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Research Article

The formal demography of kinship VII: Lifetime kin overlap within and across generations

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The formal demography of kinship VII: Lifetime kin overlap within and across generations

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Abstract

BACKGROUND
Interactions among kin have important consequences, including resource transfers, alloparenting, health care, and economic support. Some interactions require that the lives of the interacting relatives overlap. The overlap over a lifetime (lifetime kin overlap, LKO) depends on mortality (longer lives give more opportunity for overlap) and fertility (higher fertility produces more kin with which to overlap). Here we provide a general solution to the problem of calculating lifetime kin overlap.

OBJECTIVE
Our objective is to develop a demographic model for the mean and variance of the lifetime overlap of any types of kin over the life of a focal individual.

METHODS
The matrix kinship model is used to provide the age distribution of kin as an age-specific property of Focal. The mean and variance of lifetime overlap with kin of any type are then calculated using Markov chains with rewards.

RESULTS
The analysis provides the mean and variance of the remaining lifetime overlap with any kind of kin at every age of a focal individual. It may be measured in terms of numbers, numbers in chosen age ranges, or numbers weighted by prevalence, or by the presence of at least one kin. Overlap is defined both prospectively and retrospectively. and includes simultaneous overlap with two or more types of kin ('sandwiched kin').

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CONTRIBUTION

It is now possible to compute the mean and variance of the projected LKO with any type of kin, in one-sex or two-sex models based on age or combinations of age and stage.

1. Introduction

Interactions among relatives play critical roles in social and family life. Some are within generations and others between generations, and the types of interactions and their effects are diverse. Examples are many, including resource transfers by bequests (Zagheni and Wagner 2015; Brennan, James, and Morrill 1982), support provided by grandparents to children and grandchildren (e.g., Stecklov 2002; Wachter 1997; Tu, Freedman, and Wolf 1993; Himes 1992), and intergenerational effects on social mobility (Song 2016; Song and Mare 2017; Mare and Song 2015). The presence of relatives can affect infant and child survival (Sear and Mace 2008), particularly when relatives act as alloparents (Hrdy 2009). The provision for care across generations imposes costs on those providing the care, especially in the case of 'sandwich' families, in which individuals care for both dependent children and aging parents (DeRigne and Ferrante 2012; Alburez-Gutierrez, Mason, and Zagheni 2021). Orphanhood, and more generally bereavement, can be a major disruption of intergenerational interactions during pandemics (e.g., Zagheni 2010; Snyder et al. 2022). A rich anthropological literature on grandmothers documents their role in caring for grandchildren and the role of such care in the evolution of the human postmenopausal lifespan (e.g., Voland, Chasiotis, and Schiefenhovel 2005; Hrdy 2005; Tanskanen and Danielsbacka 2019). Page and French (2020) point to the importance of kinship structures in determining the balance of kin- and non-kin selection in hunter-gatherer populations. In his PAA presidential address, Mare (2011) emphasized the many possibilities for kin effects among more distantly related individuals, effects encompassing two, three, or more generations.

Some of these interactions can take place only if the participants are alive at the same time; that is, that their lives overlap. The amount of kin overlap to be experienced over a lifetime depends on the schedules of mortality and fertility, and this has led naturally to attempts to calculate the overlap implied by such a set of demographic rates. We refer to this as 'lifetime kin overlap,' abbreviated as LKO.[3] As we will see, 'overlap' can be defined in many ways.

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[3] This notation is an intentional analogy to terms such as lifetime reproductive success (LRS), lifetime reproductive output (LRO), net reproductive rate (NRR), total fertility rate (TFR), and healthy life expectancy (HE or HALE). The calculation of these indices all begin with an age- or stage-specific property (fertility, healthy life, and so on) and then integrate that property over all or part of a lifetime.

The most sophisticated analysis of LKO to date is that of Song and Mare (2019), who used the kinship model of Goodman, Keyfitz, and Pullum (1974) to calculate the expected lifetime overlap of grandparents with their grandchildren from both prospective and retrospective points of view. Other approaches have been used. Margolis (2016) calculated the time spent with at least one grandchild from prevalence data using the Sullivan method. Microsimulations have been used by Verdery and Margolis (2017) to project older adults without close kin in the United States and by Margolis and Verdery (2019) for a detailed analysis of grandparenthood.

Our goal here is to provide a general solution to the lifetime overlap problem. That solution requires two demographic calculations. First, we need to know the nature of the kinship network experienced by an individual of any specified age. For example, a very young person will have no children but is likely to have parents and even grandparents. An old person is more likely to have children and grandchildren but unlikely to have living parents and grandparents. The kinship network is a high-dimensional age-specific property of an individual.

Second, we need to integrate this age-specific property over the life of an individual. The individual overlaps, at every age until death, with a set of kin. LKO is the lifetime accumulation of this overlap; it reflects the kin available at each age and the probability of living through that age.

The age-specific kinship network is provided by the matrix kinship model. That model has been presented in a series of papers (Caswell 2019, 2020; Caswell and Song 2021; Caswell 2022; Caswell, Verdery, and Margolis 2023; Caswell 2024) and is implemented in an R package for those desiring such (Williams et al. 2023). It has been applied to analysis of demographic transitions (Jiang et al. 2023), projections of future kinship networks (Alburez-Gutierrez, Williams, and Caswell 2023), to prevalences of unemployment (Song and Caswell 2022) and dementia (Feng, Song, and Caswell 2024), and even African elephant social interactions (Croll and Caswell 2025). In this paper we will use a two-sex version of the model that can, if desired, compute the LKO of female and male individuals with female and male kin (Section 2).

Given the age-specific abundance of kin, the lifetime overlap is calculated using a Markov chain with rewards (MCWR).[4] The MCWR treats the kinship network experienced at each age as a 'reward' and computes the mean and variance (and higher mo-

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[4] This is the first application of MCWR to kinship analysis. The basic idea of Markov chains with rewards was introduced by Howard (1960) as the basis for stochastic dynamic programming (e.g., Puterman 1994; Sheskin 2010). Extensions of the theory to random rewards (i.e., treated as random variables with defined statistical properties) and to demographic models were presented by Caswell (2011) and have since been extended with applications to lifetime reproductive output (Caswell 2011; van Daalen and Caswell 2015; van Daalen and Caswell 2017), evolutionary biodemography (van Daalen and Caswell 2024), income and expenditures (Caswell and Kluge 2015), and healthy longevity in both prevalence-based (Caswell and Zarulli 2018; Owoeye, Oseni, and Gayawan 2020; Dudel and Myrskylä 2020; Zarulli and Caswell 2024) and incidence-based models (Caswell and van Daalen 2021).

ments if desired) of the lifetime accumulation of this reward (Caswell 2011; van Daalen and Caswell 2017) to give the LKO.

The minimal data needed for these calculations are a mortality schedule and a fertility schedule. If separate schedules are available for men and women, so much the better, but approximations are available if that is not the case. In the example we will explore here, we use separate male and female mortality schedules, which are often available, but only a single female fertility schedule, because male and female fertility are not always available.

Our analyses:

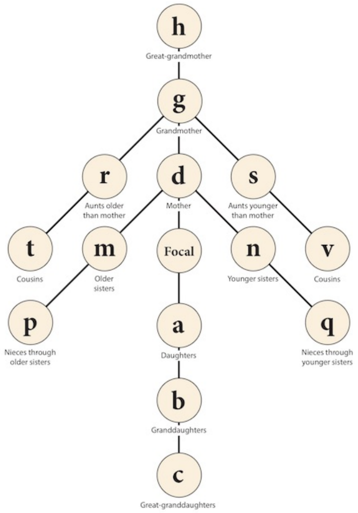
- apply to any type of kin,
- are easily applied to chosen age groups of kin (e.g., parents older than some age, or children younger than some age),
- accommodate weighted numbers of kin (e.g., kin numbers weighted by prevalence of a disease) and overlap with at least one kin,
- are readily applied to some multistate models (e.g., age×parity),
- are flexible in their definition of ‘lifetime,’ including LKO from birth to death (lifetime sensu stricto), remaining LKO starting from any initial age, and LKO up to some specified age (e.g., overlap prior to retirement age),
- provide ‘sandwich’ overlap with two or more types of kin,
- provide not only the mean LKO but also the variance and other statistics,
- make it possible to partition variance in LKO into within- and between-group components.

The model can provide both prospective and retrospective LKO, in the sense of Song and Mare (2019). We describe this in Section 4.5, but unless otherwise indicated, all results presented are for prospective LKO.

2. The matrix model for the kinship network

The matrix kinship model, which we describe briefly here, projects the expected age distribution of male and female relatives of each of the types of kin alive at each age of a focal individual, referred to as Focal. See Figure 1 for the types of kin surrounding Focal. Focal is a member (assumed female here) of a population characterized by a mortality and a fertility schedule that apply to all individuals. As Focal ages, the number and age distribution of her kin will change. The model, in various extensions, has been described in a series of papers (Caswell 2019, 2020; Caswell and Song 2021; Caswell 2022; Caswell, Verdery, and Margolis 2023; Caswell 2024). For details on the two-sex version we use, see Caswell (2022).

Figure 1: The kinship network showing kin of Focal and the symbols used to identify them



Source: Reproduced from Caswell (2019) under a CC-BY license.

2.1 Notation

Matrices are denoted by uppercase bold characters (e.g., $\mathbf{U}$) and vectors by lowercase 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 the matrix $\mathbf{I}$ is the identity matrix. When necessary, subscripts are used to denote the size of a vector or matrix; for example, $\mathbf{I}_\omega$ is an identity matrix of size $\omega \times \omega$. The notation $\|\mathbf{x}\|$ denotes the 1-norm of $\mathbf{x}$ (i.e., the sum of the absolute values of the entries).

The symbol $\circ$ denotes the Hadamard, or element-by-element product. On occasion, MATLAB notation will be used to refer to rows and columns; for example, $\mathbf{F}(i,:)$ and $\mathbf{F}(:,j)$ refer to the ith row and jth column of the matrix $\mathbf{F}$.

Matrices and vectors with a tilde (e.g., $\tilde{\mathbf{U}}$, $\tilde{\mathbf{k}}$) are block-structured in some way, which is specified when they are defined.

2.2 Projecting the kinship network: One sex

The kinship network considered here is shown in Figure 1. The network can be extended to longer chains of descendants if desired. In the one-sex model, each type of kin is denoted by a letter, and the bold-faced letter denotes the age distribution vector of that type of kin. For example, $\mathbf{a}(x)$ denotes the age distribution of the daughters of Focal at age x of Focal.

The kin of Focal are a population, which is projected by a survival matrix $\mathbf{U}$ and a fertility matrix $\mathbf{F}$. For three age classes,

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

The entry in the lower right corner of $\mathbf{U}$ is an optional open-ended final age class.

Let $\mathbf{k}(x)$ be the age distribution vector of a generic kin type at age x of Focal. The kinship model projects $\mathbf{k}(x)$ by

$$\mathbf{k}(x+1) = \mathbf{U}\mathbf{k}(x) + \boldsymbol{\beta}(x), \tag{2}$$

where $\boldsymbol{\beta}(x)$ is a recruitment vector. For some types of kin, no recruitment is possible (e.g., Focal can accumulate no new older sisters). For others, recruitment comes from the fertility of another type of kin (e.g., new granddaughters come from the reproduction of daughters). Thus

$$\boldsymbol{\beta}(x) = \left\{ \begin{array}{cl} 0 & \text{no recruitment} \\ \mathbf{F}\mathbf{k}^*(x) & \text{recruitment from type } \mathbf{k}^* \end{array} \right. . \tag{3}$$

The model is supplemented by an initial condition $\mathbf{k}_0$ that specifies the kin present when Focal is born into the first age class. This is zero for some types of kin (e.g., Focal has no children when she is born), and is calculated for other types from the distribution of ages of mothers at birth. See Caswell (2019) for details.

2.3 Projecting the kinship network: Two sexes

The one-sex version of the kinship model (Caswell 2019) describes female kin through female lines of descent. To fully account for both female and male kin (e.g., both grandsons and granddaughters) through all lines of descent (e.g., sons of daughters, sons of sons, daughters of daughters, and daughters of sons) would require both male and female mortality and fertility schedules (Caswell 2022). In the absence of male and female fertility, we use a model with separate male and female survival, but with female fertility applied to both males and females. This approximation is called Model 2 in Section 5 of Caswell (2022).[5]

In the two-sex model, the age distribution vector includes both females and males

$$\tilde{\mathbf{k}}(x) = \left(\frac{\mathbf{k}_\mathrm{f}}{\mathbf{k}_\mathrm{m}} \right)(x). \tag{4}$$

The survival and fertility matrices for Model 2 are block-structured, using female fertility and male and female survival:

$$\tilde{\mathbf{U}} = \begin{pmatrix} \mathbf{U}_\mathrm{f} & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_\mathrm{m} \end{pmatrix} \qquad \tilde{\mathbf{F}} = \begin{pmatrix} \bar{\alpha}\mathbf{F}_\mathrm{f} & \bar{\alpha}\mathbf{F}_\mathrm{f} \\ \alpha\mathbf{F}_\mathrm{f} & \bar{\alpha}\mathbf{F}_\mathrm{f} \end{pmatrix} \qquad \tilde{\mathbf{F}}^* = \begin{pmatrix} \bar{\alpha}\mathbf{F}_\mathrm{f} & \mathbf{0} \\ \alpha\mathbf{F}_\mathrm{f} & \mathbf{0} \end{pmatrix}, \tag{5}$$

where α is the fraction of births that are male and $\bar{\alpha} = 1 - \alpha$. The fertility matrix $\tilde{\mathbf{F}}^*$ applies to reproduction by direct ancestors (parents, grandparents, and so on). The matrix $\tilde{\mathbf{F}}$ applies to all other kin. See Caswell (2022) for details.

Projecting the kinship model yields the expected age-sex distribution of each type of kin over the life of Focal. This age-sex distribution can be aggregated in various ways (see Section 3.1).

3. Markov chain with rewards as a model for overlap

A Markov chain is a stochastic model for the movement of entities among states. In our case, the entities are individuals and the states are a sequence of age classes and one or more absorbing states corresponding to death.[6] Eventual death is certain. The transitions of an individual are given by the transition matrix[7]

$$\tilde{\mathbf{P}} = \left(\begin{array}{c|c} \tilde{\mathbf{U}} & \mathbf{0} \\ \hline \tilde{\mathbf{M}} & \mathbf{I} \end{array} \right), \tag{6}$$

where $\tilde{\mathbf{U}}$ is the survival matrix in Equation (5) and $\tilde{\mathbf{M}}$ is a matrix containing transitions from each living state to the dead state. The tilde notation indicates that the matrices are

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[5] If neither sex-specific mortality or fertility schedules are available, female rates can be applied to both sexes (the androgynous approximation) to obtain male and female kin numbers (Caswell 2022).

[6] Markov chain models can also describe multistate demography in which the states correspond to stages (e.g., health conditions or parity classes) in combination with age classes. We do not consider these further here, but it is important that the methods we present apply to them as well.

[7] The transition matrix is written in column-to-row orientation to agree with the orientation of population projection matrices.

block-structured to include both sexes. The $\mathbf{0}$ in the upper right corner says that the dead never return to life, and the identity matrix in the lower right corner says that the dead stay dead. The life of an individual is a stochastic sequence of state transitions that continues until eventual death. Although all individuals are identically subject to the probabilities in $\tilde{\mathbf{P}}$, some will experience longer and some shorter lives.

In a Markov chain with rewards (MCWR) the individual collects a 'reward' at each step of its life. The reward is a random variable, specified by its moments. Although all individuals collect rewards from the same distributions, some will gather more and some less by chance. The individual accumulates the reward over the course of its life until death. The model assumes that the reward, whatever it may be, stops accumulating at death. The variation among individuals in LKO accounts for both sources of stochasticity: the variation of the overlap at each age and the variation in the length of life over which overlap is accumulated.

The age-specific rewards are incorporated into a set of reward matrices. Let r_{ij} denote the random reward accumulated when an individual makes the transition $j \mapsto i$. There is a reward matrix for each of the moments of the reward; $\mathbf{R}_1$ contains the first moments, $\mathbf{R}_2$ the second moments, and so on:

$$\mathbf{R}_1 = \left(\; E(r_{ij}) \;\right) \qquad \mathbf{R}_2 = \left(\; E(r_{ij}^2) \;\right). \tag{7}$$

The higher moment matrices are defined similarly. See van Daalen and Caswell (2017) for details on specifying reward moments.

The lifetime accumulation of rewards is given in a set of vectors, $\tilde{\boldsymbol{\rho}}_1$ for the first moments and $\tilde{\boldsymbol{\rho}}_2$ for the second moments. The ith entry of $\tilde{\boldsymbol{\rho}}_1$ is the mean remaining lifetime reward for an individual in age-sex class i and similarly for the second moments in $\tilde{\boldsymbol{\rho}}_2$. The formulae for these moment vectors are given by van Daalen and Caswell (2017: Theorem 1). In our case they are block-structured for males and females:

$$\tilde{\boldsymbol{\rho}}_1 = \left(\frac{\boldsymbol{\rho}_{1,\mathrm{f}}}{\boldsymbol{\rho}_{1,\mathrm{m}}}\right) = \tilde{\mathbf{N}}^{\mathsf{T}}\mathbf{Z}\left(\mathbf{P}\circ\mathbf{R}_1\right)^{\mathsf{T}}\mathbf{1}_{\omega} \tag{8}$$

$$\tilde{\boldsymbol{\rho}}_2 = \left(\frac{\boldsymbol{\rho}_{2,\mathrm{f}}}{\boldsymbol{\rho}_{2,\mathrm{m}}}\right) = \tilde{\mathbf{N}}^{\mathsf{T}}\left[\mathbf{Z}\left(\tilde{\mathbf{P}}\circ\mathbf{R}_2\right)^{\mathsf{T}}\mathbf{1}_{\omega} + 2\left(\tilde{\mathbf{U}}\circ\mathbf{R}_1\right)^{\mathsf{T}}\tilde{\boldsymbol{\rho}}_1\right], \tag{9}$$

where $\tilde{\mathbf{N}}$ is the fundamental matrix

$$\tilde{\mathbf{N}} = \left(\mathbf{I}-\tilde{\mathbf{U}}\right)^{-1}. \tag{10}$$

The matrix $\mathbf{Z}$ is a matrix of zeros and ones that slices off the rows and columns of $\mathbf{P}$ and $\mathbf{R}_i$ corresponding to the absorbing states; these reduced matrices are denoted $\tilde{\mathbf{P}}$ and $\tilde{\mathbf{R}}$.

The first two moments shown here suffice to calculate the mean, variance, standard deviation, and other statistical properties of LKO:

$$\begin{aligned} E(LKO) &= \tilde{\boldsymbol{\rho}}_1 && (11)\\ V(LKO) &= \tilde{\boldsymbol{\rho}}_2 - (\tilde{\boldsymbol{\rho}}_1 \circ \tilde{\boldsymbol{\rho}}_1) && (12)\\ SD(LKO) &= \sqrt{V(\tilde{\boldsymbol{\rho}})}. && (13) \end{aligned}$$

The means, variances, and so on are taken element-wise. These quantities are vectors whose entries give the statistics of remaining LKO.

3.1 Measures of age-specific kin abundance

When the question is posed about overlap with some type of kin, one must specify the measure of kin abundance that is of interest. Do we want to know overlap with all grandchildren? Or with young grandchildren for whom you might babysit? Or with teen grandchildren who you might help with education? Whatever the choice, we denote this measure as ξ. Some possibly interesting choices include the following

- The age distributions of female and male kin are given by the blocks $\mathbf{k}_{\mathrm{f}}(x)$ and $\mathbf{k}_{\mathrm{m}}(x)$ in $\tilde{\mathbf{k}}(x)$. To calculate LKO with both sexes combined, we define the age-specific abundance as

$$\xi(x) = \begin{pmatrix} \mathbf{I}_\omega & \mathbf{I}_\omega \end{pmatrix} \tilde{\mathbf{k}}(x). \tag{14}$$

- Overlap with female and male kin separately are given by

$$\xi_{\mathrm{f}}(x) = \|\mathbf{k}_{\mathrm{f}}(x)\| \qquad \xi_{\mathrm{m}}(x) = \|\mathbf{k}_{\mathrm{m}}(x)\|, \tag{15}$$

  and the total number of kin, female and male combined, is

$$\xi(x) = \|\tilde{\mathbf{k}}(x)\| \tag{16}$$

- We might be interested in overlap with the number of kin in selected age ranges (e.g., school-age children); this is given by using as the measure of abundance

$$\xi(x) = \mathbf{c}^{\mathsf{T}} \tilde{\mathbf{k}}(x), \tag{17}$$

  where **c** is a 0–1 vector that selects the age classes and sexes of interest.

- We might be interested in overlap with kin weighted by some measure of importance. If $\mathbf{w}$ is a vector of age-specific weights, then

  $$\xi(x) = \mathbf{w}^{\mathsf{T}}\tilde{\mathbf{k}}(x). \tag{18}$$

  The weights might be measures of prevalence of, for example, employment, disability, health conditions, or, as in Song and Mare (2019), grandparents weighted by educational attainment. In an evolutionary context, kin might be weighted by their degree of relatedness to the focal individual; overlap with more closely related kin permits more intense selection on traits related to kin interactions.

3.2 Reward matrices for kin overlap

The matrix containing the first moments of the age-specific rewards is

$$\mathbf{R}_1 = \left(\begin{array}{ccc|c} E[\xi(1)] & \dots & E[\xi(\omega)] & 0 \\ \vdots & \dots & \vdots & \vdots \\ E[\xi(1)] & \dots & E[\xi(\omega)] & 0 \\ \hline 0.5E[\xi(1)] & \dots & 0.5E[\xi(\omega)] & 0 \end{array}\right). \tag{19}$$

The entries in the last row are the rewards collected if Focal dies during that year, assuming that on average, she lives half the time step. The second moment reward matrix is then

$$\mathbf{R}_2 = \left(\begin{array}{ccc|c} V[\xi(1)] & \dots & V[\xi(\omega)] & 0 \\ \vdots & \dots & \vdots & \vdots \\ V[\xi(1)] & \dots & V[\xi(\omega)] & 0 \\ \hline 0.25V[\xi(1)] & \dots & 0.25V[\xi(\omega)] & 0 \end{array}\right) + \mathbf{R}_1 \circ \mathbf{R}_1, \tag{20}$$

where the entries in the last row are the variances resulting from multiplying the kin numbers by 0.5.

The matrices for the second and higher moments depend on the moments of the frequency distribution of kin numbers. That distribution has often been assumed to be Poisson (e.g., Schoen 2019; Song, Campbell, and Lee 2015). However, the stochastic kinship model (Caswell 2024) provides support for that choice. It found that the numbers of kin are well fit by a Poisson distribution except for direct ancestors (parents, grandparents, and great-grandparents), which are well described by a binomial distribution. Both of these distributions provide variances for the kin numbers at every age; the variances of the age-specific abundance indices in Section 3.1 can be calculated from these.

3.3 LKO is measured in units of person-years

Place yourself, for a moment, in the shoes of an individual progressing through their life. At each age your life overlaps with some number of, say, cousins. As each year goes by, you accumulate more overlap, and add that years overlap to the overlap already accumulated. LKO thus has units of person-years. This implies that spending one year with 10 cousins is equivalent, as far as you are concerned, to spending 10 years with one cousin.

An alternative would be to ask, in each year, "Do I have any cousins?" and to accumulate overlap with at least one cousin (see Section 4.2). This version of LKO is also measured in person-years, but since there is only one person, it can equally be treated as being measured in years.[8] Song and Mare (2019) refer to these two choices as "overlap with all kin" and "overlap with any kin."

4. Kin overlap during a demographic transition in Japan

As an example of the LKO calculations and their results, we present an analysis of kin overlap for the population of Japan (as in Caswell 2019 and Caswell 2024). Japan underwent a dramatic demographic transition between 1947 and 2019. Under 1947 rates, period life expectancy in Japan was low (53.7 years) and fertility was high (period TFR of 4.6). By 2019, Japan had one of the highest life expectancies in the world (87.4 years) and one of the lowest fertilities (TFR of 1.3). This dramatic transition translates into important differences in the kinship network (Caswell 2019, 2024).

As an example, expected LKO with grandchildren and grandparents is shown in Figure 2. Lifetime overlap at birth with grandchildren is higher under 1947 rates than under 2019 rates (about 125 person-years compared to 50 person-years). LKO with grandparents is about 45 person-years under 1947 rates and about 100 person-years under 2019 rates.

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[8] Perhaps a more general analysis would define a utility function for the number of kin. Consider cousins. The age-specific number of cousins is a utility function with constant returns; each additional cousin increases the abundance in that year by 1. The presence of at least one cousin is an extreme case of a utility function with diminishing returns; once a single cousin is present, additional cousins add nothing to the overlap in that year. A utility function could easily be devised that would exhibit either increasing or decreasing returns. This is an open research problem.

For convenience, figures showing the LKO results for all types of kin are collected in Appendix B. For ready reference, the expected kin numbers for each type of kin, under the 1947 and 2019 rates, are given in Appendix C

4.1 Lifetime, remaining lifetime, and partial lifetime overlap

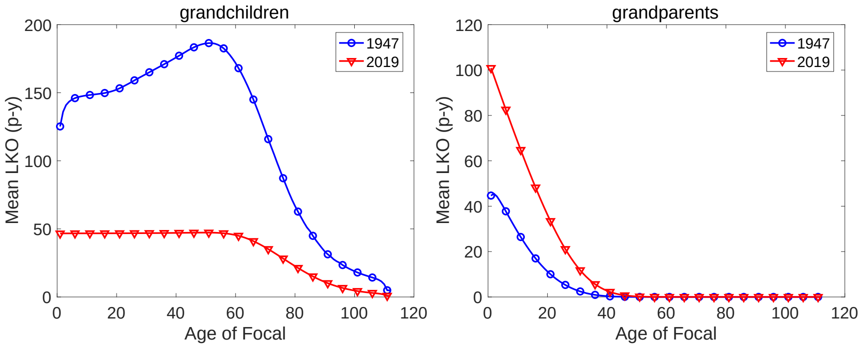
The vectors $\tilde{\boldsymbol{\rho}}_1$ and $\tilde{\boldsymbol{\rho}}_2$ defined in Equations (8) and (9) give the statistics of remaining lifetime overlap, starting from every age. Partial LKO, up to some specified age $x_{\max}$ rather than to death, is calculated by terminating the overlap calculation at $x_{\max}$. This can be done in two ways. One is to artificially ‘kill’ Focal at age $x_{\max}$ by setting the survival probability used in the MCWR calculation (the subdiagonal entries in **U** in Equation (6)) to 0 for ages $x > x_{\max}$. Equivalently, one could set the reward matrices to zero for ages greater than $x_{\max}$,

$$\mathbf{R}_m(:, x) = \mathbf{0} \qquad \text{for } x > x_{\max}, \; m = 1, 2. \tag{21}$$

This would allow Focal to live beyond age $x_{\max}$, but would prevent the accumulation of further rewards after that age.

Mean LKO results for all types of kin are collected in Figure B-1. As with grandparents in Figure 2, LKO with parents and great-grandparents is higher under 2019 rates than under 1947 rates, reflecting the higher survival in 2019. LKO with all other types of kin is higher under 1947 rates, reflecting the higher fertility in 1947.

Figure 2: Mean remaining lifetime overlap with grandchildren and grandparents, in person-years, as a function of the age of Focal. Note different scales on the y-axes



Notes: Japanese rates for 1947 and 2019; male and female kin combined.

4.2 Overlap with at least one kin

Instead of focusing on age-specific number of kin, consider the question of overlap with at least one relative (e.g., at least one child, or at least one sibling). Song and Mare (2019) refer to this as overlap with ”any kin.” This calculation treats the overlap as identical regardless of the number of children or siblings involved.

The condition of having at least one relative is a prevalence measure, formally similar to the condition of having a disability or a disease. Our task is to calculate the age-specific prevalence of having at least one kin, given the mean and variance in the age-specific number of kin provided by the kinship model. This requires information on the probability distribution of kin numbers at each age. Even if the expected number of kin is less than one, there is still some probability that at least one kin is present. Similarly, even if the expected number is large, there is still some probability to have none.

Given the prevalence of at least one kin, we then compute the reward matrices $\mathbf{R}_1$ and $\mathbf{R}_2$. See Caswell and Zarulli (2018) and Zarulli and Caswell (2024) for examples of computing reward matrices for the prevalences of health conditions.

If the number of kin follows a Poisson distribution, then the prevalence of having at least one relative at age j is

$$\mathbf{R}_1(:,j) = 1 - \exp\Big(- \|\mathbf{k}(j)\| \Big). \tag{22}$$

The Poisson distribution is appropriate for all categories of kin except for direct ancestors (parents $\mathbf{d}(x)$, grandparents $\mathbf{g}(x)$, and great-grandparents $\mathbf{h}(x)$ in the current model). For them, the appropriate distribution of kin numbers is binomial, with sample sizes $N = 2, 4, 8$, respectively (see Caswell 2024). The prevalence of having at least one relative in the binomial case is

$$\mathbf{R}_1(:,j) = 1 - \left(1 - \frac{\|\mathbf{k}(j)\|}{N}\right)^N. \tag{23}$$

Because a relative is either present or not present, the presence of kin has a Bernoulli (0–1) distribution,[9] and the second moment reward matrix is the same as the first:

$$\mathbf{R}_2 = \mathbf{R}_1. \tag{24}$$

Lifetime overlap with at least one kin calculated from these matrices has units person-years, but because only one person is considered, the units can also be treated as years.

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[9] Please do not become confused between the Poisson or binomial distribution of kin numbers and the Bernoulli distribution of the presence of at least one kin.

Figure 3 shows the mean LKO with at least one grandchild and at least one grandparent. It is interesting to compare the results with those for LKO counting all kin in Figure 2. Focusing on LKO measured from birth, we have

LKO with grandchildren

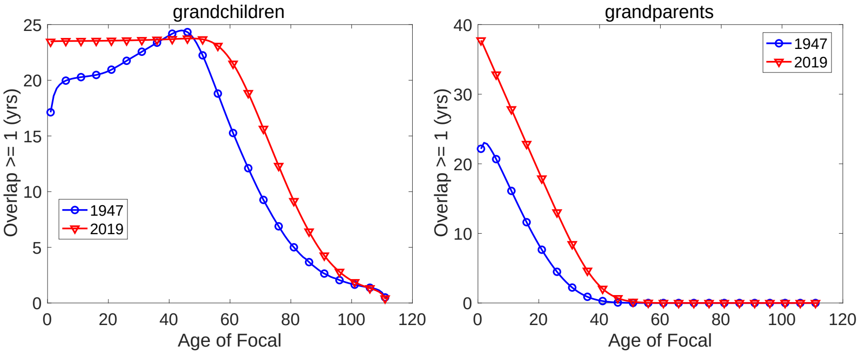
	1947	2019
All kin	125.2	46.6
At least one kin	17.1	23.4

LKO with grandparents

	1947	2019
All kin	44.7	100.9
At least one kin	22.2	37.7

Even though 1947 rates produce far more grandchildren than 2019 rates, the longer life of grandchildren under 2019 rates more than makes up for the smaller number when LKO is calculated for at least one grandchild. In contrast, LKO with grandparents is unaffected by changes in fertility because no new grandparents are born to Focal. Thus LKO with grandparents is greater under 2019 rates than 1947 rates for both all kin and at least one kin.

Figure 3: Mean LKO with at least one grandchild (left) and at least one grandparent (right). Compare with Figure 2, which shows LKO with numbers of kin. Note different y-axis scales



Notes: Japanese rates for 1947 and 2019, male and female kin combined.

4.3 Overlap with female and male kin

The extent of overlap with female and male kin may differ because of fertility and mortality differences between the sexes. Instead of combining the sexes as in Figure 2, in Figure B-2 we show results for each sex of each type of kin (e.g., sons and daughters, mothers and fathers, and so on).

The differences in overlap between the sexes are small. They are nearly invisible for children, grandchildren, and great-grandchildren. Even under 1947 rates these kin are unlikely to be old enough for sex differences in longevity to have an impact. The biggest differences between LKO with female and male kin are for parents, grandparents, and great-grandparents. Focal will experience more person-years of LKO with mother than father, with grandmothers than grandfathers, and great-grandmothers than great-grandfathers.

The model in Equations (4) and (5) contains sex differences only in mortality. A model that also included female and male fertility would probably not change these LKO patterns because while births may differ between the sexes, the sex ratio of offspring will not. On the other hand, sex differences in the age pattern of fertility might affect the pattern of LKO.

4.4 Variation and prediction intervals for LKO

The MCWR provides the second moments, and thus the variances and standard deviations of LKO, in Equations (9), (12), and (13). These measure the variation among individuals in their experience of LKO. Figure B-4 shows the standard deviation as a function of the age of Focal for all kin types. These standard deviations are almost always much higher under 1947 than under 2019 rates. Thus, under 1947 rates not only do individuals have higher expected overlap with their families, but there is more variation among individuals in this family experience.

The variance in LKO implies a prediction interval surrounding the expected value.[10] Calculating such an interval requires an assumption of a probability distribution of LKO. Lifetime kin overlap is often, but not always, overdispersed relative to a Poisson distribution, and is not necessarily a discrete distribution (for example, if some weighted set of kin numbers is used, or when the square root is applied in a sandwich overlap). An attractive choice of a probability distribution for this case is the gamma distribution. It is known to be a more flexible approximation to the negative binomial distribution (e.g., Ord 1967; Best and Gipps 1974; Ramalho 2013). It has support on the nonnegative real line and includes the exponential, Weibull, χ^2, and Erlang distributions as special cases. The

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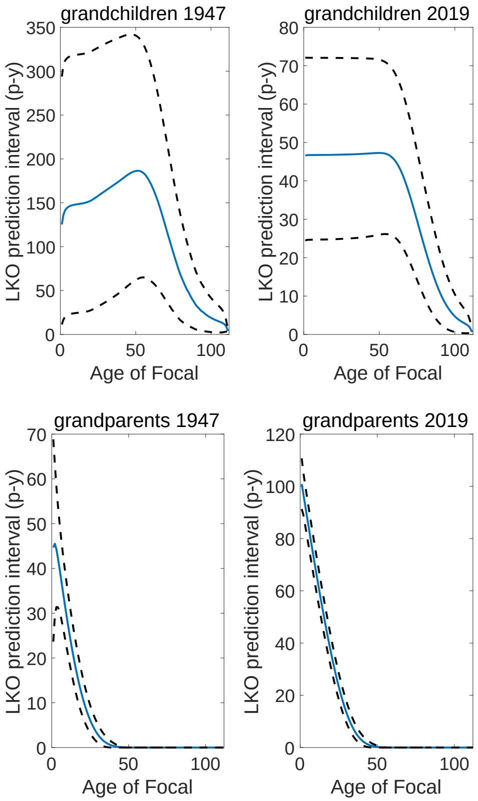
[10] This intervals are not confidence intervals surrounding an estimated mean, but rather intervals capturing a specified percentage of the distribution of LKO. The mean itself is calculated exactly from the mortality and fertility schedules and is not subject to sampling variation.

method of moments provides estimates of the shape parameter a and the scale parameter b of the Gamma distribution of a variable ξ as

$$\hat{b} = \frac{V(\xi)}{E(\xi)^2} \qquad \hat{a} = \frac{E(\xi)^2}{V(\xi)}. \tag{25}$$

The desired prediction intervals are then obtained from the inverse of the cumulative Gamma distribution, and are shown in Figure 4.

Figure 4: The mean and 90% prediction intervals for LKO with grandparents and grandchildren under Japan rates in 1947 and 2019. Note different y-axis scales



Notes: Japanese rates for 1947 and 2019, both sexes combined.

The 90% prediction intervals for LKO with grandchildren are wide: from about 10 to about 300 person-years under 1947 rates. There is much less variation around the mean for grandparents. For completeness, the prediction intervals for all kin are given in Figure B-5.

4.5 Prospective and retrospective overlap

Song and Mare (2019) make an important distinction between what they term 'prospective' and 'retrospective' overlap with kin. Prospective LKO projects Focal's overlap with her kin forward from her birth (or some other starting age) until death. It is as if the researcher is a wizard equipped with a crystal ball, making a prediction informed by mortality and fertility rates. The calculation must account for both the abundance of kin at each future age and Focal's potential of living to experience that overlap. The results we have shown so far are all prospective overlap measures.

Retrospective LKO can be thought of as the response of an individual (let us call her Respondent) to a survey question at some age a, asking how much overlap she has had with kin up to that age. The calculation must be conditional on Respondent's survival to age a so that she is available to respond to the survey, but must exclude any overlap after age a, because Respondent has no knowledge of that.

To condition on Respondent's survival to age a, we modify the $\mathbf{U}$ matrix in Equations (6), (8), and (9) to contain ones on the subdiagonal and zeros elsewhere, up to age a. Because overlap after age a has no impact on Respondent's retrospective overlap up to age a, we may as well calculate as if Respondent dies, or stops collecting rewards, immediately after answering the retrospective survey question at age a. To do this, set the columns of the reward matrices to 0 for all columns greater than a:

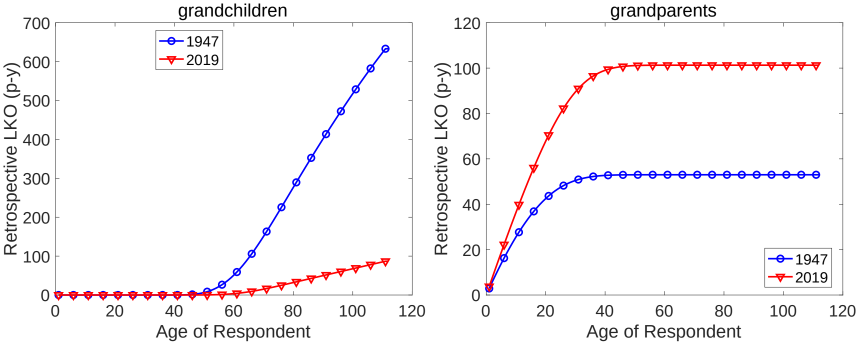
$$\mathbf{R}(:, a+1:\omega) = \mathbf{0}. \tag{26}$$

It is as if the researcher conducting the survey is an anthropomorphized personification of Death, equipped with a scythe and a clipboard.

As an example, the retrospective LKO of Respondent with her grandchildren and grandparents is shown in Figure 5. Retrospective overlap results for all kin are shown in Figure B-6. Retrospective LKO is by necessity a non-decreasing function of Respondent's age. In Figure 5, the retrospective LKO with grandchildren is zero until Respondent is about age 50, after which it increases with Respondent's age. The increase is more rapid, and reaches much higher levels, under 1947 rates than under 2019 rates.

Retrospective LKO with grandparents increases to an asymptote at about age 30 under 1947 rates and about age 40 under 2019 rates. After those ages, Respondent's grandparents are likely not alive and so Respondent's LKO with them cannot increase further. The overlap is higher under 2019 rates than under 1947 rates.

Figure 5: **Mean retrospective LKO with grandchildren and grandparents, in person-years, as a function of the age of Respondent. Note different scales on the y-axes**



Notes: Japanese rates for 1947 and 2019, both sexes combined.

4.6 Simultaneous overlap: The case of sandwiched kin

Focal experiences overlaps with many types of kin, and sometimes those simultaneous overlaps create problems or opportunities. The term 'sandwich generation' has been introduced to describe an individual sandwiched between simultaneous overlap with, and associated care burdens for, young children and old parents (e.g., Lei, Leggett, and Maust 2023; DeRigne and Ferrante 2012; Alburez-Gutierrez, Mason, and Zagheni 2021).

The sandwich concept can be generalized to other types of kin and need not always have negative connotations of burdens of care. Being sandwiched between young children and parents who are loving grandparents to those children can be a benefit rather than a burden to Focal (e.g., Eibich and Zai 2024). Similarly, simultaneous overlap of Focal with children and siblings might measure the opportunity for alloparental care of Focal's children by their aunts or uncles (Nitsch, Faurie, and Lummaa 2014). Kinlessness is a particular null case of overlap where Focal's simultaneous overlap with some specified type(s) of kin is zero (e.g., Verdery and Margolis 2017; Margolis and Verdery 2017; Margolis et al. 2022).

To be sandwiched at age x is to overlap simultaneously, at age x, with two types of kin. Consider two types (parents and children, for example) and define weighted kin numbers $\xi_1(x)$ and $\xi_2(x)$ at each age

$$\begin{aligned} \xi_1(x) &= \mathbf{c}_1^{\mathsf{T}} \mathbf{k}_1(x) \\ \xi_2(x) &= \mathbf{c}_2^{\mathsf{T}} \mathbf{k}_2(x), \end{aligned} \tag{27}$$

where $\mathbf{c}_1$ and $\mathbf{c}_2$ are vectors of weights, as in Section 3.1.

An appropriate measure of the simultaneous overlap of Focal with two types, at age x, is given by the geometric mean[11] of the two abundances

$$v(x) = \sqrt{\xi_1(x)\,\xi_2(x)}. \tag{28}$$

The first moment reward matrix for 'sandwichedness' is then

$$\mathbf{R}_1 = \left(\begin{array}{ccc|c} v(1) & \cdots & v(\omega) & 0 \\ \vdots & \cdots & \vdots & 0 \\ v(1) & \cdots & v(\omega) & 0 \\ \hline 0.5v(1) & \cdots & 0.5v(\omega) & 0 \end{array} \right). \tag{29}$$

As a measure of simultaneous overlap, the product of the numbers of two types of kin has the desirable property of being zero in the absence of either type of kin, and of being an increasing function of either type of kin for a fixed value of the other. The square root in the geometric mean standardizes the units of $v(x)$ to individuals rather than individuals squared.

The entries of the vector $\tilde{\boldsymbol{\rho}}_1$ from Equation (8) are the mean LKO, in units of person-years, over the lifetime of Focal. The second moment matrix $\mathbf{R}_2$ would require the variance of the geometric mean of kin numbers at each age. This variance could be found using a series expansion, but will not be explored here.

The different types of kin, and the age weights in Equation (27) define the layers of the sandwich. Attention has usually focused on the young of one type of kin and the old of another, and a variety of definitions of the young and old have been proposed. Some analyses define young dependent children as those less than 18 years of age and old dependent adults as older than 65 years. A particularly interesting definition by Alburez-Gutierrez, Mason, and Zagheni (2021) defines the young as less than or equal to 15 and defines the old as those within 5 years of death, using the prospective longevity approach

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[11] The product appears in various contexts as a measure of simultaneous occurrence. It corresponds to the AND operator in symbolic logic (two statements being simultaneously true) and to the intersection operator in set theory (for elements to belong simultaneously to two sets). In the algebra of events underlying probability theory, the product of two events describes the occurrence of both events (Rényi 1970).

of Sanderson and Scherbov (2019). We do not explore that definition here, but it will be interesting to eventually incorporate it into the MCWR framework.

It is possible to define sandwichedness in terms of any set of kin. Alburez-Gutierrez, Mason, and Zagheni (2021) examine parent-child sandwiches and parent-grandchild 'grand-sandwiches.' It is possible to define multilayer sandwiches with more than two types of kin: for example, simultaneous overlap with parents, siblings, children, and nieces-nephews. These four kin types would capture a three-generation family configuration that may be of interest in family care. The geometric mean measure of overlap in such a case would be

$$v(x) = \sqrt[4]{k_1(x)\, k_2(x)\, k_3(x)\, k_4(x)}. \tag{30}$$

Hünteler (2022) and Hünteler, Nutz, and Wörn (2024) define and explore a range of generational family structures, ranging from childlessness through one-, two-, three-, and four-generation families. The patterns of LKO in such multilayer sandwiches would be interesting to explore.

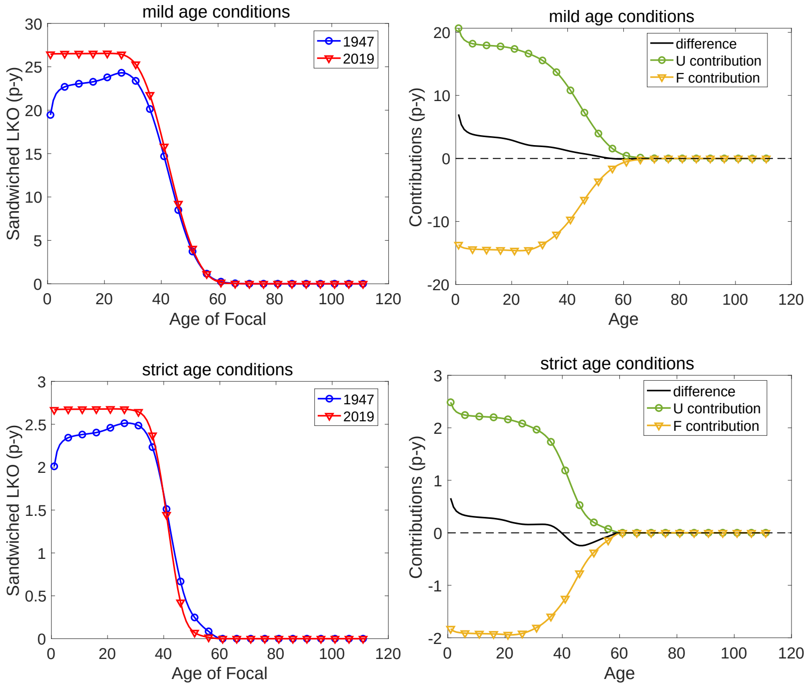
For the case of Japan, Figure 6 shows the expected LKO, in units of person-years, for two definitions of the sandwich under 1947 and 2019 rates. A set of 'mild' conditions defines Focal as sandwiched when she overlaps simultaneously with children younger than 18 and parents older than 65. A more strict definition is for simultaneous overlap with children younger than 5 and parents older than 75. The age patterns of LKO with these sandwiches are very similar, but of course the amount of sandwichedness is greater when the definitions are relaxed to include a wider age range of children and parents.

5. Decomposing differences in overlap: Contributions of mortality and fertility

The difference in LKO between two populations (or two time periods) is influenced by both fertility and survival. When both fertility and survival differ, as in the comparison of Japan under 1947 and 2019 rates, the difference in LKO can be decomposed into contributions of mortality and fertility using the classic Kitagawa-Keyfitz decomposition method (Kitagawa 1955; Keyfitz 1968).

It is often supposed that sandwiched families will become more common under recent conditions of higher survival and longer life expectancy. However, that has not happened in the comparison of Japan under 1947 and 2019 rates, despite the dramatic difference in those rates. Under either mild or strict age conditions, the mean sandwiched LKO is quite similar between the 1947 and 2019 rates.

Figure 6: Left: Mean sandwiched LKO between parents and children under mild (parents aged > 65, children aged < 18) and strict (parents aged > 75, children aged < 5) age conditions. Right: Contributions of survival and fertility differences to the change in LKO between 2019 and 1947. Units are person-years



Notes: Japanese rates for 1947 and 2019, both sexes combined.

To decompose this difference, consider two populations, each with its own survival and fertility matrices, and let $\boldsymbol{\rho}_1$ be the vector of mean sandwiched LKO calculated using the reward matrix in Equation (29). In our case the two populations are Japan in 1947 and in 2019. The difference in overlap is

$$\Delta \boldsymbol{\rho}_1 = \boldsymbol{\rho}_1 \left(\mathbf{U}_2, \mathbf{F}_2 \right) - \boldsymbol{\rho}_1 \left(\mathbf{U}_1, \mathbf{F}_1 \right). \tag{31}$$

We partition this difference into contributions from the difference in $\mathbf{U}$ and the difference in $\mathbf{F}$. These contributions are

$$C(\mathbf{U}) = \frac{1}{2}\left[\boldsymbol{\rho}_1(\mathbf{U}_2,\mathbf{F}_2) - \boldsymbol{\rho}_1(\mathbf{U}_1,\mathbf{F}_2)\right] + \frac{1}{2}\left[\boldsymbol{\rho}_1(\mathbf{U}_2,\mathbf{F}_1) - \boldsymbol{\rho}_1(\mathbf{U}_1,\mathbf{F}_1)\right] \quad (32)$$

$$C(\mathbf{F}) = \frac{1}{2}\left[\boldsymbol{\rho}_1(\mathbf{U}_2,\mathbf{F}_2) - \boldsymbol{\rho}_1(\mathbf{U}_2,\mathbf{F}_1)\right] + \frac{1}{2}\left[\boldsymbol{\rho}_1(\mathbf{U}_1,\mathbf{F}_2) - \boldsymbol{\rho}_1(\mathbf{U}_1,\mathbf{F}_1)\right]. \quad (33)$$

The first term on the right-hand side of $C(\mathbf{U})$ is the difference in LKO that would be produced by the difference in survival matrices $\mathbf{U}_2 - \mathbf{U}_1$ under the fertility schedule $\mathbf{F}_2$. The second term is the same, but under the fertility schedule $\mathbf{F}_1$. The contribution of differences in $\mathbf{U}$ is the average of these two. The calculation is the same for the effects of the differences in $\mathbf{F}$.

If $\boldsymbol{\rho}_1$ is a vector (e.g., a vector of remaining lifetime overlap as a function of age), the contributions $C(\mathbf{U})$ and $C(\mathbf{F})$ will also be vectors. The decomposition is exact.

The decomposition result applied to Japanese rates in 1947 and 2019 is shown in the right-hand panels of Figure 6. The increased survival in 2019 would, on its own, have created a large increase in sandwiched LKO (+25 person-years with the mild age definition, +3 person-years with the more strict age definition). The reduced fertility in 2019 would, on its own, have created an almost equal reduction in sandwiched LKO. The contributions of survival and fertility differences nearly cancel each other out, leaving little difference in sandwiched LKO.

Is there something special about the comparison of these two particular years in this particular country that leads to such a close balance between increases and decreases? We do not know.

6. Discussion

Humans are a social species. Our interactions with immediate family, ancestors, descendants, and other relatives affect many aspects of our lives and family dynamics. Many of the interactions require shared lives; they take place only if the lives of both parties overlap. This calls for a way to calculate the patterns of lifetime kin overlap (LKO) implied by a set of demographic rates. Such calculations have previously been approached by formal models (e.g., Song and Mare 2019) and by microsimulations (e.g., Margolis and Verdery 2019; Alburez-Gutierrez, Mason, and Zagheni 2021). Valuable as those analyses are, they have been limited to a few types of kin and indices of overlap, and have been provided only expected values of kin overlap. A more general and flexible framework that can incorporate a wider range of demographic outcomes and provide variances as well as means has been lacking.

6.1 Overview

We have approached the problem by combining two analyses: (1) the kinship network surrounding Focal at each age and (2) the life course of Focal as she experiences that network over a lifetime. The first of these is provided by the matrix kinship model, the second by a Markov chain with rewards. The rewards accumulated at each age (or more generally each transition) are given by (some function of) the age-specific kinship network.

The rewards are incorporated in matrices defined in Equations (19) and (20) for kin abundance, by (22) and (23) for presence of at least one kin, and by (29) for sandwiched kin. The MCWR calculations are given by Equations (8) and (9). Higher moments are available if desired.

Our comparison of Japan under 1947 and 2019 rates highlights changes in LKO produced by the dramatic demographic transition that occurred over that period. The rates of 1947 produced much greater LKO with all types of kin except parents, grandparents, and great-grandparents, compared to 2019 rates. In contrast, the rates of 2019 produced greater LKO with at least one relative. The variance in LKO among individuals is much greater under 1947 rates than 2019 rates. The reduction in fertility and increase in survival between 1947 and 2019 work in opposite directions. In the case of sandwich overlap with parents and children, the contribution of these two changes almost cancel each other out.

6.2 Evolutionary demography

In evolutionary and anthropological contexts, overlap with kin who have different degrees of genetic relatedness influences the outcome of kin selection (Tanskanen and Danielsbacka 2019). For example, alloparenting of kin in humans allowed us to have shorter birth intervals when compared to other primates with altricial offspring (Hrdy 2009). In turn, Hrdy (2009) argues that this complicated and social form of childrearing led to the evolution of our unique prosocial tendencies.

The evolutionary importance of overlap with kin is not limited to humans, but applies more broadly to other social species. For example, Ellis et al. (2024) argue that the evolution of menopause in toothed whales (one of the few mammalian groups that share this property with humans) is related to their kinship networks. The toothed whales are projected to have more kin than other groups of whales, increasing the opportunity for post-reproductive females to benefit their relatives and thus increase inclusive fitness. Refining those analyses to consider kin overlap as well as kin abundance might provide additional insight.

The mortality and fertility of elephants are also influenced by the overlap with relatives (e.g., Lahdenperä et al. 2012; Lahdenperä, Mar, and Lummaa 2016a,b; Berger et al. 2021; Croll and Caswell 2025). Analyzing LKO and its response to poaching pressure, as was done for population growth by Croll and Caswell (2025), would be an exciting addition.

The LKO calculation also provides a potential starting point for empirical estimates of the lifetime accumulated benefits due to helping – that is, estimates of one side of Hamilton's equation (Hamilton 1964). Consider sibling helping in elephants as an example. Lynch et al. (2019) find that living near a younger sister significantly increases the likelihood of annual reproduction among female elephants, and that this effect is strongest when living near a sister 0–5 years younger. The analysis presented here might be used to calculate the lifetime accumulated additional nephews and nieces born due to a focal female overlapping with sisters. Incorporating reproductive value (which describes the relative importance of a stage from the perspective of natural selection; see Rodrigues and Gardner 2022) would allow an estimate of the benefit of sister helping – that is, the benefit side of Hamilton's equation. Obtaining empirical estimates of Hamilton's equation has been challenging (see Bourke 2014 and van Veelen et al. 2017 for reviews), so this would be an exciting development.

6.3 Extensions

Several issues are not yet addressed in the method we present here. The model for kinship currently treats only biological kin. Although male and female rates are included, spouses, blended families, and kin by marriage are not. Including these aspects of kinship networks is very much an open research problem. However, both Focal and Focal's spouse are subject to the same demographic rates, so the patterns found here are expected to be mirrored in a model including affinal kin.

Our analysis uses time-invariant period rates, and thus apply to synthetic cohorts following those rates over a lifetime. The time-varying version of the kinship model exists (Caswell and Song 2021) and has been used to project future kinship sizes and health patterns (Alburez-Gutierrez, Williams, and Caswell 2023; Feng, Song, and Caswell 2025). The MCWR method has been developed for some types of time-varying rates (Caswell 2011). However, combining the two is very much an open research question. In this paper, we have used age-classified demographic rates. Multistate or stage-classified models could be analyzed as was done for age×parity by Caswell (2020), provided that all offspring are born into a single stage. Analysis of cases in which offspring may be born into multiple different stages (e.g., spatial models) requires further extensions. To date, analyses of such cases require the approach introduced by Coste et al. (2021) and Butterick et al. (2025). Extending the matrix kinship model to cover these cases is an open research problem; see Butterick et al. (2025) for some promising developments.

Focal's overlap with kin as defined here is a fact of her being alive and having living kin at the same time. The implications of that overlap may depend on many properties of the coexisting kin. A particularly important dimension of LKO, yet to be addressed, is spatial proximity, especially coresidence. Interactions with nearby kin and distant kin can be very different, and patterns of dispersal of kin have changed in recent times. Incorporating information on the prevalence of coresidence (e.g., Amorim, Pilkauskas, and Dunifon 2017; Healy and Dunifon 2025) into a weighted kin abundance measure, as in Equation 18, would be a first step, but only that, toward examining LKO with age-weighted coresident kin.

The MCWR analysis yields the moments, as many as desired, of the distribution of LKO (van Daalen and Caswell 2017). We have focused on the mean and variance of LKO here; the skewness of LKO could be calculated from the third moments of LKO. An alternative approach to lifetime calculations was introduced by Tuljapurkar et al. (2020) in the context of lifetime reproductive success. That approach provides the complete distribution; it may be possible to extend this approach from lifetime reproductive output to LKO.

Many demographic processes operate differentially over age and carry particular significance when accumulated over a lifetime. The event of survival, or of survival in some particular state of health, when compounded over a lifetime becomes longevity or healthy longevity. The event of reproducing, when compounded over a lifetime, yields lifetime reproductive output. The kinship network experienced by an individual is an equally important age-specific property. The methodology presented here gives the result of accumulating that overlap over a (suitably defined) lifetime.

These lifetime outcomes are random variables. They necessarily vary among individuals due to the stochasticity of survival, reproduction, health, and so on. Even so, they are all too often discussed only in terms of mean values (life expectancy, health expectancy, net reproductive rate, total fertility rate). The MCWR approach is one powerful way to obtain all the moments of lifetime accumulated outcomes. It is now applicable to the kinship network, which is projected as an age-specific property of Focal.

The flexibility of the LKO analysis (Section 4.1) makes our results possibly useful in a variety of practical applications. The LKO measure could help assess potential family support across an individual's entire life span. Remaining LKO as a function of age could help assess available family support resources during later life stages (e.g., retirement and elderly care), and partial lifetime overlap highlights the availability of kin during critical life periods, such as during parenting years or midlife when caregiving demands are high.

We have indicated some of the potential applications of this analysis and shown some examples of how LKO changes over a demographic transition. More patterns await exploration.

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Appendices

Appendix A: Notes on Markov chains with rewards

This Appendix provides a bit more discussion of the MCWR method for calculating LKO. It is modified from Caswell and van Daalen (2021) and Caswell and Zarulli (2018), in both cases under the terms of CC-BY licenses.

Life is a Markov chain; the things that happen during that life are rewards. An individual in a Markov chain makes transitions among states. A Markov chain with rewards (MCWR) imagines that the individual collects a ‘reward’ r_{ij} when making the transition from state j to state i. In our case, this is the transition of Focal from age j to age $i = j + 1$. These rewards accumulate over the lifetime of the individual. The concept is extraordinarily flexible. The lifetime accumulation of the reward might measure lifetime occupancy of, or transitions among, health stages, lifetime reproductive output, lifetime accumulation of income, or, in our case, lifetime overlap with a specified type of kin.

A simple example may clarify the concept. Suppose that over a lifetime of four units the mean age-specific number of kin $k(x)$ is

$$\begin{array}{r|cccc} x & 1 & 2 & 3 & 4 \\ k(x) & 0 & 2 & 4 & 0 \end{array} . \tag{34}$$

A Focal individual who lives through all four years of life will die with a lifetime accumulated overlap of $2+4=6$ person-years. Should Focal die in age class 2, she will have a lifetime accumulated overlap of $0+1=1$ person-years, receiving credit for one half of the year in which she dies.

Individuals will live different lengths of time. This is accounted for by describing the life cycle by the absorbing Markov chain transition matrix in Equation (6).

In reality, the age-specific number of kin at each age of Focal is a random variable. The transition from state j to state i collects a random reward r_{ij} and we must specify its moments. The moments of the r_{ij} are placed in a series of reward matrices; the matrix containing the kth moments of the r_{ij} is denoted $\mathbf{R}_k$:

$$\mathbf{R}_k = \left(\; E\left[r_{ij}^k\right] \; \right) . \tag{35}$$

If $k(x)$ in Equation (34) is the means of a Poisson distributed number of kin, then the first moment reward matrix is

$$\mathbf{R}_1 = \left(\begin{array}{cccc|c} 0 & 2 & 4 & 0 & 0 \\ 0 & 2 & 4 & 0 & 0 \\ 0 & 2 & 4 & 0 & 0 \\ 0 & 2 & 4 & 0 & 0 \\ \hline 0 & (0.5)(2) & (0.5)(4) & 0 & 0 \end{array}\right), \tag{36}$$

where transitions to death have been credited with 1/2 of the overlap that would be obtained from surviving through the interval.

The matrix of second moments is

$$\mathbf{R}_2 = \left(\begin{array}{cccc|c} 0 & 6 & 20 & 6 & 0 \\ 0 & 6 & 20 & 6 & 0 \\ 0 & 6 & 20 & 6 & 0 \\ 0 & 6 & 20 & 6 & 0 \\ \hline 0 & (0.25)(6) & (0.25)(20) & 0 & 0 \end{array}\right). \tag{37}$$

The upper left block of $\mathbf{R}_2$ follows from the fact that if $X \sim$ Poisson(λ), then $E(X^2) = \lambda + \lambda^2$. The lower left block follows from the fact that if $Y = cX$, then $E(Y^2) = c^2 E(X^2)$.

Rewards accumulate over time. The MCWR method calculates the statistical properties of lifetime accumulation of rewards (LKO in our context) accounting for the randomness of the lifetime of Focal and of the age-specific abundance of kin. Define $\boldsymbol{\rho}_k$ as the vector containing the kth moments of accumulated rewards as a function of the initial age of the individual

$$\boldsymbol{\rho}_k = \left(\; E\left[\rho_i^k\right] \; \right). \tag{38}$$

A recursive formula for these moments is given by Caswell (2011), and an exact solution derived by van Daalen and Caswell (2017). Because rewards are not collected in the absorbing states (in our context, this is the eminently reasonable assumption that the dead do not accumulate any further kin overlap), we need only compute that part of $\boldsymbol{\rho}$ corresponding to the transient, living states $1, \ldots, \omega$. van Daalen and Caswell (2017) denote this vector by $\tilde{\mathbf{p}}$, but in this paper we use the tilde to denote the block-structured matrices and vectors including both males and females. For the sake of clarity we denote the reward vector by $\boldsymbol{\rho}^\dagger$.

Denoting this subvector by $\boldsymbol{\rho}_k^\dagger$, of dimension $\omega \times 1$, we write

$$\boldsymbol{\rho}_k^\dagger = \mathbf{Z}\boldsymbol{\rho}, \tag{39}$$

where

$$\mathbf{Z} = \left(\begin{array}{c|c} \mathbf{I}_{\omega\times\omega} & \mathbf{0}_{\omega\times\alpha} \end{array} \right). \tag{40}$$

Then the moments of remaining lifetime rewards for individuals starting in any of the transient states are given by the entries of the moment vectors $\boldsymbol{\rho}_i^\dagger$, where

$$\boldsymbol{\rho}_1^\dagger = \mathbf{N}^\mathsf{T}\mathbf{Z}\left(\mathbf{P}\circ\mathbf{R}_1\right)^\mathsf{T}\mathbf{1}_\omega \tag{41}$$

$$\boldsymbol{\rho}_2^\dagger = \mathbf{N}^\mathsf{T}\left[\mathbf{Z}\left(\mathbf{P}\circ\mathbf{R}_2\right)^\mathsf{T}\mathbf{1}_\omega + 2\left(\mathbf{U}\circ\mathbf{R}_1^\dagger\right)^\mathsf{T}\boldsymbol{\rho}_1^\dagger\right] \tag{42}$$

$$\begin{aligned}\boldsymbol{\rho}_3^\dagger = \mathbf{N}^\mathsf{T}\Big[&\mathbf{Z}\left(\mathbf{P}\circ\mathbf{R}_3\right)^\mathsf{T}\mathbf{1}_\omega + 3\left(\mathbf{U}\circ\mathbf{R}_2^\dagger\right)^\mathsf{T}\boldsymbol{\rho}_1^\dagger \\ &+ 3\left(\mathbf{U}\circ\mathbf{R}_1^\dagger\right)^\mathsf{T}\boldsymbol{\rho}_2^\dagger\Big]\end{aligned} \tag{43}$$

and, in general,

$$\begin{aligned}\boldsymbol{\rho}_m^\dagger = {} & \mathbf{N}^\mathsf{T}\mathbf{Z}\left(\mathbf{P}\circ\mathbf{R}_m\right)^\mathsf{T}\mathbf{1}_\omega \\ & + \sum_{k=1}^{m-1}\binom{m}{k}\mathbf{N}^\mathsf{T}\left(\mathbf{U}\circ\mathbf{R}_{m-k}^\dagger\right)^\mathsf{T}\boldsymbol{\rho}_k^\dagger,\end{aligned} \tag{44}$$

where

$$\mathbf{R}_i^\dagger = \mathbf{Z}\mathbf{R}_i\mathbf{Z}^\mathsf{T} \tag{45}$$

is the $\omega \times \omega$ submatrix of $\mathbf{R}_i$ corresponding to the transient states. Proofs of (41)–(44) are given in van Daalen and Caswell (2017: Theorem 1).

These expressions do not admit any facile interpretation, but it may be helpful to focus on the ingredients. The first moment vector $\boldsymbol{\rho}_1^\dagger$ depends on the time spent in each stage ($\mathbf{N}$) and the Hadamard product of the transition matrix ($\mathbf{P}$) and the first moments of the age-specific rewards ($\mathbf{R}_1$). The second moment vector $\boldsymbol{\rho}_2^\dagger$ depends on $\mathbf{N}$ and the product $\mathbf{P}\circ\mathbf{R}_2$, as well as on the first moments. The pattern continues to all the higher moments.

Note that the moments of lifetime rewards (LKO in our case) depend only on the moments of the age-specific rewards (age-specific kin abundances in our case), not on the total distribution of those age-specific rewards.

The variance, standard deviation, coefficient of variation, and skewness of lifetime overlap are calculated from the moment vectors, as

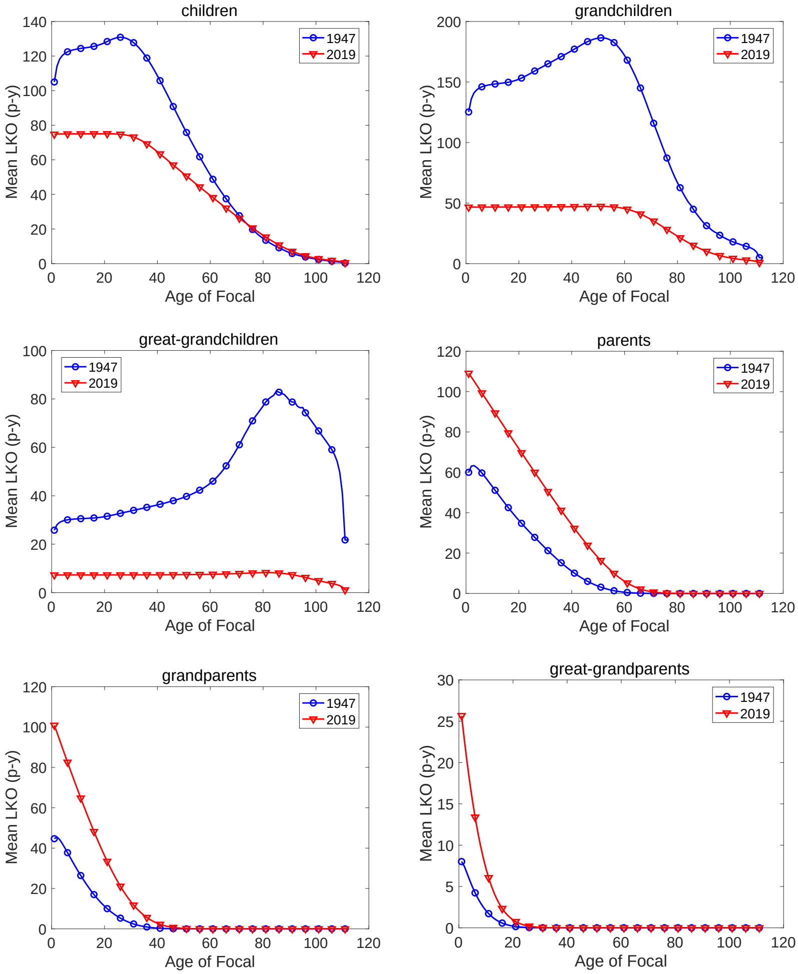
$$\begin{aligned} V\left(\boldsymbol{\rho}\right) &= \boldsymbol{\rho}_2 - \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1 && (46) \\ SD\left(\boldsymbol{\rho}\right) &= \sqrt{V\left(\boldsymbol{\rho}\right)} && (47) \\ CV\left(\boldsymbol{\rho}\right) &= \mathcal{D}\left(\boldsymbol{\rho}_1\right)^{-1} SD\left(\boldsymbol{\rho}\right) && (48) \\ Sk\left(\boldsymbol{\rho}\right) &= \mathcal{D}\left[V(\boldsymbol{\rho})\right]^{-3/2} \, \big(\boldsymbol{\rho}_3 - 3\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_2 \\ &\quad +2\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1\big) \, . && (49) \end{aligned}$$

For those interested in derivations and proofs and a detailed discussion of choices of reward distributions, we suggest van Daalen and Caswell (2017). For those interested in a demographically rich extension of MCWR models to healthy longevity in multistate health models, we recommend the paper of Caswell and van Daalen (2021) on incidence-based models.

Appendix B: Collected figures: LKO results for all kin

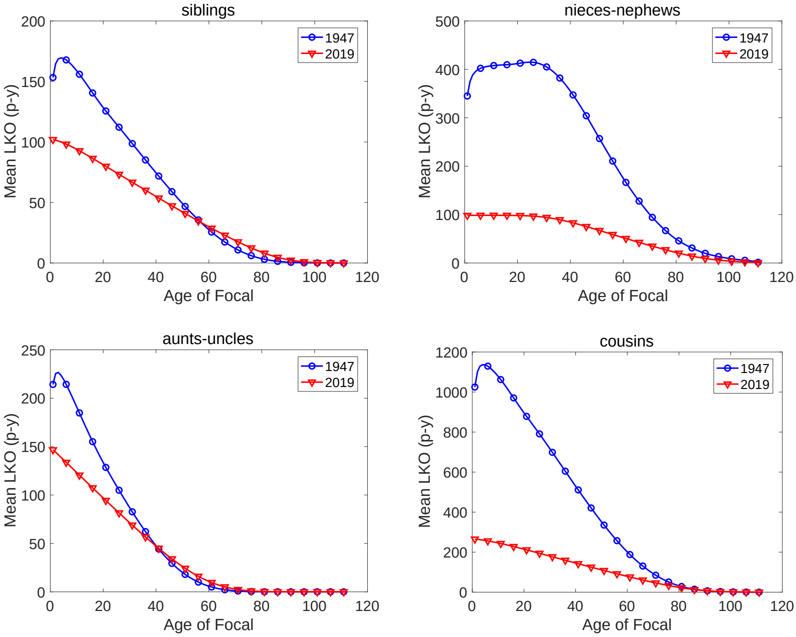
Mean prospective lifetime overlap with kin

Figure B-1: (Part 1) Mean remaining LKO with each type of kin as a function of the age of Focal. LKO is measured in person-years



Notes: Japanese rates for 1947 and 2019, both sexes combined.

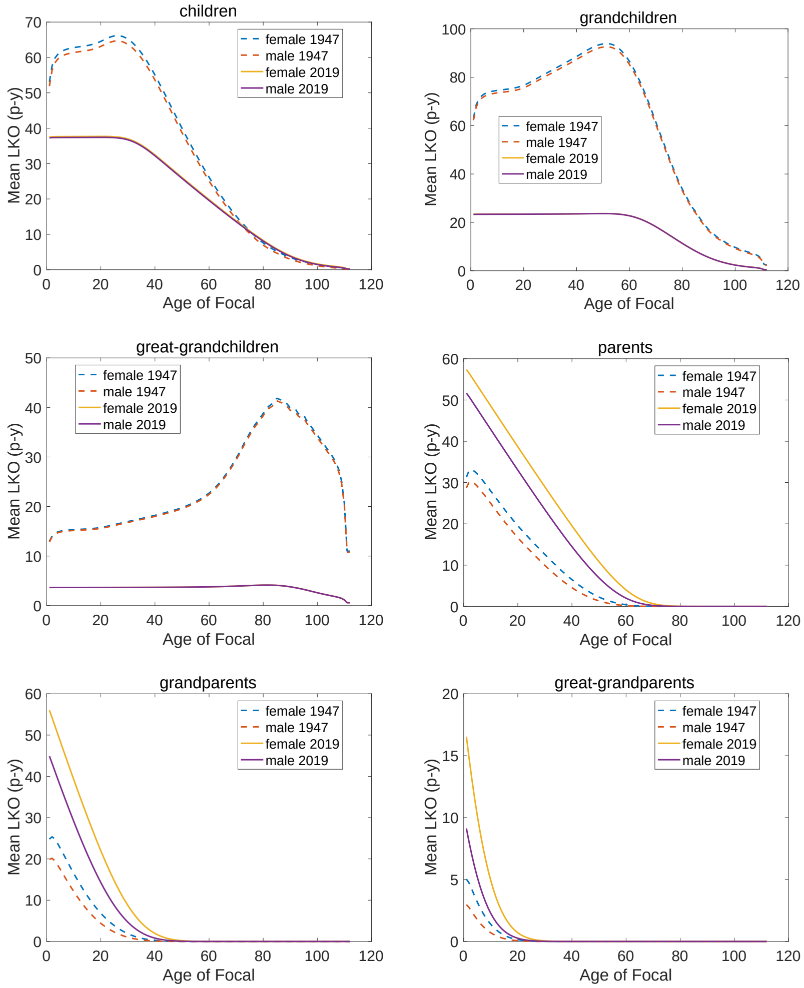
Figure B-1: (Part 2) Mean remaining LKO with each type of kin as a function of the age of Focal. LKO is measured in person-years



Notes: Japanese rates for 1947 and 2019, both sexes combined.

Overlap with female and male kin

Figure B-2: (Part 1) Mean remaining LKO with male and female members of each type of kin, as a function of the age of Focal. LKO is measured in person-years



children

grandchildren

great-grandchildren

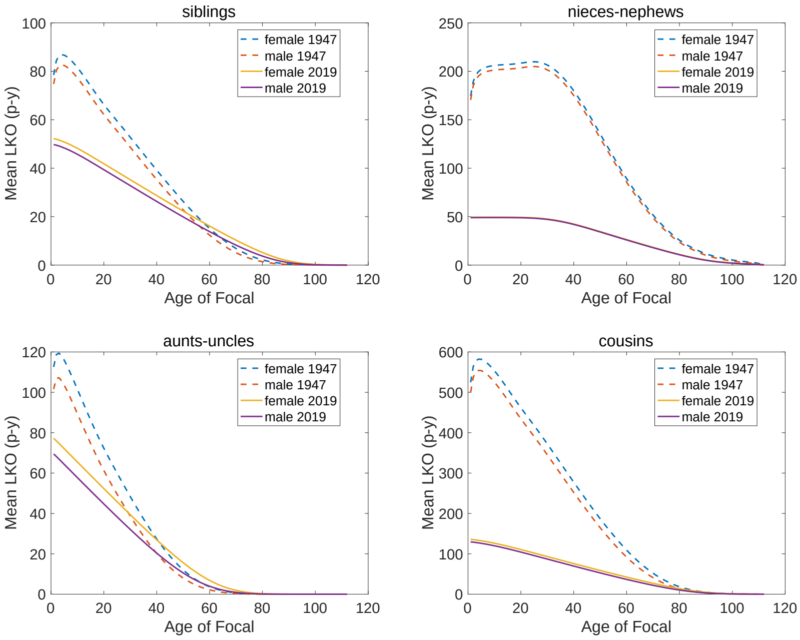
parents

grandparents

great-grandparents

Notes: Japan rates for 1947 and 2019.

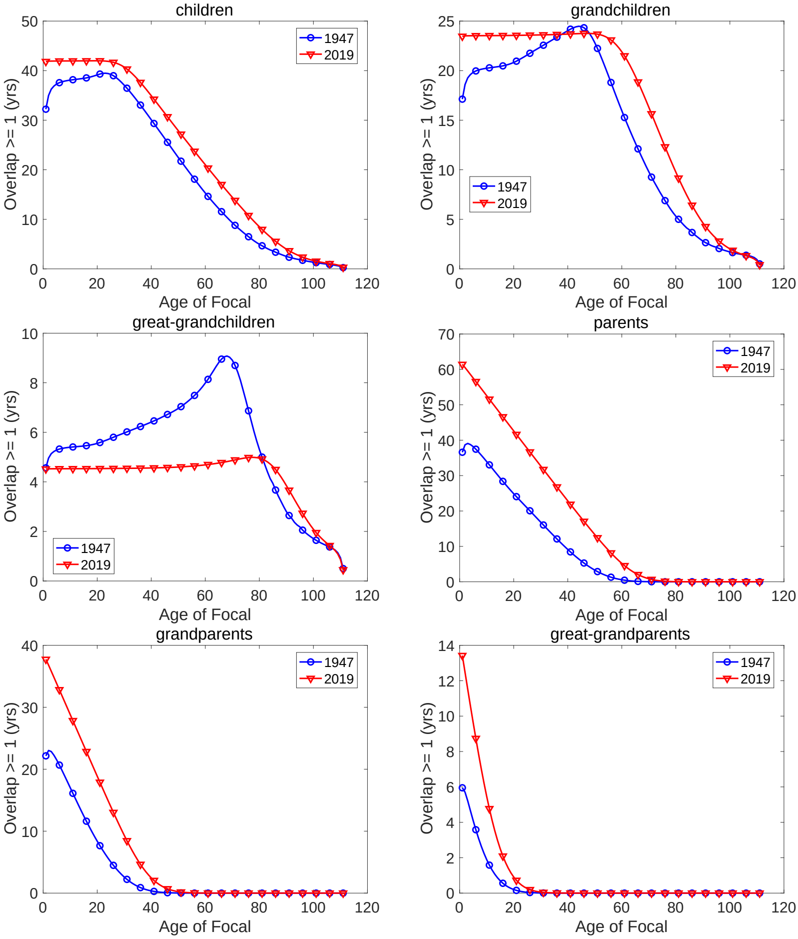
Figure B-2: (Part 2) Mean remaining LKO with male and female members of each type of kin, as a function of the age of Focal. LKO is measured in person-years



Notes: Japan rates for 1947 and 2019.

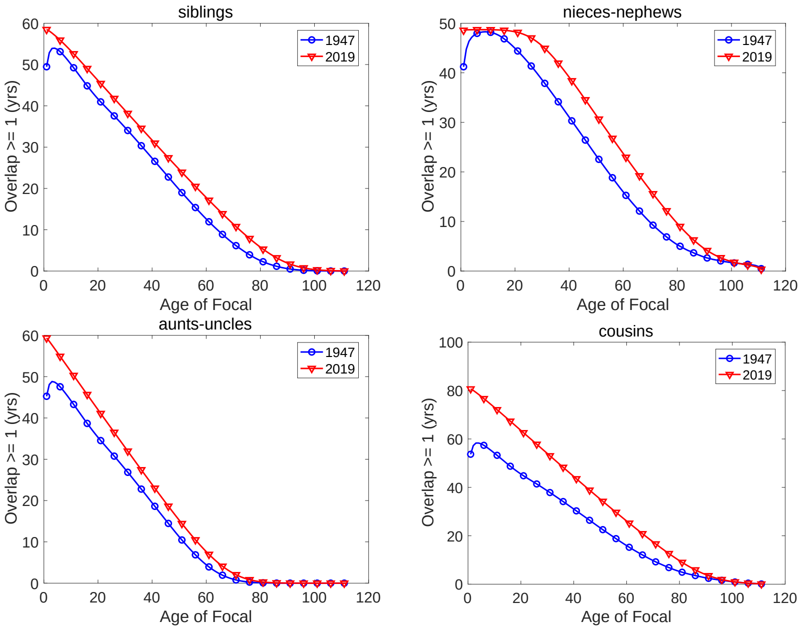
Overlap with at least one kin

Figure B-3: **(Part 1.) Mean remaining LKO, with at least one individual of each type of kin, as a function of the age of Focal. LKO is measured in years**



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

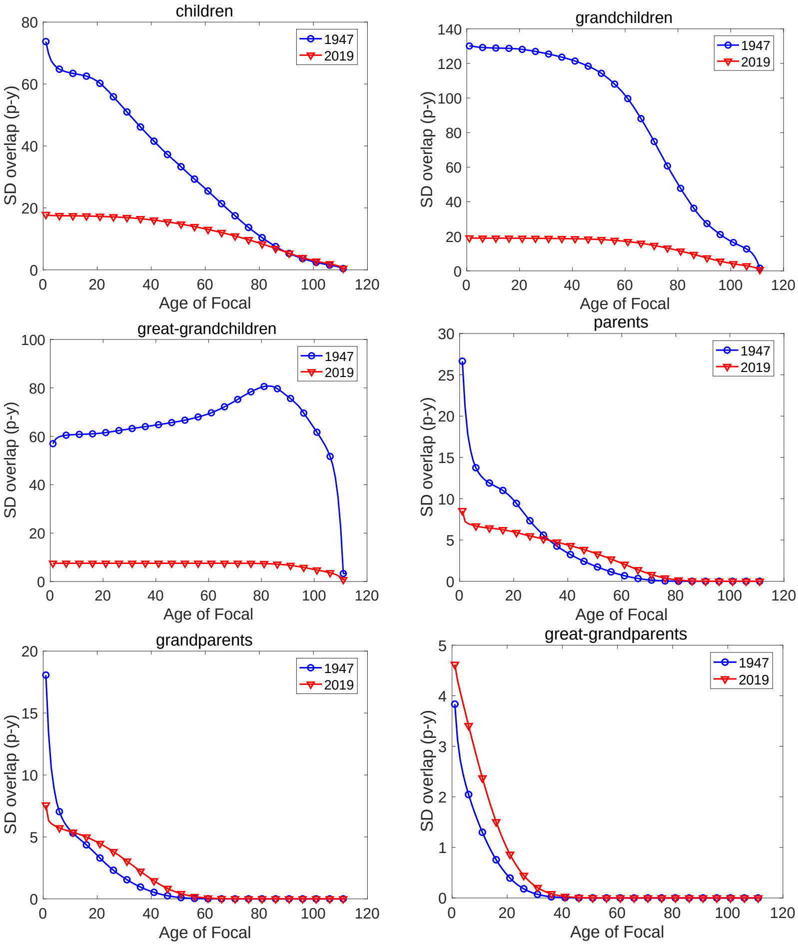
Figure B-3: (Part 2) Mean remaining LKO with at least one individual of each type of kin, as a function of the age of Focal. LKO is measured in years



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

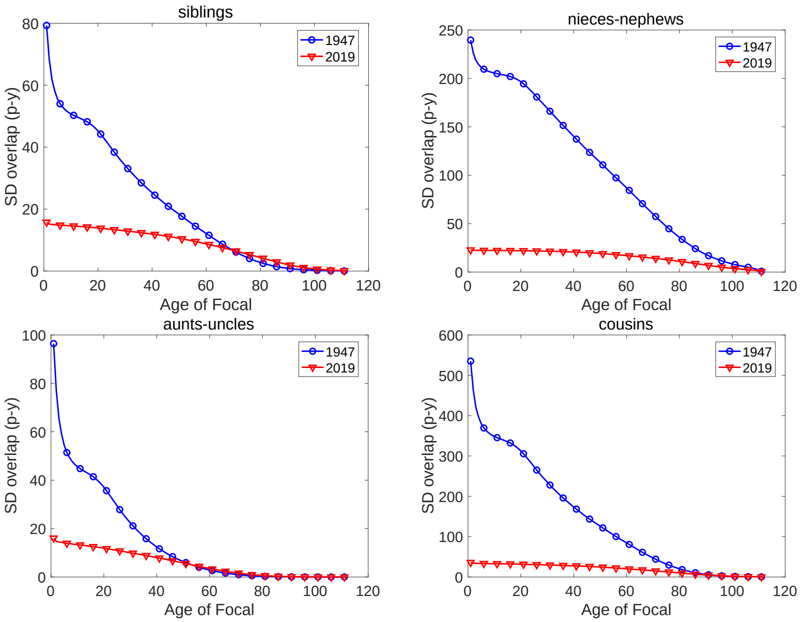
Standard deviation of kin overlap

Figure B-4: **(Part 1) Standard deviation (SD) of remaining LKO with each type of kin as a function of the age of Focal. SD is measured in person-years**



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

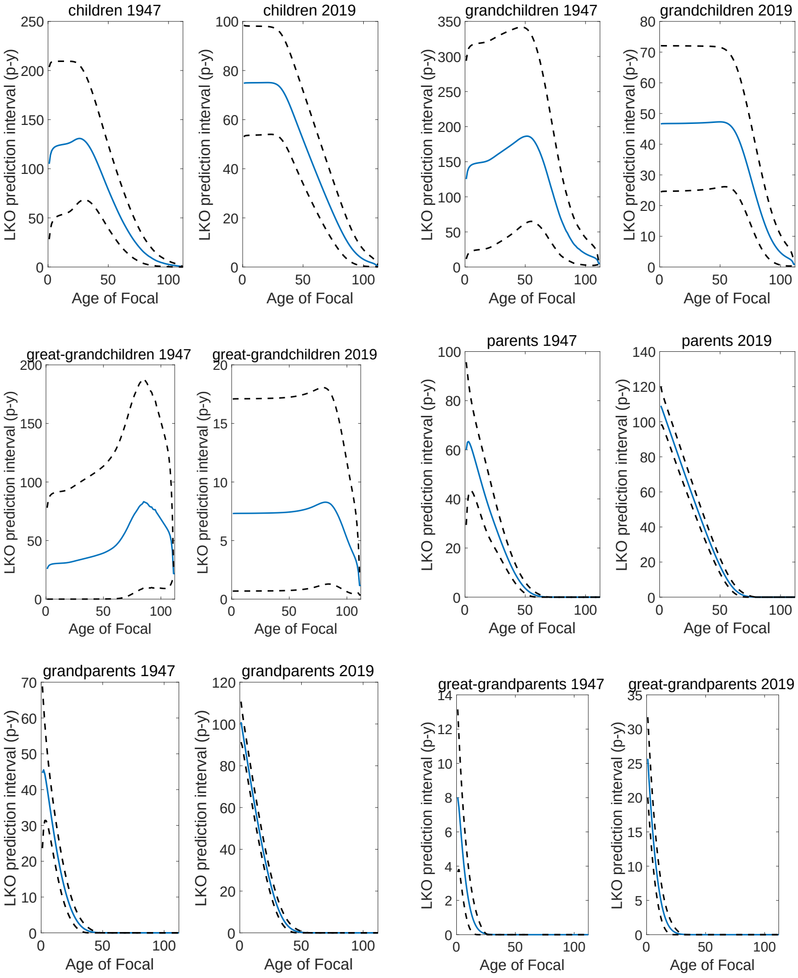
Figure B-4: (Part 2) Standard deviation (SD) of remaining LKO with each type of kin as a function of the age of Focal. SD is measured in person-years



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

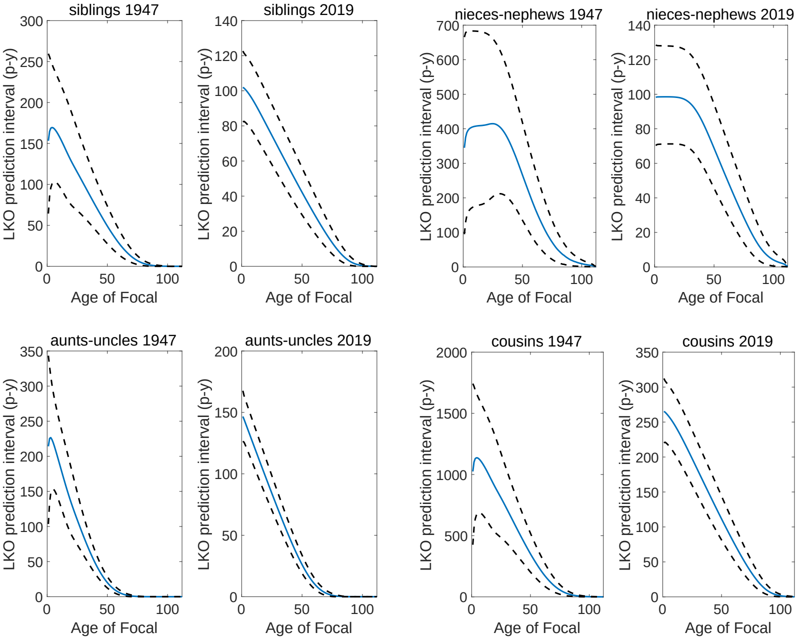
Prediction intervals for kin overlap

Figure B-5: (Part 1) Expected remaining LKO and 90% prediction intervals for each kind of kin. LKO is measured in person-years



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

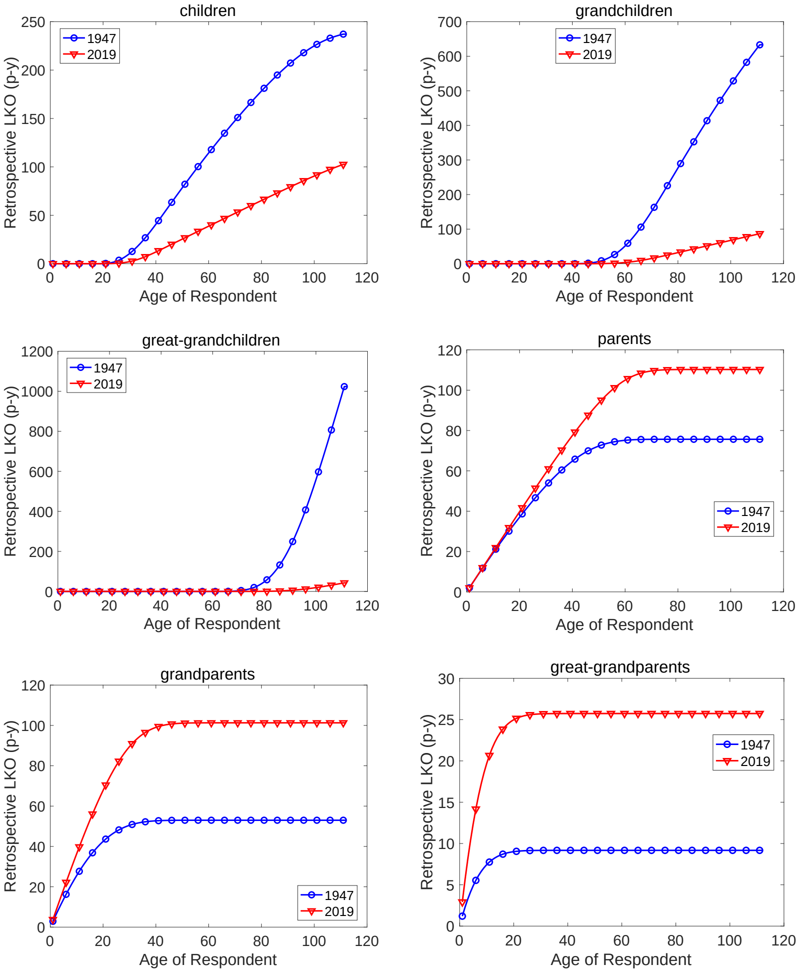
Figure B-5: (Part 2) Expected remaining LKO and 90% prediction intervals for each kind of kin. LKO is measured in person-years



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

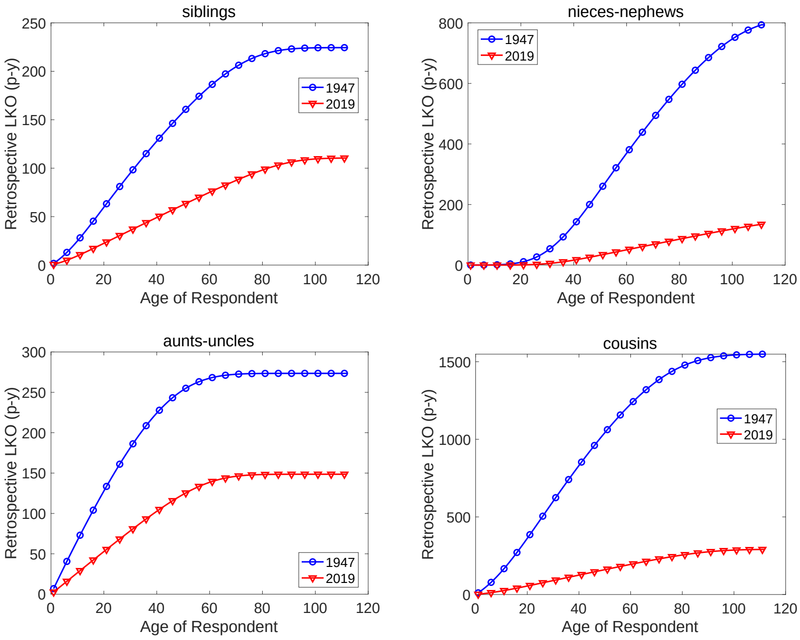
Mean retrospective lifetime overlap with kin

Figure B-6: **(Part 1) Mean retrospective LKO with each type of kin, as a function of the age of Respondent. LKO is measured in person-years**



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

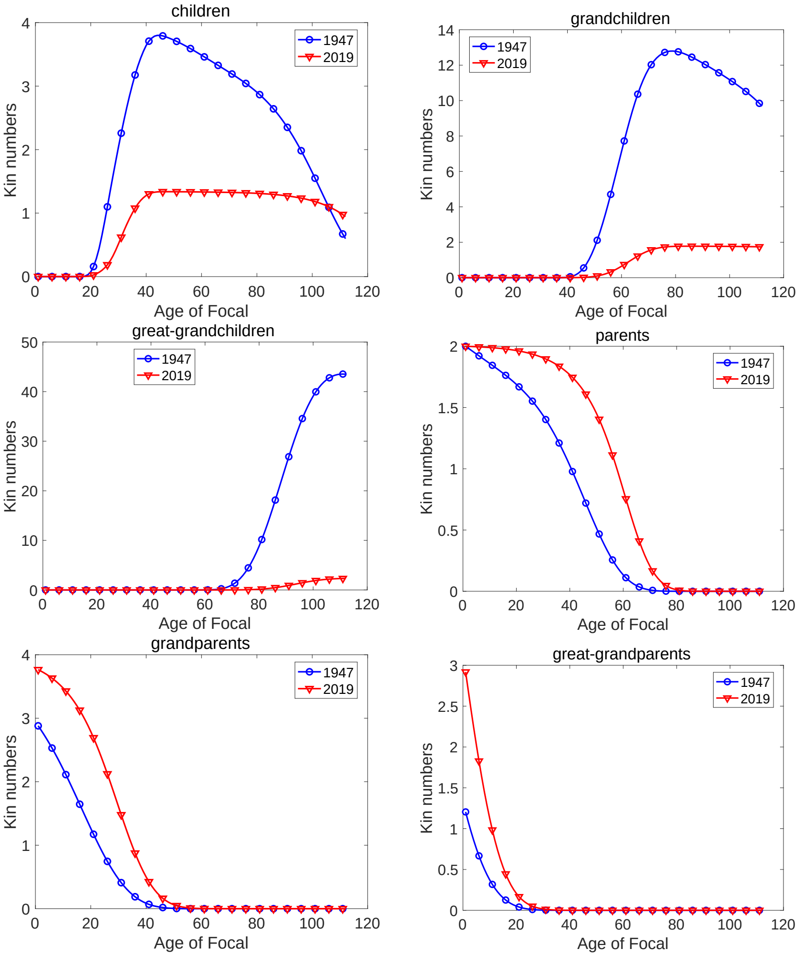
Figure B-6: (Part 2) Mean retrospective LKO with each type of kin, as a function of the age of Respondent. LKO is measured in person-years



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

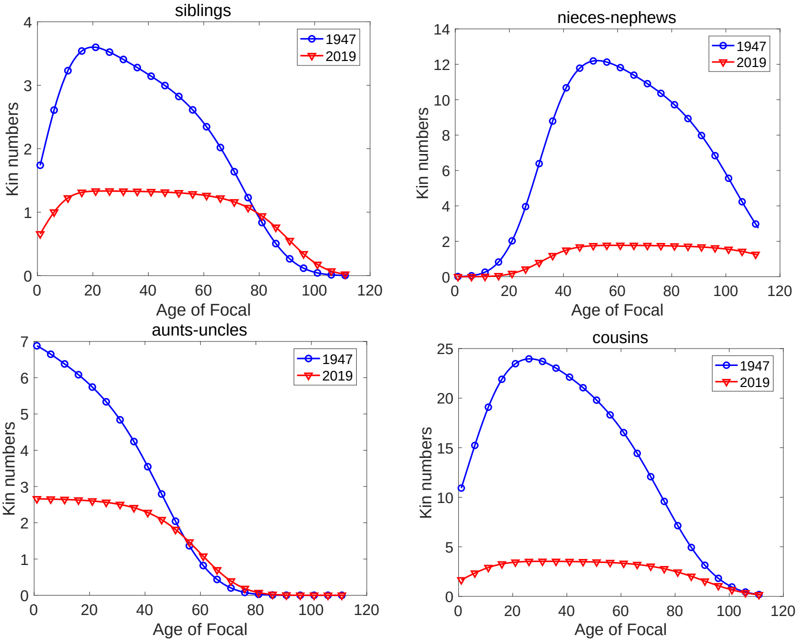
Appendix C: Projected mean kin numbers: Japan 1947 and 2019

Figure C-1: **(Part 1.) Expected numbers of each type of kin as a function of the age of Focal**



Notes: Japanese rates for 1947 and 2019. Both sexes combined.

Figure C-1: (Part 2.) Expected numbers of each type of kin as a function of the age of Focal



Notes: Japanese rates for 1947 and 2019. Both sexes combined.