mother aged $1, 2, 3$ are all independent and their measures convolve to yield distribution for the sum – that is, the term $\boldsymbol{\psi}_2 \star \boldsymbol{\psi}_1$ gives the distribution for the number of sisters as the sum of those born when mother was 2 and those born when she was 1.

Cousins from aunts older than mother (t) or $(g = 2, q = 2)$-kin

Appealing to Equation (13) we obtain the pmf for cousins of age $s_2 \in \Sigma$, who descend through aunts who are older than Focal's mother:

$$\mathbf{k}_{s_2}^{2,2}(y) \equiv \; \mathbf{t}_{s_2}(y) \\ = \sum_{b_1} \sum_{b_2} \rho_{b_1} \rho_{b_2} \mathop{\circledast}\limits_{s_2 \in \Sigma} \mathbb{U}(0, s_2) \mathop{\circledast}\limits_{s_1=y+b_1+1}^{\bar{n}+s_2} \mathbb{F}(s_1 - s_2)\mathbb{U}(0, s_1 - s_2)\boldsymbol{\psi}_{b_1+b_2+y-s_1}. \tag{36}$$

Equation (36) reads that cousins of Focal at age s_2 when Focal is y were produced by Focal's older aunts when Focal was $y - s_2$ and when aunt was age $s_1 - s_2$ (at least $y + b_1 + 1 - s_2$ or older).

In more detail, each term within the double summation is defined by a conditional sequence of ancestral reproductions, (b_1, b_2). For each condition, we calculate the pmf for Focal's grandmother's reproduction 'before' producing Focal's mother, $\psi_{b_1+b_2+y-s_1}$. We pre-multiply through $\mathbb{F}(s_1 - s_2)\mathbb{U}(0, s_1 - s_2)$ to obtain the total reproduction of Focal's aunts at age $s_1 - s_2$. Here Focal's aunt's possible age is constrained such that she is older than Focal's mother (i.e., $s_1 - s_2 > y - s_2 + b_1$). Reproduction of aunt results in the newborn cousins of Focal. Through $\mathbb{U}(0, s_2)$ the pmf of newborn cousins is projected to age s_2. Doing this procedure for all ages $s_2 \in \Sigma$ and convolving the measures of these independent random variables gives a total pmf for cousins, conditioned on b_1, b_2. Summing over all b_1, b_2 with probability $\rho_{b_1}\rho_{b_2}$ gives the unconditional pmf.

Illustration of independence

Following on from the example of Appendix E (Illustration of independence), we find

$$\begin{aligned}
\sum_{b_1=1}^{4}\sum_{b_2=1}^{4} \rho_{b_1}\rho_{b_2} \mathop{\circledast}_{s_2=1}^{4} \mathop{\circledast}_{s_1=2}^{4} \mathbb{F}(s_1 - s_2)\boldsymbol{\psi}_{b_1+b_2+y-s_1}& \\
&= \rho_1\rho_1 \mathop{\circledast}_{s_2=1}^{4} \big(\mathbb{F}(2-s_2)\boldsymbol{\psi}_1 \star \mathbb{F}(3-s_2)\boldsymbol{\psi}_0 \star \mathbb{F}(4-s_2)\boldsymbol{\psi}_{-1}\big) \\
&+ \rho_1\rho_2 \mathop{\circledast}_{s_2=1}^{4} \big(\mathbb{F}(2-s_2)\boldsymbol{\psi}_2 \star \mathbb{F}(3-s_2)\boldsymbol{\psi}_1 \star \mathbb{F}(4-s_2)\boldsymbol{\psi}_0\big) \\
&+ \rho_1\rho_3 \mathop{\circledast}_{s_2=1}^{4} \big(\mathbb{F}(2-s_2)\boldsymbol{\psi}_3 \star \mathbb{F}(3-s_2)\boldsymbol{\psi}_2 \star \mathbb{F}(4-s_2)\boldsymbol{\psi}_1\big) \\
&+ \rho_1\rho_4 \mathop{\circledast}_{s_2=1}^{4} \big(\mathbb{F}(2-s_2)\boldsymbol{\psi}_4 \star \mathbb{F}(3-s_2)\boldsymbol{\psi}_3 \star \mathbb{F}(4-s_2)\boldsymbol{\psi}_2\big) \\
&+ \dots.
\end{aligned} \tag{37}$$

Importantly, for each conditioning of ancestral sequence, e.g., $b_1 = 1, b_2 = 2$, then for each age of cousin $s_2 \in [1, 4]$ the random variables for age-specific kin number are independent – in this case with distribution $\mathbb{F}(2-s_2)\boldsymbol{\psi}_4$ and $\mathbb{F}(3-s_2)\boldsymbol{\psi}_3$ and $\mathbb{F}(4-s_2)\boldsymbol{\psi}_2$. Convolving over ages of cousin thus results in

$$\begin{aligned}
\rho_1\rho_2\Big\{&\mathbb{F}(1)\boldsymbol{\psi}_2 \star \mathbb{F}(2)\boldsymbol{\psi}_1 \star \mathbb{F}(3)\boldsymbol{\psi}_0 \star \mathbb{F}(0)\boldsymbol{\psi}_2 \\
&\star \mathbb{F}(1)\boldsymbol{\psi}_1 \star \mathbb{F}(2)\boldsymbol{\psi}_0 \star \mathbb{F}(-1)\boldsymbol{\psi}_2 \star \mathbb{F}(0)\boldsymbol{\psi}_1 \\
&\star \mathbb{F}(1)\boldsymbol{\psi}_0 \star \mathbb{F}(-2)\boldsymbol{\psi}_2 \star \mathbb{F}(-1)\boldsymbol{\psi}_1 \star \mathbb{F}(0)\boldsymbol{\psi}_0\Big\},
\end{aligned} \tag{38}$$

where we recall that $\mathbb{F}(s)$ is a matrix with top-row ones and zeros elsewhere and $\boldsymbol{\psi}_s$ is the unit vector with mass in the first entry $\forall s \notin [1, 2, 3]$.

Younger sisters (n) or $(q = 1, g = 1)$-kin

In relation to the established model Caswell (2019), we have from appealing to Equation (16) the pmf of younger sisters of age s_1 of Focal age y:

$$\mathbf{k}^{1,1}_{s_1}(y) \equiv \mathbf{n}_{s_1}(y) = \sum_{b_1} \rho_{b_1} \mathbb{U}(0, s_1)\mathbb{F}(b_1 + y - s_1)\mathbb{U}(b_1, b_1 + y - s_1)\mathbf{e}_2. \tag{39}$$

We condition on b_1 the age when Focal's mother has Focal in Equation (39). For each b_1, Focal's mother's number pmf is a unit vector with mass in the 1-kin-number class (mother is certainly alive when having Focal). Mother survives $y - s_1$ years (through the $\mathbb{U}$-matrix), up to age $b_1 + y - s_1$, when she produces a younger sister of Focal (through the $\mathbb{F}$-matrix). The younger sister survives from birth up to age s_1. We compute these age-specific pmfs for sisters of age $s_1 \in \Sigma$, and convolve them. This gives a conditional pmf for sisters of age in Σ. Summing over all probable ages of mother with probability ρ_{b_1} gives the unconditional pmf for such kin.

Cousins from aunts younger than Focal's mother (v) or $(q = 2, g = 1)$-kin

We have from Equation (16)

$$\begin{aligned} \mathbf{k}^{1,2}_{s_2}(y) \equiv \mathbf{v}_{s_2}(y) = \sum_{b_1}\sum_{b_2} \rho_{b_1}\rho_{b_2} \mathop{\circledast}_{s_2\in\Sigma} \mathbb{U}(0, s_2)\times \\ \left\{ \mathop{\circledast}_{s_1=\underline{n}+s_2}^{y+b_1-1} \mathbb{F}(s_1 - s_2)\mathbb{U}(0, s_1 - s_2)\mathbb{F}(y + b_1 + b_2 - s_1)\mathbb{U}(b_2, y + b_1 + b_2 - s_1)\mathbf{e}_2 \right\}. \end{aligned} \tag{40}$$

In Equation (40), each term within the double summation is defined by a conditional sequence of ancestral reproductions, (b_1, b_2). For each condition, we calculate the pmf for Focal's grandmother's reproduction 'after' producing Focal's mother, $\mathbb{F}(y + b_1 + b_2 - s_1)\mathbb{U}(b_2, y + b_1 + b_2 - s_1)\mathbf{e}_2$. We pre-multiply through $\mathbb{F}(s_1 - s_2)\mathbb{U}(0, s_1 - s_2)$ to obtain the total reproduction of Focal's aunt at age $s_1 - s_2$. Here, Focal's aunt's possible age is constrained such that she is younger than Focal's mother (i.e., $s_1 - s_2 < y - s_2 + b_1$). Reproduction of aunt results in the newborn cousins of Focal. Through $\mathbb{U}(0, s_2)$ the pmf of newborn cousins is projected to age s_2. Doing this procedure for all ages $s_2 \in \Sigma$ and convolving the measures of these independent random variables gives a total pmf for cousins, conditioned on b_1, b_2. Summing over all b_1, b_2 with probability $\rho_{b_1}\rho_{b_2}$ gives the unconditional pmf.

Daughters (a) or $(g = 1, q = 0)$-kin

At each age i of Focal's reproductive life she gives birth to a non-negative integer $j = 0, 1, \dots, Q$ of offspring with respective probabilities $\psi_i(j)$. The pmfs for daughters aged s_1 when Focal is aged y are calculated using Equation (19):

$$\mathbf{k}^{0,1}_{s_1}(y) \equiv \mathbf{a}_{s_1}(y) = \mathbb{U}(0, s_1)\boldsymbol{\psi}_{y-s_1}. \tag{41}$$

Notice that for Focal's daughter to be aged s_1 when Focal is aged y, Focal's reproductive probability mass function must have been defined when Focal was at age $y - s_1$, hence $\boldsymbol{\psi}_{y-s_1}$.

Granddaughters (b) or $(g = 2, q = 0)$-kin

We apply Equation (19) with $g = 2$ to obtain the age-specific pmf for granddaughters of age s_2 when Focal is y. The equation below demonstrates that the granddaughters of Focal currently aged s_2 are produced through Focal's daughter over all possible ages of s' when Focal was age $y - s_2$ (in the past):

$$\mathbf{k}^{2,0}_{s_2}(y) \equiv \mathbf{b}_{s_2}(y) = \mathbb{U}(0, s_2) \underset{s_1=\underline{n}+s_2}{\overset{y-s_2}{\circledast}} \mathbb{F}(s_1 - s_2)\mathbb{U}(0, s_1 - s_2)\boldsymbol{\psi}_{y-s_1}, \tag{42}$$

where $s_1 - s_2$ represents Focal's daughter's age at reproduction of Focal's granddaughter (at which time Focal was age $y - s_2$).

Mother (d) or $(g = 0, q = 1)$-kin

From Equation (20) we see that when Focal is age y, the age-specific probability distribution for a mother of age s_0 reduces to

$$\mathbf{k}^{0,1}_{s_0}(y) \equiv \mathbf{d}_{s_0}(y) = \begin{pmatrix} 1-\rho_{b_1} \\ 0 \\ 0 \\ \vdots \\ 0 \end{pmatrix} + \rho_{b_1}\mathbb{U}(b_1, s_0)\begin{pmatrix} 0 \\ 1 \\ 0 \\ \vdots \\ 0 \end{pmatrix}, \tag{43}$$

where the summation term in Equation (20) is over one element (i.e., $b_1 = s_0 - y$ by definition) because the age at which mother gives birth to Focal is uniquely defined by mother's age s_0 when Focal is y.

Grandmother (g) or $(g = 0, q = 2)$-kin

From Equation (20) we see that when Focal is age y, the age-specific probability distribution for a mother of age s_0 is given by

$$\mathbf{k}^{0,2}_{s_0}(y) \equiv \mathbf{g}_{s_0}(y) = \begin{pmatrix} 1-\mu \\ 0 \\ 0 \\ \vdots \\ 0 \end{pmatrix} + \mu \sum_{b_1+b_2=s_0-y} \mathbb{U}(b_2, s_0) \begin{pmatrix} 0 \\ 1 \\ 0 \\ \vdots \\ 0 \end{pmatrix}, \mu = \sum_{b_1+b_2=s_0-y} \rho_{b_1}\rho_{b_2}. \quad (44)$$

Note that now we are summing over possible ages at which grandmother produced mother (b_2) and mother produced Focal (b_1), which result in grandmother being age s_0 when Focal is y.