Research Article

The formal demography of kinship IV: Two-sex models and their approximations

Hal Caswell

Contents

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Hal Caswell[1]

Abstract

BACKGROUND
Previous kinship models analyze female kin through female lines of descent, neglecting male kin and male lines of descent. Because males and females differ in mortality and fertility, including both sexes in kinship models is an important unsolved problem.

OBJECTIVE
The objectives are to develop a kinship model including female and male kin through all lines of descent, to explore approximations when full sex-specific rates are unavailable, and to apply the model to several populations as an example.

METHODS
The kin of a focal individual form an age×sex-classified population and are projected as Focal ages using matrix methods, providing expected age-sex structures for every type of kin at every age of Focal. Initial conditions are based on the distribution of ages at maternity and paternity.

RESULTS
The equations for two-sex kinship dynamics are presented. As an example, the model is applied to populations with large (Senegal), medium (Haiti), and small (France) differences between female and male fertility. Results include numbers and sex ratios of kin as Focal ages. An approximation treating female and male rates as identical provides some insight into kin numbers, even when male and female rates are very different.

CONTRIBUTION
Many demographic and sociological parameters (e.g., aspects of health, bereavement, labor force participation) differ markedly between the sexes. This model permits analysis of such parameters in the context of kinship networks. The matrix formulation makes it possible to extend the two-sex analysis to include kin loss, multistate kin demography, and time varying rates.

[1] Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, PO Box 94240, 1090GE Amsterdam, The Netherlands. h.caswell@uva.nl.

1. Introduction

That men and women live and reproduce differently is a demographic truism. However, the kinship models of Caswell (2019a, 2020) and Caswell and Song (2021), following those of Goodman, Keyfitz, and Pullum (1974), and including the model of Coste et al. (2021), describe the kinship network of a female focal individual subject to female demographic rates. The result is a projection of female kin (e.g., daughters, granddaughters, . . .) through female lines of descent (e.g., granddaughters include daughters of daughters, but not daughters of sons). This paper removes this limitation and presents a complete two-sex version of the matrix analytic kinship model. The kinship network is defined relative to a focal individual, referred to as Focal. The model provides the age and sex structures of all types of kin through all lines of descent. Female and male rates generally differ, and this model makes it possible for the first time to explore the effects of these differences on the kinship network.

Differences between female and male rates are well known. Female longevity almost always exceeds male longevity. The female advantage in life expectancy, on the order of 2–10 years, has long been documented (Dublin, Lotka, and Spiegelman 1949). In a multi-country analysis Raftery, Lalic, and Gerland (2014) found the median female advantage, from 1950 to 2010, to range from 2.5 to 6 years, with some values as high as 10–12 years. Clark and Peck (2012) found life expectancy gaps of 3–8 years in the late 20th century in an analysis of 195 countries, and related the gap to factors including women's status, traditional male hazards, development, income inequality, and female representation in government. Glei and Horiuchi (2007), analyzing 29 high income countries, found the gap affected by changes not only in the levels but also in the age patterns of male and female mortality. The gaps in life expectancy are also reflected in differences between women and men in healthy longevity and the proportion of life spent in poor health (Luy and Minagawa 2014; Oksuzyan et al. 2014).

Male and female fertility can also differ substantially. The most obvious difference is that men can reproduce at much later ages than women (Kühnert and Nieschlag 2004; Bribiescas 2016; Paget and Timaeus 1994). This difference has been used to great effect by Tuljapurkar, Puleston, and Gurven (2007) as a compelling explanation for the evolution of post-reproductive survival in human females. They showed that extended male fertility will favor extended male lifetime and that, when expressed in females, such genes will lead to extended female lifetime even though female reproduction ends at menopause.

In addition to differences in timing, the levels of male and female reproduction often differ.[2] In a valuable recent review, Schoumaker (2019) analyzes male and female fertility, ages at maternity and paternity, and trends in these quantities, for 160 countries, and

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[2] An extreme case is that of Moulay Ismael the Bloodthirsty, the Emperor of Morocco (1672–1727), who is reported to have sired 888 children. A recent analysis by Oberzaucher and Grammer (2014) has concluded that it is indeed possible to that he could have done so.

provides an extensive source of data in the online appendices to the article. He reports that male TFR (total fertility rate) almost always exceeds female TFR, by an amount that increases with female TFR. Thus as a population goes through the demographic transition, female and male fertility become more similar. The mean age at paternity (the mean age of childbearing for men) is always greater than the mean age at maternity (mean age of childbearing for women), by five to fifteen years. Schoumaker presents the age-specific fertility rates for men and women in Senegal, Haiti, and France (his Figure 4; these will be used below in Section 4), as typical results for high, medium, and low fertility populations and explores the roles of overall fertility, economics, and polygyny in determining these patterns.

Incorporating the demographic rates of both sexes makes it possible to explore the consequences of such differences between female and male rates. In particular, questions about the sex composition of various kinds of kin, as a function of the age of Focal, can be addressed in this new framework. It is known that differential mortality leads to a female-skewed population structure among the elderly (e.g., 10.8 females per male among supercentenarians; Robine and Vaupel 2001). We can ask how this skew will differ among the various kinds of kin,

The attentive reader is no doubt aware that complete sets of male and female rates are not exactly common, which is true. With this in mind, the model presented here accepts any level of sex-specificity in the data: (a) age-specific mortality and fertility schedules for both women and men, (b) sex-specificity in only mortality or only fertility, or (c) no sex-specific data at all, treating the sexes as identical. The last option does away with all the interesting effects of the differences between women and men, but still allows an approximate accounting for the numbers of male and female kin through male and female lines of descent. Section 5 evaluates the adequacy of this approximation.

The model presented here is linear. In principle, two-sex fertility rates in sexually reproducing species must depend on the relative abundance of males and females. This leads to frequency-dependent nonlinearities embodied in a marriage or mating function (e.g., Keyfitz 1972; Iannelli, Martcheva, and Milner 2005; Shyu and Caswell 2018). However, this effect would operate not within a particular type of kin, but in the population as a whole, which would require an additional model, not considered here. This model, as with most demographic analyses, is conditional on the hypothesis that male and female fertility schedules remain in effect throughout the calculation. The incorporation of a fully nonlinear two-sex model remains an open research problem.

1.1 Notation and terminology

Matrices are denoted by upper case bold characters (e.g., $\mathbf{U}$) and vectors by lower case bold characters (e.g., $\mathbf{a}$). Female and male rates are distinguished by subscripts (e.g., $\mathbf{U}_\mathrm{f}$

and $\mathbf{U}_{\mathrm{m}}$). Vectors are column vectors by default; $\mathbf{x}^{\mathsf{T}}$ is the transpose of $\mathbf{x}$. The ith unit vector (a vector with a 1 in the ith location and zeros elsewhere) is $\mathbf{e}_i$. The vector $\mathbf{1}$ is a vector of ones, and the matrix $\mathbf{I}$ is the identity matrix. When necessary, subscripts are used to denote the size of a vector or matrix; e.g., $\mathbf{I}_\omega$ is an identity matrix of size $\omega \times \omega$. Matrices and vectors with a tilde (e.g., $\tilde{\mathbf{U}}$ or $\tilde{\mathbf{a}}$) are block-structured, containing blocks for females and males.

The symbol $\circ$ denotes the Hadamard, or element-by-element product (implemented by .* in MATLAB and by * in R). The symbol $\otimes$ denotes the Kronecker product. The vec operator stacks the columns of a $m \times n$ matrix into a $mn \times 1$ column vector. The notation $\|\mathbf{x}\|$ denotes the 1-norm of $\mathbf{x}$. On occasion, MATLAB notation will be used to refer to rows and columns; e.g., $\mathbf{F}(i,:)$ and $\mathbf{F}(:,j)$ refer to the ith row and jth column of the matrix $\mathbf{F}$.

1.2 The basic one-sex kinship model

The one sex (female) kinship network, as shown in Figure 1, consists of descendants of Focal (daughters, granddaughters, etc.), ancestors of Focal (mothers, grandmothers, etc.), and descendants of ancestors (sisters, aunts, cousins, etc.). Each kin type is identified by a letter; these become variables in the model.

Let $\mathbf{k}(x)$ denote the age structure vector of some kin type at age x of Focal. The dynamics are given by

$$\mathbf{k}(x+1) \;=\; \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x) \tag{1}$$
$$\mathbf{k}(0) \;=\; \mathbf{k}_0. \tag{2}$$

Here, $\mathbf{U}$ is a survival matrix, with age-specific survival probabilities on the subdiagonal and zeros elsewhere; $\boldsymbol{\beta}(x)$ is the recruitment of kin of type $\mathbf{k}$. Because kin do not reproduce themselves (e.g., the reproduction of children produces grandchildren) the population of one type of kin is said to be subsidized by the fertility of some other kin type. In some cases, the subsidy is zero (e.g., Focal can gain no new older sisters after her birth). Thus

$$\boldsymbol{\beta}(x) = \begin{cases} \mathbf{F}\mathbf{k}^*(x) & \text{reproduction by } \mathbf{k}^* \\ \mathbf{0} & \text{no recruitment} \end{cases} \tag{3}$$

where $\mathbf{F}$ is a matrix with age-specific fertility in the first row and zeros elsewhere. See Caswell (2019a, 2020) for a full discussion. In the one sex version of the model, fertility is measured in units of daughters per female.

Figure 1: **The kinship network surrounding the Focal individual. Symbols (a, b, etc.) denote the age structure vectors of each type of kin of Focal. Modified from Caswell (2019a) based on network defined in Goodman, Keyfitz, and Pullum (1974) and Keyfitz and Caswell (2005).**
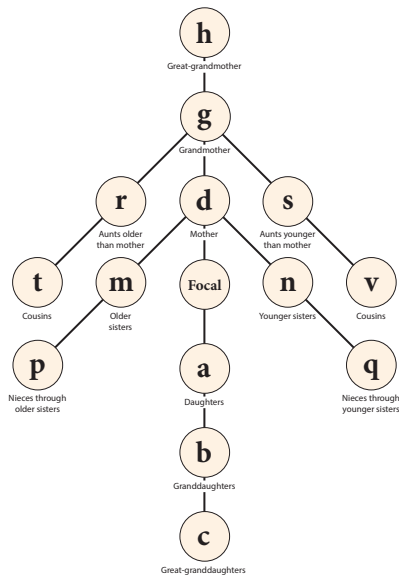
2. Principles of the two-sex kinship model

Before presenting the complete derivation (Section 3), it is helpful to consider the principles along which the two-sex model is organized. Each kin type contains a set of subtypes defined by sex and line of descent. These will be compressed, under a reasonable set of assumptions, to individuals classified by age and sex.

We begin by specifying notation. Define

$$
\begin{aligned}
\mathbf{U}_{\mathrm{f}}, \ \mathbf{U}_{\mathrm{m}} &= \text{female and male survival matrices} & (4)\\
\mathbf{F}_{\mathrm{f}}. \ \mathbf{F}_{\mathrm{m}} &= \text{female and male fertility matrices} & (5)\\
\boldsymbol{\pi}_{\mathrm{f}}, \ \boldsymbol{\pi}_{\mathrm{m}} &= \text{distribution of ages at maternity and paternity} & (6)\\
\alpha &= \text{proportion males among offspring} & (7)\\
\bar{\alpha} &= 1 - \alpha & (8)
\end{aligned}
$$

The survival matrices contain age-specific survival probabilities on the subdiagonal and zeros elsewhere. Fertility matrices contain age-specific fertility rates on the first row and zeros elsewhere. Fertility includes both female and male children of female and male parents. The proportion of males at birth is set to $\alpha = 0.5$ here, but it could be otherwise. The distributions $\boldsymbol{\pi}_{\mathrm{f}}$ and $\boldsymbol{\pi}_{\mathrm{m}}$ are defined below in Section 3.1.

2.1 Descendants of Focal

Figure 2 shows three implementations of the descendants of Focal. In Figure 2(a), Focal produces two types of children: daughters and sons. These give rise to four types of grandchildren: daughters of daughters, daughters of sons, sons of daughters, and sons of sons. This chain of descendants extends naturally to eight types of great-grandchildren, and so on.

The vectors $\mathbf{a}_1', \mathbf{a}_2', \mathbf{b}_1', \ldots, \mathbf{b}_4'$ are the age structure vectors of children and grand-children. My convention is to number females $(1, 3, 5, \ldots)$ first and males $(2, 4, 6, \ldots)$ second. The primes appearing in Figure 2(a) indicate that those vectors are specific to both sex and line of descent. We will eliminate the primes shortly by combining lines of descent.

Figure 2: **Reproduction in the two-sex model. (a) Female and male children (a_1' and a_2') and grandchildren ($b_1', \ldots, b_4'$) of Focal. The primes indicate that kin are defined by sex and line of descent. (b) Female and male children, grandchildren, and great-grandchildren of Focal, obtained from (a) by combining kin regardless of line of descent. (c) The female and male kin in (b), combined into the block-structured vectors $\tilde{a}$, $\tilde{b}$, and $\tilde{c}$.**

(a)

(b)   **(c)**
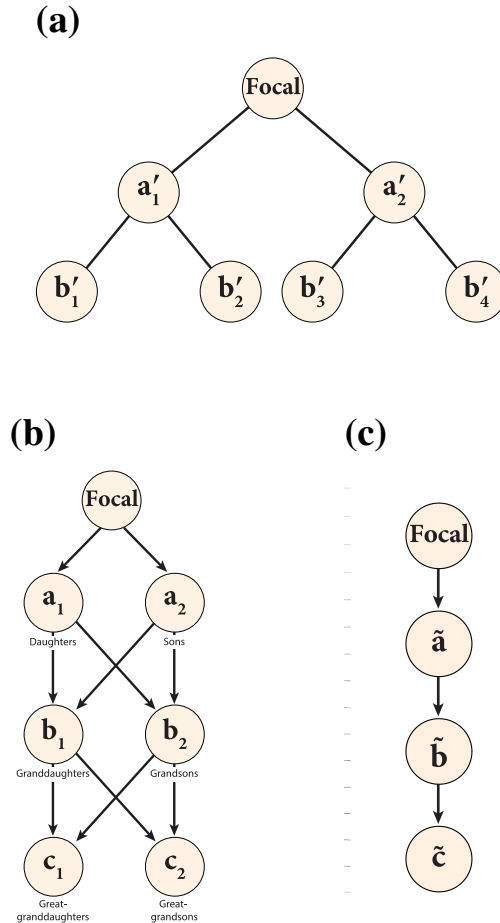
For the case of the children in Figure 2(a), we write

$$\begin{pmatrix} \mathbf{a}_1' \\ \mathbf{a}_2' \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_{\mathrm{f}} & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \mathbf{a}_1' \\ \mathbf{a}_2' \end{pmatrix}(x) + \begin{pmatrix} \bar{\alpha}\mathbf{F}_{\mathrm{f}} & \bar{\alpha}\mathbf{F}_{\mathrm{m}} \\ \alpha\mathbf{F}_{\mathrm{f}} & \alpha\mathbf{F}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \boldsymbol{\phi}_{\mathrm{f}} \\ \boldsymbol{\phi}_{\mathrm{m}} \end{pmatrix}(x) \quad (9)$$

Daughters and sons survive according to the matrices $\mathbf{U}_{\mathrm{f}}$ and $\mathbf{U}_{\mathrm{m}}$. New children are produced by the fertility of Focal. If Focal is a female, then $\boldsymbol{\phi}_{\mathrm{f}}(x) = \mathbf{e}_x$, where $\mathbf{e}_x$ is a unit vector of length ω, and $\boldsymbol{\phi}_{\mathrm{m}}(x) = \mathbf{0}$. If Focal is male, then these vectors are reversed.

The dynamics of grandchildren must account for all four types of grandchildren shown in Figure 2(a):

$$\begin{pmatrix} \mathbf{b}_1' \\ \mathbf{b}_2' \\ \mathbf{b}_3' \\ \mathbf{b}_4' \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_1 & & & \\ & \mathbf{U}_2 & & \\ & & \mathbf{U}_3 & \\ & & & \mathbf{U}_4 \end{pmatrix} \begin{pmatrix} \mathbf{b}_1' \\ \mathbf{b}_2' \\ \mathbf{b}_3' \\ \mathbf{b}_4' \end{pmatrix}(x) + \begin{pmatrix} \bar{\alpha}\mathbf{F}_{\mathrm{f}} & \mathbf{0} \\ \alpha\mathbf{F}_{\mathrm{f}} & \mathbf{0} \\ \mathbf{0} & \bar{\alpha}\mathbf{F}_{\mathrm{m}} \\ \mathbf{0} & \alpha\mathbf{F}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \mathbf{a}_1' \\ \mathbf{a}_2' \end{pmatrix}(x) \quad (10)$$

Equation (10) permits each of the four types of grandchildren to experience its own survival schedule, and each of the two types of children to contribute according to its own fertility schedule. The corresponding model for great-grandchildren would include eight survival matrices, $\mathbf{U}_1, \ldots, \mathbf{U}_8$ and four fertility matrices $\mathbf{F}_1, \ldots, \mathbf{F}_4$. And so on.

We now make the usual assumption that the demographic rates may be affected by sex but not by line of descent from an arbitrarily defined Focal individual. Then

$$\mathbf{U}_1 = \mathbf{U}_3 = \mathbf{U}_{\mathrm{f}} \tag{11}$$

$$\mathbf{U}_2 = \mathbf{U}_4 = \mathbf{U}_{\mathrm{m}} \tag{12}$$

Under this assumption, the four types of grandchildren can be aggregated into granddaughters and grandsons, ignoring their lines of descent from Focal. Define

$$\mathbf{b}_1 = \mathbf{b}_1' + \mathbf{b}_3' \quad \text{(granddaughters)} \tag{13}$$

$$\mathbf{b}_2 = \mathbf{b}_2' + \mathbf{b}_4' \quad \text{(grandsons).} \tag{14}$$

The dynamics then become

$$\begin{pmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_{\mathrm{f}} & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{pmatrix}(x) + \begin{pmatrix} \bar{\alpha}\mathbf{F}_{\mathrm{f}} & \bar{\alpha}\mathbf{F}_{\mathrm{m}} \\ \alpha\mathbf{F}_{\mathrm{f}} & \alpha\mathbf{F}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{pmatrix}(x) \quad (15)$$

This continues for subsequent generations of descendants, leading to the pattern shown in Figure 2(b), in which female and male children, female and male grandchildren, and so on are produced by the female and male survival and fertility matrices.

A final notational simplification follows from writing the vectors containing female and male age distributions as block-structured vectors

$$\begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{pmatrix} = \tilde{\mathbf{a}} \qquad \begin{pmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{pmatrix} = \tilde{\mathbf{b}}. \tag{16}$$

If appropriate block-structured matrices are defined, Figure 2(b) reduces to Figure 2(c) and equations (9) and (15) simplify to the projections of a single vector. Section 3 develops the entire kinship model in these terms.

2.2 Accounting for ancestors

Focal has a network of female and male ancestors, as shown in Figure 3. She has two parents (mothers $\mathbf{d}_1'$ and fathers $\mathbf{d}_2'$), four grandparents (maternal $\mathbf{g}_1'$ and $\mathbf{g}_2'$; paternal $\mathbf{g}_3'$ and $\mathbf{g}_4'$). The pattern continues for as many levels as desired, the number of types of ancestors doubling with each level.

Figure 3: **Accounting for the parents ($\mathbf{d}_1'$ and $\mathbf{d}_2'$) and grandparents ($\mathbf{g}_1', \ldots, \mathbf{g}_4'$) of Focal. Symbols represent age structure vectors; primes indicate that individuals are characterized by both sex and chains of ancestry.**
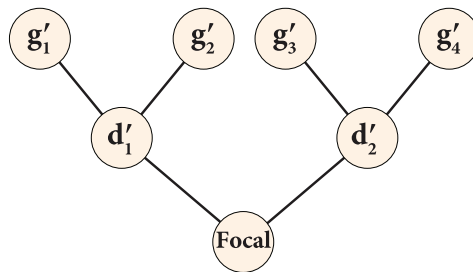
Consider the grandparents. Their dynamics satisfy

$$
\begin{pmatrix} \mathbf{g}_1' \\ \mathbf{g}_2' \\ \mathbf{g}_3' \\ \mathbf{g}_4' \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_1 & & & \\ & \mathbf{U}_2 & & \\ & & \mathbf{U}_3 & \\ & & & \mathbf{U}_4 \end{pmatrix} \begin{pmatrix} \mathbf{g}_1' \\ \mathbf{g}_2' \\ \mathbf{g}_3' \\ \mathbf{g}_4' \end{pmatrix}(x) + \mathbf{0} \qquad (17)
$$

where the recruitment term is zero because Focal accumulates no new biological ancestors after her birth. Combining the maternal and paternal grandparents of each sex yields

$$
\begin{pmatrix} \mathbf{g}_1 \\ \mathbf{g}_2 \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_\mathrm{f} & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_\mathrm{m} \end{pmatrix} \begin{pmatrix} \mathbf{g}_1 \\ \mathbf{g}_2 \end{pmatrix}(x) + \mathbf{0}. \qquad (18)
$$

2.3 Reproduction by ancestors

The reproduction of the ancestors of Focal produces the side chains in Figure 1. In the two-sex model, reproduction must account for the lack of independence of pairs of ancestors. Consider Focal's daughters and sons. They can be assumed to reproduce independently to produce grandchildren, and are treated so in Figure 2(b) and equation (15). But Focal's mother and father do not reproduce independently to produce her siblings. Therefore, as shown in Figure 4, we credit the reproduction of Focal's parents to her mother, following the female fertility schedule (a kind of female dominance assumption). This gives

$$
\begin{pmatrix} \mathbf{m}_1 \\ \mathbf{m}_2 \end{pmatrix}(x+1) = \begin{pmatrix} \mathbf{U}_\mathrm{f} & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_\mathrm{m} \end{pmatrix} \begin{pmatrix} \mathbf{m}_1 \\ \mathbf{m}_2 \end{pmatrix}(x) + \begin{pmatrix} \bar{\alpha}\mathbf{F}_\mathrm{f} & \mathbf{0} \\ \alpha\mathbf{F}_\mathrm{m} & \mathbf{0} \end{pmatrix} \begin{pmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \end{pmatrix}(x) \qquad (19)
$$

Notice the difference between the block-structured fertility matrices in (19) and (15).

3. The two-sex kinship model

This section derives the dynamics of each type of kin. For some type $\mathbf{k}$ of kin, we write

$$
\tilde{\mathbf{k}}(x) = \begin{pmatrix} \mathbf{k}_\mathrm{f} \\ \mathbf{k}_\mathrm{m} \end{pmatrix}(x) \qquad (20)
$$

Figure 4: **An example of reproduction by ancestors (parents, in this case) of Focal. All reproduction by Focal's parents, producing older and younger sisters and brothers, is attributed to Focal's mother.**
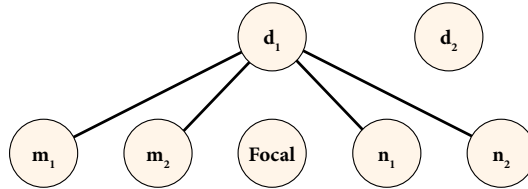
where x is the age of Focal. The tilde denotes block structured vectors and matrices composed of female and male parts. Define the block-structured matrices

$$\tilde{\mathbf{U}} = \left(\begin{array}{cc} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_m \end{array} \right) \qquad \tilde{\mathbf{F}} = \left(\begin{array}{cc} \bar{\alpha}\mathbf{F}_f & \bar{\alpha}\mathbf{F}_m \\ \alpha\mathbf{F}_f & \bar{\alpha}\mathbf{F}_m \end{array} \right) \qquad \tilde{\mathbf{F}}^* = \left(\begin{array}{cc} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{array} \right) \qquad (21)$$

The dynamics of $\tilde{\mathbf{k}}(x)$ are

$$\left(\begin{array}{c} \mathbf{k}_f \\ \mathbf{k}_m \end{array} \right)(x+1) = \left(\begin{array}{cc} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_m \end{array} \right) \left(\begin{array}{c} \mathbf{k}_f \\ \mathbf{k}_m \end{array} \right)(x) + \left(\begin{array}{c} \boldsymbol{\beta}_f \\ \boldsymbol{\beta}_m \end{array} \right)(x) \qquad (22)$$

$$\tilde{\mathbf{k}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{k}}(x) + \tilde{\boldsymbol{\beta}}(x). \qquad (23)$$

The recruitment subsidy term $\tilde{\boldsymbol{\beta}}(x)$ depends on the nature of the kin that provide the recruitment.

1. If the subsidy is provided by reproduction of one of the direct ancestors of Focal (parents, grandparents, etc.), then, as in equation (19)

$$\left(\begin{array}{c} \boldsymbol{\beta}_f \\ \boldsymbol{\beta}_m \end{array} \right)(x) = \left(\begin{array}{cc} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{array} \right) \left(\begin{array}{c} \mathbf{k}^*_{\ f} \\ \mathbf{k}^*_{\ m} \end{array} \right)(x) \qquad (24)$$

$$\tilde{\boldsymbol{\beta}}(x) = \tilde{\mathbf{F}}^*\tilde{\mathbf{k}}(x) \qquad (25)$$

where $\mathbf{k}^*$ denotes the source kin. The matrix $\tilde{\mathbf{F}}^*$ includes reproduction of both female and male offspring by females.

2. If the subsidy is provided by any other kin type, then as in equation (15)

$$
\begin{pmatrix} \boldsymbol{\beta}_{\mathrm{f}} \\ \boldsymbol{\beta}_{\mathrm{m}} \end{pmatrix}(x) = \begin{pmatrix} \bar{\alpha}\mathbf{F}_{\mathrm{f}} & \bar{\alpha}\mathbf{F}_{\mathrm{m}} \\ \alpha\mathbf{F}_{\mathrm{f}} & \bar{\alpha}\mathbf{F}_{\mathrm{m}} \end{pmatrix} \begin{pmatrix} \mathbf{k}^{*}_{\mathrm{f}} \\ \mathbf{k}^{*}_{\mathrm{m}} \end{pmatrix}(x) \tag{26}
$$

$$
\tilde{\boldsymbol{\beta}}(x) = \tilde{\mathbf{F}}\tilde{\mathbf{k}}(x) \tag{27}
$$

where $\mathbf{k}^{*}$ again denotes the source kin.

3. If there is no recruitment subsidy, as in (18), then $\tilde{\boldsymbol{\beta}} = \mathbf{0}$.

3.1 Ages at maternity and paternity

The matrices $\mathbf{F}_{\mathrm{f}}$ and $\mathbf{F}_{\mathrm{m}}$ contain age-specific fertilities for females and males respectively. The distributions of the ages of mothers and of fathers are obtained by applying these per capita rates to age distributions of women and men, respectively. Let

$$
\tilde{\mathbf{z}} = \begin{pmatrix} \mathbf{z}_{\mathrm{f}} \\ \mathbf{z}_{\mathrm{m}} \end{pmatrix} \tag{28}
$$

be the age structure of the population. The age distributions of maternity and paternity are

$$
\boldsymbol{\pi}_{\mathrm{f}} = \frac{\mathbf{F}_{\mathrm{f}}(1,:)^{\mathsf{T}} \circ \mathbf{z}_{\mathrm{f}}}{\|\mathbf{F}_{\mathrm{f}}(1,:)^{\mathsf{T}} \circ \mathbf{z}_{\mathrm{f}}\|} \tag{29}
$$

$$
\boldsymbol{\pi}_{\mathrm{m}} = \frac{\mathbf{F}_{\mathrm{m}}(1,:)^{\mathsf{T}} \circ \mathbf{z}_{\mathrm{m}}}{\|\mathbf{F}_{\mathrm{m}}(1,:)^{\mathsf{T}} \circ \mathbf{z}_{\mathrm{m}}\|} \tag{30}
$$

and we write

$$
\tilde{\boldsymbol{\pi}} = \begin{pmatrix} \boldsymbol{\pi}_{\mathrm{f}} \\ \boldsymbol{\pi}_{\mathrm{m}} \end{pmatrix}. \tag{31}
$$

The age structure $\tilde{\mathbf{z}}$ could be obtained from projection of a previous population (Caswell and Song 2021) or from an observed population structure. Here, following Goodman, Keyfitz, and Pullum 1974; Caswell 2019a, 2020, we use the stable population defined by the demographic rates in $\tilde{\mathbf{U}}$ and $\tilde{\mathbf{F}}$. Define a projection matrix for the female dominant

population

$$\tilde{\mathbf{A}} = \left(\begin{array}{cc} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_m \end{array} \right) + \left(\begin{array}{cc} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{array} \right). \tag{32}$$

The stable sex-age structure is given by the eigenvector $\tilde{\mathbf{w}}$ corresponding to the dominant eigenvalue of $\tilde{\mathbf{A}}$. Without loss of generality, we scale $\tilde{\mathbf{w}}$ so that its entries are non-negative, write

$$\tilde{\mathbf{w}} = \left(\begin{array}{c} \mathbf{w}_f \\ \mathbf{w}_m \end{array} \right) \tag{33}$$

and substitute $\tilde{\mathbf{w}}$ for $\tilde{\mathbf{z}}$ in (28). Notice the use of $\tilde{\mathbf{F}}^*$ rather than $\tilde{\mathbf{F}}$; this corresponds to the usual female dominance assumption in stable population theory.

3.2 Dynamics of each type of kin

We turn now to the model for each type of kin. These models are summarized in Table 1, in terms of the initial population, the distribution of ages at maternity and paternity, and survival and fertility.

3.2.1 Focal

Focal is an individual of specified sex, alive at age x. The state of Focal is given by the vector

$$\tilde{\phi}(x) = \left(\begin{array}{c} \phi_f \\ \phi_m \end{array} \right) (x) \tag{34}$$

This can be extended to cases where Focal is classified by stage as well as age, following the methods in Caswell (2020).

3.2.2 Children and descendants of Focal

The dynamics of the children of focal are given by

$$\begin{aligned} \tilde{\mathbf{a}}(x+1) &= \tilde{\mathbf{U}}\tilde{\mathbf{a}}(x) + \tilde{\mathbf{F}}\tilde{\phi}(x) \tag{35} \\ \tilde{\mathbf{a}}(0) &= \mathbf{0} \tag{36} \end{aligned}$$

The dynamics of the grandchildren of focal are given by

$$\tilde{\mathbf{b}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{b}}(x) + \tilde{\mathbf{F}}\tilde{\mathbf{a}}(x) \tag{37}$$
$$\tilde{\mathbf{b}}(0) = \mathbf{0} \tag{38}$$

The dynamics of the great-grandchildren of focal are given by

$$\tilde{\mathbf{c}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{c}}(x) + \tilde{\mathbf{F}}\tilde{\mathbf{b}}(x) \tag{39}$$
$$\tilde{\mathbf{c}}(0) = \mathbf{0} \tag{40}$$

In each case, the initial condition is zero (Focal has no children, grandchildren, etc. when she is born). The recruitment of each generation of descendants comes from the fertility of the previous generation.

The chain of descendants can be extended as far as desired. To do so, let $\tilde{\mathbf{k}}_i(x)$ be the state vector of the ith generation of descendants, with Focal defined as generation 0. Then

$$\tilde{\mathbf{k}}_i(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{k}}_i(x) + \tilde{\mathbf{F}}\tilde{\mathbf{k}}_{i-1}(x) \qquad i = 1, \dots \tag{41}$$
$$\tilde{\mathbf{k}}_i(0) = \mathbf{0} \tag{42}$$

3.2.3 Parents and ancestors of Focal

Counting the ancestors (parents, grandparents, etc.) of Focal involves going up the branching network shown in Figure 3. We know that, at birth, Focal had exactly one living mother. We will assume that she also has one living father, thus ignoring paternal mortality in the nine months between conception and birth.

The ages of Focal's parents at her birth are unknown, so we treat her mother and father as being selected at random from the distributions $\boldsymbol{\pi}_{\mathrm{f}}$ and $\boldsymbol{\pi}_{\mathrm{m}}$ of the ages of mothers and fathers at the birth of children. Under these assumptions, the dynamics of the parents of Focal are given by

$$\tilde{\mathbf{d}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{d}}(x) + \mathbf{0} \tag{43}$$
$$\tilde{\mathbf{d}}(0) = \tilde{\boldsymbol{\pi}} \tag{44}$$

Focal accumulates no new parents after her birth, so the recruitment term is zero.

The dynamics of the grandparents of Focal are given by

$$\tilde{\mathbf{g}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{g}}(x) + \mathbf{0} \tag{45}$$

$$\tilde{\mathbf{g}}(0) = \sum_i \left[\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)\right] \tilde{\mathbf{d}}(i) \tag{46}$$

The initial condition $\tilde{\mathbf{g}}(0)$ is obtained by noting that the grandparents of Focal are the parents of Focal's parents. Thus we could write

$$\tilde{\mathbf{g}}(0) = \left(\begin{array}{c} \text{mothers of mom} \\ \text{fathers of mom} \end{array}\right)(0) + \left(\begin{array}{c} \text{mothers of dad} \\ \text{fathers of dad} \end{array}\right)(0) \tag{47}$$

We do not know the ages of Focal's mother or father, but we know their distributions, so

$$\tilde{\mathbf{g}}(0) = \left(\begin{array}{c} \sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\mathbf{d}_{\mathrm{f}}(i) \\ \sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\mathbf{d}_{\mathrm{m}}(i) \end{array}\right) + \left(\begin{array}{c} \sum_i \boldsymbol{\pi}_{\mathrm{m}}(i)\mathbf{d}_{\mathrm{f}}(i) \\ \sum_i \boldsymbol{\pi}_{\mathrm{m}}(i)\mathbf{d}_{\mathrm{m}}(i) \end{array}\right) \tag{48}$$

$$= \sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\tilde{\mathbf{d}}(i) + \sum_i \boldsymbol{\pi}_{\mathrm{m}}(i)\tilde{\mathbf{d}}(i) \tag{49}$$

$$= \sum_i \left[\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)\right] \tilde{\mathbf{d}}(i) \tag{50}$$

The dynamics of the great-grandparents of Focal follow the same pattern. The great-grandparents of Focal at her birth are the grandparents of Focal's parents, so

$$\tilde{\mathbf{h}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{h}}(x) + \mathbf{0} \tag{51}$$

$$\tilde{\mathbf{h}}(0) = \sum_i \left[\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)\right] \tilde{\mathbf{g}}(i) \tag{52}$$

As with descendants, the ancestors can be calculated back as far as desired. For this calculation, let $\tilde{\mathbf{k}}_j$ be the kin vector of the jth generation of ancestors, where parents are generation zero. Then, for $j \geq 1$,

$$\tilde{\mathbf{k}}_j(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{k}}_j(x) + \mathbf{0} \tag{53}$$

$$\tilde{\mathbf{k}}_j(0) = \sum_i \left[\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)\right] \tilde{\mathbf{k}}_{i-1}(j) \tag{54}$$

3.2.4 Siblings, nieces, and nephews of Focal

We turn next to the siblings, nieces, and nephews of Focal.

Siblings. The older and younger siblings of Focal are treated separately because they have different dynamics.

It is possible for Focal to be born with older siblings, but she can accumulate no more of them after she is born, so the recruitment term is zero. Older siblings at Focal's birth are the children of Focal's mother at Focal's birth. Focal's mother and father do not reproduce independently, so the initial condition is credited to Focal's mother and calculated as an average over $\boldsymbol{\pi}_\mathrm{f}$ only. Thus

$$\tilde{\mathbf{m}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{m}}(x) + \mathbf{0} \tag{55}$$

$$\tilde{\mathbf{m}}(0) = \sum_i \boldsymbol{\pi}_\mathrm{f}(i)\tilde{\mathbf{a}}(i) \tag{56}$$

Focal can have no younger siblings at her birth,[3] but can accumulate younger siblings through her mother's reproduction. Thus

$$\tilde{\mathbf{n}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{n}}(x) + \tilde{\mathbf{F}}^* \, \tilde{\mathbf{d}}(x) \tag{57}$$

$$\tilde{\mathbf{m}}(0) = \mathbf{0} \tag{58}$$

The matrix $\tilde{\mathbf{F}}^*$ ensures that the recruitment of new younger siblings comes from the reproduction of Focal's mother following the female fertility schedule, as in Figure 4.

Nieces and nephews. Then nieces and nephews of Focal are the children of Focal's older and younger siblings.[4]

The recruitment of nieces and nephews through older siblings comes from the reproduction of those siblings, with the brothers and sisters of Focal contributing independently. The initial condition follows from the fact that, at the time of Focal's birth, these nieces and nephews are the grandchildren of Focal's mother. Thus, the dynamics of nieces

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[3] A slight modification of the initial conditions for older and younger siblings can account for the possibility of multiple births.

[4] English seems to have no gender-inclusive collective term for nieces and nephews, as in 'children' as a collective for daughters and sons, 'parent' for mothers and fathers, and 'sibling' for brothers and sisters. The term 'nibling' has been suggested, according to the internet. German has such a term, 'Geschwisterkind,' meaning child of a sibling. There also seems to be no gender-inclusive collective term for aunts and uncles.

and nephews through older siblings are

$$\tilde{\mathbf{p}}(x+1) \;=\; \tilde{\mathbf{U}}\tilde{\mathbf{p}}(x) + \tilde{\mathbf{F}}\,\tilde{\mathbf{m}}(x) \tag{59}$$

$$\tilde{\mathbf{p}}(0) \;=\; \sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\tilde{\mathbf{b}}(i) \tag{60}$$

This line of descent can be continued indefinitely. Each generation receives its recruitment from the generation before (grand-nieces and grand-nephews from nieces and nephews, etc.). The initial condition for each generation is the corresponding descendant of Focal's mother: nieces and nephews are the grandchildren of Focal's mother; grand-nieces and grand-nephews are the great-grandchildren, and so on.

The recruitment of nieces and nephews through younger siblings of Focal comes from the reproduction of those younger siblings. The initial condition is zero, because Focal has no younger siblings at birth, and hence can have no nieces or nephews through them at that time. The resulting dynamics are

$$\tilde{\mathbf{q}}(x+1) \;=\; \tilde{\mathbf{U}}\tilde{\mathbf{q}}(x) + \tilde{\mathbf{F}}\,\tilde{\mathbf{n}}(x) \tag{61}$$

$$\tilde{\mathbf{q}}(0) \;=\; \mathbf{0} \tag{62}$$

3.2.5 Aunts and uncles of Focal

The aunts and uncles of Focal are the siblings of Focal's parents. The aunts and uncles through the older siblings receive no recruitment subsidy because once Focal is born, her parents cannot add any older siblings. The initial condition combines the older siblings of the mother and father of Focal, following the steps above for the grandparents of focal. The resulting dynamics are

$$\tilde{\mathbf{r}}(x+1) \;=\; \tilde{\mathbf{U}}\tilde{\mathbf{r}}(x) + \mathbf{0} \tag{63}$$

$$\tilde{\mathbf{r}}(0) \;=\; \sum_i \left[\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)\right] \tilde{\mathbf{m}}(i) \tag{64}$$

Aunts and uncles through younger siblings receive a recruitment subsidy from the reproduction of the grandmothers of Focal. Grandmothers and grandfathers do not reproduce independently, so only input from grandmothers is counted. The initial condition combines the younger siblings of Focal's mother and of Focal's father, at the time of Focal's birth.

The resulting dynamics are

$$\tilde{\mathbf{s}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{s}}(x) + \tilde{\mathbf{F}}^{*}\,\tilde{\mathbf{g}}(x) \tag{65}$$

$$\tilde{\mathbf{s}}(0) = \sum_{i} [\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)]\,\tilde{\mathbf{n}}(i) \tag{66}$$

3.2.6 Cousins of Focal

The cousins of Focal are the children of the aunts and uncles of Focal. The cousins through the older aunts/uncles receive a recruitment subsidy from the reproduction of older aunts and uncles. These cousins are the nieces and nephews of Focal's mother through her older siblings.

The resulting dynamics are

$$\tilde{\mathbf{t}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{t}}(x) + \tilde{\mathbf{F}}\,\tilde{\mathbf{r}}(x) \tag{67}$$

$$\tilde{\mathbf{t}}(0) = \sum_{i} [\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)]\,\tilde{\mathbf{p}}(i) \tag{68}$$

The cousins through the aunts/uncles younger than mother receive a recruitment subsidy from the reproduction of those aunts and uncles. These cousins are the nieces and nephews of Focal's mother through her younger siblings.

The resulting dynamics are

$$\tilde{\mathbf{v}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{v}}(x) + \tilde{\mathbf{F}}\,\tilde{\mathbf{s}}(x) \tag{69}$$

$$\tilde{\mathbf{v}}(0) = \sum_{i} [\boldsymbol{\pi}_{\mathrm{f}}(i) + \boldsymbol{\pi}_{\mathrm{m}}(i)]\,\tilde{\mathbf{q}}(i) \tag{70}$$

The chains of descendants through these cousins can be extended indefinitely. Recruitment into each generation comes from the generation before it, and the initial condition consists of the corresponding level of nieces/nephews of Focal's mother.

Table 1: The two-sex kinship model. In this table, $\boldsymbol{\pi}_{\mathrm{fm}} = \boldsymbol{\pi}_{\mathrm{f}} + \boldsymbol{\pi}_{\mathrm{m}}$. Fertility $\tilde{\mathbf{F}}$ includes both female and male offspring. Compare with the age-classified, multistate, and time-varying models in Appendix A.

Symbol	Kin	initial condition $\mathbf{k}_0$	Subsidy $\boldsymbol{\beta}(x)$
$\tilde{\mathbf{a}}$	children	$\mathbf{0}$	$\tilde{\mathbf{F}}\boldsymbol{\phi}(x)$
$\tilde{\mathbf{b}}$	grandchildren	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{a}}(x)$
$\tilde{\mathbf{c}}$	great-grandchildren	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{b}}(x)$
$\tilde{\mathbf{d}}$	parents	$\tilde{\boldsymbol{\pi}}$	$\mathbf{0}$
$\tilde{\mathbf{g}}$	grandparents	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\tilde{\mathbf{d}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{h}}$	great-grandparents	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\tilde{\mathbf{g}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{m}}$	older siblings	$\sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\,\tilde{\mathbf{a}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{n}}$	younger siblings	$\mathbf{0}$	$\tilde{\mathbf{F}}^*\,\tilde{\mathbf{d}}(x)$
$\tilde{\mathbf{p}}$	nieces/nephews via older siblings	$\sum_i \boldsymbol{\pi}_{\mathrm{f}}(i)\,\tilde{\mathbf{b}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{m}}(x)$
$\tilde{\mathbf{q}}$	nieces/nephews via younger siblings	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{n}}(x)$
$\tilde{\mathbf{r}}$	aunts/uncles older than mother	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\tilde{\mathbf{m}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{s}}$	aunts/uncles younger than mother	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\mathbf{n}(i)$	$\tilde{\mathbf{F}}^*\,\tilde{\mathbf{g}}(x)$
$\tilde{\mathbf{t}}$	cousins from aunts/uncles older than mother	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\tilde{\mathbf{p}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{r}}(x)$
$\tilde{\mathbf{v}}$	cousins from aunts/uncles younger than mother	$\sum_i \boldsymbol{\pi}_{\mathrm{fm}}(i)\,\tilde{\mathbf{q}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{s}}(x)$

4. Some two-sex kinship patterns: Senegal, Haiti, France

As an example, I explore some two-sex kinship patterns using mortality and fertility schedules for Senegal (2013), Haiti (2010), and France (2012). These were presented by Schoumaker (2019) as examples of populations with large, medium, and small differences between female and male mortality and fertility schedules; see Table 2. In Senegal, male TFR is much greater than female TFR and mean age at paternity is much greater than mean age at maternity. In Haiti, the differences are smaller and in France the differences are reduced even further. The three populations also differ in mortality, with all three showing typical differences between female and male life expectancy at birth. MATLAB code for the two-sex calculations is provided as an online supplement.

4.1 Fertility schedules

Age-specific fertility schedules in five-year age classes were kindly provided by Bruno Schoumaker based on information in Schoumaker (2019). The five-year age classes were interpolated to one-year age intervals, using the MATLAB function `interp1` with cubic spline interpolation (MATLAB method `akemi`). The observed fertility rates and the interpolated rates used in the model are shown in Figure 5.

Figure 5: **The observed (circles) and interpolated (lines) age-specific fertility rates for Senegal (2013), Haiti (2010), and France (2012). Based on data from Schoumaker (2019).**
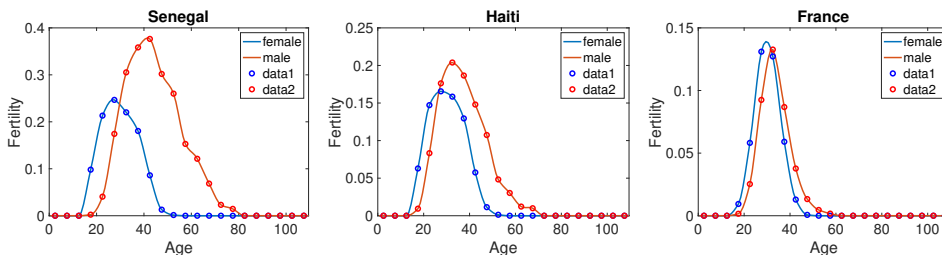

Table 2: **Male and female life expectancy at birth (e_0) and at age 60 ($e(60)$), total fertility rate (TFR), and mean ages at maternity and paternity for the data used in the example calculations. Fertility figures from Schoumaker (2019: Appendix A). Life expectancy data for the period 2010–2015 from United Nations (2019).**

	Senegal	Haiti	France
e_0 female	67.5	64.4	85.0
e_0 male	63.8	60.2	78.7
$e(60)$ female	17.4	18.7	27.3
$e(60)$ male	15.7	16.9	22.9
TFR female	5.3	3.7	2.0
TFR male	11.0	5.1	2.0
age at maternity	29.8	30.0	30.1
age at paternity	44.1	37.0	33.5

4.2 Mortality schedules

Mortality data for the three countries were obtained from United Nations compilations[5] (United Nations 2019). Survival probabilities were taken from abridged male and female life tables for the time period 2010–2015. These five-year survival probabilities were transformed to one-year probabilities, and then interpolated to one-year age intervals using the MATLAB function `interp1` with cubic spline interpolation (MATLAB method `akemi`). The UN life tables are truncated at 85 years of age; I extended them to age 100

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[5] https://population.un.org/wpp/Download/Archive/Standard/

by assuming that survival declined to 0 at age 100 and extrapolating the values between age 85 and 100 using cubic splines.

4.3 Numbers of female and male kin

Of the many results that could be calculated from the model, here I show the numbers of female and male kin and the sex ratios for each kind of kin, as a function of the age of Focal.

Results for kin numbers are shown in Figure 6. The three vertical columns represent, from left to right, Senegal, Haiti, and France. Each row is a different type of kin.

Looking down columns in Figure 6 we see the expected increase in grandchildren over children, and great-grandchildren over grandchildren. The increase is most marked in Senegal, which has the highest fertility. Similarly, we see the expected reduction in grandparents relative to parents, and great-grandparents relative to grandparents. The reduction is most marked in Senegal. This may reflect the degrees of mortality. While life expectancy at birth is lowest in Haiti, suggesting that it has the highest mortality, life expectancy at older ages (e.g., age 60) is lowest in Senegal. The mortality at old ages will, of course, be most relevant to the survival of grandparents and great-grandparents.

The remaining kin types are affected by both fertility and mortality and the patterns are diverse. Nieces and nephews, compared to siblings, behave much like grandchildren compared to children. Aunts and uncles behave much like parents because by the time of Focal's birth, new aunts and uncles are not likely to be produced, so the trajectory is dominated by mortality.

Comparing countries across rows in Figure 6, the main differences are those to be expected in comparisons of high and low fertility or high and low mortality populations. The numbers of children, grandchildren, and great-grandchildren decrease from Senegal to France. Parents, grandparents, and great-grandparents decline most rapidly with age in Senegal, and most slowly in France.

Siblings, nieces and nephews, aunts and uncles, and cousins are affected, in different ways, by both mortality and fertility schedules. Focal accumulates more of these kin, more rapidly, and loses them more precipitously in Senegal than in Haiti and France.

In general, comparisons across the three countries emphasize the great difference in the sizes and structures of the kinship network created by the differences in mortality and fertility.

Figure 6:   **(part 1 of 3) The numbers of male and female kin as a function of the age of Focal. Data for Senegal (left column), Haiti (middle column), and France (right column). For clarity, the y-axes are the same across countries, but differ among kin types.**
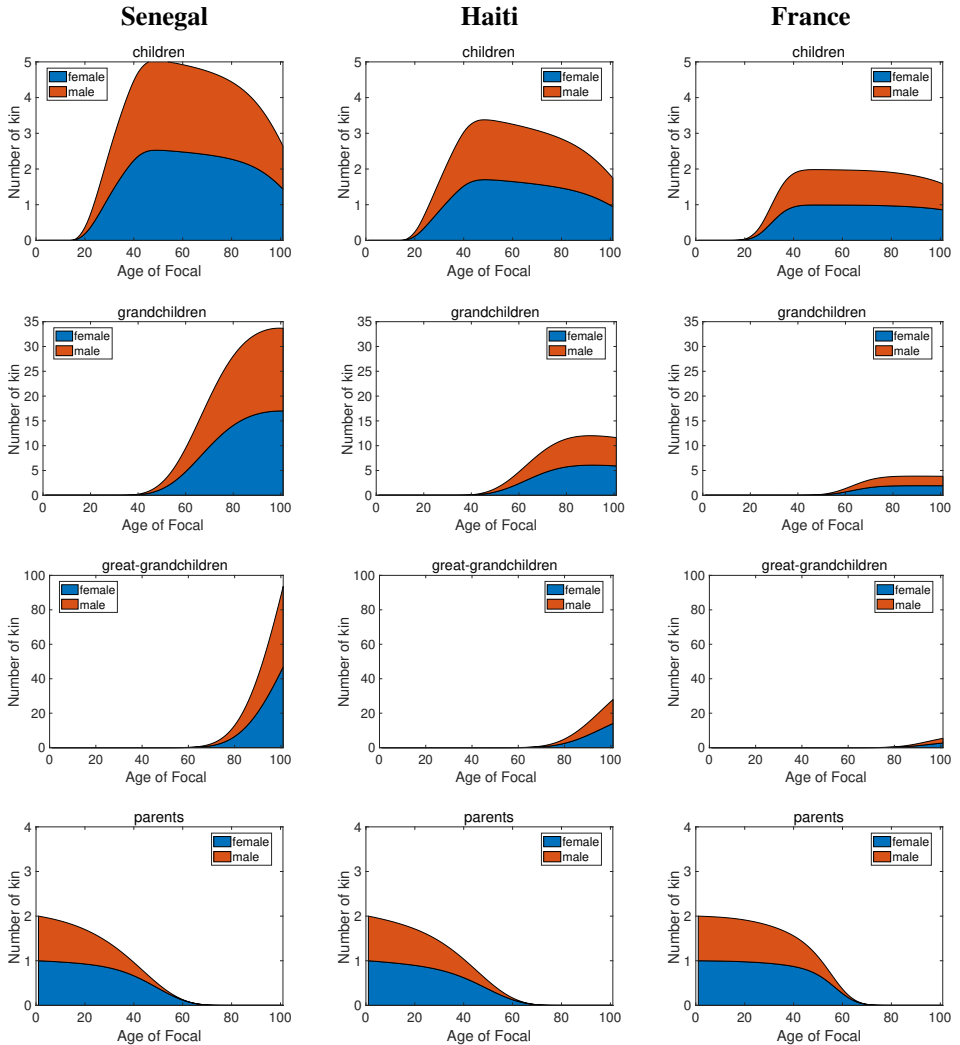
Figure 6: **(part 2 of 3) The numbers of male and female kin as a function of the age of Focal. Data for Senegal (left column), Haiti (middle column), and France (right column).**
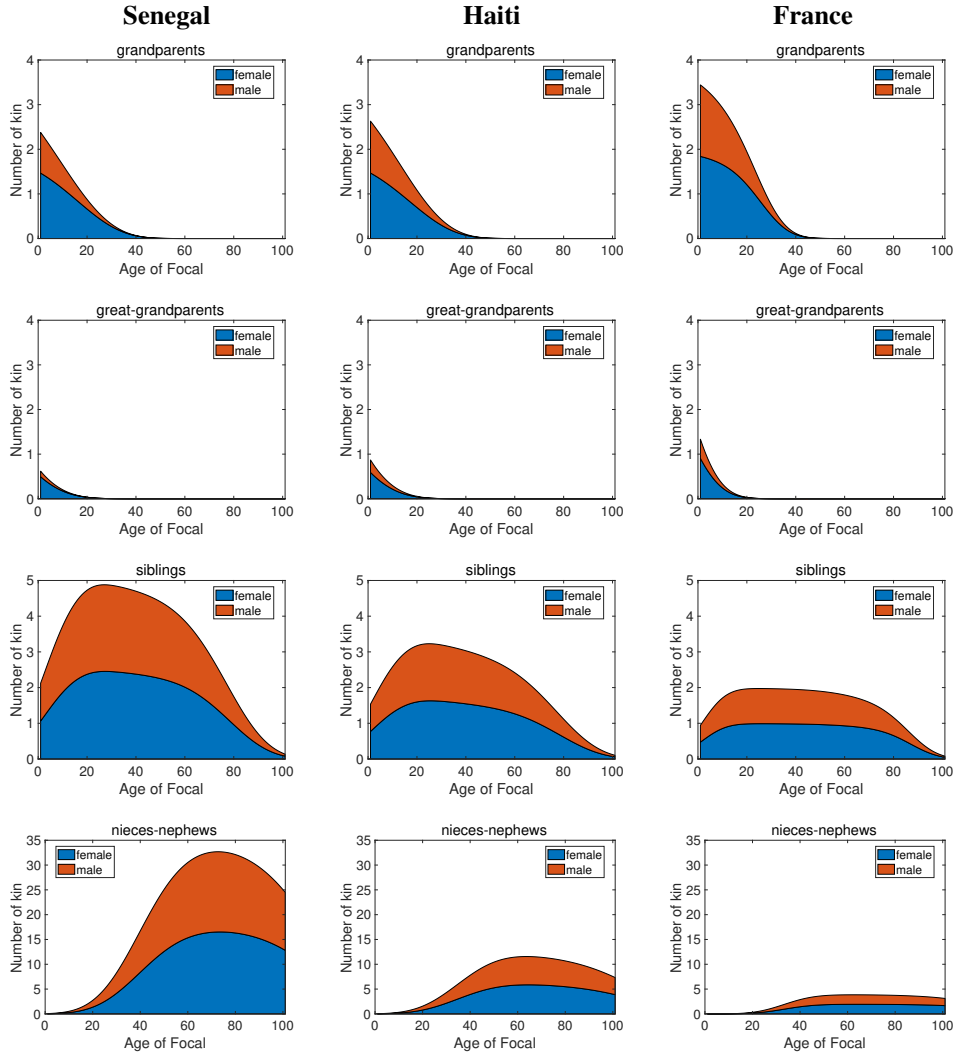
Figure 6:   **(part 3 of 3) The numbers of male and female kin as a function of the age of Focal. Data for Senegal (left column), Haiti (middle column), and France (right column).**
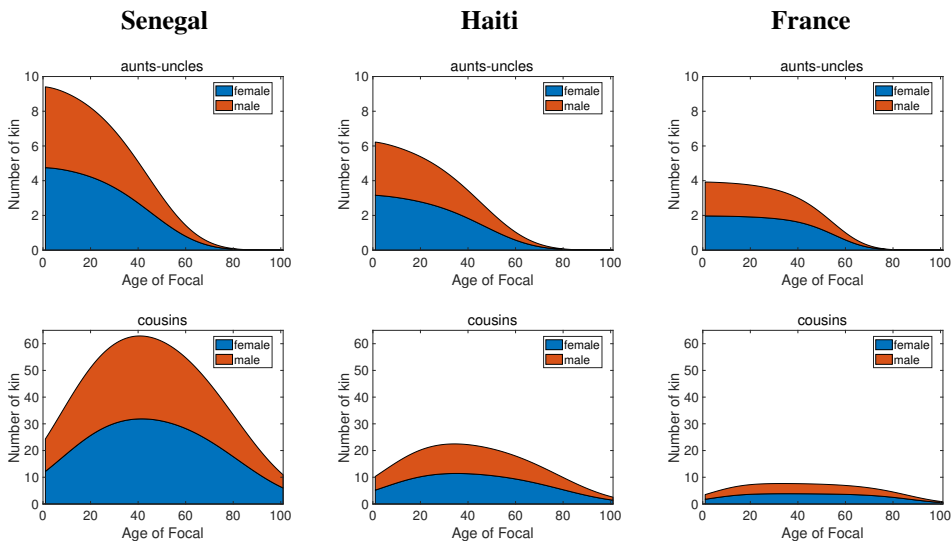
**Senegal**   **Haiti**   **France**

4.4 Kin sex ratios

What is hinted at, but not clearly apparent, in Figure 6 is a shift in the sex composition as Focal ages. Figure 7 shows the sex ratio (number of males divided by number of females), for each type of kin, as a function of the age of Focal.

The sex ratio declines (i.e., females increasingly outnumber males) with increasing age of Focal in all cases. Children are of necessity younger than Focal; grandchildren and great-grandchildren even younger. Thus the reduction in sex ratio of these kin is small. Parents, grandparents, and great-grandparents are correspondingly older than Focal, and their sex ratios decline dramatically with age of Focal. The declines among siblings (children of Focal's mother) and cousins (children of Focal's siblings) are similar. The sex ratios of nieces and nephews (the children of Focal's siblings) are similar to those of the children of Focal herself.

A comparison of the three countries hints at some processes that warrant further investigation. Of the three countries, France shows the largest sex difference in life expectancy (Table 2). Its sex ratio might thus be expected to decline the most rapidly. This is true for some kin (aunts-uncles, cousins) but not for others (children, grandchildren). This suggests that the details of age-specific differences in mortality, rather than overall

life expectancy, interact with the age structure of kin to determine the details of the sex ratio patterns. A sensitivity analysis of the kinship model, using methods similar to those of Caswell (2019b) would reveal the importance of mortality differences at every age to the changes in sex ratios.

Figure 7:   **Sex ratios of kin as a function of the age of Focal. The y-axis scale for children, grandchildren, and great-grandchildren differs from that of other kin.**
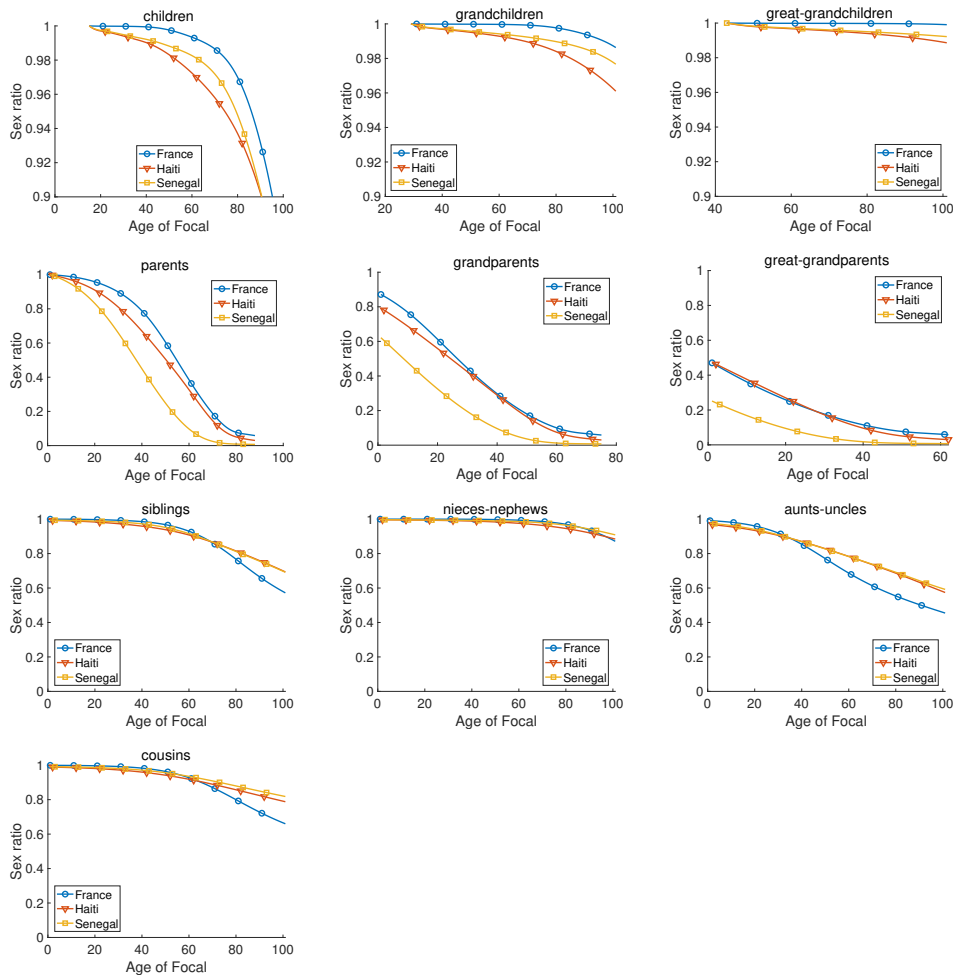
5. Approximations to the two-sex model

Complete age- and sex-specific mortality and fertility schedules are not always available. In particular, male fertility data are less commonly reported than female fertility data (e.g., Coleman 2000, but see Schoumaker 2019). Fortunately, the structure of the two-sex kinship model readily admits approximations that utilize whatever mortality and fertility data are available. Four such approximations are

Model 1. The full two-sex model. It utilizes the fertility matrices $\mathbf{F}_f$ and $\mathbf{F}_m$ and the survival matrices $\mathbf{U}_f$ and $\mathbf{U}_m$, as described in Section 3.

Model 2. In the absence of male fertility data, this approximation uses $\mathbf{F}_f$ for both female and male fertility, setting

$$\tilde{\mathbf{U}} = \begin{pmatrix} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_m \end{pmatrix} \qquad \tilde{\mathbf{F}} = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \bar{\alpha}\mathbf{F}_f \\ \alpha\mathbf{F}_f & \alpha\mathbf{F}_f \end{pmatrix} \qquad \tilde{\mathbf{F}}^* = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{pmatrix} \quad (71)$$

Schoumaker (2019) reports that the difference between male and female fertility is least in countries with low fertility rates; this approximation should, therefore, be most successful in such populations.

Model 3. In the absence of male mortality data, this approximation uses $\mathbf{U}_f$ for both female and male survival, setting

$$\tilde{\mathbf{U}} = \begin{pmatrix} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_f \end{pmatrix} \qquad \tilde{\mathbf{F}} = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \bar{\alpha}\mathbf{F}_m \\ \alpha\mathbf{F}_f & \bar{\alpha}\mathbf{F}_m \end{pmatrix} \qquad \tilde{\mathbf{F}}^* = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{pmatrix} \quad (72)$$

Model 4. In the absence of male rates of any kind, this approximation treats males and females as indistinguishable. I refer to this as the *androgynous approximation*, in which female rates are used for both sexes, leading to

$$\tilde{\mathbf{U}} = \begin{pmatrix} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_f \end{pmatrix} \qquad \tilde{\mathbf{F}} = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \bar{\alpha}\mathbf{F}_f \\ \alpha\mathbf{F}_f & \bar{\alpha}\mathbf{F}_f \end{pmatrix} \qquad \tilde{\mathbf{F}}^* = \begin{pmatrix} \bar{\alpha}\mathbf{F}_f & \mathbf{0} \\ \alpha\mathbf{F}_f & \mathbf{0} \end{pmatrix} \quad (73)$$

In each of these cases, the calculations proceed as prescribed in Section 3, but using the matrices specified here. The symmetrical cases in which male rates are used in place of missing female rates are an obvious extension.

5.1 How good is the androgynous approximation?

The androgynous approximation deserves special consideration because it requires a minimum amount of data. It uses female rates only, treating males and females as identical. Even so, it retains female and male kin as categories, which can be a useful if, e.g., one wants to subject the kinship network to sex-specific prevalences of a disease. To evaluate the approximation in an extreme case, we can compare the full two-sex model and the androgynous approximation for Senegal, with its large differences between male and female fertility. The differences between the two models are a measure of how much the sex-specific rates contribute to the structure of the kinship network (at least, as measured by numbers of kin).

Figure 8 shows the numbers of female and male kin as a function of the age of Focal, for Model 1 and Model 4. In general, the differences are small, at most a fraction of an individual. A few kin types (female children, parents, and siblings) show no differences at all.

The differences between the two models reflect the differences in mortality (two-sex vs. female only) and fertility (two-sex vs. female only). Small as the are, the differences can be decomposed into contributions from these two sources using the Kitagawa-Keyfitz decomposition (Kitagawa 1955; Keyfitz 1968: Section 7.4); see Caswell (2010) for description. Figure 9 shows the result of the decomposition for each kin type as a function of the age of Focal.

The sum of the contributions is positive in all cases: the androgynous Model 4 overestimates the kin numbers obtained from the two-sex Model 1. The overall error from the androgynous model is less than one-half of an individual for all kin types except for great-grandchildren at old ages of Focal. Because children and siblings are unaffected by male fertility rates, the differences in kin numbers are totally due to the assumption of identical female and male mortality. All the other kin types are affected by both mortality and fertility assumptions.

Figure 8: **Male and female kin as calculated from the full two-sex Model 1 and the androgynous approximation Model 4. The latter model applies the same (female) rates to both sexes, based on the rates of Senegal.**
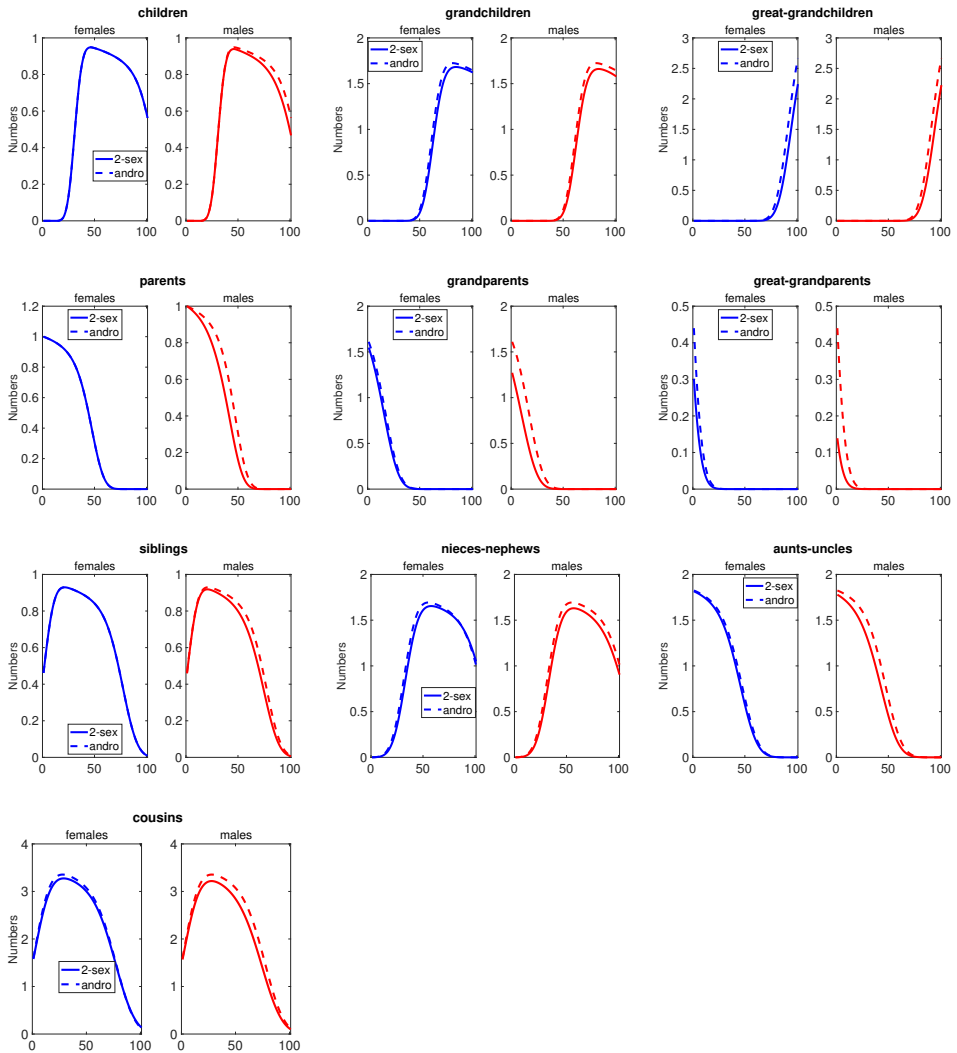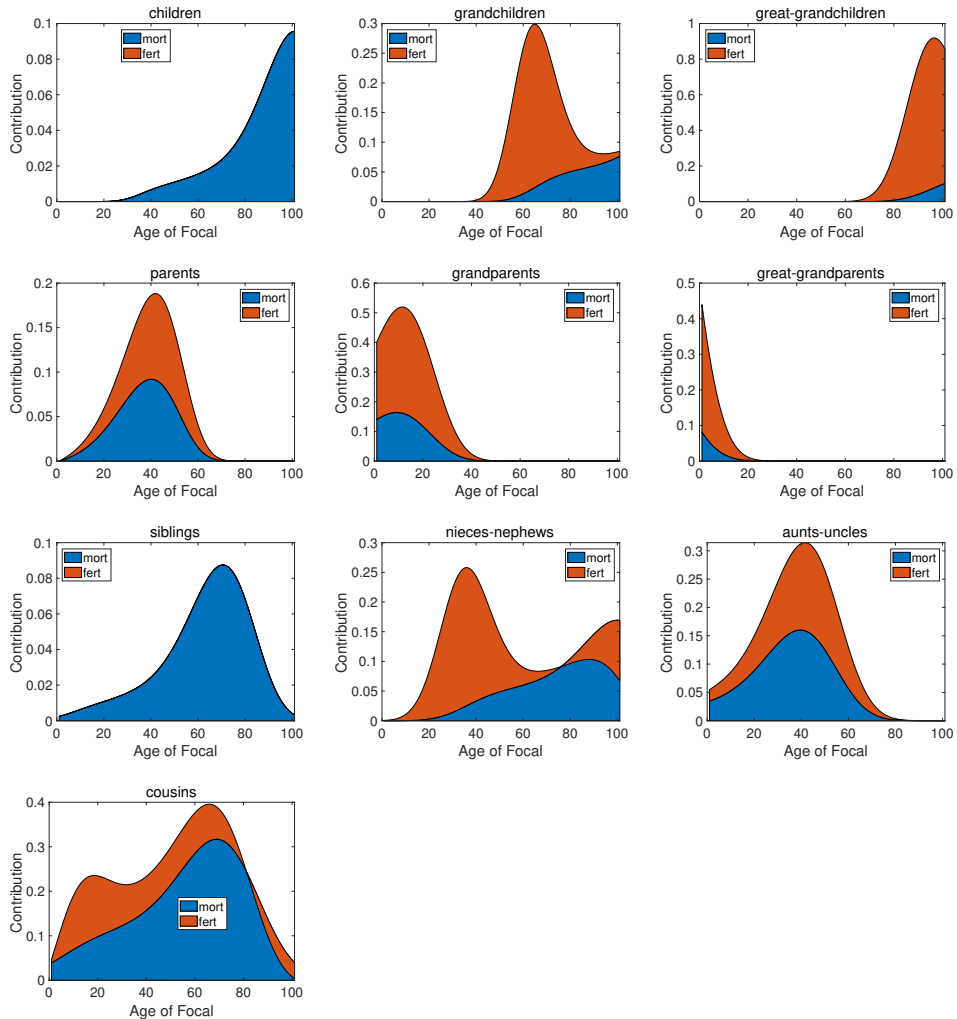
Figure 9: **Decomposition analysis. The difference in kin numbers between the androgynous approximation Model 4 and the two-sex Model 1 is decomposed into contributions of differences in mortality and differences in fertility. Based on rates of Senegal.**

5.2 Total kin numbers: the GKP factors

In the absence of information on male rates, Goodman, Keyfitz, and Pullum (1974) suggested multiplying the results of a one-sex model by a set of factors (I refer to these as the GKP factors) to obtain kin numbers for a scenario in which female and male rates were identical (i.e., our androgynous approximation Model 4). The GKP factors multiply daughters by 2, granddaughters by 4, great-granddaughters by 8, mothers by 2, grandmothers by 4, great-grandmothers by 8, sisters by 2, nieces by 4, aunts by 4, and cousins by 8. Calculations under the Senegal rates show, not surprisingly, that the GKP factors do give exactly the androgynous Model 4 kin numbers. Thus the results of Figure 9) also give the error resulting from using the GKP factors to approximate the results of the full two-sex model.

It should be noted that these comparisons are based on numbers of kin. Other results, especially those concerning sex ratios and sex-specific prevalences, cannot be approximated by one-sex models.

6. Discussion

The two-sex kinship model treats sex as an individual state variable in addition to age. As is generally true of such multistate models (Caswell et al. 2018) the form of the model is unchanged[6] but the vectors and matrices take on a structure that reflects the enlarged state space: (a) the age structure vector $\mathbf{k}(x)$ is replaced by the age×stage vector $\tilde{\mathbf{k}}(x)$, (b) the survival matrix $\mathbf{U}$ is replaced by the block-structured matrix $\tilde{\mathbf{U}}$, (c) the fertility matrix $\mathbf{F}$ is replaced with the block structured matrices $\tilde{\mathbf{F}}$ and $\tilde{\mathbf{F}}^*$, and (d) the age at maternity distribution $\boldsymbol{\pi}$ is replaced by the maternity and paternity distributions $\boldsymbol{\pi}_{\mathrm{f}}$ and $\boldsymbol{\pi}_{\mathrm{m}}$.

The two-sex model accounts for the independence of reproduction by some kin (e.g., sons and daughters of Focal producing grandchildren independently) but dependence in others (e.g., Focal's mother and father do not produce siblings of Focal independently). The summaries in Table 1 (two-sex) and Tables A-1 (the one-sex model of Caswell 2019a), A-2 (the age×stage -classified model of Caswell 2020), and A-3 (the time-varying model of Caswell and Song 2021) emphasize this formal similarity.

Formal similarity is more than a mathematical nicety. It is an important goal because it permits the two-sex model to be extended to arbitrary kin types just as the one-sex model has been. Dead kin and the experience of kin loss can be included as of Caswell (2019a). Additional state variables can be added as in the age×parity model of Caswell (2020). And, time variation can be incorporated as in the models of Caswell and Song (2021) and Song and Caswell (2022).

This paper has focused on the numbers and sex ratios of kin. But because the model

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[6] This invariance of form, and hence of analysis, is one part of the definition of "formal" in formal demography.

provides the full age×sex structure for each type of kin, many other kinds of weighted numbers (e.g., dependency ratios) are easily computed. Of particular interest are quantities that might, in general, be called "prevalences" — measures of the occurrence of some property, at specified ages, for each sex. The properties are often medical or health conditions (e.g., Caswell 2019a: for an analysis of dementia). The prevalences of many conditions are strongly sex dependent. Some cancers, for example, exhibit highly skewed prevalences. In the United States in 2021, new cases of lung cancer, per capita, were 25% higher in men than in women. New cases of kidney cancer were twice as frequent in men, and of bladder cancer four times as frequent (National Cancer Institute 2021). The prevalence of obstructive sleep apnea in a population in Brazil is both strongly age-dependent (increasing by about three-fold from age 20 to age 80) and sex-dependent (by four-fold controlling for age and other variables) (Tufik et al. 2010).

Sex-specific prevalences, in a more general sense, also appear in non-medical conditions. For example, the income level of kin could be an important issue for Focal, and the gender gap in pay rates is widespread and well known. In the EU as of 2014, women earned from 1% (Romania) to 24% (Estonia) less than men, with an average gap of 14% (Boll and Lagerman 2018). Song and Caswell (2022) analyzed unemployment among kin, but had to rely on applying the GKP factors to a one-sex model, and thus could not incorporate sex-specific unemployment. Such an analysis would be possible using the two-sex model.

I have not explored it here, but the kinship structure shown in Figure 2(a) can be incorporated, accounting for all lines of descent in each generation, at the cost of larger matrices for each generation. There exist situations in which this structure and the resulting equation (10) would be of interest. For example, evolutionary calculations based on kin selection depend on the sharing of genes between individuals. Because maternity is more certain than paternity, Focal can be more certain that she shares 1/4 of her genes with the children of her daughters, $\mathbf{b}_1'$ and $\mathbf{b}_2'$ than she is for the children of her sons, $\mathbf{b}_3'$ and $\mathbf{b}_4'$. In general, each passage through a male descendant introduces additional uncertainty into the inheritance.

A related issue arises with respect to mitochondrial DNA, which is passed from mothers to offspring, and Y chromosomes, which are transmitted from fathers to sons; calculations involving these forms of inheritance might benefit from being able to distinguish kin by lines of descent. See Tanskanen and Danielsbacka (2019), especially their Table 2.2, for a summary of these issues.

Many gender-specific demographic and sociological variables can be related to kinship structures using this model. In light of this goal, the apparent adequacy of the androgynous approximation to the full two-sex model, in a case (Senegal) with quite large male-female differences, is encouraging. It appears safe to use the approximations listed in Section 5, especially in cases where both male and female mortality are available, but male fertility is lacking. Notice that the differences in numbers of kin between the two-

sex model and the androgynous approximation (Figures 8 and 9) are much smaller than the differences in kin numbers among the three countries examined here (Figure 6). More comparative research is warranted.

The possible use of model fertility schedules (e.g., Coale and Trussell 1974) when measured fertility data are lacking deserves further research. Paget and Timaeus (1994), extending work of Booth (1984), describe a relational model for male fertility that produces fertility patterns (their Figure 2) not unlike those in Figure 5.

Despite the growing list of factors included in the matrix kinship models, limitations and open research questions remain. Multiple births, for example, are not included. This is easily addressed and is especially important in biodemography and population biology if one is interested in the kinship structure of species whose fertility patterns are very different from ours (Caswell 2021).

The distributions of ages at maternity and paternity of Focal's mother and father determine initial conditions for kin. These ages have been treated here as independent; an obvious extension would be to use a joint distribution reflecting the age distribution of couples.

This model, like previous models, is limited to consanguineal, biological kin. The challenge of incorporating affinal kin, stepkin, kin by marriage, and blended families is an open research question. Perhaps a first step towards a solution would be to combine the kinship networks of two Focal individuals of different ages to provide a picture of a blended set of kin.[7] The ages of the Focal individuals to be combined might be chosen from a distribution of the ages of parents forming blended families.

Finally, it is important to recall that the projections of the kin populations provide mean age-sex structures, over the distributions produced by the survival and fertility probabilities. Because the kin populations are small, there will be an (as yet unknown) degree of stochastic variation around those means.

By treating kinship dynamics as a population projection problem, the matrix-based theory permits a variety of demographic extensions: from age distributions to age×stage multistate distributions, from time-invariant to time-varying demographic rates, and now from one-sex to two-sex rates. The theory yields a rich collection of demographic outcomes, including bereavement, prevalences of health or social conditions, parity, family sizes, and sex ratios. Such quantities are now open to analysis in terms of demographic rates in a kinship setting.

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[7] The successful television comedy series *The Brady Bunch*, which aired from 1969 to 1974 and is, at the time of this writing, still internationally broadcast in syndication, was premised on just such a blending. In the show, fate (remember, this is a television show) brings together a single mother of three daughters and a widowed father of three sons. They marry, resulting in a blended family of six children. Hilarity ensues. Setting aside the historically dated social setting, it provides an example of a way in which such blended families could be incorporated into theory.

7. Acknowledgments

Correction. The originally published version of the paper contained a graphics error in Figure 5. The plot for Senegal was printed twice and that for Haiti was omitted. The error has been corrected.

References

Boll, C. and Lagerman, A. (2018). *Gender pay gap in EU countries based on SES (2014)*. Tech. rep., European Commission, Luxembourg: Publications Office of the European Union.

Booth, H. (1984). Transforming Gompertz's function for fertility analysis: The development of a standard for the relational Gompertz function. *Population Studies* 38(3): 495–506. doi:10.1080/00324728.1984.10410306.

Bribiescas, R.G. (2016). *How men age: What evolution reveals about male health and mortality*. Princeton, New Jersey, USA: Princeton University Press. doi:doi.org/10.2307/j.ctt1wf4cmx.

Caswell, H. (2010). Life table response experiment analysis of the stochastic growth rate. *Journal of Ecology* 98(2): 324–333. doi:10.1111/j.1365-2745.2009.01627.x.

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

Caswell, H. (2019b). *Sensitivity analysis: Matrix methods for demography and ecology*. Demographic Research Monographs. Cham, Switzerland: Springer Nature. doi:10.1007/978-3-030-10534-1.

Caswell, H. (2020). The formal demography of kinship. II. Multistate models, parity, and sibship. *Demographic Research* 42: 1097–1144. doi:10.4054/DemRes.2020.42.38.

Caswell, H. (2021). The demography of kinship: A new axis for exploring life histories and population structure. Presention at Annual Meeting of Ecological Society of America, August 2021.

Caswell, H., de Vries, C., Hartemink, N., Roth, G., and van Daalen, S.F. (2018). Age×stage-classified demographic analysis: A comprehensive approach. *Ecological Monographs* 88(4): 560–584. doi:10.1002/ecm.1306.

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

Clark, R. and Peck, B.M. (2012). Examining the gender gap in life expectancy: A cross-national analysis, 1980–2005. *Social Science Quarterly* 93(3): 820–837. doi:10.1111/j.1540-6237.2012.00881.x.

Coale, A.J. and Trussell, T.J. (1974). Model fertility schedules: Variations in the age structure of childbearing in human populations. *Population Index* 185–258. doi:10.2307/2733910.

Coleman, D.A. (2000). Male fertility trends in industrial countries: Theories in search of some evidence. In: Bledsoe, C., Lerner, S., and Guyer, J. (eds.). *Fertility and the male life cycle in the era of fertility decline*. Oxford, U.K.: Oxford University Press: 29–60.

Coste, C.F., 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.

Dublin, L.I., Lotka, A.J., and Spiegelman, M. (1949). *Length of life*. New York, New York: Ronald.

Glei, D.A. and Horiuchi, S. (2007). The narrowing sex differential in life expectancy in high-income populations: Effects of differences in the age pattern of mortality. *Population Studies* 61(2): 141–159. doi:10.1080/00324720701331433.

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.

Iannelli, M., Martcheva, M., and Milner, F.A. (2005). *Gender-structured population modeling: Mathematical methods, numerics, and simulations*. Philadelphia, Pennsylvania, USA: SIAM. doi:10.1137/1.9780898717488.

Keyfitz, N. (1972). The mathematics of sex and marriage. *Proceedings of the Fourth Berkeley Symposium on Mathematical Statistics and Probability* 6: 89–108.

Keyfitz, N. (1968). *Introduction to the mathematics of population*. Reading, Massachusetts, USA: Addison-Wesley.

Keyfitz, N. and Caswell, H. (2005). *Applied mathematical demography*. New York, New York: Springer, 3rd ed.

Kitagawa, E.M. (1955). Components of a difference between two rates. *Journal of the American Statistical Association* 50: 1168–1194. doi:10.1080/01621459.1955.10501299.

Kühnert, B. and Nieschlag, E. (2004). Reproductive functions of the ageing male. *Human Reproduction Update* 10(4): 327–339. doi:10.1080/01621459.1955.10501299.

Luy, M. and Minagawa, Y. (2014). Gender gaps—Life expectancy and proportion of life in poor health. *Health Reports* 25(12): 12–19.

National Cancer Institute (2021). Surveillance, epidemiology, and end results program: Cancer stat facts. [electronic resource]. URL https://seer.cancer.gov/statfacts/.

Oberzaucher, E. and Grammer, K. (2014). The case of Moulay Ismael—Fact or fancy? *PloS ONE* 9(2): e85292. doi:10.1371/journal.pone.0085292.

Oksuzyan, A., Shkolnikova, M., Vaupel, J.W., Christensen, K., and Shkolnikov, V.M. (2014). Sex differences in health and mortality in Moscow and Denmark. *European Journal of Epidemiology* 29(4): 243–252. doi:10.1007/s10654-014-9893-4.

Paget, W.J. and Timaeus, I.M. (1994). A relational Gompertz model of male fertility: Development and assessment. *Population Studies* 48(2): 333–340. doi:10.1080/0032472031000147826.

Raftery, A.E., Lalic, N., and Gerland, P. (2014). Joint probabilistic projection of female and male life expectancy. *Demographic Research* 30: 795–822. doi:10.4054/DemRes.2014.30.27.

Robine, J.M. and Vaupel, J.W. (2001). Supercentenarians: Slower ageing individuals or senile elderly? *Experimental Gerontology* 36(4-6): 915–930. doi:10.1016/S0531-5565(00)00250-3.

Schoumaker, B. (2019). Male fertility around the world and over time: How different is it from female fertility? *Population and Development Review* 45(3): 459–487. doi:10.1111/padr.12273.

Shyu, E. and Caswell, H. (2018). Mating, births, and transitions: A flexible two-sex matrix model for evolutionary demography. *Population Ecology* 60:21–36. doi:10.1007/s10144-018-0615-8.

Song, X. and Caswell, H. (2022). The role of racial differences in exposure to unemployment. *Demography* 59(4): 1325–1352. doi:10.1215/00703370-10057831.

Tanskanen, A.O. and Danielsbacka, M. (2019). *Intergenerational family Relations: An evolutionary social science approach*. Routledge Advances in Sociology. New York, New York, USA: Routledge. doi:10.4324/9781315107806.

Tufik, S., Santos-Silva, R., Taddei, J.A., and Bittencourt, L.R.A. (2010). Obstructive sleep apnea syndrome in the Sao Paulo epidemiologic sleep study. *Sleep Medicine* 11(5): 441–446. doi:10.1016/j.sleep.2009.10.005.

Tuljapurkar, S.D., Puleston, C.O., and Gurven, M.D. (2007). Why men matter: Mating patterns drive evolution of human lifespan. *PLoS ONE* 2(8): e785. doi:10.1371/journal.pone.0000785.

United Nations (2019). *World population prospects 2019*. Tech. Rep. Revision 2019, United Nations Department of Economic and Social Affairs, Population Division.

Appendix

A. One-sex, time-varying, and multistate kinship models

This appendix presents tables showing the expressions for the kinship dynamics in one-sex, multistate, and time-varying kinship models. Comparison of these tables with with Table 1 shows the formal similarity of the four models. Tables are modified from their cited sources under the terms of a Creative Commons Attribution license.

Table A-1: **The age-classified, time-invariant, one-sex kinship model of Caswell (2019a).**

Symbol	Kin	initial condition $\mathbf{k}_0$	Subsidy $\beta(x)$
$\mathbf{a}$	daughters	$\mathbf{0}$	$\mathbf{Fe}_x$
$\mathbf{b}$	granddaughters	$\mathbf{0}$	$\mathbf{Fa}(x)$
$\mathbf{c}$	great-granddaughters	$\mathbf{0}$	$\mathbf{Fb}(x)$
$\mathbf{d}$	mothers	$\boldsymbol{\pi}$	$\mathbf{0}$
$\mathbf{g}$	grandmothers	$\sum_i \pi_i \mathbf{d}(i)$	$\mathbf{0}$
$\mathbf{h}$	great-grandmothers	$\sum_i \pi_i \mathbf{g}(i)$	$\mathbf{0}$
$\mathbf{m}$	older sisters	$\sum_i \pi_i \mathbf{a}(i)$	$\mathbf{0}$
$\mathbf{n}$	younger sisters	$\mathbf{0}$	$\mathbf{Fd}(x)$
$\mathbf{p}$	nieces via older sisters	$\sum_i \pi_i \mathbf{b}(i)$	$\mathbf{Fm}(x)$
$\mathbf{q}$	nieces via younger sisters	$\mathbf{0}$	$\mathbf{Fn}(x)$
$\mathbf{r}$	aunts older than mother	$\sum_i \pi_i \mathbf{m}(i)$	$\mathbf{0}$
$\mathbf{s}$	aunts younger than mother	$\sum_i \pi_i \mathbf{n}(i)$	$\mathbf{Fg}(x)$
$\mathbf{t}$	cousins from aunts older than mother	$\sum_i \pi_i \mathbf{p}(i)$	$\mathbf{Fr}(x)$
$\mathbf{v}$	cousins from aunts younger than mother	$\sum_i \pi_i \mathbf{q}(i)$	$\mathbf{Fs}(x)$

Table A-2: **The age×stage-classified kinship model of Caswell (2020). Matrices and vectors bearing tildes (e.g., ã) are age×stage block-structured.**

Symbol	Kin	initial condition $\mathbf{k}_0$	Subsidy $\beta(x)$
$\tilde{\boldsymbol{\phi}}$	Focal	$\tilde{\boldsymbol{\phi}}_0$	$\mathbf{0}$
$\tilde{\mathbf{a}}$	daughters	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\boldsymbol{\phi}}(x)$
$\tilde{\mathbf{b}}$	granddaughters	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{a}}(x)$
$\tilde{\mathbf{c}}$	great-granddaughters	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{b}}(x)$
$\tilde{\mathbf{d}}$	mothers	$\tilde{\boldsymbol{\pi}}$	$\mathbf{0}$
$\tilde{\mathbf{g}}$	grandmothers	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{d}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{h}}$	great-grandmothers	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{g}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{m}}$	older sisters	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{a}}(i)$	$\mathbf{0}$
$\tilde{\mathbf{n}}$	younger sisters	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{d}}(i)$
$\tilde{\mathbf{p}}$	nieces via older sisters	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{b}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{m}}(x)$
$\tilde{\mathbf{q}}$	nieces via younger sisters	$\mathbf{0}$	$\tilde{\mathbf{F}}\tilde{\mathbf{n}}(i)$
$\tilde{\mathbf{r}}$	aunts older than mother	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{m}}(x)$	$\mathbf{0}$
$\tilde{\mathbf{s}}$	aunts younger than mother	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{n}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{g}}(x)$
$\tilde{\mathbf{t}}$	cousins: aunts older than mother	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{p}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{r}}(x)$
$\tilde{\mathbf{v}}$	cousins: aunts younger than mother	$\sum_i \boldsymbol{\pi}_i^{\mathrm{age}}\tilde{\mathbf{q}}(i)$	$\tilde{\mathbf{F}}\tilde{\mathbf{s}}(x)$

Table A-3: **The time-varying kinship model of Caswell and Song (2021). Age of Focal and time are denoted by x and t, respectively. For each type of kin, the relevant age boundary condition, survival dynamics, and reproductive subsidy are shown.**

Kin	age boundary	survival	subsidy $\beta(x)$
$\mathbf{a}(x,t)$ daughters	$\mathbf{0}$	$\mathbf{U}_t\mathbf{a}(x,t)$	$\mathbf{F}_t\mathbf{e}_x$
$\mathbf{b}(x,t)$ granddaughters	$\mathbf{0}$	$\mathbf{U}_t\mathbf{b}(x,t)$	$\mathbf{F}_t\mathbf{a}(x,t)$
$\mathbf{c}(x,t)$ great-granddaughters	$\mathbf{0}$	$\mathbf{U}_t\mathbf{c}(x,t)$	$\mathbf{F}_t\mathbf{b}(x,t)$
$\mathbf{d}(x,t)$ mothers	$\boldsymbol{\pi}(t)$	$\mathbf{U}_t\mathbf{d}(x,t)$	$\mathbf{0}$
$\mathbf{g}(x,t)$ grandmothers	$\sum_i \pi_i(t)\mathbf{d}(i,t)$	$\mathbf{U}_t\mathbf{g}(x,t)$	$\mathbf{0}$
$\mathbf{h}(x,t)$ great-grandmothers	$\sum_i \pi_i(t)\mathbf{g}(i,t)$	$\mathbf{U}_t\mathbf{h}(x,t)$	$\mathbf{0}$
$\mathbf{m}(x,t)$ older sisters	$\sum_i \pi_i(t)\mathbf{a}(i,t)$	$\mathbf{U}_t\mathbf{m}(x,t)$	$\mathbf{0}$
$\mathbf{n}(x,t)$ younger sisters	$\mathbf{0}$	$\mathbf{U}_t\mathbf{n}(x,t)$	$\mathbf{F}_t\mathbf{d}(x,t)$
$\mathbf{p}(x,t)$ nieces via older sisters	$\sum_i \pi_i(t)\mathbf{b}(i,t)$	$\mathbf{U}_t\mathbf{p}(x,t)$	$\mathbf{F}_t\mathbf{m}(x,t)$
$\mathbf{q}(x,t)$ nieces via younger sisters	$\mathbf{0}$	$\mathbf{U}_t\mathbf{q}(x,t)$	$\mathbf{F}_t\mathbf{n}(x,t)$
$\mathbf{r}(x,t)$ aunts older than mother	$\sum_i \pi_i(t)\mathbf{m}(i,t)$	$\mathbf{U}_t\mathbf{r}(x,t)$	$\mathbf{0}$
$\mathbf{s}(x,t)$ aunts younger than mother	$\sum_i \pi_i(t)\mathbf{n}(i,t)$	$\mathbf{U}_t\mathbf{s}(x,t)$	$\mathbf{F}_t\mathbf{g}(x,t)$
$\mathbf{t}(x,t)$ cousins; aunts older than mother	$\sum_i \pi_i(t)\mathbf{p}(i,t)$	$\mathbf{U}_t\mathbf{t}(x,t)$	$\mathbf{F}_t\mathbf{r}(x,t)$
$\mathbf{v}(x,t)$ cousins; aunts younger than mother	$\sum_i \pi_i(t)\mathbf{q}(i,t)$	$\mathbf{U}_t\mathbf{v}(x,t)$	$\mathbf{F}_t\mathbf{s}(x,t)$