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

DEMOGRAPHIC RESEARCH

VOLUME 41, ARTICLE 24, PAGES 679–712
PUBLISHED 10 SEPTEMBER 2019
http://www.demographic-research.org/Volumes/Vol41/24/
DOI: 10.4054/DemRes.2019.41.24

Research Article

The formal demography of kinship: A matrix formulation

Hal Caswell

Contents

Demographic Research: Volume 41, Article 24
Research Article

The formal demography of kinship: A matrix formulation

Hal Caswell[1]

Abstract

BACKGROUND
Any individual is surrounded by a network of kin that develops over her lifetime. In a justly famous paper, Goodman, Keyfitz, and Pullum (1974) presented formal calculations of the mean numbers of (female, matrilineal) kin implied by a mortality and fertility schedule.

OBJECTIVE
The aim of this paper is a new theory of kinship demography that provides age distributions as well as expected numbers, permits calculation of properties (e.g., dependency) of kin, is easily computable, and does not require simulation.

METHODS
The analysis relies on a novel application of the matrix formulation of cohort component population projection to describe the dynamics of a kinship network. The approach arises from the observation that the kin of a focal individual form a population, and can be modelled as one.

RESULTS
Kinship dynamics are described by a coupled system of non-autonomous matrix equations. I show how to calculate age distributions, total numbers, prevalence, dependency, and the experience of the death of relatives. As an example, I compare the kinship networks implied by the period vital rates of Japanese women in 1947 and 2014. Over this interval, fertility declined by 70% while life expectancy increased by 60%. The implications of these changes for kinship structure are profound; a lifetime dominated, under 1947 rates, by the experience of the death of kin has changed to one in which the death of kin is a rare event. On the other hand, the burden of dependent aged kin, including those suffering from dementia, is many-fold larger under 2014 rates.

[1] Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, Netherlands. Email: h.caswell@uva.nl.

CONCLUSIONS
This new theory opens to investigation hitherto inaccessible aspects of kinship, with potential applications to many problems in family demography.

1. Introduction

Birth and death are universals of demography. Every individual, without exception, will eventually die. Every individual, without exception, was born and most individuals will have the experience of producing children during their lives. No surprise then, that there exists a rich and powerful formal demographic theory of mortality, fertility, and how their interactions determine population growth and structure.

The third universal of human demography is kinship and family. The children of humans are unusually dependent, compared to other species (Hrdy 2009), and every individual human has some experience of family (or an attempted institutional substitute, as in orphanages). These family interactions reflect, in various ways in different cultures, the degrees of kinship among individuals. The development of a formal demography of kinship and families is challenging, because it requires accounting not only for individuals, but also for relations among individuals.

The analysis of kinship is a venerable problem (e.g., Greenwood and Yule 1914; Lotka 1931).[2] The modern approach to kinship was derived in a justly famous paper by Goodman, Keyfitz, and Pullum (1974; see also Keyfitz and Caswell 2005: Chap. 15). Their analysis takes as input an age schedule of mortality and fertility, and calculates from these schedules the mean numbers of specified kin [daughters, granddaughters (and further generations of descendants), mothers, grandmothers (and more remote generations of ancestors), sisters, nieces, maternal aunts, and cousins] of an individual at a specified age x. Their methodology is a tour de force of multiple integration over the survival and reproduction of all individuals involved in a type of kin, tracking the routes by which individuals of one type can produce surviving individuals of another type. Later extensions have led to more elaborate integral formulations (Krishnamoorthy 1979). Alternative calculations have been presented by Burch (1995), and important stochastic extensions by Pullum (Pullum 1982; Pullum and Wolf 1991).

As powerful as it is, the approach of Goodman, Keyfitz, and Pullum (1974) has limitations. It provides numbers of kin, but not their age distributions. It provides mean numbers of kin, but not variances or covariances. It describes living kin, but provides no information on the dead. It relies on age-classified vital rates, and does not generalize easily to stage-classified or multistate models. Its implementation requires multiple

[2] Perhaps the early interest in kinship was motivated because, in 1914, much of the world was ruled, at least nominally, by hereditary monarchs, a context in which kinship is of central political importance.

integrals to be approximated by high dimensional summations (Goodman, Keyfitz, and Pullum 1974) with a confusing proliferation of subscripts. This paper is the first report on a new approach to kinship demography that overcomes these limitations.

Kinship and kinship structures appear in diverse applications throughout demography (and, although it is not the focus here, population biology; see Tanskanen and Danielsbacka 2019). To cite just a few examples, consider (1) intergenerational transfers by bequests (Zagheni and Wagner 2015; Brennan, James, and Morrill 1982); (2) economic support for kin, including support of grandparents by children and grandchildren (e.g., Stecklov 2002; Wachter 1997; Tu, Freedman, and Wolf 1993; Himes 1992) and grandparents acting as a safety net for grandchildren (Bengtson 2001); (3) intergenerational reproductive conflict as a factor in the evolution of menopause (Lahdenperä et al. 2012; Croft et al. 2017); (4) the estimation of demographic parameters from limited data (Harpending and Draper 1990; McDaniel and Hammel 1984; Goldman 1978); (5) the medical and psychological implications of the experience of death of close kin (Umberson et al. 2017); (6) changes in generational overlap as populations age (Dykstra 2010); (7) social unrest fueled by the age distribution of children within families in societies where children of different orders have different social roles (Roche 2010, 2014); (8) "sandwich" families, where individuals care for both dependent children and aging parents (DeRigne and Ferrante 2012); (9) "boomerang" families in which adult children return to live with parents (Farris 2016); (10) orphanhood (e.g., due to HIV/AIDS) and its attendant social consequences (Jones and Morris 2003; Zagheni 2010; Kazeem and Jensen 2017); (11) the interaction of population aging and the likelihood of living ancestors (Gisser and Ediev 2019); and (12) intergenerational social mobility (Song 2016; Song and Mare 2017; Song and Campbell 2017; Mare and Song 2015).

This paper presents a new formulation of the demography of kinship. It provides not only the mean numbers of kin of an individual of any age, but also age distribution of the kin and a variety of demographic properties calculated from those distributions. It also calculates the experience of the death of kin and their ages at death.

Notation: In what follows, matrices are denoted by upper case bold characters (e.g., $\mathbf{U}$) and vectors by lower case bold characters (e.g., $\mathbf{a}$). 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 $\mathbf{I}$ is the identity matrix. The symbol $\circ$ denotes the Hadamard, or element-by-element product (implemented by .* in MATLAB and by * in R). The notation $\|\mathbf{x}\|$ denotes the 1-norm of $\mathbf{x}$. When necessary, subscripts may be used to denote the size of a vector or matrix; e.g., $\mathbf{I}_\omega$ is an identity matrix of size $\omega \times \omega$. On occasion, MATLAB notation will be used to refer to rows and columns; e.g., $\mathbf{F}(i,:)$ and $\mathbf{F}(:,j)$ referring to the ith row and jth column of the matrix $\mathbf{F}$.

2. The demography of kinship

Introducing Focal. The analysis is organized in terms of the kin of a focal individual. This individual appears so often as to deserve a name, so I will refer to her/him as Focal. Focal is an individual of a specified age and sex (female, for this paper), who might also be characterized by other properties, such as education, health, partnership status, parity, etc. Focal is a member of a population subject to a mortality and fertility schedule, and by any age will have developed a network of kin of different kinds and degrees of relatedness. The kin are the product of the reproduction of Focal (in the case of children), or of other kin (e.g., the sisters of Focal are the children of Focal's mother). In this paper, as in Goodman, Keyfitz, and Pullum (1974), calculations refer to female kin through female lineages.

The analysis here, like that of Goodman, Keyfitz, and Pullum (1974), makes three assumptions: (1) Homogeneity. All individuals in the population are subject to the same schedules of mortality and fertility. (2) Time invariance. The vital rates to which the individuals are subject do not change, and have not changed, over time. (3) Stability. The population is at the stable age (or age$\times$stage) structure implied by the mortality and fertility schedules. This assumption is implied by the assumptions of homogeneity and time invariance.

To relax the time-invariance assumption would require writing quantities as joint functions of time and the age of Focal, and will not be considered here. To relax the homogeneity assumption would require enlarging the i-state space to include the numbers and ages of kin of different kinds, each with its own rates. This will be pursued elsewhere. The stability assumption is used to obtain the mixing distribution of the ages of the mothers of Focal at the time of her birth. This could be relaxed by using an empirically measured distribution of ages of mothers.

The population of which Focal is a part is characterized by a mortality and a fertility schedule. The mortality schedule is incorporated into a matrix $\mathbf{U}$, of dimension $\omega \times \omega$, with survival probabilities on the subdiagonal and zeros elsewhere. The fertility schedule is incorporated into a matrix $\mathbf{F}$, of dimension $\omega \times \omega$, with effective fertility on the first row and zeros elsewhere. For example, if $\omega = 3$,

$$\mathbf{U} = \begin{pmatrix} 0 & 0 & 0 \\ p_1 & 0 & 0 \\ 0 & p_2 & [p_3] \end{pmatrix} \qquad \mathbf{F} = \begin{pmatrix} f_1 & f_2 & f_3 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}. \tag{1}$$

The optional entry in the ω, ω position in $\mathbf{U}$ describes an open final age interval. Effective fertility refers to the production of daughters. Stage-classified models would lead to other structures for $\mathbf{U}$ and $\mathbf{F}$. The population projection matrix describing Focal's population is

$$\mathbf{A} = \mathbf{U} + \mathbf{F}. \tag{2}$$

It has the familiar Leslie matrix structure, with non-zero entries only on the subdiagonal and the first row (e.g., Leslie 1945; Caswell 2001).

The vital rates in $\mathbf{A}$ imply an asymptotic population growth rate λ given by the dominant eigenvalue of $\mathbf{A}$ (or the corresponding continuous-time rate $r = \log \lambda$), and a stable age distribution given by the associated right eigenvector $\mathbf{w}$, scaled to sum to 1. The net reproductive rate R_0 is given by the dominant eigenvalue of the matrix $\mathbf{F}\left(\mathbf{I} - \mathbf{U}\right)^{-1}$.

An important role in kinship calculations is played by the distribution of the ages of the mothers of offspring produced in the population, which is denoted $\boldsymbol{\pi}$. Here, this distribution is taken to be that implied by the stable population, which is given by

$$\boldsymbol{\pi} = \frac{\mathbf{F}(1,:)^{\mathsf{T}} \circ \mathbf{w}}{\|\mathbf{F}(1,:)^{\mathsf{T}} \circ \mathbf{w}\|} \tag{3}$$

The mean age over this distribution is the generation time (Coale 1972). Other distributions could be substituted for this stable population if desired.

2.1 The kin of Focal are a population

The key to the what follows is the recognition that *the kin, of any specified degree, of Focal comprise a population*, albeit one with some special properties. Being a population, the kin might as well be modeled as such. This deceptively simple observation is key to the analysis.

Let the vector $\mathbf{k}(x)$ denote the age distribution of the population of some specified type of kin, at age x of Focal. This vector $\mathbf{k}(x)$ contains the survivors of the population at Focal's age $x - 1$, with survival accounted for by the matrix $\mathbf{U}$.

The kin of Focal subsidized population. That is, new members of the population arise not from reproduction of current members, but from elsewhere (Pascual and Caswell 1991; Caswell 2008).[3] For example, new daughters of Focal do not arise from reproduction of current daughters (those are grand-daughters), but from the reproduction of Focal.

The kin of Focal at birth provide the initial condition for the dynamics. This initial condition, $\mathbf{k}(0) = \mathbf{k}_0$, depends on the type of kin considered. Focal will, for example, have no daughters at birth, but may very well have older sisters.

Combining survival, subsidy, and initial conditions yields the model for the dynamics of the kin $\mathbf{k}(x)$:

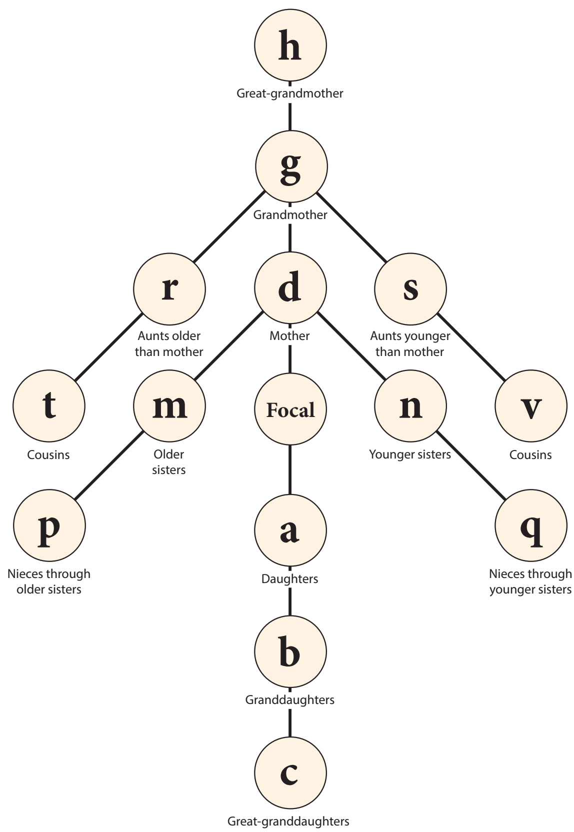
$$\mathbf{k}(x+1) = \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x) \tag{4}$$

$$\mathbf{k}(0) = \mathbf{k}_0 \tag{5}$$

[3] Subsidy is common in species with widely dispersed offspring, such as many marine invertebrates, and also appears in models of recruitment to organizations (e.g., Pollard 1968); such systems are referred to as 'open' by Bartholomew (1982). Now subsidy appears also in the dynamics of kin.

where x is the age of Focal and $\boldsymbol{\beta}(x)$ is a vector giving the age distribution of the subsidy of these kin at age x of Focal.

Figure 1: The kinship network. The network of kin defined in Goodman, Keyfitz, and Pullum (1974) and Keyfitz and Caswell (2005). The symbols (a, b, etc.) are used here to denote the age distribution vectors of each type of kin of Focal. That is, e.g., $\mathrm{a}(x)$ is the expected age distribution of daughters at age x of Focal.



Focal is surrounded by a network of kin of different types and different degrees of relatedness. My goal here is to describe the dynamics of this network; the model is a coupled system of non-autonomous matrix difference equations of the form (4) and (5).

Figure 1, modified from Goodman, Keyfitz, and Pullum (1974), shows a portion of this network. I consider only direct matrilineal descent (mothers, daughters, granddaughters, etc.) and only consanguineal relationships. Each of these 14 types of kin is described by a population vector ($\mathbf{a}(x)$, $\mathbf{b}(x)$, $\ldots$), as indicated in Figure 1. Keeping track of 14 types of kin poses notational challenges, because some symbols need to be used for other purposes. The rationale behind the exclusion of some letters from the assignments in Figure 1 is as follows. The symbol $\mathbf{e}_j$ is already in use as the jth unit vector (i.e., a vector with a 1 in the jth entry and zeros elsewhere), $\mathbf{F}$ is the fertility matrix, i and j are reserved for indices and counters, $\mathbf{k}$ is used to refer to a generic kin, ℓ is the survivorship function, $\mathbf{o}$ is generally confusing as a symbol, $\mathbf{U}$ is the transition and survival matrix, $\mathbf{w}$ the stable age distribution, and x is age.

The network in Figure 1 can be extended further in the direction of descendants, ancestors, and chains derived from the siblings of ancestors (as, for example, cousins are the descendants of the siblings of the mother of Focal). I will discuss some of these descendants below.

Armed with these definitions and the general model in (4) and (5), we can proceed to derive models for the dynamics of each type of kin.

2.1.1 Daughters and descendants

Each type of descendent depends on the reproduction of another type of descendent, or of Focal herself.

$\mathbf{a}(x)$ **= daughters of Focal.** Daughters are the result of the reproduction of Focal. Since Focal is assumed to be alive at age x, the subsidy vector is $\boldsymbol{\beta}(x) = \mathbf{F}\mathbf{e}_x$, where $\mathbf{e}_x$ is the unit vector for age x. Because we may be sure that Focal has no daughters when she is born, the initial condition is $\mathbf{a}_0 = \mathbf{0}$. Thus

$$\begin{aligned} \mathbf{a}(x+1) &= \mathbf{U}\mathbf{a}(x) + \mathbf{F}\mathbf{e}_x && (6) \\ \mathbf{a}_0 &= \mathbf{0}. && (7) \end{aligned}$$

$\mathbf{b}(x)$ **= granddaughters of Focal.** Granddaughters are the children of the daughters of Focal. At age x of Focal, these daughters have age distribution $\mathbf{a}(x)$, so $\boldsymbol{\beta}(x) = \mathbf{F}\mathbf{a}(x)$. Because Focal has no granddaughters at birth, the initial condition is $\mathbf{0}$;

$$\begin{aligned} \mathbf{b}(x+1) &= \mathbf{U}\mathbf{b}(x) + \mathbf{F}\mathbf{a}(x) && (8) \\ \mathbf{b}_0 &= \mathbf{0}. && (9) \end{aligned}$$

$\mathbf{c}(x)$ **= great-granddaughters of Focal.** Similarly, great-granddaughters are the result of reproduction by the granddaughters of Focal, with an initial condition of $\mathbf{0}$.

$$\begin{aligned} \mathbf{c}(x+1) &= \mathbf{U}\mathbf{c}(x) + \mathbf{F}\mathbf{b}(x) \qquad (10) \\ \mathbf{c}_0 &= \mathbf{0}. \qquad (11) \end{aligned}$$

The extension to arbitrary levels of direct descendants is obvious. Let $\mathbf{k}_n$, in this case, be the age distribution of descendants of level n, where $n = 1$ denotes children. Then

$$\mathbf{k}_{n+1}(x+1) = \mathbf{U}\mathbf{k}_{n+1}(x) + \mathbf{F}\mathbf{k}_n(x) \qquad (12)$$

with the initial condition

$$\mathbf{k}_{n+1}(0) = \mathbf{k}_n(0) = 0$$

2.1.2 Mothers and ancestors

The surviving mothers and other direct ancestors depend on the age of those ancestors at the time of the birth of Focal.

$\mathbf{d}(x)$ **= mothers of Focal.** The population of mothers of focal consists of at most a single individual (step-mothers are not considered here). It has an expected age distribution, and is subject to survival according to $\mathbf{U}$. No new mothers arrive after Focal's birth, so the subsidy term is $\boldsymbol{\beta}(x) = \mathbf{0}$.
At the time of Focal's birth, she has exactly one mother, but we do not know her age. Hence the initial age distribution $\mathbf{d}_0$ of mothers is a mixture of unit vectors $\mathbf{e}_i$; the mixing distribution is the distribution $\boldsymbol{\pi}$ of ages of mothers given by (3). Thus,

$$\begin{aligned} \mathbf{d}(x+1) &= \mathbf{U}\mathbf{d}(x) + \mathbf{0} \qquad (13) \\ \mathbf{d}_0 &= \sum_i \pi_i \mathbf{e}_i = \boldsymbol{\pi}. \qquad (14) \end{aligned}$$

$\mathbf{g}(x)$ **= grandmothers of Focal.** The grandmothers of Focal are the mothers of the mother of Focal. No new grandmothers appear, so once again the subsidy term $\boldsymbol{\beta}(x) = \mathbf{0}$. The age distribution of grandmothers at the birth of Focal is the age distribution of the mothers of Focal's mother, at the age of Focal's mother when Focal is born. The age of Focal's mother at Focal's birth is unknown, so the initial age distribution of grandmothers is a mixture of the age distributions $\mathbf{d}(x)$ of mothers, with mixing distribution $\boldsymbol{\pi}$:

$$\begin{aligned} \mathbf{g}(x+1) &= \mathbf{U}\mathbf{g}(x) + \mathbf{0} \qquad (15) \\ \mathbf{g}_0 &= \sum_i \pi_i \mathbf{d}(i). \qquad (16) \end{aligned}$$

$\mathbf{h}(x)$ **= great-grandmothers of Focal.** Again, the subsidy term is $\boldsymbol{\beta}(x) = \mathbf{0}$. The initial condition is a mixture of the age distributions of the grandmothers of Focal, with mixing distribution $\boldsymbol{\pi}$:

$$\begin{aligned} \mathbf{h}(x+1) &= \mathbf{U}\mathbf{h}(x) + \mathbf{0} && (17) \\ \mathbf{h}_0 &= \sum_i \pi_i \mathbf{g}(i). && (18) \end{aligned}$$

The extension to arbitrary levels of direct ancestry is clear. Let $\mathbf{k}_n$ be, in this case, the age distribution of ancestors of level n, where $n = 1$ denotes mothers. Then the dynamics and initial conditions are

$$\begin{aligned} \mathbf{k}_{n+1}(x+1) &= \mathbf{U}\mathbf{k}_{n+1}(x) + \mathbf{0} && (19) \\ \mathbf{k}_{n+1}(0) &= \sum_i \pi_i \mathbf{k}_n(i). && (20) \end{aligned}$$

Note that, because Focal has at most one mother, grandmother, etc., the expected number of mothers, grandmothers, etc. is also the probability of having a living mother, grandmother, etc.

2.1.3 Sisters and nieces

The sisters of Focal, and their children, who are the nieces of Focal, form the first set of side branches in the kinship network of Figure 1. Following Goodman, Keyfitz, and Pullum (1974), it is convenient to divide the sisters of Focal into older and younger sisters, because they follow different dynamics.

$\mathbf{m}(x)$ **= older sisters of Focal.** Once Focal is born, she accumulates no more older sisters, so the subsidy term is $\boldsymbol{\beta}(x) = \mathbf{0}$. At Focal's birth, her older sisters are the children $\mathbf{a}(i)$ of the mother of Focal at the age i of Focal's mother at Focal's birth. This age is unknown, so the initial condition $\mathbf{m}_0$ is a mixture of the age distributions of children with mixing distribution $\boldsymbol{\pi}$.

$$\begin{aligned} \mathbf{m}(x+1) &= \mathbf{U}\mathbf{m}(x) + \mathbf{0} && (21) \\ \mathbf{m}_0 &= \sum_i \pi_i \mathbf{a}(i). && (22) \end{aligned}$$

$\mathbf{n}(x)$ **= younger sisters of Focal.** Focal has no younger sisters when she is born, so the initial condition is $\mathbf{n}_0 = \mathbf{0}$. Younger sisters are produced by reproduction of Focal's mother, so the subsidy term is the reproduction of the mothers at age x of Focal.

$$\begin{aligned} \mathbf{n}(x+1) &= \mathbf{U}\mathbf{n}(x) + \mathbf{F}\mathbf{d}(x) && (23) \\ \mathbf{n}_0 &= \mathbf{0}. && (24) \end{aligned}$$

$\mathbf{p}(x)$ **= nieces through older sisters of Focal.** At the birth of Focal, these nieces are the granddaughters of the mother of Focal, so the initial condition is mixture of granddaughters with mixing distribution $\boldsymbol{\pi}$. New nieces through older sisters are the result of reproduction by the older sisters, at age x, of Focal.

$$\mathbf{p}(x+1) = \mathbf{U}\mathbf{p}(x) + \mathbf{F}\mathbf{m}(x) \tag{25}$$
$$\mathbf{p}_0 = \sum_i \pi_i \mathbf{b}(i). \tag{26}$$

$\mathbf{q}(x)$ **= nieces through younger sisters of Focal.** At the birth of Focal she has no younger sisters, and hence has no nieces through these sisters. Thus the initial condition is $\mathbf{q}_0 = \mathbf{0}$. New nieces are produced by reproduction of the younger sisters of Focal.

$$\mathbf{q}(x+1) = \mathbf{U}\mathbf{q}(x) + \mathbf{F}\mathbf{n}(x) \tag{27}$$
$$\mathbf{q}_0 = \mathbf{0}. \tag{28}$$

2.1.4 Aunts and cousins

Aunts and cousins form another level of side branching on the kinship network; their dynamics follow the same principles as those for sisters and nieces.

$\mathbf{r}(x)$ **= aunts older than mother of Focal.** These are the older sisters of the mother of Focal. Once Focal is born, her mother accumulates no new older sisters, so the subsidy term is $\boldsymbol{\beta}(x) = \mathbf{0}$. The initial age distribution of these aunts, at the birth of Focal, is a mixture of the age distributions $\mathbf{m}$ of older sisters, with mixing distribution $\boldsymbol{\pi}$

$$\mathbf{r}(x+1) = \mathbf{U}\mathbf{r}(x) + \mathbf{0} \tag{29}$$
$$\mathbf{r}_0 = \sum_i \pi_i \mathbf{m}(i). \tag{30}$$

$\mathbf{s}(x)$ **= aunts younger than mother of Focal.** These are the younger sisters of the mother of Focal. These aunts are the children of the grandmother of Focal, and thus the subsidy term comes from reproduction by the grandmothers of Focal. The initial age distribution of these aunts, at the birth of Focal, is a mixture of the age distributions $\mathbf{n}$ of younger sisters, with mixing distribution $\boldsymbol{\pi}$.

$$\mathbf{s}(x+1) = \mathbf{U}\mathbf{s}(x) + \mathbf{F}\mathbf{g}(x) \tag{31}$$
$$\mathbf{s}_0 = \sum_i \pi_i \mathbf{n}(i). \tag{32}$$

$\mathbf{t}(x)$ **= cousins from aunts older than mother of Focal.** These are the children of the older sisters of the mother of Focal, and thus the nieces of the mother of Focal through her older sisters. The subsidy term comes from reproduction by the older sisters of the mother of Focal.The initial condition is a mixture of the age distributions of nieces through older sisters, with mixing distribution $\boldsymbol{\pi}$.

$$\mathbf{t}(x+1) = \mathbf{U}\mathbf{t}(x) + \mathbf{F}\mathbf{r}(x) \tag{33}$$

$$\mathbf{t}_0 = \sum_i \pi_i \mathbf{p}(i). \tag{34}$$

$\mathbf{v}(x)$ **= cousins from aunts younger than mother of Focal.** These are the nieces of the mother of Focal through her younger sisters. The subsidy term comes from reproduction by the younger sisters of the mother of Focal. The initial condition is a mixture of the age distributions of nieces through younger sisters, with mixing distribution $\boldsymbol{\pi}$.

$$\mathbf{v}(x+1) = \mathbf{U}\mathbf{v}(x) + \mathbf{F}\mathbf{s}(x) \tag{35}$$

$$\mathbf{v}_0 = \sum_i \pi_i \mathbf{q}(i). \tag{36}$$

2.1.5 Model summary

The dynamics of the entire network of 14 types of consanguineal kin in Figure 1 are summarized in Table 1. Note that each kin type depends only on kin types above it in the table. Thus there are no circular dependencies to render the model insoluble. Note also that the side chains through nieces, cousins, etc. can be extended just as the chains of descendants and ancestors are extended in equations (12) and (19).

Table 1: Summary of the components of the kin model given in equations (4) and (5)

Symbol	Kin	Initial condition	Subsidy $\boldsymbol{\beta}(x)$
$\mathbf{a}$	daughters	$\mathbf{0}$	$\mathbf{F}\mathbf{e}_x$
$\mathbf{b}$	granddaughters	$\mathbf{0}$	$\mathbf{F}\mathbf{a}(x)$
$\mathbf{c}$	great-granddaughters	$\mathbf{0}$	$\mathbf{F}\mathbf{b}(x)$
$\mathbf{d}$	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	$\mathbf{0}$	$\mathbf{F}\mathbf{d}(x)$
$\mathbf{p}$	nieces via older sisters	$\sum_i \pi_i \mathbf{b}(i)$	$\mathbf{F}\mathbf{m}(x)$
$\mathbf{q}$	nieces via younger sisters	$\mathbf{0}$	$\mathbf{F}\mathbf{n}(x)$
$\mathbf{r}$	aunts older than mother	$\sum_i \pi_i \mathbf{m}(i)$	$\mathbf{0}$
$\mathbf{s}$	aunts younger than mother	$\sum_i \pi_i \mathbf{n}(i)$	$\mathbf{F}\mathbf{g}(x)$
$\mathbf{t}$	cousins from aunts older than mother	$\sum_i \pi_i \mathbf{p}(i)$	$\mathbf{F}\mathbf{r}(x)$
$\mathbf{v}$	cousins from aunts younger than mother	$\sum_i \pi_i \mathbf{q}(i)$	$\mathbf{F}\mathbf{s}(x)$

3. Derived properties of kin

Because the model provides the age distributions of all types of kin, it makes it possible to compute what might be called derived properties of the age distribution of kin. These might be linear functions of the age distribution, leading to a model

$$\mathbf{k}(x+1) = \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x) \tag{37}$$

$$\mathbf{k}(0) = \mathbf{k}_0 \tag{38}$$

$$\mathbf{y}(x) = \boldsymbol{\Psi}(x)\mathbf{k}(x) \tag{39}$$

where $\mathbf{y}(x)$ is a vector of the property in question at age x of focal, and $\boldsymbol{\Psi}(x)$ is the matrix of a linear transformation from the age distribution to the property vector. Examples of such derived properties include

1. Numbers of kin, in which case $\boldsymbol{\Psi}(x) = \mathbf{1}_\omega^\mathsf{T}$.
2. Prevalence, in which case $\boldsymbol{\Psi}(x)$ is a vector containing, e.g., age-specific prevalence of some condition, such as disease, disability, health, labor force participation, etc.
3. Measures of economic dependency. For example, if three dependency categories are defined (young-age dependency, old-age dependency, and independence), then each row of $\boldsymbol{\Psi}$ would pick out the ages corresponding to one of the dependency groups. For six age classes, with two classes in each dependency category, the resulting matrix would be

$$\boldsymbol{\Psi} = \begin{pmatrix} 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{pmatrix} \tag{40}$$

4. Coresidence probability. This is actually a special case of prevalence, where the condition is “coresiding with Focal.”

Nonlinear functions of $\mathbf{k}(x)$ (e.g., dependency ratios) can also be calculated. One important set of such derived properties are the mean, and other moments, of the age of a particular set of relatives.

5. Moments of age distribution. Define vectors

$$\mathbf{c}_i = \begin{pmatrix} 0.5^i & 1.5^i & \cdots & (\omega - 0.5)^i \end{pmatrix}^{\mathsf{T}} \qquad i = 1, 2, \ldots. \tag{41}$$

   Define μ_i as the ith moment of age (so that the mean age is μ_1). The ith moment of the age of the kin $\mathbf{k}(x)$ is

$$\mu_i(x) = \mathbf{c}_i^{\mathsf{T}} \frac{\mathbf{k}(x)}{\|\mathbf{k}(x)\|} \tag{42}$$

   (provided, of course, that $\|\mathbf{k}(x)\| > 0$). In particular, the mean and variance of the age of kin are

$$E\left(\mu(x)\right) = \mu_1(x) \tag{43}$$

$$V\left(\mu(x)\right) = \mu_2(x) - \mu_1(x)^2. \tag{44}$$

A useful operation is the aggregation of kin types. It is possible to aggregate the kinship network in Figure 1 by adding the appropriate vectors.

6. Aggregation of kin.
   Figure 1 disaggregates the older and younger sisters of Focal. The total number of sisters is the sum of the older and younger sisters,

$$\text{sisters} = \mathbf{m}(x) + \mathbf{n}(x). \tag{45}$$

   An important aggregation is that based on degree. Degrees of kinship are defined in both civil and religious law, and determine ability to marry, aspects of inheritance, jury selection, restrictions on nepotism in hiring, and other fascinating things. According to one version,

$$\text{first degree kin} = \mathbf{a}(x) + \mathbf{d}(x) \tag{46}$$

$$\text{second degree kin} = \mathbf{b}(x) + \mathbf{g}(x) + \mathbf{m}(x) + \mathbf{n}(x) \tag{47}$$

$$\text{third degree kin} = \mathbf{h}(x) + \mathbf{c}(x) + \mathbf{r}(x) + \mathbf{s}(x) + \mathbf{p}(x) + \mathbf{q}(x). \tag{48}$$

4. Death of kin

The experience of the death of close relatives can have long-lasting effects on an individual (e.g., Umberson et al. 2017). The experience by Focal of the death of kin can be calculated directly from the kinship model. To do so, we expand the kin population vector $\mathbf{k}$ to include dead as well as living kin, creating a new vector

$$\tilde{\mathbf{k}} = \left(\begin{array}{c} \mathbf{k}_{\text{living}} \\ \hline \mathbf{k}_{\text{dead}} \end{array} \right). \tag{49}$$

The tilde distinguishes this multistate vector from the vector containing only living relatives.

Two possibilities present themselves for calculations with deceased relatives. We can calculate the deaths of kin experienced by Focal at a given age x, or the cumulative deaths experienced by Focal up to a given age x. The calculations require only a simple change to the matrices $\mathbf{U}$ and $\mathbf{F}$, and the vector $\mathbf{k}_0$, in order to account for both living and dead kin.

In order for $\mathbf{k}_{\text{dead}}(x)$ to capture the age distribution of the deaths experienced by Focal at age x, $\mathbf{U}$ is replaced by the block-structured matrix

$$\tilde{\mathbf{U}} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{0} \end{array} \right). \tag{50}$$

The mortality matrix $\mathbf{M}$ contains the transition probabilities from ages of kin (columns of $\mathbf{M}$) to the state of being dead at a particular age (rows of $\mathbf{M}$). Thus

$$\mathbf{M} = \mathcal{D}(\mathbf{q}). \tag{51}$$

The matrix $\mathbf{0}$ in the lower right corner of $\tilde{\mathbf{U}}$ removes the dead individuals after a single time step. The result is the projection

$$\tilde{\mathbf{k}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{k}}(x) + \tilde{\boldsymbol{\beta}}(x). \tag{52}$$

The fertility matrix $\mathbf{F}$ that appears in $\boldsymbol{\beta}(x)$ is replaced by the matrix

$$\tilde{\mathbf{F}} = \left(\begin{array}{c|c} \mathbf{F} & \mathbf{0} \\ \hline \mathbf{0} & \mathbf{0} \end{array} \right) \tag{53}$$

which asserts no dead offspring are produced (this could be modified to account for stillbirth) and that the dead do not reproduce.

To calculate the cumulative deaths experienced by Focal up to age x, rather than the deaths experienced at a given age, the matrix $\mathbf{U}$ is replaced by

$$\tilde{\mathbf{U}} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{I} \end{array} \right) \tag{54}$$

where again

$$\mathbf{M} = \mathcal{D}(\mathbf{q}).$$

The identity matrix in the lower right corner of $\tilde{\mathbf{U}}$ keeps the dead kin in an absorbing state corresponding to their age at death.

The initial condition $\tilde{\mathbf{k}}_0$ for the partitioned kin vector accounts for the fact that Focal has experienced no deaths at the time of her birth. Thus,

$$\tilde{\mathbf{k}}_0 = \left(\begin{array}{c} \mathbf{k}_0 \\ \hline \mathbf{0} \end{array} \right) \tag{55}$$

where $\mathbf{k}_0$ is the initial vector for kin $\mathbf{k}$ as described in Table 1.

These calculations can be extended to include deaths that occur before the birth of Focal (e.g., "your grandmother died before you were born") or after the death of Focal (e.g., Queen Victoria died in 1901 at the age of 81, but of her 87 great-grandchildren, several were born after 1901, and of course other descendants continue to appear). These extensions will be presented elsewhere.

5. An example: Changes in the kinship network of Japan

As an example of the model, I explore the implications for the kinship network of changes in the mortality and fertility schedules of Japanese women from 1947 and 2014. This period saw dramatic changes in both mortality (life expectancy increased by about 60%) and fertility (total fertility rate decreased by 70% and the net reproductive rate declined by about 60%), as shown in Figure 2.

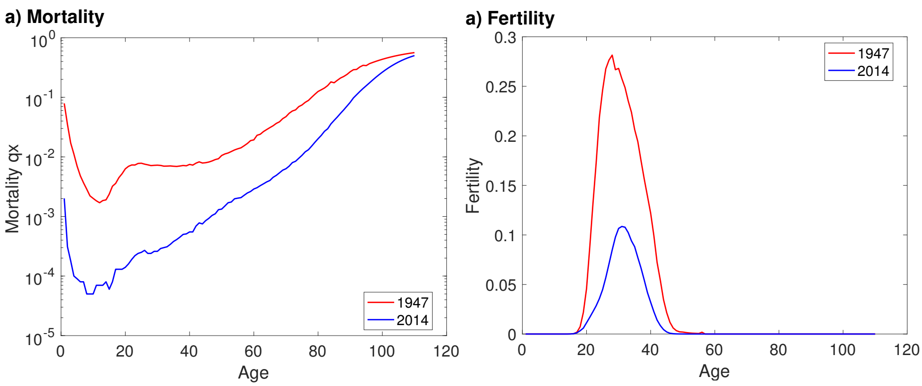
	1947	2014	% change
life exp	54	87	+61%
TFR	4.6	1.4	−70%
R_0	1.7	0.7	−59%

The matrices $\mathbf{U}$ and $\mathbf{F}$ are created from the mortality (q_x) schedules and the age-specific fertility schedules from the Human Mortality Database and Human Fertility Database (Human Mortality Database 2018; Human Fertility Database 2018). MATLAB code for the calculations is given in the online materials.

Note that this is just an example; it is not intended as a detailed examination of the kinship demography of Japan. Also note that for convenience I will speak of, e.g., "Japan in 1947" instead of the more correct "a stable population subject to the period mortality and fertility schedules of Japan as measured in 1947."

For the convenience of the reader, results of the calculations are collected together, in graphical form, for selected types of kin, in Section 7. For the truly curious, an Online Supplementary collection contains figures for all types of kin for each of the categories examined here.

Figure 2: Mortality and fertility. The mortality and fertility schedules for Japanese women in 1947 and 2014



Source: Data from Human Mortality Database (2018) and Human Fertility Database (2018).

5.1 Age distributions

Figure 4 shows the age distributions of mothers, grandmothers, daughters, granddaughters, sisters, and cousins, for a Focal individual aged 30 and aged 70. The mothers of Focal at 30 are slightly older under 2014 rates than under 1947 rates, and far more common. Focal at age 70 has essentially no chance of a living mother in 1947, but still some chance of a very elderly living mother in 2014 (Figure 4a). The situation with grandmothers is similar (Figure 4b), but more extreme. No living grandmothers remain at age 70 of Focal, but at age 30 grandmothers are about 4 times more likely and about 10 years older in 2014 compared to 1947.

Daughters and granddaughters (Figures 4c and d) are less abundant in 2014 than in 1947, reflecting the lower fertility in 2014. Granddaughters are more abundant than daughters in 1947, but less abundant in 2014, reflecting the net reproductive rates at those two times (population increase in 1947, population decline in 2014).

The age distributions of sisters and cousins (Figure 4e and f) show the effects of the mortality difference between 1947 and 2014. In 1947, Focal loses about 40% of her sisters and cousins between the ages of 30 and 70. In 2014, there is almost no loss of sisters or cousins between these ages.

5.2 Numbers of kin

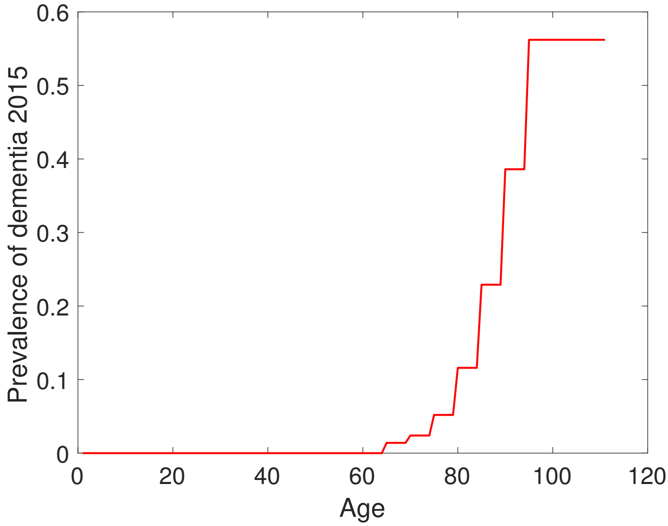
Figure 5 shows the numbers of living kin as a function of the age of Focal. Comparing daughters, granddaughters, and great-granddaughters (Figures 5a, c, and e) shows the integrated effects of mortality and fertility changes between 1947 and 2014. In 1947, Focal reaches a peak of about 3 times more daughters than does Focal in 2014, but the number of living daughters declines after about age 40 of Focal. In 2014, fewer daughters are produced, and there is hardly any decline in the number of daughters due to mortality. Comparing the numbers of granddaughters and great-granddaughters shows the pattern hinted at in Figure 4: Focal in 1947 has progressively more descendants in each generation, while Focal in 2014 has fewer.

For ancestors (Figures 5b, d, and f), the intergenerational pattern is reversed. Focal in 2014 is more likely to have a surviving mother than Focal in 1947; the differential increases for grandmothers and great-grandmothers.

5.3 Prevalence of dementia

As an example of using equation (39) to map from age distributions to the prevalence of some condition, consider kin suffering from dementia. Figure 3 shows the age-specific prevalence of dementia in Japanese females in 2015 (Fukawa 2018): a roughly exponential increase starting at age 60. In the absence of information on the prevalence pattern in 1947, I will use this prevalence schedule for both years.

Figure 3: Dementia prevalence. Age-specific prevalence of dementia among Japanese women in 2015



Source: Data from Fukawa (2018).

Figure 6 shows the numbers of kin with dementia, as a function of the age of Focal, in 1947 and 2014. Focal is far more likely to have a mother, grandmother, or great-grandmother with dementia in 2014 than in 1947 (Figures 6a, c, and d). The difference is large (about 7-fold for mothers, even greater for grandmothers and great-grandmothers). The same holds for sisters (Figure 6b) and aunts (Figure 4d). Among cousins, the difference is not as great, but the prevalence of dementia among kin is still higher in 2014 than 1947.

5.4 Mean and variance of ages of kin

The means and standard deviations of the ages of several types of kin are shown in Figures 7 and 8. Mean ages naturally increase with the age of Focal. For both ancestors (mothers, grandmothers, etc.) and descendants (daughters, granddaughters, etc.) there is little difference between 1947 and 2014, perhaps because the timing of fertility does not change much between those years.

The standard deviation of descendants increases with age of Focal, and is slightly higher under 1947 rates than 2014 rates, presumably because of the higher mortality rates in 1947. The standard deviation of the age of ancestors decreases with the age of

Focal, with no consistent differences between 1947 and 2014 rates. Maximum standard deviations are on the order of 6 to 8 years. Differences between 1947 and 2014 rates are small relative to other properties, because the timing of reproduction shows only minor changes.

5.5 Dependency of kin

Figure 9 shows, as a function of the age of Focal, the numbers of kin in three categories of dependence. Young dependence is defined here as ages 0–15, old dependence as ages greater than 65, and independence as ages 16–65. These could easily be replaced with more detailed descriptors of economic contribution.

Figure 9 shows results for 1947 in solid lines, and 2014 in dashed lines. Dependent children, grandchildren, and great-grandchildren accumulate earlier, and much more rapidly, for Focal in 1947 than in 2014. Focal in 1947 was much more likely to have dependent great-granddaughters than in 2014, reflecting the greater numbers of descendants under those conditions (cf. Figure 5).

The pattern is reversed when considering dependent mothers, grandmothers, and great-grandmothers, which are much more abundant in 2014 than in 1947. A short description of the pattern would be that Focal in 1947 confronts more dependent children and descendants, but in 2014 she is faced with more dependent parents and ancestors.

5.6 Death of kin

Turning now to the death of kin, Figure 10 shows the experience of death of kin at each age of Focal, and Figure 11 shows the cumulative deaths experienced up to each age of Focal. As far as deaths of kin are concerned, the world changed dramatically between 1947 and 2014. The deaths of daughters, granddaughters, mothers, sisters, and aunts occur earlier and far more frequently under the rates of 1947. Focal in 2014 will almost never experience the death of a daughter or granddaughter (Figures 10a, b; 11a and b). It is rare for Focal in 2014 to experience the death of a sister before the age of 60, but in 1947 such deaths occur frequently from the birth of Focal.

6. Discussion

The model of Goodman, Keyfitz, and Pullum (1974) relies on multiple integrals to calculate expected numbers of kin of different kinds, at a specified age of a focal individual. The method presented here, in contrast, is a coupled system of matrix equations that projects the population of kin forward as Focal ages. The mathematics (formally, a coupled system of non-autonomous matrix difference equations) may sound more complicated. It is not. As with any dynamical system, the dynamic equations carry out the necessary integrations, but with much more flexibility. Together, the assumptions of homogeneity and time invariance make it possible to extend the equations for parents and children to include all the kin shown in Table 1, and even beyond that, as in equation (12) for arbitrary levels of descendants. A brief comparison of the results given by Goodman, Keyfitz, and Pullum (1974) and those produced by this model shows qualitative agreement, but with quantitative differences probably due to the (unspecified) choice of numerical integration methods applied to the coarsely-resolved (5 year age intervals) life tables available in 1974. The freedom from the need to carry out such numerical integration, and from the error propagation involved with multiple integrals, is a strength of the present method.

One advantage of formal mathematical specification is that it makes explicit the assumptions underlying an analysis. As Goodman, Keyfitz, and Pullum (1974) pointed out repeatedly, these results are not expected to give the same results as a census of the kin of individuals of different ages, precisely because the assumptions are counterfactuals. The value of comparing calculated kinship structures with empirical kinship censuses is not to test the mathematics, but to see how the actual kinship network is warped by violation of the assumptions.

It will be interesting to relax the assumptions. Relaxing the assumption of homogeneity will require extending the state space to include additional dimensions affecting kinship (marital status is one obvious possibility) in age$\times$stage or multistate models (Caswell et al. 2018). Parity dependence is another important dimension. Schoen (2019) presents theory for close kin in terms of parity progression, under the assumption that all women live to the end of their reproductive years and that mortality does not affect children. He emphasizes that parity progression, when used as a model for fertility, automatically captures some important aspects of sibship and family formation. Incorporating age and parity into the reproductive component of the model here will permit exploration of these effects under less restrictive assumptions.

The analysis here, and the example in Section 5, are formulated in terms of female survival and fertility, and relatives through the female line. It is clearly possible to carry out the same analysis using male survival and fertility; it will be interesting to do so to see the effect of the extended timing of male fertility, especially in hunter–gatherer populations (e.g., Tuljapurkar, Puleston, and Gurven 2007). A generalization to include both male and female kin, through both male and female lines of descent, will be presented elsewhere.

In addition to extensions to male as well as female kin, several other extensions are under active investigation. The present model is age-classified, which implies that age alone determines mortality and fertility. Stage-classified and multistate models will allow age to interact with other characteristics (marital status, health status, etc.). Relaxing the assumption of time invariance will require the extension of the time domain to include not only the age x of Focal but also the time before or after the birth of Focal.

Finally, note that the results of these calculations, like those of Goodman, Keyfitz, and Pullum (1974), provide *expected* age distributions. While the kin of Focal form a population, that population is small and thus subject to demographic stochasticity. Stochastic versions of the model could be constructed using branching process methods, as discussed by Pullum (1982). Connections of multitype branching processes to matrix population models are explored by Pollard (1966), Caswell (2001), and Caswell and Vindenes (2018). Alternatively, stochastic realizations of the dynamic models here, or even complete microsimulation models (e.g., Wachter 1997), can provide information on variances and higher moments.

The analysis, presented here as an example, using vital rates for Japan shows how this method can reveal differences in the kinship patterns implied by different mortality and fertility schedules. The differences, using rates in 1947 and 2014, are dramatic. In 1947, the kinship structure of a Japanese woman was full of the experience of the death of close kin, often at young ages. In 2014, such experiences are rare or non-existent. On the other hand, a Japanese woman in 2014 is many times more likely to experience elderly dependent kin, or kin suffering from dementia, than was the case under 1947 rates. These results are presented here as examples of the use of the kinship theory presented here, but they make it obvious that using the theory to explore the effects of changes in mortality and fertility is an important next step.

7. Figures

Figure 4: Age distributions. The age distributions of several types of kin, at ages 30 (solid lines) and 70 (dashed lines) of Focal. Calculated from the vital rates of Japan in 1947 (red) and 2014 (blue).

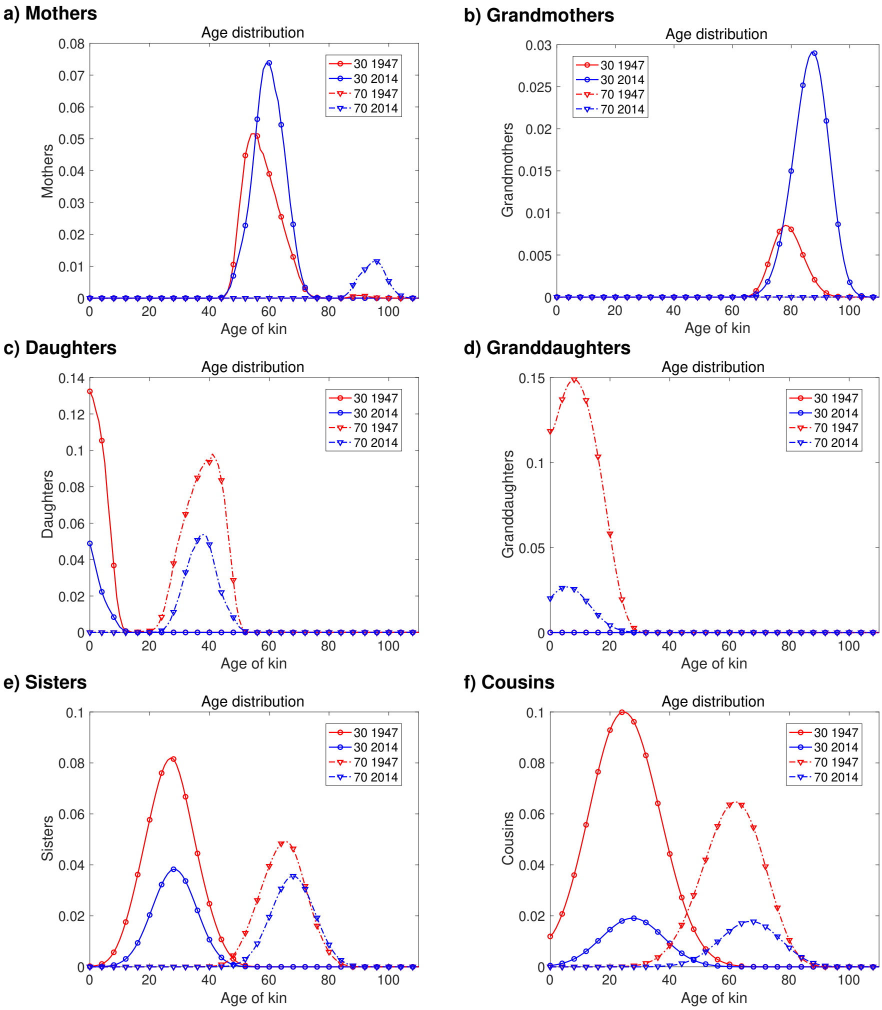


Figure 5: Numbers. Numbers of kin of several types, as a function of the age of Focal. Calculated from the vital rates of Japan in 1947 (red) and 2014 (blue).

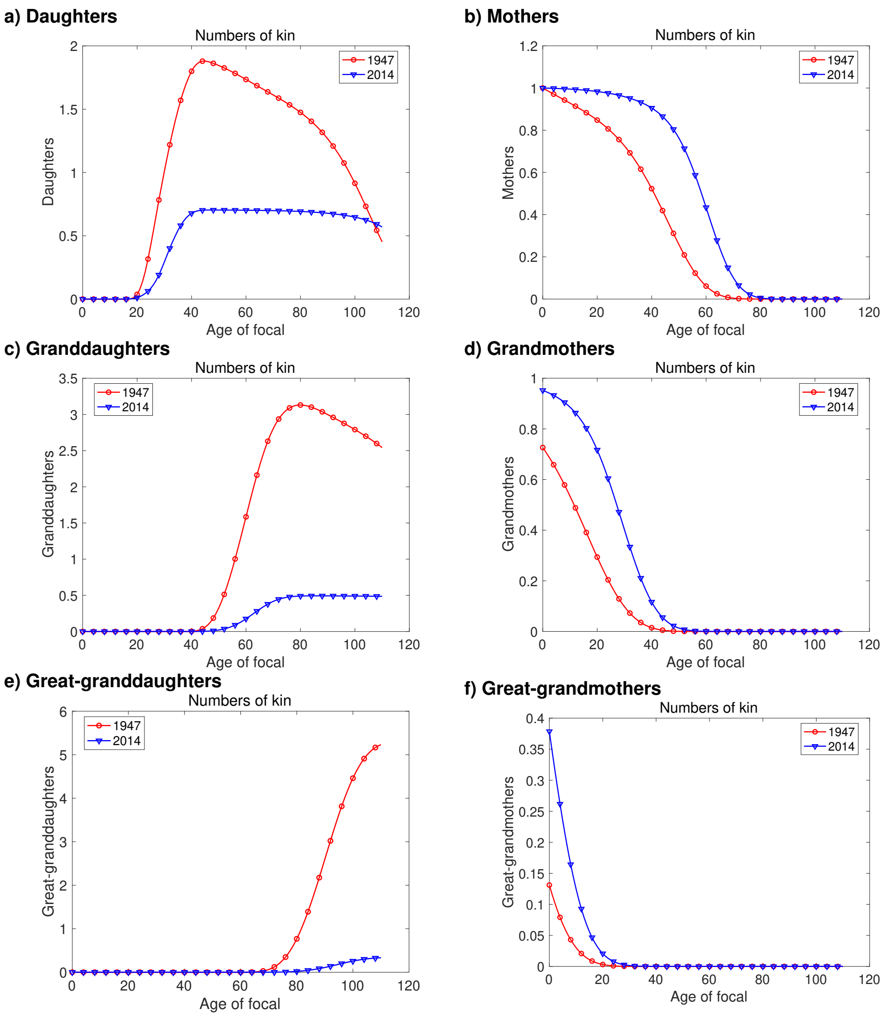


Figure 6: Kin with dementia. Numbers of kin of several types suffering from dementia, as a function of the age of Focal. Calculated from the vital rates of Japan in 1947 (red) and 2014 (blue), using dementia prevalence rates for Japanese females in 2015.

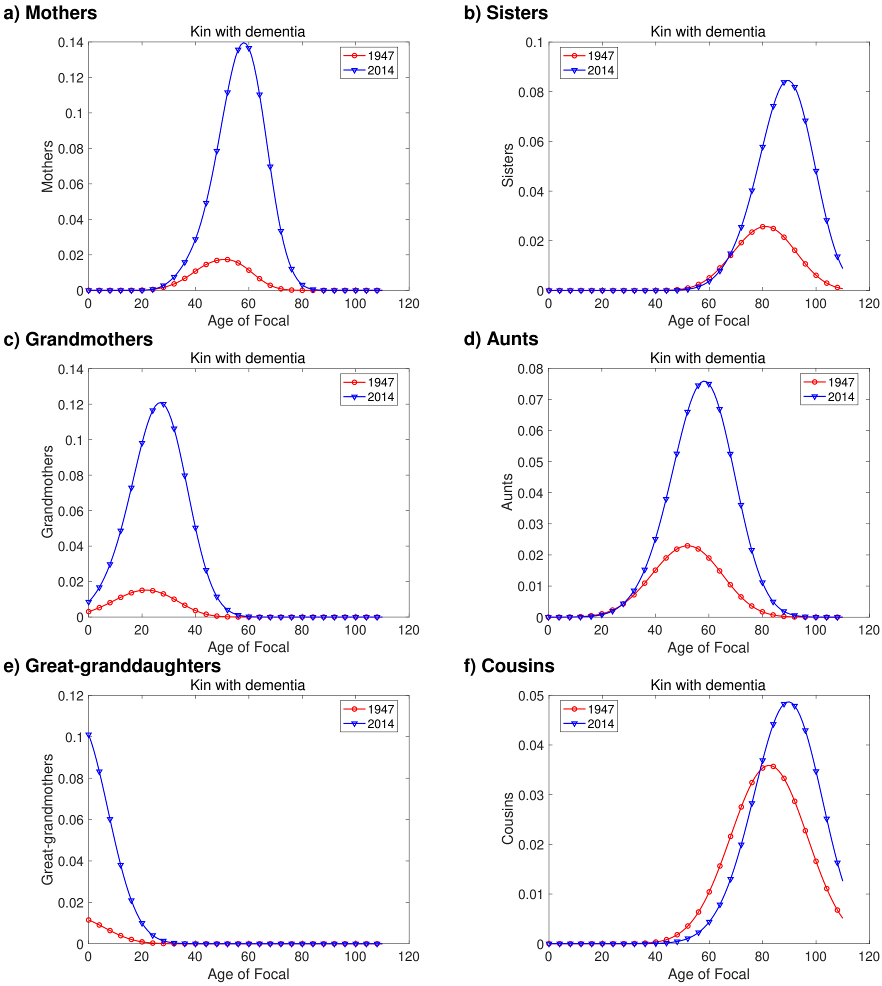


Figure 7: Mean age. The mean age of kin of several types, as a function of the age of Focal. Calculated from the vital rates of Japan in 1947 (red) and 2014 (blue). The mean age is set to zero when the number of kin drops below 10^{-9}.

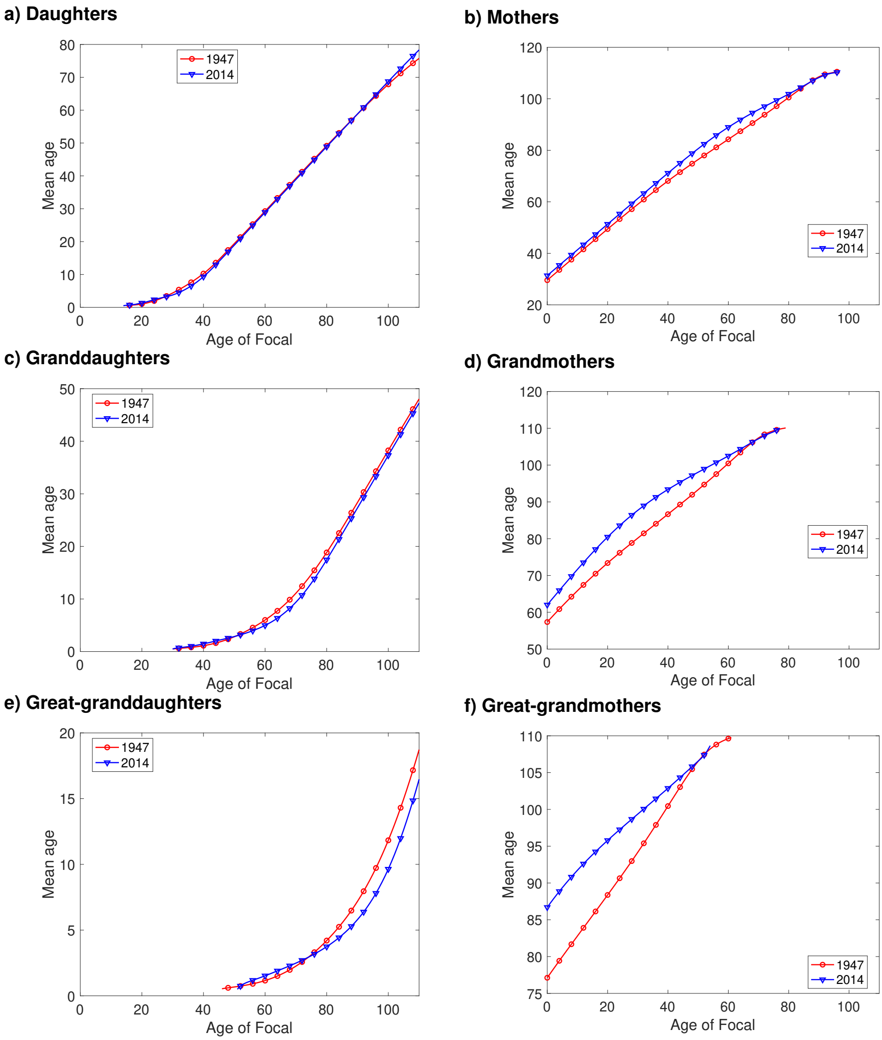


Figure 8: Standard deviation of age. The standard deviation (in years) of the age of kin of several types, as a function of the age of Focal. Calculated from the vital rates of Japan in 1947 (red) and 2014 (blue).

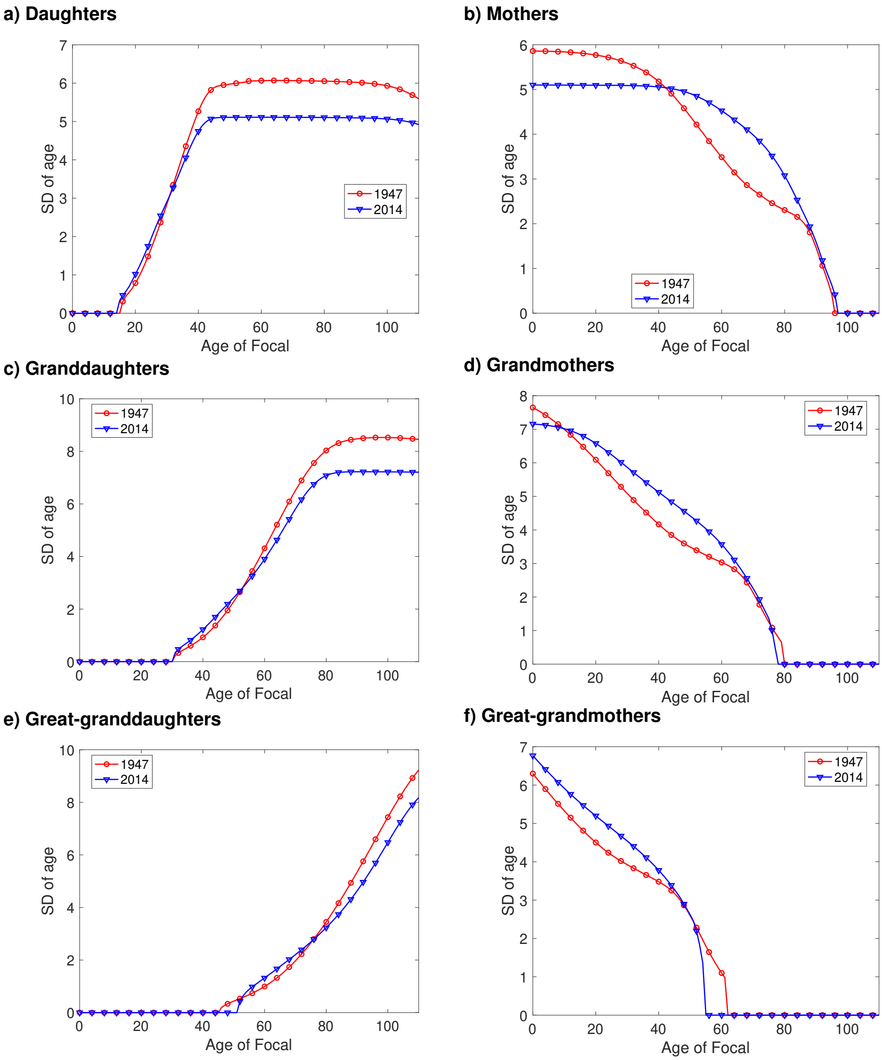


Figure 9: Dependency of kin. Numbers of kin, of several types, in three different dependency categories: young dependents aged 0–16, old dependents aged more than 65, and independent kin aged 16–65, as a function of the age of Focal. Calculated from the vital rates of Japan in 1947 (solid lines) and 2014 (dashed lines).

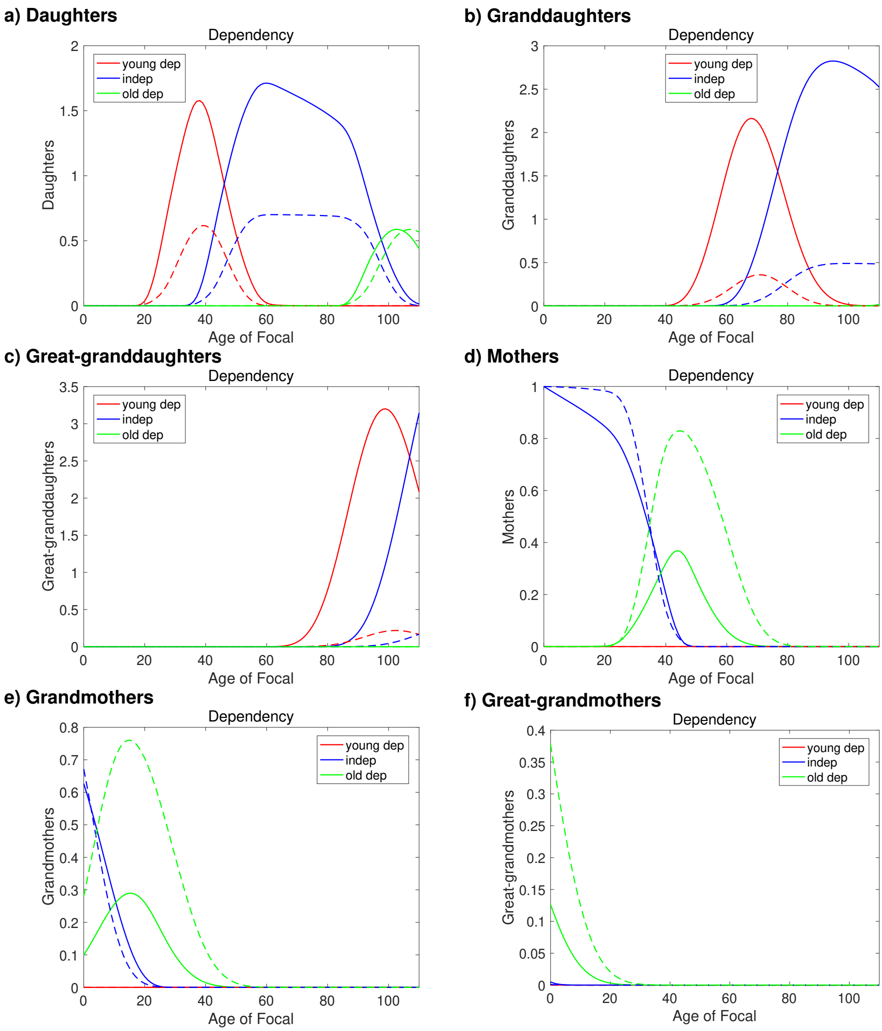


Figure 10: **Experienced deaths. Numbers of deaths of kin, of several types, experienced by Focal at each age. Calculated from the vital rates of Japan in 1947 and 2014.**

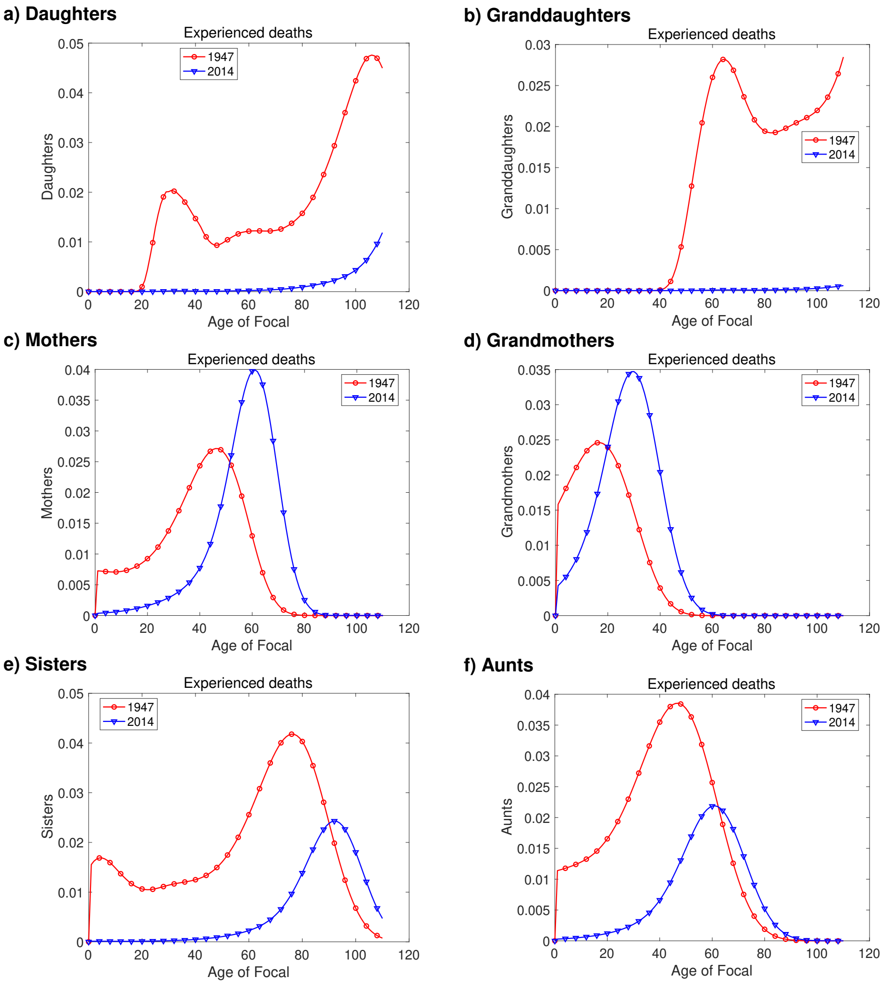
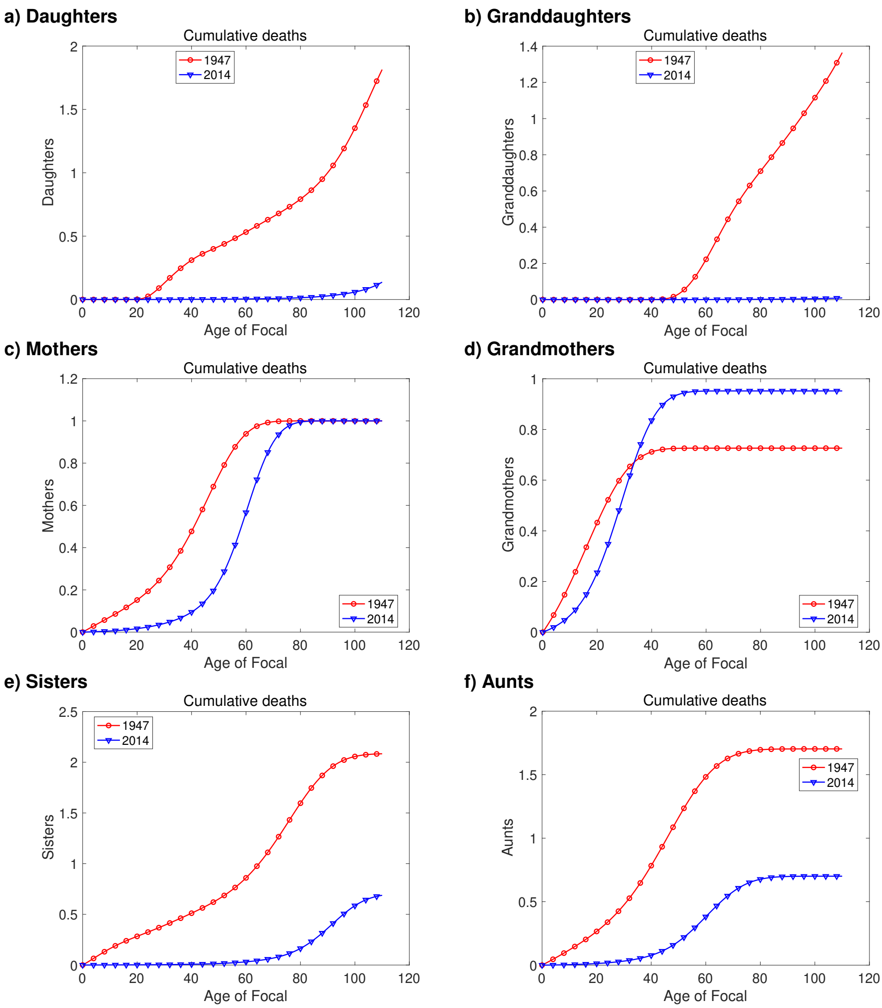


Figure 11: Cumulative deaths. The cumulative numbers of deaths of kin experienced by Focal up to each age. Calculated from the vital rates of Japan in 1947 and 2014.



8. Acknowledgments

This research was supported by the European Research Council under the European Union's Horizon 2020 research and innovation program, ERC Advanced Grant 788195. I thank Thomas Pullum, Andrew Noymer, and two anonymous reviewers for helpful comments. Discussions with Jim Oeppen, Xi Song, Silke van Daalen, Lotte de Vries, Robert Schoen, and the Theoretical Ecology group at the University of Amsterdam were helpful throughout. Thanks to Motion Coffee, Amsterdam, and to Emilio Zagheni for the casual conversation, years ago, in which the question of a matrix approach was first raised.

References

Bartholomew, D.J. (1982). *Stochastic models for social processes*. New York: Wiley.

Bengtson, V.L. (2001). Beyond the nuclear family: The increasing importance of multigenerational bonds. *Journal of Marriage and Family* 63(1): 1–16. doi:10.1111/j.1741-3737.2001.00001.x.

Brennan, E.R., James, A.V., and Morrill, W.T. (1982). Inheritance, demographic structure, and marriage: A cross-cultural perspective. *Journal of Family History* 7(3): 289–298. doi:10.1177/036319908200700304.

Burch, T.K. (1995). Estimating the Goodman, Keyfitz, Pullum kinship equations: An alternative procedure. *Mathematical Population Studies* 5(2): 161–170. doi:10.1177/036319908200700304.

Caswell, H. (2001). *Matrix population models: Construction, analysis, and interpretation*. Sunderland: Sinauer, 2nd ed.

Caswell, H. (2008). Perturbation analysis of nonlinear matrix population models. *Demographic Research* 18(3): 59–116. doi:10.4054/DemRes.2008.18.3.

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 Vindenes, Y. (2018). Demographic variance in heterogeneous populations: Matrix models and sensitivity analysis. *Oikos* 127(5): 648–663. doi:10.1111/oik.04708.

Coale, A.J. (1972). *The growth and structure of human populations: A mathematical approach*. Princeton: Princeton University Press.

Croft, D.P., Johnstone, R.A., Ellis, S., Nattrass, S., Franks, D., Brent, L.J., Mazzi, S., Balcomb, K.C., Ford, J.K., and Cant, M.A. (2017). Reproductive conflict and the evolution of menopause in killer whales. *Current Biology* 27(2): 298–304. doi:10.1016/j.cub.2016.12.015.

DeRigne, L. and Ferrante, S. (2012). The sandwich generation: A review of the literature. *Florida Public Health Review* 9: 95–104.

Dykstra, P.A. (2010). Intergenerational family relationships in ageing societies. New York: United Nations. https://www.unece.org/fileadmin/DAM/pau/_docs/age/2010/Intergenerational-Relationships/ECE-WG.1-11.pdf.

Farris, D.N. (2016). *Boomerang kids: The demography of previously launched adults*. Cham: Springer. doi:10.1007/978-3-319-31227-9.

Fukawa, T. (2018). Prevalence of dementia among the elderly population of japan. *Health and Primary Care* 2(4): 1–6. doi:10.15761/HPC.1000147.

Gisser, R. and Ediev, D.M. (2019). Having ancestors alive: Trends and prospects in ageing Europe. In: Schoen, R. (ed.). *Analytical family demography*. Cham: Springer: 241–274. doi:10.1007/978-3-319-93227-9_11.

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.

Greenwood, M. and Yule, G.U. (1914). On the determination of size of family and of the distribution of characters in order of birth from samples taken through members of the sibships. *Journal of the Royal Statistical Society* 77(2): 179–199. doi:10.2307/2339801.

Harpending, H. and Draper, P. (1990). Estimating parity of parents: Application to the history of infertility among the !Kung of Southern Africa. *Human Biology* 62(2): 195–203.

Himes, C.L. (1992). Future caregivers: Projected family structures of older persons. *Journal of Gerontology* 47(1): S17–S26. doi:10.1093/geronj/47.1.S17.

Hrdy, S.B. (2009). *Mothers and others*. Cambridge: Harvard University Press.

Human Fertility Database (2018). Human fertility database [electronic resource]. Rostock and Vienna: Max Planck Institute for Demographic Research and the Vienna Institute of Demography. http://www.humanfertility.org.

Human Mortality Database (2018). Human mortality database [electronic resource]. Berkeley and Rostock: University of California, Berkeley and Max Planck Institute for Demographic Research. http://www.mortality.org.

Jones, J.H. and Morris, M. (2003). *Orphans and 'grandorphans' in sub-Saharan Africa: The consequences of dependent mortality*. Paper presented at the Annual Meeting of the Population Association of America, Minneapolis, USA, May 1–3, 2003.

Kazeem, A. and Jensen, L. (2017). Orphan status, school attendance, and relationship to household head in Nigeria. *Demographic Research* 36(22): 659–690. doi:10.4054/DemRes.2017.36.22.

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

Krishnamoorthy, S. (1979). Family formation and the life cycle. *Demography* 16(1): 121–129. doi:10.2307/2061083.

Lahdenperä, M., Gillespie, D.O., Lummaa, V., and Russell, A.F. (2012). Severe intergenerational reproductive conflict and the evolution of menopause. *Ecology Letters* 15(11): 1283–1290. doi:10.1111/j.1461-0248.2012.01851.x.

Leslie, P.H. (1945). On the use of matrices in certain population mathematics. *Biometrika* 33(3): 183–212. doi:10.1093/biomet/33.3.183.

Lotka, A.J. (1931). Orphanhood in relation to demographic factors. *Metron* 9: 37–109.

Mare, R.D. and Song, X. (2015). *The changing demography of multigenerational relationships*. Paper presented at the Annual Meeting of the Population Association of America, San Diego, USA, April 30–May 2, 2015.

McDaniel, C. and Hammel, E. (1984). A kin-based measure of r and an evaluation of its effectiveness. *Demography* 21(1): 41–51. doi:10.2307/2061026.

Pascual, M. and Caswell, H. (1991). The dynamics of a size-classified benthic population with reproductive subsidy. *Theoretical Population Biology* 39(2): 129–147. doi:10.1016/0040-5809(91)90032-B.

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:10.1093/biomet/53.3-4.397.

Pollard, J.H. (1968). A note on the age structures of learned societies. *Journal of the Royal Statistical Society Series A: General* 131(4): 569–578. doi:10.2307/2343724.

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

Pullum, T.W. and Wolf, D.A. (1991). Correlations between frequencies of kin. *Demography* 28(3): 391–409. doi:10.2307/2061018.

Roche, S. (2010). From youth bulge to conflict: The case of Tajikistan. *Central Asian Survey* 29(4): 405–419. doi:10.1080/02634937.2010.533968.

Roche, S. (2014). *Domesticating youth: Youth bulges and their socio-political implications in Tajikistan*. New York: Berghahn Books.

Schoen, R. (2019). Parity progression and the kinship network. In: Schoen, R. (ed.). *Analytical family demography*. Cham: Springer: 189–199.

Song, X. (2016). Diverging mobility trajectories: Grandparent effects on educational attainment in one- and two-parent families in the United States. *Demography* 53(6): 1905–1932. doi:10.1007/s13524-016-0515-5.

Song, X. and Campbell, C.D. (2017). Genealogical microdata and their significance for social science. *Annual Review of Sociology* 43: 75–99. doi:10.1146/annurev-soc-073014-112157.

Song, X. and Mare, R.D. (2017). Short-term and long-term educational mobility of families: A two-sex approach. *Demography* 54(1): 145–173. doi:10.1007/s13524-016-0540-4.

Stecklov, G. (2002). The economic boundaries of kinship in Côte d'Ivoire. *Population Research and Policy Review* 21(4): 351–375. doi:10.1023/A:1020072023054.

Tanskanen, A.O. and Danielsbacka, M. (2019). *Intergenerational family relations: An evolutionary social science approach*. New York: Routledge.

Tu, E.J.C., Freedman, V.A., and Wolf, D.A. (1993). Kinship and family support in taiwan: A microsimulation approach. *Research on Aging* 15(4): 465–486. doi:10.1177/0164027593154006.

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.

Umberson, D., Olson, J., Crosnoe, R., Liu, H., Pudrovska, T., and Donnelly, R. (2017). Death of family members as an overlooked source of racial disadvantage in the United States. *Proceedings of the National Academy of Sciences* 114(5): 915–920. doi:10.1073/pnas.1605599114.

Wachter, K.W. (1997). Kinship resources for the elderly. *Philosophical Transactions of the Royal Society of London Series B: Biological Sciences* 352(1363): 1811–1817. doi:10.1098/rstb.1997.0166.

Zagheni, E. (2010). The impact of the HIV/AIDS epidemic on orphanhood probabilities and kinship structure in Zimbabwe [PhD Thesis]. Berkeley: University of California, Berkeley.

Zagheni, E. and Wagner, B. (2015). The impact of demographic change on intergenerational transfers via bequests. *Demographic Research* 33(18): 525–534. doi:10.4054/DemRes.2015.33.18.