The formal demography of kinship: a matrix formulation*
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Abstract

Background. Any individual is surrounded by a network of kin that develops over her life. 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.

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

Results. The dynamics of the kinship network is described by a coupled system of non-autonomous matrix difference equations. They arise from the observation that the kin of a focal individual form a population, and can be modelled as one. 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.

Contribution. This theory opens to investigation hitherto inaccessible aspects of kinship, with potential applications to many problems in family demogaphy.

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).[1] 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 descendents), 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 et al. (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

[1] 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.

or multistate models. Its implementation requires multiple integrals to be approximated by high dimensional summations (Goodman et al., 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 (i) intergenerational transfers by bequests (Zagheni and Wagner, 2015; Brennan et al., 1982); (ii) economic support for kin, including support of grandparents by children and grandchildren (e.g., Stecklov, 2002; Wachter, 1997; Tu et al., 1993; Himes, 1992) and grandparents acting as a safety net for grandchildren (Bengtson, 2001); (iii) intergenerational reproductive conflict as a factor in the evolution of menopause (Lahdenperä et al., 2012; Croft et al., 2017); (iv) network and group formation in anthropological populations (Hammel, 2005; Alvard, 2011); (v) the estimation of demographic parameters from limited data (Harpending and Draper, 1990; McDaniel and Hammel, 1984; Goldman, 1978); (vi) the medical and psychological implications of the experience of death of close kin (Umberson et al., 2017); (vii) 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); (viii) "sandwich" families, where individuals care for both dependent children and aging parents (DeRigne and Ferrante, 2012); (ix) "boomerang" families in which adult children return to live with parents (Farris, 2016); (x) impact of orphanhood (e.g., due to HIV/AIDS) and its attendant social consequences (Jones and Morris, 2003; Zagheni, 2010; Kazeem and Jensen, 2017); and (xi) intergenerational social mobility, particularly effects of grandparents (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., $\mathbf{a}$). 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. The symbol

$\circ$ denotes the Hadamard, or element-by-element product. The notation $\|\mathbf{x}\|$ denotes the 1-norm of $\mathbf{x}$.

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).

The analysis here, like that of Goodman et al. (1974), makes three assumptions:(1) *Uniformity.* 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 $\mathbf{U}$ and $\mathbf{F}$. 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 uniformity 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. Stage-classified models would lead to other structures for $\mathbf{U}$ and $\mathbf{F}$. The population projection matrix describing Focal's population is

$$\mathbf{A} = \mathbf{U} + \mathbf{F}. \tag{1}$$

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 $\mathbf{A}$, 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, with is given by

$$\boldsymbol{\pi} = \frac{\mathbf{F}(1,:)^{\mathsf{T}} \circ \mathbf{w}}{\|\mathbf{F}(1,:)^{\mathsf{T}} \circ \mathbf{w}\|} \tag{2}$$

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 modelled 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 $\mathbf{k}(x)$ are a *subsidized* population. That is, new members of the population do not arise from reproduction of current members, but come from elsewhere (Pascual and Caswell, 1991; Caswell, 2008).[2] For example, new daughters of Focal do not arise from reproduction of current daughters (those would be grand-daughters), but from the reproduction of Focal. The kin of Focal at birth

[2]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). Now it appears also in the dynamics of kin.

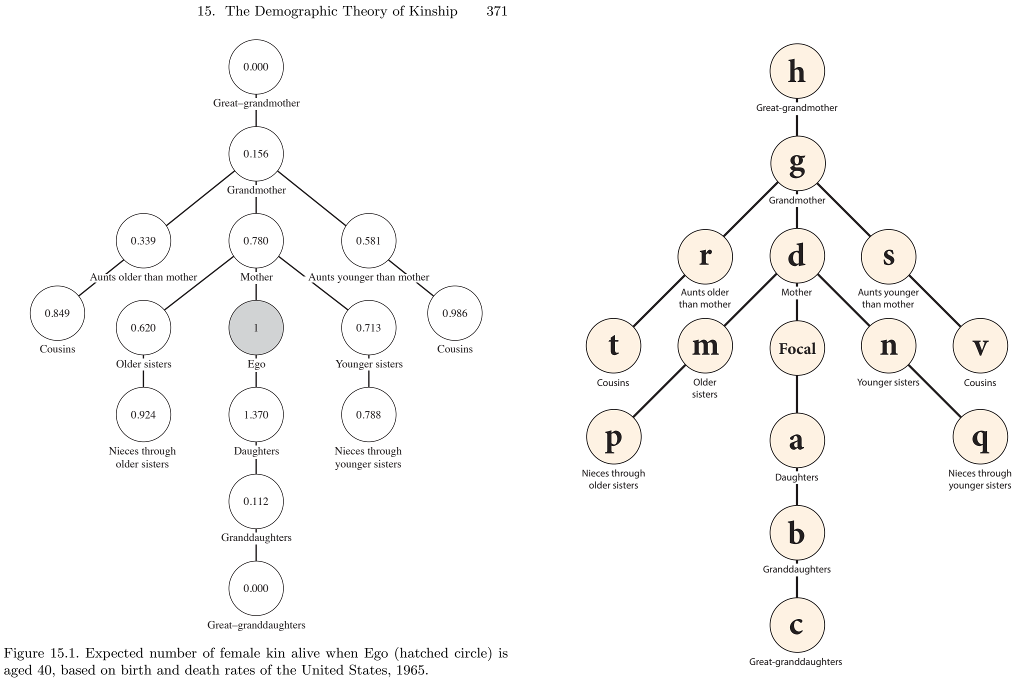


Figure 1: Left: The network of kin defined in Goodman et al. (1974) and Keyfitz and Caswell (2005). Right: The symbols ($\mathbf{a}$, $\mathbf{b}$, etc.) used here to denote the age distribution vectors of each type of kin of Focal.

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 a model for the dynamics of the kin $\mathbf{k}(x)$ is

$$\mathbf{k}(x+1) = \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x) \tag{3}$$

$$\mathbf{k}(0) = \mathbf{k}_0 \tag{4}$$

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.

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 (3) and (4). Figure 1, modified from Goodman et al. (1974), shows a portion of this network. I consider only direct matrilineal descent (mothers, daughters, granddaughters, ...) and only consanguineal relationships. Each of these 14 types of kin is described by a population vector ($\mathbf{a}(x)$, $\mathbf{b}(x)$,...), 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 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 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 descendents, ancestors, and chains derived from the siblings of ancestors (as, for example, cousins are the descendents of the siblings of the mother of Focal). I will discuss some of these descendents below.

Armed with these definitions and the general model in (3) and (4), we can proceed to derive models for the dynamics of each type of kin.

2.1.1 Daughters and descendents

$\mathbf{a}(x)$ = 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 $\boldsymbol{\beta}(x) = \mathbf{F}\mathbf{e}_x$. Because we may be sure that Focal has no daughters when she is born, the initial condition is $\mathbf{a}_0 = \mathbf{0}$. Thus

$$\mathbf{a}(x+1) = \mathbf{U}\mathbf{a}(x) + \mathbf{F}\mathbf{e}_x \tag{5}$$

$$\mathbf{a}_0 = \mathbf{0} \tag{6}$$

$\mathbf{b}(x)$ = 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 $\mathbf{0}$.

$$\mathbf{b}(x+1) = \mathbf{U}\mathbf{b}(x) + \mathbf{F}\mathbf{a}(x) \tag{7}$$

$$\mathbf{b}_0 = \mathbf{0} \tag{8}$$

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

$$
\begin{aligned}
\mathbf{c}(x+1) &= \mathbf{U}\mathbf{c}(x) + \mathbf{F}\mathbf{b}(x) & (9)\\
\mathbf{c}_0 &= \mathbf{0} & (10)
\end{aligned}
$$

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

$$
\mathbf{k}_{n+1}(x+1) = \mathbf{U}\mathbf{k}_{n+1}(x) + \mathbf{F}\mathbf{k}_n(x) \tag{11}
$$

with the initial condition $\mathbf{k}_{n+1}(0) = \mathbf{k}_n(0) = \mathbf{0}$.

2.1.2 Mothers and ancestors

$\mathbf{d}(x)$ **= mothers of Focal.** The population of mothers of focal consists of at most a single individual (step-mothers are not considered here), but has an age distribution, and is subject to survival according to $\mathbf{U}$. No new mothers arrive, 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 (2). Thus,

$$
\begin{aligned}
\mathbf{d}(x+1) &= \mathbf{U}\mathbf{d}(x) + \mathbf{0} & (12)\\
\mathbf{d}_0 &= \sum_i \pi_i \mathbf{e}_i \;=\; \boldsymbol{\pi} & (13)
\end{aligned}
$$

$\mathbf{g}(x)$ **= 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

$\boldsymbol{\pi}$:

$$\begin{aligned} \mathbf{g}(x+1) &= \mathbf{U}\mathbf{g}(x) + \mathbf{0} & (14) \\ \mathbf{g}_0 &= \sum_i \pi_i \mathbf{d}(i) & (15) \end{aligned}$$

$\mathbf{h}(x)$ = 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 $\boldsymbol{\pi}$:

$$\begin{aligned} \mathbf{h}(x+1) &= \mathbf{U}\mathbf{h}(x) + \mathbf{0} & (16) \\ \mathbf{h}_0 &= \sum_i \pi_i \mathbf{g}(i) & (17) \end{aligned}$$

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

$$\begin{aligned} \mathbf{k}_{n+1}(x+1) &= \mathbf{U}\mathbf{k}_{n+1}(x) + \mathbf{0} & (18) \\ \mathbf{k}_{n+1}(0) &= \sum_i \pi_i \mathbf{k}_n(i) & (19) \end{aligned}$$

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. Following Goodman et al. (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 $\boldsymbol{\pi}$.

$$\mathbf{m}(x+1) = \mathbf{U}\mathbf{m}(x) + \mathbf{0} \tag{20}$$

$$\mathbf{m}_0 = \sum_i \pi_i \mathbf{a}(i) \tag{21}$$

$\mathbf{n}(x)$ **= younger sisters of Focal.** Focal can have no younger sisters at the time of her birth, 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.

$$\mathbf{n}(x+1) = \mathbf{U}\mathbf{n}(x) + \mathbf{F}\mathbf{d}(x) \tag{22}$$

$$\mathbf{n}_0 = \mathbf{0} \tag{23}$$

$\mathbf{p}(x)$ **= 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.

$$\mathbf{p}(x+1) = \mathbf{U}\mathbf{p}(x) + \mathbf{F}\mathbf{m}(x) \tag{24}$$

$$\mathbf{n}_0 = \sum_i \pi_i \mathbf{b}(i) \tag{25}$$

$\mathbf{q}(x)$ **= 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 through reproduction by the younger sisters of Focal.

$$\mathbf{q}(x+1) = \mathbf{U}\mathbf{q}(x) + \mathbf{F}\mathbf{n}(x) \tag{26}$$

$$\mathbf{q}_0 = \mathbf{0} \tag{27}$$

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 $\boldsymbol{\pi}$

$$\mathbf{r}(x+1) = \mathbf{U}\mathbf{r}(x) + \mathbf{0} \tag{28}$$

$$\mathbf{r}_0 = \sum_i \pi_i \mathbf{m}(i) \tag{29}$$

$\mathbf{s}(x)$ **= 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 $\boldsymbol{\pi}$.

$$\mathbf{s}(x+1) = \mathbf{U}\mathbf{s}(x) + \mathbf{F}\mathbf{g}(x) \tag{30}$$

$$\mathbf{s}_0 = \sum_i \pi_i \mathbf{n}(i) \tag{31}$$

$\mathbf{t}(x)$ **= 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 $\boldsymbol{\pi}$.

$$\mathbf{t}(x+1) = \mathbf{U}\mathbf{t}(x) + \mathbf{F}\mathbf{r}(x) \tag{32}$$

$$\mathbf{t}_0 = \sum_i \pi_i \mathbf{p}(i) \tag{33}$$

$\mathbf{v}(x)$ **= 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 distri-

Symbol	Kin	i.c. $\mathbf{k}_0$	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	$\mathbf{0}$	$\mathbf{F}\mathbf{d}(i)$
$\mathbf{p}$	nieces via older sisters	$\sum_i \pi_i \mathbf{b}(i)$	$\mathbf{F}\mathbf{m}(x)$
$\mathbf{q}$	nieces via younger sisters	$\mathbf{0}$	$\mathbf{F}\mathbf{n}(i)$
$\mathbf{r}$	aunts older than mother	$\sum_i \pi_i \mathbf{m}(x)$	$\mathbf{0}$
$\mathbf{s}$	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	$\sum_i \pi_i \mathbf{q}(i)$	$\mathbf{F}\mathbf{s}(x)$

Table 1: Summary of the components of the kin model given in equations (3) and (4).

bution $\boldsymbol{\pi}$.

$$\mathbf{v}(x+1) = \mathbf{U}\mathbf{v}(x) + \mathbf{F}\mathbf{s}(x) \tag{34}$$

$$\mathbf{v}_0 = \sum_i \pi_i \mathbf{q}(i) \tag{35}$$

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 proceeding through nieces, cousins, etc. can be extended just as the chains of descendents and ancestors are extended in equations (11) and (18).

3 Derived properties of kin

Because the model provides the age distributions of all types of kin, it is straightforward to compute what might be called *properties* of the age distribution of kin. In the simple case, these are linear functions of the age distribution, leading to a model

$$\mathbf{k}(x+1) = \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x) \tag{36}$$

$$\mathbf{k}(0) = \mathbf{k}_0 \tag{37}$$

$$\mathbf{y}(x) = \boldsymbol{\Phi}(x)\mathbf{k}(x) \tag{38}$$

where $\mathbf{y}(x)$ is a vector of the property in question at age x of focal, and $\boldsymbol{\Phi}(x)$ 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 $\boldsymbol{\Phi}(x) = \mathbf{1}_\omega^\mathsf{T}$.

2. Weighted numbers of kin, in which case $\boldsymbol{\Phi}(x)$ is a vector containing, e.g., age-specific prevalence of some condition (disease, disability, health, labor force participation...).

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 $\boldsymbol{\Phi}$ would pick out the ages corresponding to one of the dependency groups. For six age classes, with two in each dependency category, the resulting matrix would be

$$\boldsymbol{\Phi} = \begin{pmatrix} 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{pmatrix} \tag{39}$$

4. Co-residence probability; this is actually a special case of prevalence, where the condition is "co-residing with Focal."

Nonlinear functions of $\mathbf{k}(x)$ (e.g., dependency ratios) can also be calculated.

4 Death of kin

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

$$\tilde{\mathbf{k}} = \left(\begin{array}{c} \mathbf{k}_{\text{living}} \\ \hline \mathbf{k}_{\text{dead}} \end{array} \right) \tag{40}$$

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 particular age x, or the cumulative numbers of 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 $\mathbf{k}_0$, 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, then $\mathbf{U}$ is replaced by

$$\tilde{\mathbf{U}} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{0} \end{array} \right) \tag{41}$$

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

$$\mathbf{M} = \mathcal{D}(\mathbf{q}). \tag{42}$$

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

$$\tilde{\mathbf{k}}(x+1) = \tilde{\mathbf{U}}\tilde{\mathbf{k}}(x) + \tilde{\boldsymbol{\beta}}(x) \tag{43}$$

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

$$\tilde{\mathbf{F}} = \left(\begin{array}{c|c} \mathbf{F} & \mathbf{0} \\ \hline \mathbf{0} & \mathbf{0} \end{array} \right) \tag{44}$$

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

$$\tilde{\mathbf{U}} = \left(\begin{array}{c|c} \mathbf{U} & \mathbf{0} \\ \hline \mathbf{M} & \mathbf{I} \end{array}\right) \tag{45}$$

where

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

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,

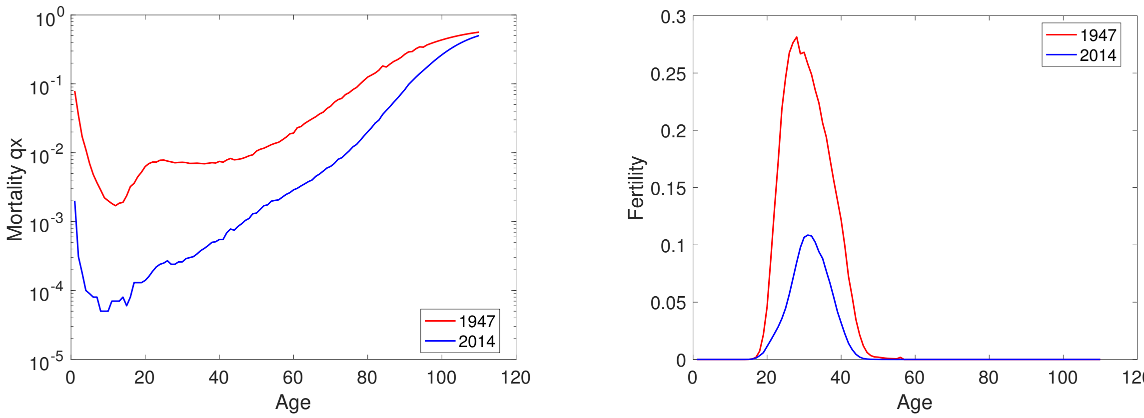
$$\tilde{\mathbf{k}}_0 = \left(\begin{array}{c} \mathbf{k}_0 \\ \hline \mathbf{0} \end{array}\right) \tag{46}$$

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

These calculations can be extended in several directions. It is possible to calculate the joint distribution of the age of the deceased kin at death and the age of Focal at the time of that death. Doing so requires a bit more work to develop the matrix $\mathbf{M}$, but no new concepts. It is also possible to construct the network of living and dead kin, including 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 descendents continue to appear). These extensions will be presented elsewhere.

5 An example: Changes in the kin network of Japan

These results invite comparison of kin networks across any dimension that modifies mortality or fertility schedules. As an example of the use of the model, I explore the implications for kin demography of changes in the mortality and fertility schedules of Japanese women from 1947 and 2014 (Human Mortality Database, 2018; Human Fertility Database, 2018). This period saw dramatic changes in both mortality (life expectancy increased by about 60%) and fertility (total fertility rate decreased by 70% while the net reproductive rate declined



(a) Mortality **(b)** Fertility

Figure 2: The mortality and fertility schedules for Japanese women in 1947 and 2014. Data from Human Mortality Database (2018) and Human Fertility Database (2018).

by about 60%), as shown in Figure 2.

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

The series of figures[3] in Section 8 show some of the kinship consequences of these changes. Note that these are examples; this 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.”

Figure 4 shows the age distributions for mothers, grandmothers, daughrters, granddaughters, sisters, and cousins, for a Focal individual aged 30 and aged 70. The mothers of Focal at 30 are lightly older under 2014 rates than under 1947 rates, and far more common. Focal at 70 has essentially no chance of a living mother in 1947, but still some chance of a very elderly living mother in 2014 (Fig. 4(a)). The situation with grandmothers is similar (Fig. 4(b)), 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.

[3]For the curious, a supplementary collection contains figures for all kin types for each of the categories examined her.

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

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

Figure 5 shows the total numbers of living kin as a function of the age of Focal. Comparing daughters, granddaughters, and great-granddaughters (Figs. 5(a,c,e)) shows the integrated effects of mortality and fertility changes. Focal in 1947 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. In 2014, fewer daughters are produced, and there is hardly any decline due to mortality. Comparing granddaughters and great-granddaughters, shows the pattern hinted at in Fig. 4; Focal in 1947 has progressively more descendents in each generation, while Focal in 2014 has fewer.

For ancestors (Fig. 5(b,d,f)), the 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.

As an example of using equation (38) to map from age distributions to prevalence of some condition, consider the problem of 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.

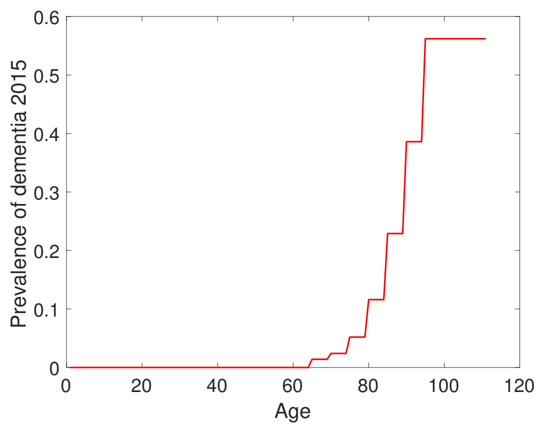


Figure 3: Age-specific prevalence of dementia among Japanese women in 2015. From Fukawa (2018)

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 (Fig. 6(a,c,d)). The difference is large (about 7-fold for mothers, greater for grandmothers and great-grandmothers). The same holds for sisters (Fig. 6(b)) and aunts (Fig. 4(d)). Among cousins, the difference is not as great, but prevalence is still higher in 2014 than 1947.

Dependency can be measured in several ways. Here, Figure 7 shows, as a function of the age of Focal, the numbers of kin in three categories of dependence. Young dependence is defined as ages 0–15, old dependence as ages greater than 65, and independence as ages 16–65. Figure 7 shows results for 1947 in solid lines, and 2014 in dashed lines. Dependent children, grandchildren, and great-grandchildren accumulate much more rapidly and earlier 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 descendents 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 descendents, but in 2014 she is faced with more dependent parents and ancestors.

Turning now to the experience of the death of kin, Figure 8 shows the experience of death of kin at each age of Focal, and Figure 9 shows the cumulative deaths experienced up to each age of Focal. The world changed dramatically between 1947 and 2014. The deaths of daughters, granddaughters, mothers, sisters, and aunts, occurs earlier and far more frequently in 1947. Focal in 2014 will essentially never experience the death of a granddaughter, and almost never the death of a daughter (Figure 8(a,b) and Figure 9(a,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 et al. (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 non-autonomous matrix difference equations. It sounds more complicated, but in fact, like any dynamical system, the 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 (11) for arbitrary levels of descendents.

One advantage of formal mathematical specification is that it makes explicit the assumptions underlying an analysis. As Goodman et al. (1974) point 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 comparisons of these results with kinship censuses will be 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 and parity are two obvious possibilities) in age×stage or multistate models (Caswell et al., 2018). 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.

The analysis here, and the example in Section 5, are formulated in terms of female survival and fertility. It is obviously 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 et al., 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 include 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 allow age to interact with other characteristics (marital status, health status, etc.). There exists a coherent approach to incorporating multiple states using matrices, and it will make multistate kinship calculations possible.

Finally, note that the results of these calculations, like those of Goodman et al. (1974), provide *expected* age distributions. While the kin of Focal form a population, they form a small population. Thus, extending the analysis to include demographic stochasticity will be important. Branching process methods, as discussed by Pullum (1982) are suited to this purpose. Connections of multitype brancing 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 complete microsimulation models, can provide information on variances.

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 Acknowledgments

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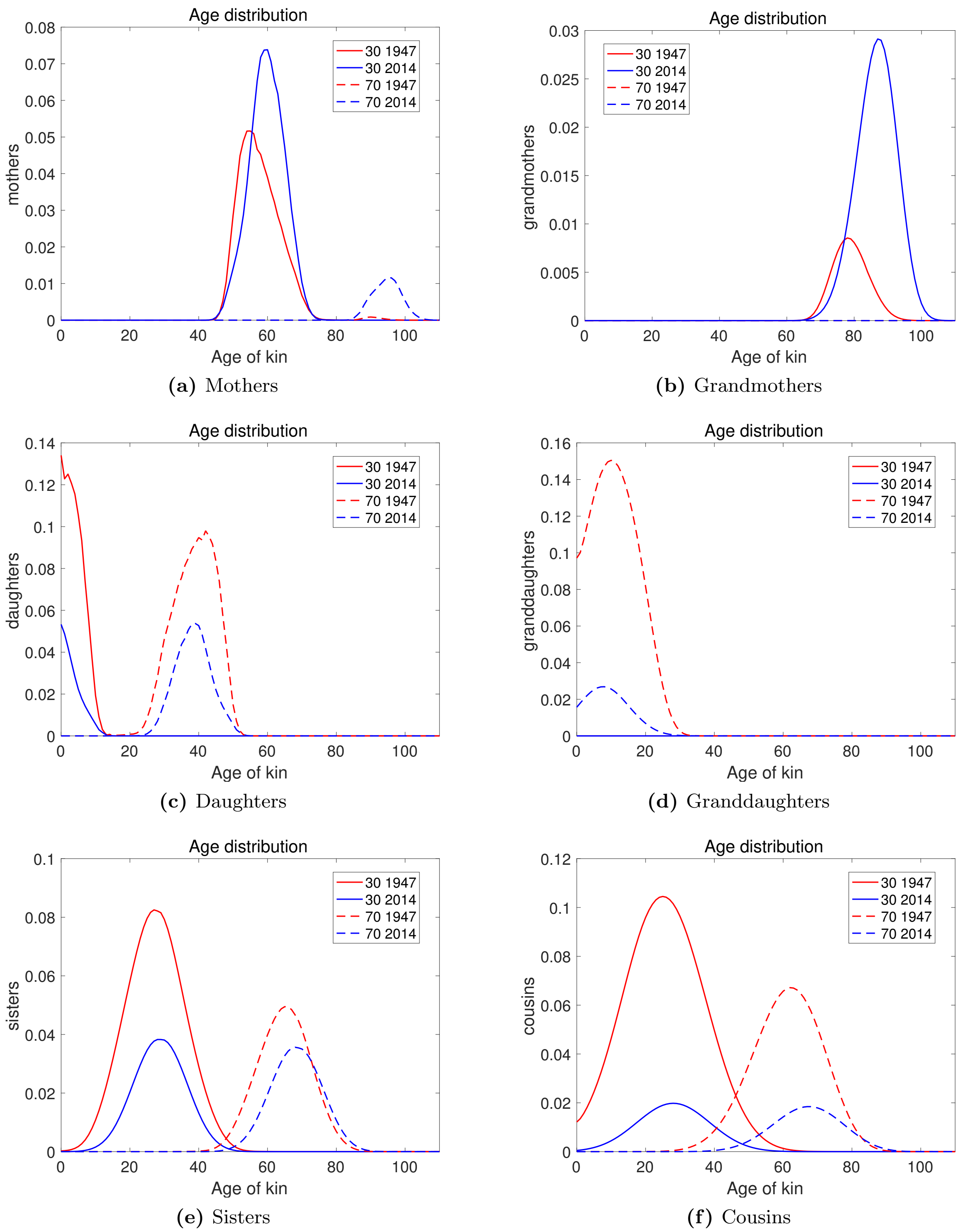
8 Figures

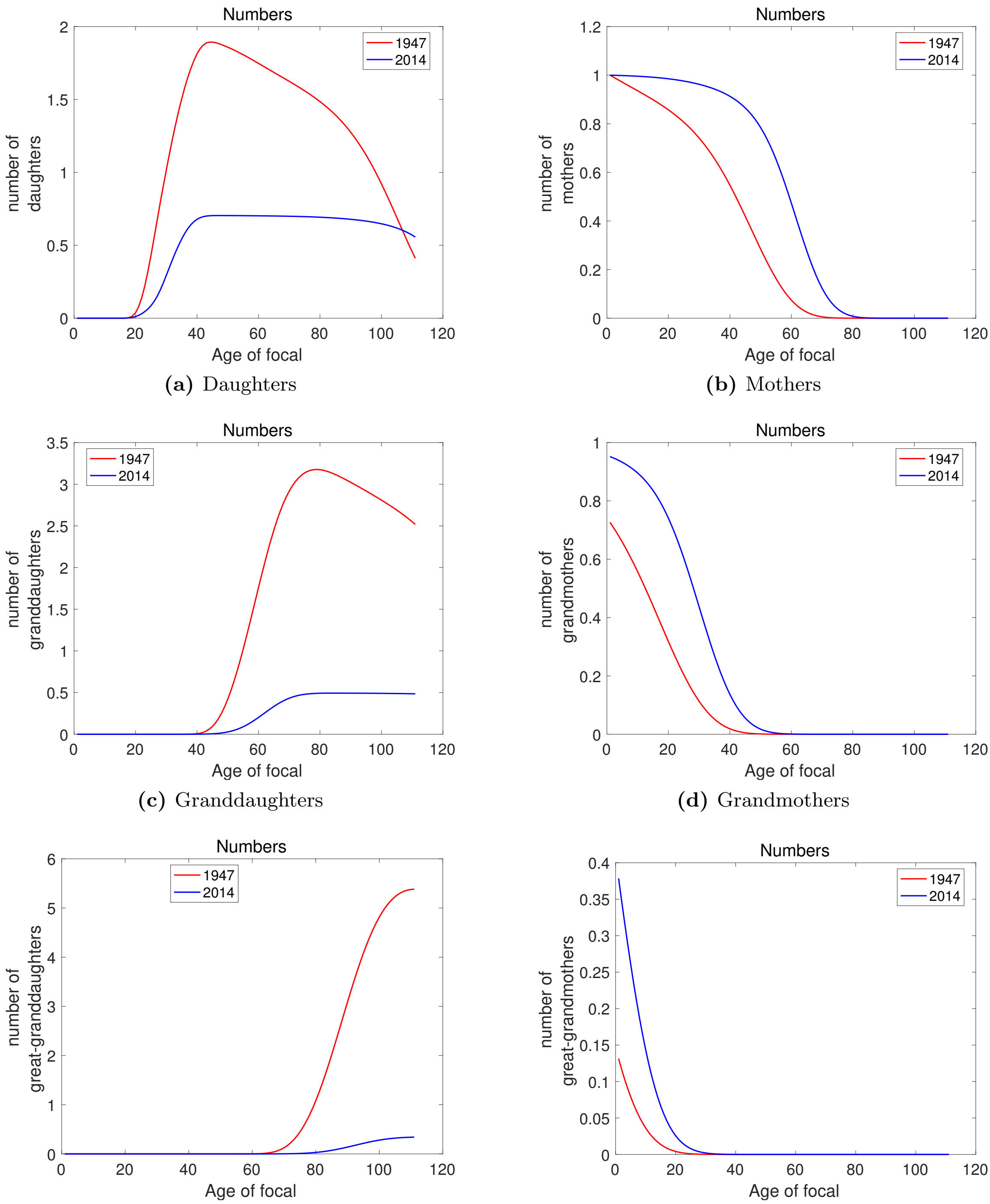
8.1 Age distributions



(a) Mothers **(b)** Grandmothers **(c)** Daughters **(d)** Granddaughters **(e)** Sisters **(f)** Cousins

Figure 4: 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).

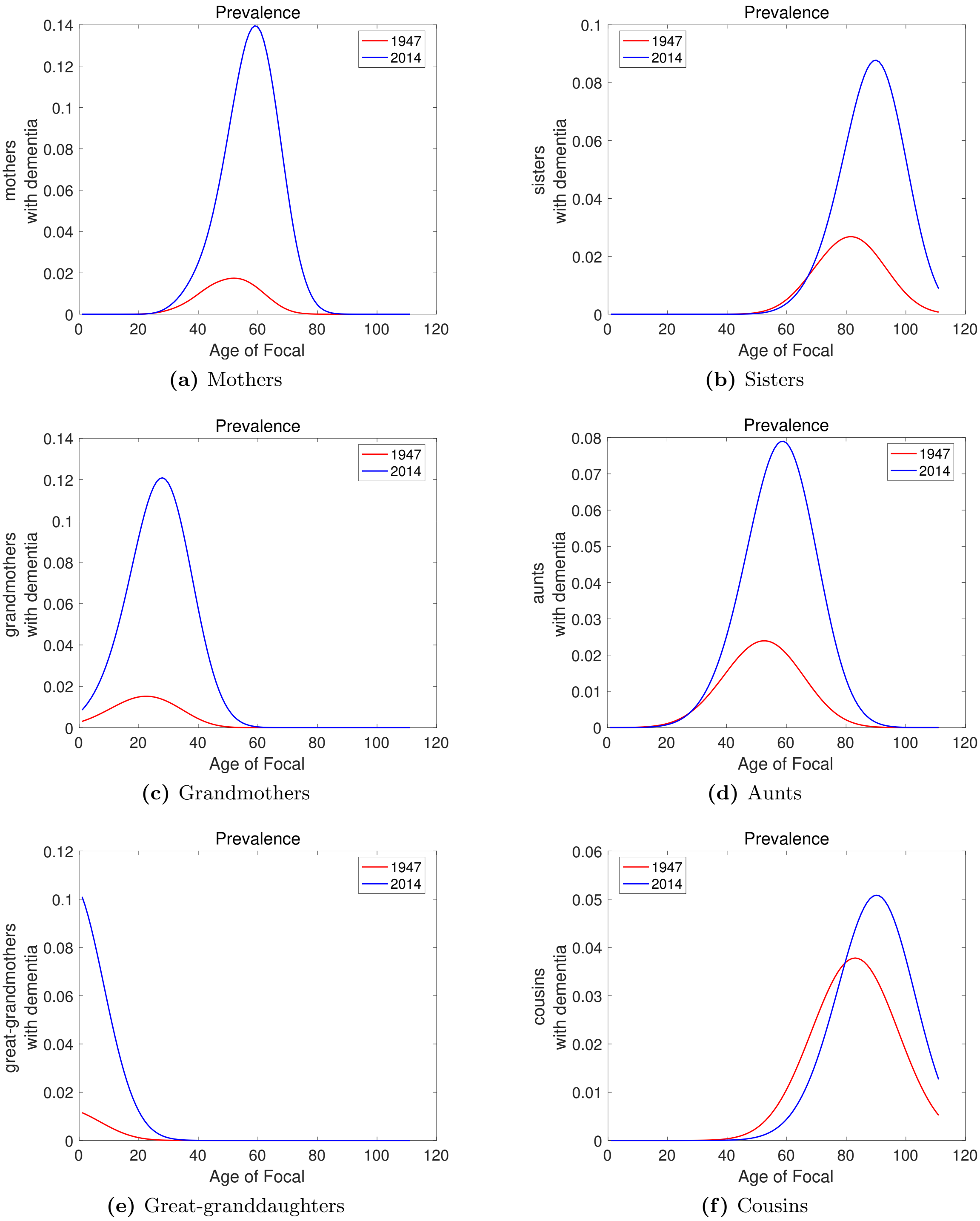
8.2 Numbers of kin



(a) Daughters (b) Mothers (c) Granddaughters (d) Grandmothers (e) Great-granddaughters (f) Great-grandmothers

Figure 5: 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).

8.3 Prevalence of dementia



(a) Mothers

(b) Sisters

(c) Grandmothers

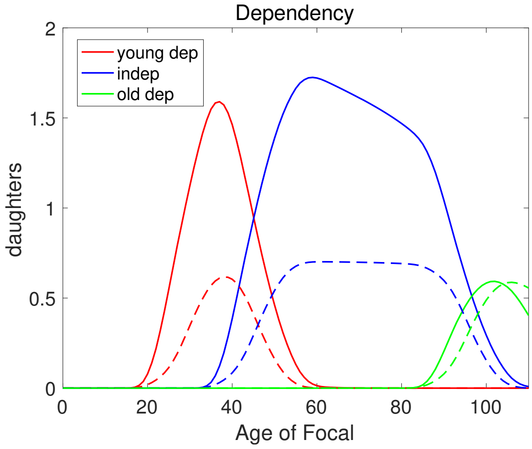
(d) Aunts

(e) Great-granddaughters

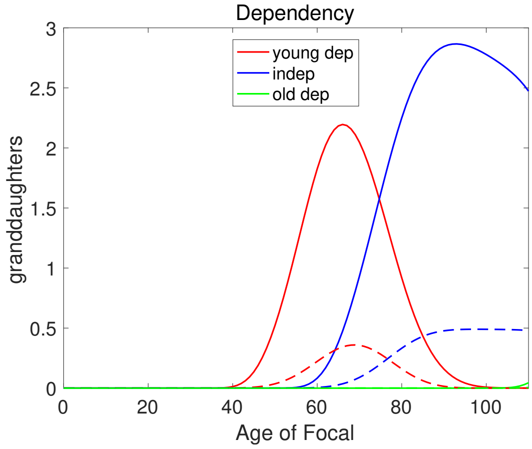
(f) Cousins

Figure 6: 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.

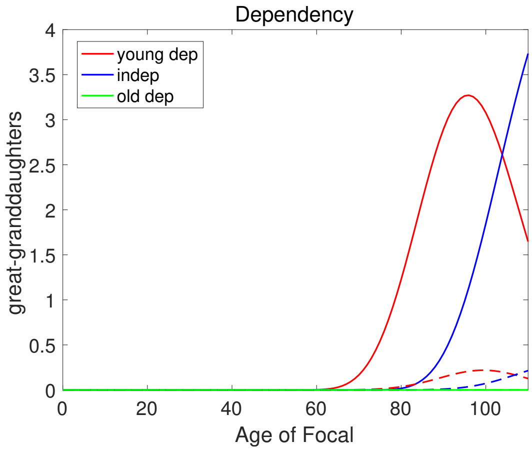
8.4 Dependency



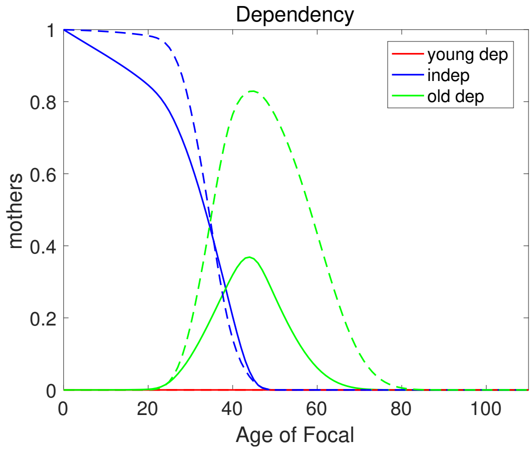
(a) Daughters



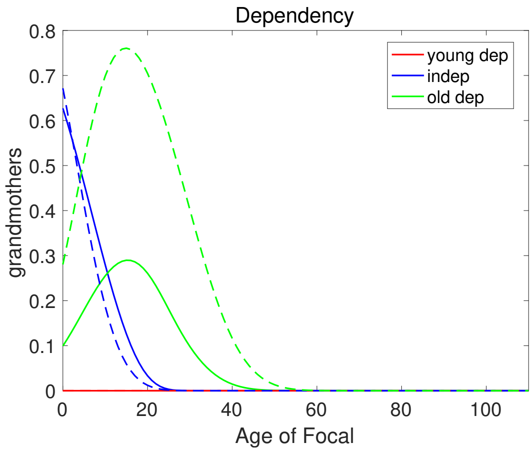
(b) Granddaughters



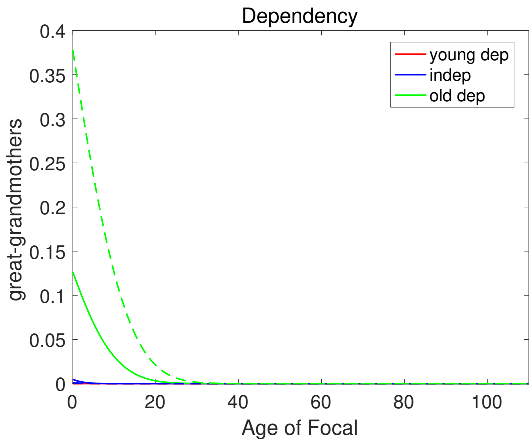
(c) Great-granddaughters



(d) Mothers



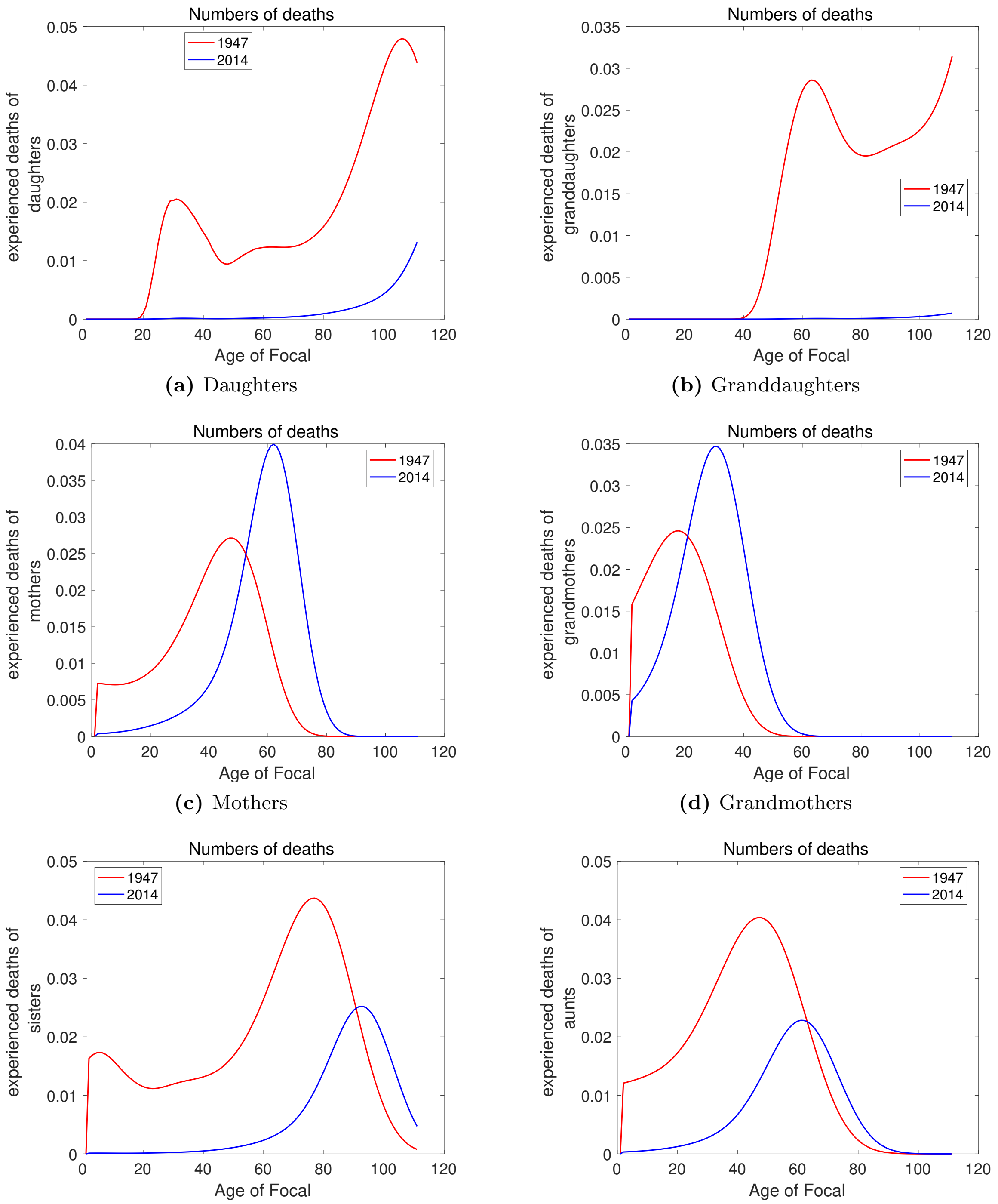
(e) Grandmothers



(f) Great-grandmothers

Figure 7: 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).

8.5 Experience of the deaths of kin



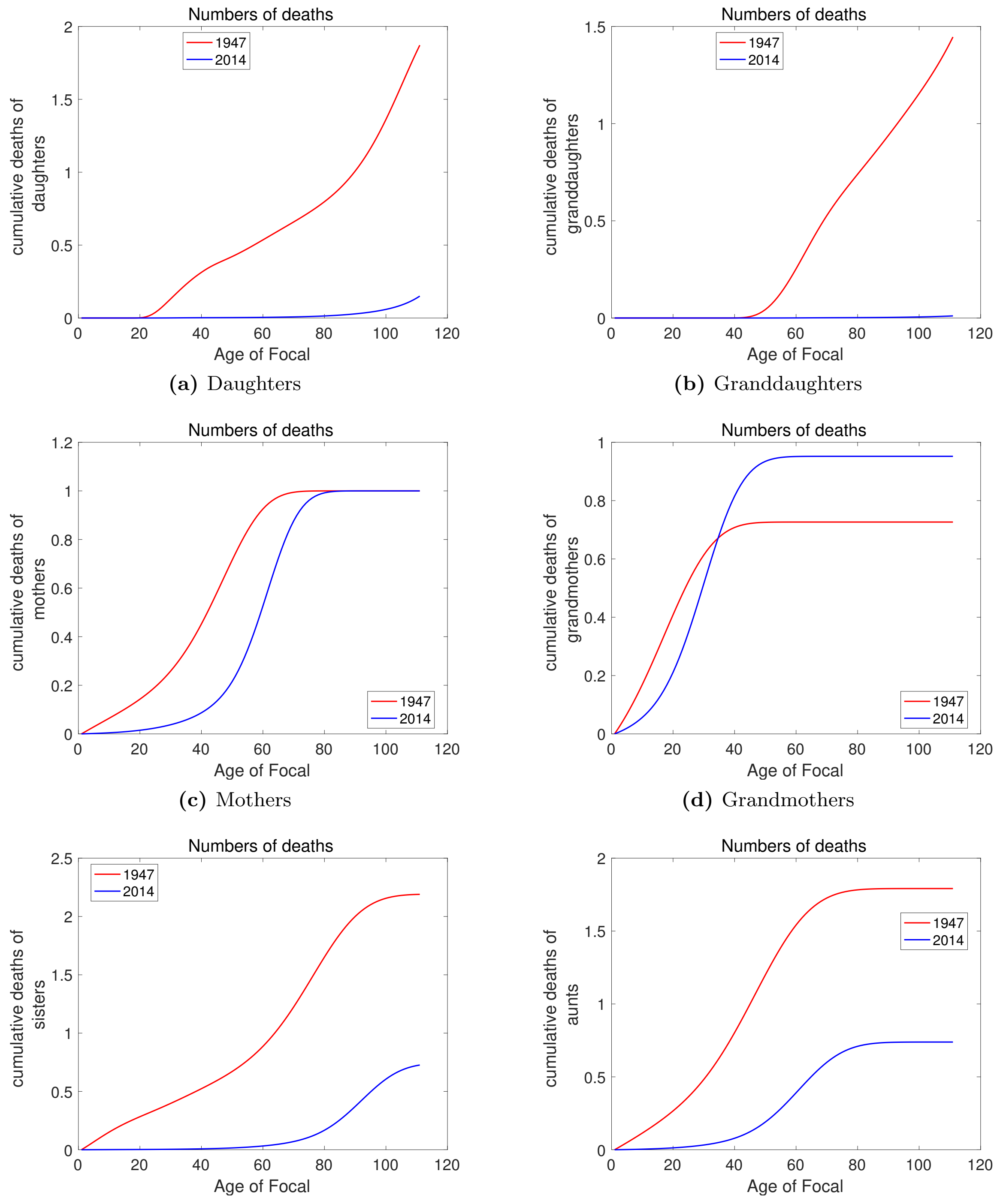
(a) Daughters **(b)** Granddaughters

(c) Mothers **(d)** Grandmothers

(e) Sisters **(f)** Aunts

Figure 8: 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.

8.6 Cumulative deaths of kin



(a) Daughters **(b)** Granddaughters **(c)** Mothers **(d)** Grandmothers **(e)** Sisters **(f)** Aunts

Figure 9: The cumulative 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.

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