

Projecting kinship networks through time in variable environments

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Acknowledgments and funding sources

This study was supported by the Research Council of Norway (Norges Forskningsråd, project 343398).

Abstract

Kinship networks shape key biological and social processes, yet their dynamics under changing environments remain poorly understood. Like population abundances, kinship structures are determined by past vital rates. Matrix population models provide a powerful framework for projecting population abundances through time and analysing the effects of environmental change on population dynamics, but no comparable framework exists for kinship networks. Here we develop a general projection framework for kinship networks in one-sex populations structured by any number of traits (e.g. age, stage, location, body mass, or genotype) under varying environments. We derive the kinship projection equation, which tracks through time the expected number of all kin, up to an arbitrary genealogical distance, structured by kin category and by the traits of both ego and its kin. By embedding kinship within the same matrix projection framework used for population dynamics, our approach provides a computationally simple and theoretically tractable tool for analysing how environmental change reshapes kinship networks. We demonstrate its analytical power by studying asymptotic, transient, and periodic kinship dynamics. Finally, we illustrate the framework by analysing how India’s demographic transition has reshaped – and will continue to reshape – kinship networks.

Running title: Kinship in varying environments

Keywords: kinship; kinship demography; relatedness; familial structure; structured populations; environmental stochasticity; population projection matrices; kin selection; kinship matrix.

Data accessibility statement: No new data are used. The demographic rates used for the illustration are publicly available from the United Nations World Population Prospects 2024 (<https://population.un.org/wpp/>). R code implementing the kinship projection equation for any one-sex model is provided in SI S12.

Competing Interests: The authors declare no conflict of interest

1 Introduction

Kinship demography is a rapidly developing branch of evolutionary demography that studies how demographic processes shape kinship networks, and how these networks in turn feed back onto demography (Pavard and Coste, 2020). Both the structured abundance of a population and the relatedness among its members are determined by past vital rates, including survival and reproduction. Consequently, changes in demographic processes leave signatures not only on population size and structure but also on the kinship networks of individuals. While projecting expected population abundance under time-varying vital rates is relatively straightforward (see eq.1 and Caswell, 2001), an analogous projection framework for kinship networks is still lacking. Yet across ecology, human demography, genetics, and anthropology, it is essential to understand how environmental change — such as demographic transitions or climate change — affects not only population dynamics but also the kinship networks of individuals (Alburez-Gutierrez et al., 2023; Shenk and Mattison, 2011; Mace and Alvergne, 2012; Hammel and Gullickson, 2004; King and Jobling, 2009). Even in species not typically considered social species, the presence, state, and number of close kin can have major consequences on individual fitness (e.g., maternal effects, see Ivimey-Cook and Moorad, 2018; Kendall et al., 2005), while inbreeding coefficients — directly determined by the kinship structure — can strongly influence population viability (McCune et al., 2002; Darwin, 1876).

Populations structured into discrete states (which may arise from discretised continuous traits; see Ellner and Rees, 2006; Metcalf et al., 2013), can be projected over a discrete time-step, via the population projection equation (Caswell, 2001):

$$\mathbf{n}_{t+1} = \mathbf{M}_t \mathbf{n}_t, \quad (1)$$

where $\mathbf{n}_t$ is the vector of expected abundances at time t and $\mathbf{M}_t$ the projection matrix (see section 2). The projection matrix may vary over time, reflecting changes in the environment (e.g., temperature) and/or in abundances (density dependence). Historically, matrix population models have been used for populations structured by a single trait, such as age (Leslie, 1945) or stage (Lefkovitch, 1965), but the projection equation applies equally to populations structured by multiple traits. These traits may be dynamic (they vary during the life trajectories of individuals, such as age, stage or location) or fixed (such as genotypes or location-at-birth). The simplicity of the population projection equation has allowed theoreticians to analyse (a) the asymptotic behaviour of population dynamics when the environment is constant (Goodman, 1967; Keyfitz, 1965), (b) the transient dynamics towards this asymptotic regime after a perturbation (Stott et al., 2011; Koons et al., 2007, 2005), (c) the dynamics of the abundance vector in periodic environments (Bacaër, 2009; Caswell et al., 1994), (d) the environmental variance of the stochastic growth rate and the composition of the population in a stationary stochastic environment (Cohen, 1976, 1977; Tuljapurkar, 1984), (e) the effects of density dependence on population dynamics (Takada and Nakajima, 1992, 1998), (f) the evolution of life-history traits (Charlesworth, 1980; Hastings, 1978) among many other results. In this manuscript, we aim to provide an analogous projection equation

for kinship structure. Such a formulation would offer two key advantages: (i) a computationally simple and efficient method for calculating kin numbers, and (ii) a framework that allows existing theoretical results for structured population dynamics to be directly extended to kinship demography.

Most analyses of the dynamics of kinship networks have relied on simulations (see, e.g., Hammel, 2005; Wachter, 1997). Two recent approaches, however, provide analytical methods for computing the expected number of kin through time under varying vital rates in one-sex models. Each of these two methods stems from an earlier study focusing on stable state demography (framework where the environment is, and has always been, constant) whose strengths and weaknesses carry over into the varying environment extension. The first approach (Caswell and Song, 2021) extends earlier work on age-structured (Caswell, 2019) and age $\times$ stage-structured (Caswell, 2020) populations and considers a few kin categories, as per the seminal study by Goodman et al. (1974) it is emulating. Recently, Butterick et al. (2025) extended the constant environment study by Coste et al. (2021) — which computes the expected number of kin, for any kin category and any population structure, but only provides an exact formula for populations structured by age (possibly combined with other stages, i.e. age $\times$ stage) — to time-varying environments. While these contributions represent important progress, both approaches treat kin categories separately rather than as components of a single kinship network. This is well suited to computing specific kin categories, but leaves the joint dynamics of the whole kinship network, and its theoretical analysis, less directly accessible.

Here, we extend the constant-environment framework of Coste (2025) to time-varying environments. That study derived a simple relationship between the expected number of kin — treated as a network extending to arbitrary genealogical depth — and the population projection matrix of the population for any structured one-sex population model (including models containing fixed (such as genetic) traits and models not structured by age). In the present manuscript, we first introduce, in section 2, the general framework: (a) the decomposition of the time-varying projection matrix into a fertility and survival component and (b) the individual kinship matrix which organises the kinship network of a focal individual, which we call *ego*, into kin categories and states (the state of *ego* and of the kin). We further introduce the population kinship matrix which counts all kin-pairs in the population and represents a subset of all pairs of individuals; we show that it can be simply inferred from the individual kinship matrix and vice versa (eq.3). This representation (via a method described in section 3) leads, in section 4, to the central result of the paper: the *kinship projection equation* (eq.10) which projects over time, and across varying environments, the kinship network of a population. We demonstrate the analytical power of this equation by studying, in section 5, two classes of environmental regime: the transient kinship dynamics (towards the asymptotic kinship network) and kinship in periodic environments. Finally, we apply the framework to quantify the effects of the demographic transition in India on the matrilineal kinship networks of its inhabitants.

2 Demographic inputs and Kinship Network

2.1 Matrix population model framework

We consider a discrete-time structured population model in which the expected abundance vector $\mathbf{n}_t$, of length s the number of states structuring the population, is projected over time (eq.1) by time-varying matrix $\mathbf{M}_t$ (dimension $s \times s$) (Caswell, 2001), decomposed into survival and fertility components:

$$\mathbf{M}_t = \mathbf{S}_t + \mathbf{F}_t \quad (2)$$

Here $S_t(i, j)$ gives the probability that an individual in state j survives and transitions to state i , and $F_t(i, j)$ the expected number of offspring in state i produced by a parent in state j . Environmental variation is incorporated through temporal variation in these demographic matrices; when the environment is itself stochastic, the expectations below are conditional on the realised sequence of demographic matrices. See SI S2, for a description of the scope of these matrices. These demographic inputs fully determine population dynamics. Throughout, individuals are assumed to survive, transition and reproduce independently of one another, conditional on the demographic matrices at time t : the population is a multitype branching process in a (possibly varying) environment (SI S2), and all kinship quantities below are expectations under this process. As kinship is also determined by demography, the projection over time of the size and structure of kinship networks (the kinship projection equation, eq. 10) also depends on $\mathbf{S}_t$ and $\mathbf{F}_t$. Unlike population abundance dynamics, expected kinship dynamics depend not only on the expectations of survival and fertility but also on higher moments of these processes. Specifically, the variance–covariance of fertility and the covariance between survival and fertility, denoted respectively $\mathbf{V}_t$ and $\mathbf{C}_t$ are required; see table 1 for all notations and definitions. This is because they determine, respectively, the formation of new sister–sister and mother–daughter relationships (more details in Section 3 and SI S6.4 and S6.5).

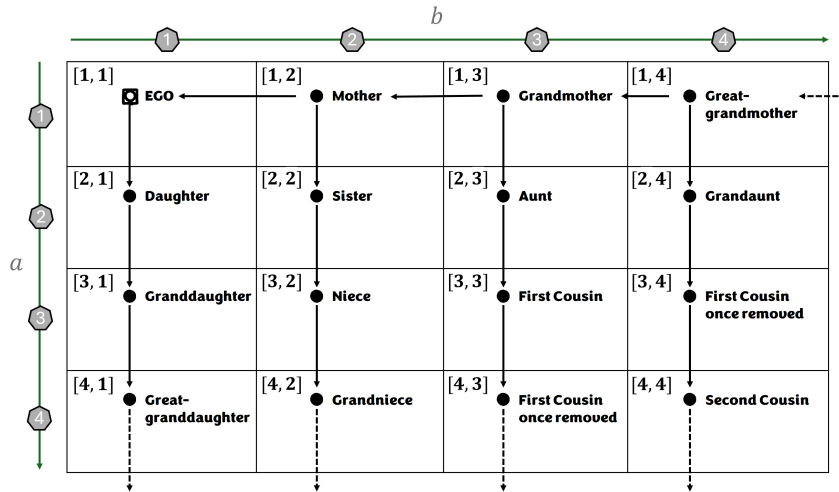


Figure 1: Characterisation of kin categories as $[a, b]$ -relationships, adapted from (Coste, 2025; Atkins, 1974).

2.2 Kinship Network

Characterisation of kin categories As per (Coste, 2025; Coste et al., 2021), we characterise the $[a, b]$ -kin of a focal individual called *ego* as the a -descendant(s) of the b -ancestor of *ego*, such that this ancestor is the most recent common ancestor of *ego* and the kin. The a -descendants (respectively the b -ancestor) lie, on the genealogical tree, $a - 1$ (respectively $b - 1$) generations away from *ego*. For instance, the 2-ancestor (or $[1, 2]$ -kin) is the mother and the 3-descendants (or $[3, 1]$ -kin), the grand-daughters, so that the $[3, 2]$ -kin are the nieces of *ego*, as per Figure 1. We call the network of all $[a, b]$ -kin such that $1 \leq a, b \leq g$: the g -kinship network. Using this denomination, Fig. 1 displays all kin accounted for in the 4-kinship network of *ego*.

The Individual Kinship Matrix The expected g -kinship network of (*ego*) is represented by the Individual Kinship Matrix (IKM) $\mathbb{K}_t$. It is a block matrix of size $sg \times sg$, with $g \times g$ blocks of size $s \times s$, where the $[a, b]$ -block corresponds to the number of $[a, b]$ -kin, structured by the states of *ego* and its kin. We denote the (i, j) entry of the $[a, b]$ -block of $\mathbb{K}_t$ as $\mathbb{K}_t[a, b](i, j)$: it is the expected number of $[a, b]$ -kin in state i , at time t , of *ego* in state j . Formal properties and stochastic interpretation are given in SI S4.

The Population Kinship Matrix The IKM corresponds to an individual metric (the number of kin of *ego*) that has been classically used in kinship demography (see, e.g., Coste et al., 2021; Goodman et al., 1974; Caswell, 2019). Here, we introduce an alternative metric at the population level; we define $\mathbb{K}_t^{(p)}[a, b](i, j)$ as expected number of directional $[a, b](i, j)$ -pairs in the population. where a directional $[a, b](i, j)$ -pair corresponds to a kin-pair linking an individual in state j and (one of) its $[a, b]$ -kin in state i . We call $\mathbb{K}_t^{(p)}$ the Population Kinship Matrix (PKM). We show in SI.S4, that there is a simple relationship between IKM and PKM:

$$\mathbb{K}_t^{(p)}[a, b](i, j) = n_t(j) \mathbb{K}_t[a, b](i, j) \quad \text{or, in matrix form,} \quad \mathbb{K}_t^{(p)} = \mathbb{K}_t \mathbb{D}_{\mathbf{n}_t}, \quad (3)$$

where $n_t(j)$ is the j^{th} entry of the abundance vector, $\mathbf{n}_t$, representing the expected number of individuals in state j at time t (see eq.1), and $\mathbb{D}_{\mathbf{n}_t}$ is the $sg \times sg$ diagonal matrix with g times vector $\mathbf{n}_t$ as its diagonal.

Population Kinship Vector For algebraic convenience we work with the vectorised population kinship matrix, $\mathbf{k}_t = \text{vec}(\mathbb{K}_t^{(p)})$, which we call the population kinship vector. This representation allows the kinship dynamics to be written as a linear projection equation as the vec operator turns a matrix into a vector by "stacking" its columns (Henderson and Searle, 1981). From $\mathbf{k}_t$, one can get back to the PKM via the reverse of the vec operator, and, further, (from eq. 3) to the IKM (see table 1):

$$\mathbb{K}_t = \mathbb{K}_t^{(p)} \mathbb{D}_{\mathbf{n}_t}^{-1} = \text{vec}^{-1}(\mathbf{k}_t) \mathbb{D}_{\mathbf{n}_t}^{-1} \quad (4)$$

Kinship Network Properties and Conditions The kinship matrices of a given population are not arbitrary. Contrary to the expected abundance vector, $\mathbf{n}_t$, which only "needs" to be a vector of non-negative real numbers, $\mathbb{K}_t$ and $\mathbb{K}_t^{(p)}$ have certain properties, that become conditions when considering the initial values of the kinship network one wishes to project over time: (a) *ego* is not a kin of *ego*; (b) the Population Kinship Matrix is symmetrical, there are as many aunts as nieces in the population; (c) the number of kin-pairs is at most equal to the number of all pairs and (d) for any $b > 1$, *ego* has at most one b -ancestor. We explore these properties further in SI S5 and make them explicit for the Population Kinship Matrix in appendix 8.1. We show, in SI S7, that these are propagated by the kinship projection equation.

2.3 Simple illustration

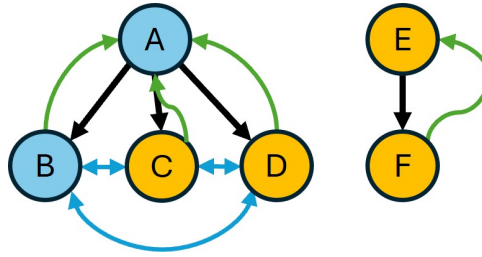


Figure 2: Kinship network of a population of 6 individuals structured by stage (juvenile, in orange, and adult in blue); directional daughter-mother relationships are marked by black/green arrows and non-directional sister-sister relationships as blue double arrows.

We now consider the population of $n_t = 6$ individuals alive at time t (labelled A to F) shown in Fig. 2, where the $g = 2$ -kinship network is represented by black arrows indicating daughter-mother (directional) relationships (e.g. B is a daughter of A). The population is structured into two states: juveniles (state 1, in orange) and adults (state 2, in blue), with $n_t(1) = 4$ and $n_t(2) = 2$. There are four $[2, 1]$ -kin pairs (black arrows), corresponding to daughter-mother relationships where *ego* is the mother and the kin the daughter. Among these pairs, two involve a juvenile daughter of an adult mother (C-A, D-A), one an adult daughter of an adult mother (B-A), and one a juvenile daughter of a juvenile mother (F-E), yielding $\mathbb{K}_t^{(p)}[2, 1](1, 2) = 2$ and $\mathbb{K}_t^{(p)}[2, 1](2, 2) = \mathbb{K}_t^{(p)}[2, 1](1, 1) = 1$. These relationships also contribute to the $[1, 2]$ -kin pairs (green arrows). There are additionally six sister-sister directional kin pairs (each blue double arrow counted twice), structured by stage as $\mathbb{K}_t^{(p)}[2, 2](1, 2) = \mathbb{K}_t^{(p)}[2, 2](2, 1) = \mathbb{K}_t^{(p)}[2, 2](1, 1) = 2$ (blue double arrows counted twice). All remaining entries of the population kinship matrix are zero, giving

$$\mathbb{K}_t^{(p)} = \begin{bmatrix} 0 & 0 & 1 & 0 \\ 0 & 0 & 2 & 1 \\ 1 & 2 & 2 & 2 \\ 0 & 1 & 2 & 0 \end{bmatrix} \quad \text{and, from eq.4} \quad \mathbb{K}_t = \begin{bmatrix} 0 & 0 & \frac{1}{4} & 0 \\ 0 & 0 & \frac{1}{2} & \frac{1}{2} \\ \frac{1}{4} & 1 & \frac{1}{2} & 1 \\ 0 & \frac{1}{2} & \frac{1}{2} & 0 \end{bmatrix}$$

In this population, an individual (*ego*) drawn at random from the juvenile class (C, D, E or F with equal probability) has probability $\mathbb{K}_t[1, 2](1, 1) + \mathbb{K}_t[1, 2](2, 1) = \frac{3}{4}$ that its mother is alive. It is also expected

to have $\mathbb{K}_t[2,1](1,1) = \frac{1}{4}$ daughters and $\mathbb{K}_t[2,2](1,1) + \mathbb{K}_t[2,2](2,1) = 1$ sisters ($\frac{1}{2}$ juvenile and $\frac{1}{2}$ adult sisters).

3 Method: towards the kinship projection equation

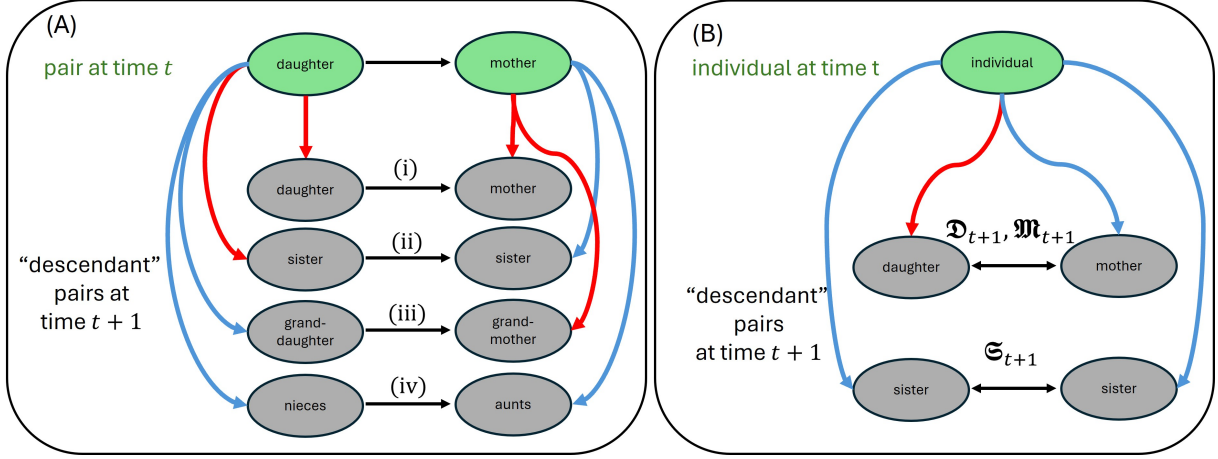


Figure 3: Diagram illustrating the method. The kin pairs in the population at time $t + 1$ arise from (A) existing pairs at time t (left side) and (B) from new pairs. (A) an existing kin pair at time t yields kin pairs at time $t + 1$ via (i) survival of both members, (ii)-(iii), survival of one member and reproduction of the other and (iv) reproduction of both members. (B) an individual at time t can generate $\mathfrak{D}_{t+1}$ (resp. $\mathfrak{M}_{t+1}$) new daughter-mother (resp. mother-daughter) kin pairs if it survives *and* reproduces and $\mathfrak{S}_{t+1}$ new sister-sister kin pairs if it produces two daughters or more.

We now derive how kinship networks evolve through time as a consequence of the survival and reproduction processes governing population dynamics. This derivation constitutes the core of the proof of the kinship projection equation (eq.10) which is the centrepiece of this manuscript, with additional computational steps in SI S6.

Overview: descendant vs. immigrant kin pairs A kin pair present in the population at time $t + 1$ is either (i) the descendant of a kin pair already present at time t (Fig. 3A), or (ii) a newly formed (“immigrant”) kin pair created by reproduction between t and $t + 1$ (Fig. 3B). We therefore decompose the population kinship matrix as

$$\mathbb{K}_{t+1}^{(p)} = \underbrace{\mathbb{A}_{t+1}^{(p)}}_{\text{descendants of existing pairs}} + \underbrace{\mathbb{B}_{t+1}^{(p)}}_{\text{"immigrant" kin pairs}}. \quad (5)$$

Descendant kin pairs As per figure 3A, existing kin pairs at time t generate descendant pairs at time $t + 1$ through survival and reproduction of their members. This yields (see SI S6), for the vectorisation of $\mathbb{A}_{t+1}^{(p)}$ (Henderson and Searle, 1981):

$$\text{vec}(\mathbb{A}_{t+1}^{(p)}) = \text{vec}(\mathbb{M}_t \mathbb{K}_t^{(p)} \mathbb{M}_t^T) = (\mathbb{M}_t \otimes \mathbb{M}_t) \text{vec}(\mathbb{K}_t^{(p)}) = (\mathbb{M}_t \otimes \mathbb{M}_t) \mathbf{k}_t, \quad (6)$$

where $\mathbb{M}_t$ is the generation-structured projection matrix induced by the structured demographic matrices: it projects over time a vector of expected abundances where individuals are structured by their states (as per $\mathbf{M}_t$) but also their generation number, which remains constant via survival but is incremented by reproduction:

$$\mathbb{M}_t = (\mathbf{I}_g \otimes \mathbf{S}_t) + (\mathbf{J}_1 \otimes \mathbf{F}_t) \quad , \text{e.g., for } g = 3, \quad \mathbb{M}_t = \begin{bmatrix} \mathbf{S}_t & \mathbf{0} & \mathbf{0} \\ \mathbf{F}_t & \mathbf{S}_t & \mathbf{0} \\ \mathbf{0} & \mathbf{F}_t & \mathbf{S}_t \end{bmatrix} \quad (7)$$

Immigrant kin pairs As per figure 3B, immigrant kin pairs at time $t + 1$ are formed by individual reproduction and survival between t and $t + 1$. If an individual produces one or more daughters and survives, this generates new daughter-mother and mother-daughter directional pairs. If an individual produces more than one daughter, this generates new sister-sister kin-pairs (same-litter sisters). The number of new mother-daughter and daughter-mother pairs is a function of the covariance between reproduction and survival ($\mathbf{C}_t$), while the number of new sister-sister pairs is a function of the reproductive variance ($\mathbf{V}_t$). Placing these three elements in the corresponding blocks of $\mathbb{B}_{t+1}^{(p)}$, we obtain (see SI S6.4, SI S6.5 and table 1):

$$\begin{cases} \text{vec}(\mathbb{B}_{t+1}^{(p)}) = \mathbb{N}_t \mathbf{n}_t & \text{with} \\ \mathbb{N}_t = \underbrace{\mathbf{J}_{2,1} ((\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J}_d + \mathbf{C}_t) + \mathbf{J}_{1,2} ((\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d + \mathbf{J}_e \mathbf{C}_t)}_{\text{"immigrant" daughter-mother and mother-daughter pairs}} + \underbrace{\mathbf{J}_{2,2} ((\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t + \mathbf{V}_t)}_{\text{"immigrant" sister-sister pairs}} \end{cases} \quad , \quad (8)$$

where the " $\mathbf{J}$ " matrices are time-invariant "dummy" matrices that place new pairs in the appropriate blocks of the kinship matrix (definitions in Table 1).

Overall, vectorising equation 5, we obtain, from equations 6 and 8

$$\mathbf{k}_{t+1} = \text{vec}(\mathbb{K}_{t+1}^{(p)}) = \text{vec}(\mathbb{A}_{t+1}^{(p)}) + \text{vec}(\mathbb{B}_{t+1}^{(p)}) = (\mathbb{M}_t \otimes \mathbb{M}_t) \mathbf{k}_t + \mathbb{N}_t \mathbf{n}_t \quad (9)$$

4 Result: the Kinship projection equation

As the demography of a population determines the time-series of its expected abundances (eq.1), it also determines the time-series of the expected kinship network. At any time t , the demographic processes therefore fully specify the expected number of $[a, b]$ -kin in state i of an *ego* individual in state j . Combining equations 9 and 1, the population kinship vector $\mathbf{k}_t$ and the abundance vector $\mathbf{n}_t$ can be projected jointly through time via a single projection equation:

$$\text{kinship projection equation: } \begin{bmatrix} \mathbf{k}_{t+1} \\ \mathbf{n}_{t+1} \end{bmatrix} = \mathcal{M}_t \begin{bmatrix} \mathbf{k}_t \\ \mathbf{n}_t \end{bmatrix} \quad (10a)$$

$$\text{with } \mathcal{M}_t = \begin{bmatrix} \mathbb{M}_t \otimes \mathbb{M}_t & \mathbb{N}_t \\ \mathbf{0} & \mathbf{M}_t \end{bmatrix} \quad (10b)$$

Equation 10 shows that kinship dynamics obey a linear projection equation formally analogous to the classical abundance projection, but acting on the joint state composed of population abundances and kinship structure. The projected vector $\begin{bmatrix} \mathbf{k}_t \\ \mathbf{n}_t \end{bmatrix}$ stacks the population kinship vector and the abundance vector, and evolves through left multiplication by the time-varying matrix $\mathcal{M}_t$. The matrix $\mathcal{M}_t$ depends on the demographic inputs $(\mathbf{S}_t, \mathbf{F}_t, \mathbf{V}_t, \mathbf{C}_t)$ through $\mathbf{M}_t$ (eq. 2), $\mathbb{M}_t$ (eq. 7) and $\mathbb{N}_t$ (eq. 8). Its construction also involves time-invariant “dummy matrices” (the $\mathbf{J}$ matrices; Table 1) that reorganise demographic quantities into kinship categories. From the projected vectors $\mathbf{k}_t$ and $\mathbf{n}_t$, the individual kinship matrix at time t follows directly from equation 4. As for any time-varying linear projection system, the state at time t is obtained simply from the initial conditions:

$$\begin{cases} \begin{bmatrix} \mathbf{k}_t \\ \mathbf{n}_t \end{bmatrix} = \mathcal{M}_{t-1} \mathcal{M}_{t-2} \cdots \mathcal{M}_0 \begin{bmatrix} \mathbf{k}_0 \\ \mathbf{n}_0 \end{bmatrix}, \\ \mathbb{K}_t = \text{vec}^{-1}(\mathbf{k}_t) \mathbb{D}_{\mathbf{n}_t}^{-1}. \end{cases} \quad (11)$$

We show in SI S7 that if the initial kinship vector $\mathbf{k}_0$ satisfies the structural conditions of appendix 8.1, these conditions remain satisfied for all subsequent times obtained via the kinship projection equation.

Particular reproductive cases In many projection models, survival and reproduction are assumed independent ($\mathbf{C}_t = \mathbf{0}$), and reproduction follows either a Bernoulli process (at most one offspring per time step) or an independent Poisson process. In these cases, $\mathbf{V}_t$ and $\mathbf{C}_t$ do not need to be specified, as $\mathbb{N}_t$ simplifies to (see SI S6.4):

$$\begin{cases} \text{Bernoulli reproduction: } \mathbb{N}_t = (\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t)) \mathbf{J}_d, \\ \text{Poisson reproduction: } \mathbb{N}_t = (\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t) + \mathbf{J}_{2,2}(\mathbf{F}_t \otimes \mathbf{F}_t)) \mathbf{J}_d. \end{cases} \quad (12)$$

Unstructured kinship, mean relatedness and non-contemporary kin In many applications, interest focuses on kin numbers irrespective of state. Following Coste (2025), we define the unstructured kinship matrix $\mathbb{K}_t^{(u)}$ (size $g \times g$), where $\mathbb{K}_t^{(u)}(a, b)$ is the expected number of $[a, b]$ -kin of an individual sampled at random in the population. Appendix 8.2 shows how to obtain this matrix from the structured kinship matrices. From structured or unstructured kinship quantities, measures of relatedness and inclusive fitness can be computed by weighting kin numbers according to genealogical distance (Coste, 2025). The framework also allows computation of non-contemporary kin. Appendix 8.3 derives $\mathbb{K}_{t,t_e}$, the

expected number of kin alive at time t for an *ego* alive at time t_e .

Emulating results of matrix projection theory Because equation 10 has the form of a classical matrix projection model, results from structured population theory can be transferred directly to kinship dynamics. In appendix 8.4, we apply results on periodic environments (e.g., Bacaër, 2009; Cushing and Henson, 2018) to derive their consequences for kinship matrices. In the next section, classical results on transient dynamics (e.g., Tuljapurkar, 1983; Koons et al., 2007) are used to analyse transient behaviour of kinship networks.

5 Asymptotic and transient dynamics of kinship networks

Asymptotic behaviour of kinship Consider an environment that fluctuates for $t \leq 0$ but becomes constant thereafter, such that for all $t \geq 0$, $\mathbf{F}_t = \mathbf{F}$, $\mathbf{S}_t = \mathbf{S}$, $\mathbf{V}_t = \mathbf{V}$ and $\mathbf{C}_t = \mathbf{C}$. Applying classical results from matrix population theory (Caswell, 2001) to equation 10 yields the following asymptotic behaviour (derivation in SI S10):

$$\left\{ \begin{array}{l} \frac{\mathbf{n}_t}{n_t} \rightarrow \hat{\mathbf{w}} \quad \text{and} \quad \frac{n_t}{\hat{\lambda}^t} \rightarrow (\hat{\mathbf{v}}^T \mathbf{n}_0) \hat{\mathbf{w}} \end{array} \right. \quad (20a)$$

$$\left\{ \begin{array}{l} \frac{\mathbf{k}_t}{n_t} \rightarrow \hat{\mathbf{k}}^{(w)} \quad \text{and} \quad \frac{\mathbf{k}_t}{\hat{\lambda}^t} \rightarrow (\hat{\mathbf{v}}^T \mathbf{n}_0) \hat{\mathbf{k}}^{(w)} \end{array} \right. \quad (20b)$$

$$\mathbb{K}_t \rightarrow \hat{\mathbb{K}} = \mathbf{vec}^{(-1)}(\hat{\mathbf{k}}^{(w)}) \mathbb{D}_{\hat{\mathbf{w}}}^{-1} \quad (20c)$$

$$\left\{ \begin{array}{l} \text{with} \quad \hat{\mathbf{k}}^{(w)} = \left(\hat{\lambda} \mathbf{I}_{s^2 g^2} - (\mathbb{M} \otimes \mathbb{M}) \right)^{-1} \mathbb{N} \hat{\mathbf{w}} \end{array} \right. \quad (20d)$$

Here $\hat{\lambda}$ is the long-term growth rate of the matrix $\mathbf{M} = \mathbf{F} + \mathbf{S}$ and $\hat{\mathbf{w}}$ and $\hat{\mathbf{v}}$ are the associated vectors of asymptotic relative abundances and reproductive values (scaled so that $\hat{\mathbf{v}}^T \hat{\mathbf{w}} = 1$). Equation 20a corresponds to the classical asymptotic behaviour of the abundance vector. Equation 20b shows that kin-pair abundance (within a given g -kinship network) grows or declines asymptotically at the same exponential rate as population abundance. Note that the total number of kin-pairs (i.e., for $g \rightarrow \infty$), like the total number of pairs, either grows asymptotically according to $\hat{\lambda}^2$ if $\hat{\lambda} > 1$ or decreases according to $\hat{\lambda}$ if $\hat{\lambda} < 1$. Finally, equation 20c demonstrates that the expected number of kin of an individual converges toward a constant individual-level kinship structure, extending the constant-environment result of Coste (2025) to the general case where survival and reproduction may covary.

Two stable states In a constant environment, equation 10 admits two nested equilibria for relative "abundances":

$$\left\{ \begin{array}{l} \text{demographic stable state :} \quad \frac{\mathbf{n}_t}{n_t} = \hat{\mathbf{w}} \\ \text{kinship stable state :} \quad \frac{\mathbf{n}_t}{n_t} = \hat{\mathbf{w}} \quad \text{and} \quad \frac{\mathbf{k}_t}{n_t} = \hat{\mathbf{k}}^{(w)} \end{array} \right. \quad (21a)$$

The first stable state is the classical *demographic stable state*, in which the vector of relative abundances remains constant over time. Because population abundances affect kinship but not conversely, the *kinship*

variable	dimension	formula/interpretation
Demographic inputs		
$\mathbf{F}_t$	$s \times s$	fertility matrix at time t : $F_t(i, j)$ is the expected number of offspring in i produced by a j individual at time t
$\mathbf{S}_t$	$s \times s$	survival matrix at time t : $S_t(i, j)$ is the probability that a j individual survives the time-step from t to $t+1$ and transitions to state i
$\mathbf{V}_t$	$s^2 \times s$	$\mathbf{V}_t = \sum_{i,j,k} Cov(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) (e_j^{(s)} \otimes e_i^{(s)}) e_k^{(s)T} \quad (13)$ j^{th} column of $\mathbf{V}_t$ is vectorised variance-covariance fertility matrix for individuals in j
$\mathbf{C}_t$	$s^2 \times s$	$\mathbf{C}_t = \sum_{i,j,k} Cov(\tilde{F}_t(i, k), \tilde{S}_t(j, k)) (e_j^{(s)} \otimes e_i^{(s)}) e_k^{(s)T} \quad (14)$ j^{th} col. of $\mathbf{C}_t$ is vectorised cross-covariance matrix between fertility and survival for j ind.
Particular Reproductive Cases		
$\mathbf{C}_t$	$s^2 \times s$	If survival and reproduction are independent: $\mathbf{C}_t = \mathbf{0}$
$\mathbf{V}_t$	$s^2 \times s$	Bernoulli reproduction: $\mathbf{V}_t = \mathbf{J}_d \mathbf{F}_t - (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d$; independent Poisson reproduction: $\mathbf{V}_t = \mathbf{J}_d \mathbf{F}_t$
Derived demographic inputs		
$\mathbf{M}_t$	$s \times s$	$\mathbf{M}_t = \mathbf{S}_t + \mathbf{F}_t$ (eq. 2); state structured projection model at time t
$\mathbf{M}_t$	$sg \times sg$	$\mathbf{M}_t = (\mathbf{I}_g \otimes \mathbf{S}_t) + (\mathbf{J}_1 \otimes \mathbf{F}_t)$ (eq.7); generation structured projection model at time t
$\mathbf{N}_t$	$s^2 g^2 \times s$	$\mathbf{N}_t = (\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t) + \mathbf{J}_{2,2}(\mathbf{F}_t \otimes \mathbf{F}_t)) \mathbf{J}_d - \mathbf{J}_{2,2} \mathbf{J}_d \mathbf{F}_t + \mathbf{J}_{2,2} \mathbf{V}_t + (\mathbf{J}_{2,1} + \mathbf{J}_{1,2} \mathbf{J}_e) \mathbf{C}_t$ (eq.8); new kin pairs formed (new sister-sister and mother-daughter kin pairs)
Kinship matrices and vectors		
$\mathbb{K}_t$	$sg \times sg$	Individual Kinship Matrix; $\mathbb{K}_t[a, b](i, j)$, the (i, j) entry of block $[a, b]$, is the expected number of $[a, b]$ -kin in state i , at time t , of ego in state j
$\mathbb{K}_t^{(p)}$	$sg \times sg$	Population Kinship Matrix; $\mathbb{K}_t^{(p)}[a, b](i, j)$, the (i, j) entry of block $[a, b]$, is expected number of directional $[a, b](i, j)$ pairs in the population
$\mathbf{k}_t$	$(sg)^2 \times 1$	population kinship vector; $\mathbf{k}_t = \text{vec}(\mathbb{K}_t^{(p)})$
Other demographic elements		
$\tilde{F}_t(i, j)$	1	random variable of the number of offspring in i produced by a j individual at time t ; $F_t(i, j)$ is the expectation, across individuals in j at time t , of $\tilde{F}_t(i, j)$
$\tilde{S}_t(i, j)$	1	random variable equal to 1 for an individual in j at time t if it survives and transitions to state i and 0 otherwise; $S_t(i, j)$ is the expectation, across individuals in j at time t , of $\tilde{S}_t(i, j)$
$\mathbf{n}_t$	$s \times 1$	abundance vector at time t
n_t	1	$n_t = \mathbf{1}^T \mathbf{n}_t$; total population abundance at time t
λ_t	1	$\lambda_t = \frac{n_{t+1}}{n_t}$; time-step population growth rate between time t and $t+1$
$\mathbf{w}_t$	$s \times 1$	$\mathbf{w}_t = \frac{1}{n_t} \mathbf{n}_t$; relative abundance vector at time t
Dummy Matrices		
$\mathbf{J}_1$	$g \times g$	$\mathbf{J}_1 = \sum_{i=1}^{g-1} e_{i+1}^{(g)} e_i^{(g)T} \quad (15)$ zero matrix except for 1s on the sub-diagonal; increases the generation number by 1.
$\mathbf{J}_d$	$s^2 \times s$	$\mathbf{J}_d = \sum_i (e_i \otimes e_i) e_i^T \quad (16)$ turns a vector into a diagonal matrix and vectorises the output: $\mathbf{J}_d \mathbf{n}_t = \text{vec}(\mathbf{D}_{\mathbf{n}_t})$
$\mathbf{J}_{a,b}$	$s^2 g^2 \times s^2$	$\mathbf{J}_{a,b} = e_b^{(g)} \otimes \mathbf{I}_s \otimes e_a^{(g)} \otimes \mathbf{I}_s \quad (17)$ places the "immigrant" (a, b) -kin in their corresponding kin categories
$\mathbf{J}_e$	$s^2 \times s^2$	$\mathbf{J}_e = \sum_{i,j} (e_j \otimes e_i) (e_i^T \otimes e_j^T) \quad (18)$
$\mathbb{J}_y$	$g \times sg$	$\mathbb{J}_y = (\mathbf{I}_g \otimes \mathbf{1}_s^T) \quad (19)$ matrix where the i^{th} $g \times s$ block is zero but for the i^{th} row filled with 1s
General notations		
$e_a^{(b)}$	$b \times 1$	$e_a^{(b)}(a) = 1$ and $i \neq a \Rightarrow e_a^{(b)}(i) = 0$; zero-vector or length b with 1 in position a .
$\mathbf{I}_b$	$b \times b$	$\sum_{i=1}^b e_i^{(b)} e_i^{(b)T}$; the identity matrix.
$\mathbb{D}_{\mathbf{n}_t}$	$sg \times sg$	$\mathbf{I}_g \otimes \mathbf{D}_{\mathbf{n}_t}$; diagonal matrix with g times $\mathbf{n}_t$ as its diagonal: that is, $\mathbb{D}_{\mathbf{n}_t}[a, b](i, j) = n_t(j)$ if $a = b$ and $i = j$, and 0 otherwise
$\mathbf{D}_{\mathbf{n}_t}$	$s \times s$	$\sum_{i=1}^s n_t(i) e_i^{(s)} e_i^{(s)T}$; the diagonal matrix with vector $\mathbf{n}_t$ as its diagonal.
$\mathbb{D}_{\mathbf{n}_t}^{-1}$	$sg \times sg$	$\mathbb{D}_{\mathbf{n}_t}^{-1}[a, b](i, j) = \frac{1}{n_t(i)}$ if $a = b$, $i = j$ and $n_t(i) \neq 0$, and 0 otherwise
$\mathbf{1}_s$	$s \times 1$	defined as the vector (of size s) of 1s
$n_t^{(-1)}(i)$	$s \times 1$	$n_t^{(-1)}(i) = \frac{1}{n_t(i)}$ if $n_t(i) \neq 0$ and 0; vector of inverse of abundance vector's entries
Operators		
notation	definition	
vec	vec operator, stacking the columns of a matrix on top of one another (to create a vertical vector)	
$\otimes$	Kronecker or direct product	
$\text{vec}^{(-1)}$	reverse operation of the vec operator for a square matrix (i.e., for $\mathbf{b}$ of length b^2 , $\text{vec}^{(-1)}(\mathbf{b})$ is the $b \times b$ matrix such that $\text{vec}[\text{vec}^{(-1)}(\mathbf{b})] = \mathbf{b}$); where, for any square matrix $\mathbf{A}$, $\text{vec}^{-1}(\text{vec}(\mathbf{A})) = \mathbf{A}$	

Table 1: Table of notations and definitions

stable state requires the *demographic stable state* but the reverse is not true. A population may therefore reach its demographic stable state while its kinship structure continues to evolve.

Kinship transient For $a, b > 1$, the number of $[a, b]$ -kin at time $t + 1$ depends on neighbouring kin categories at time t (namely $[c, d]$ -kin for $a - 1 \leq c \leq a$ and $b - 1 \leq d \leq b$). This suggests that, apart from very close kin, the kinship structure of a population converges more slowly towards equilibrium than abundances. Assuming the population is already at the demographic stable state but not at kinship equilibrium, equation 10 yields

$$\text{kinship transient:} \quad \frac{\mathbf{k}_t}{n_t} - \hat{\mathbf{k}}^{(w)} = \left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^t \left(\frac{\mathbf{k}_0}{n_0} - \hat{\mathbf{k}}^{(w)} \right), \quad (21b)$$

which converges towards 0 as $t \rightarrow \infty$, describing the transient convergence of kinship structure toward the kinship stable state. When age is a trait of the model, there exists a maximum age ω for individuals in the population; in this case, $\left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^{g\omega} = \mathbf{0}$ which leads to (derivation provided in SI S10.3.2):

$$\text{duration of kinship transient of } g\text{-kinship network:} \quad T = g\omega \quad (21c)$$

This implies that, for age-structured populations, if the population is at the *demographic stable state*, the *kinship stable state* is reached in finite time, after T time steps. This provides a heuristic for the speed of convergence of the *kinship transient* in the general case (taking ω sufficiently large so that no individual survives beyond that age). Importantly, the kinship transient duration T is a function of g , implying that the more distant the kin, the longer the transient toward equilibrium. More specifically, the duration of the kinship transient for a given $[a, b]$ -kin category increases with $a + b$ (SI S10.3.2), so that the slowest kin to converge to its equilibrium in the g -kinship network are the $[g, g]$ -kin (that is, the sisters for $g = 2$ and for $g \geq 3$, the $(g - 2)^{th}$ cousins). The number of distant kin of *ego* can therefore reflect deep historical vital rates, so that strong demographic disturbances (catastrophes) can leave a signature in kinship networks far into the future.

6 Illustration: India's demographic transition

To illustrate the kinship projection equation (eq.10) under realistic environmental variation and the kinship transient study (eqs S10.2), we consider India's demographic transition. The choice of India stems from its relatively late demographic transition, which provides high-quality data spanning most of the transition, and from the social importance of kinship networks of multiple genealogical depths. Kinship networks of several genealogical depths matter in Indian society, from nuclear families ($g = 2$) to joint families ($g = 3$) and deeper kin groups that regulate marriage patterns (Säävälä, 1998; Chandrasekhar, 1943; Sequeira et al., 2025; Sanghvi, 1966); see Figure 5d. Because the model is one-sex (female), it counts only female kin related through female lines, whereas joint families and gotras are largely patri-

lineal: quantifying the latter requires the two-sex extension outlined in the Discussion.

Female age-specific survival and fertility rates (ages 0–100) were obtained from the United Nations World Population Prospects for 1950–2023 together with medium-variant projections for 2024–2100 (Fig. 4a,b). For years prior to 1950 and after 2100, vital rates were assumed constant at their boundary values. Using eq.1, we projected population abundances to derive the birth rate, mean annual survival, population growth rate, and mean age (Fig. 4c,d). These quantities summarise the demographic forces characterising the demographic transition and driving kinship dynamics through time.

In contrast with the study by Jiang et al. (2023) which uses a 5y time-step, a Bernoulli reproduction (so that a female cannot give birth to more than one offspring every five years) and computes asymptotic kinship for each year separately, we use annual age-classes, assume Poisson reproduction (allowing twinning) and track the realised expectation of kin numbers through time, allowing transient departures from equilibrium to be quantified. Indeed, as we have seen in section 5 and shall now illustrate, realised kinship can differ strongly from asymptotic kinship even long after vital rates stabilise.

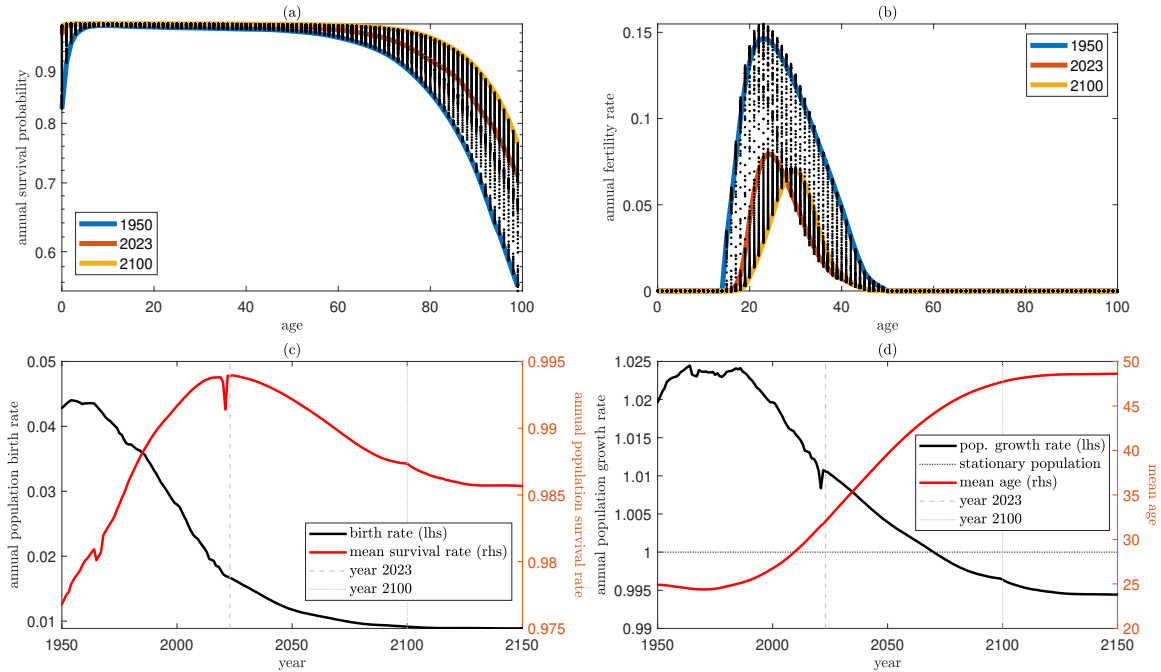


Figure 4: India's female demography; for years < 2023 , vital rates correspond to observation, for $2023 < \text{years} < 2100$ to projections and for years > 2100 vital rates correspond to their 2100 value; (a) annual survival rates per age, (b) annual fertility rates by age (c) population birth rate and mean annual survival rate (rhs axis) , (d) population annual growth rate and mean age (rhs axis)

India's demographic transition is characterised by a nearly four-fold decline in birth rate since 1950 and sustained increases in age-specific survival (Fig. 4c). Together these trends reduce population growth, which is projected to fall below zero around 2070 (Fig. 4d), while simultaneously increasing population mean age. Despite increasing survival at all ages (Fig. 4a), mean survival is projected to decline in the future because demographic ageing shifts population weight toward older age classes with lower survival

probabilities. This contrast between age-specific and population-level survival is central for interpreting kinship patterns shown below.

Kinship networks of India

We project India's kinship network through time using eq.10, initialised at the asymptotic kinship corresponding to 1950 vital rates (eq.20c).

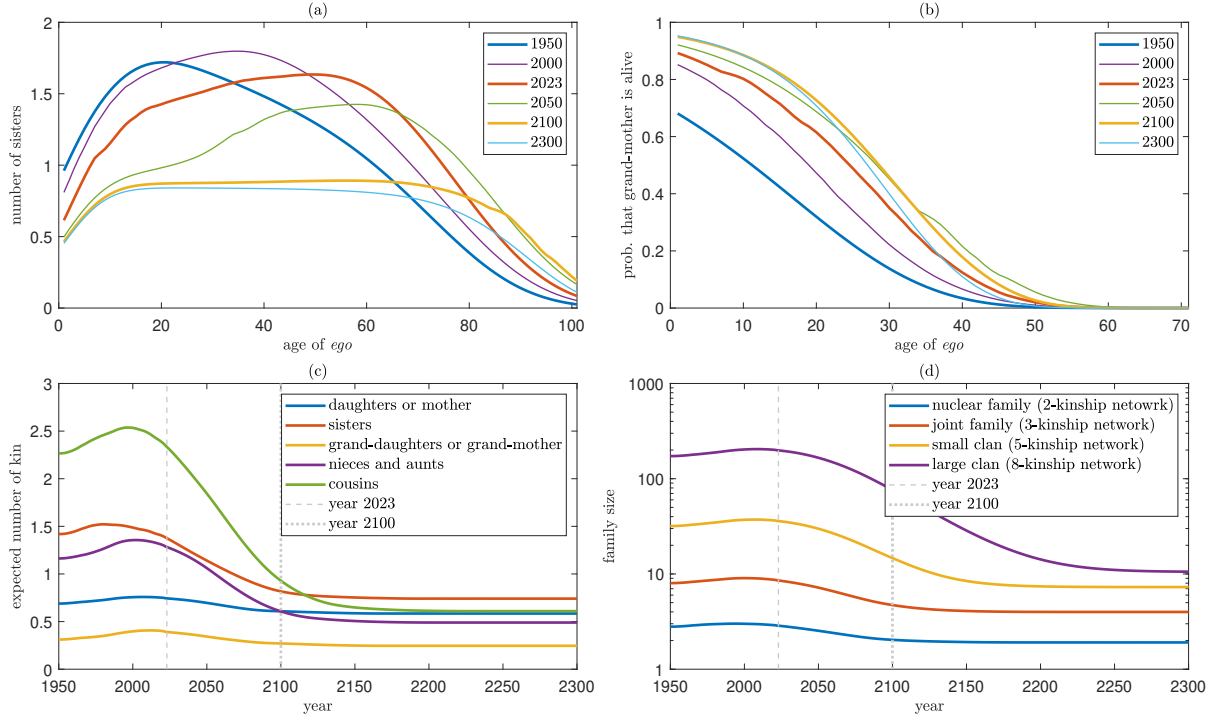


Figure 5: India's female kinship; for years < 2023 , vital rates correspond to observation, for $2023 < \text{years} < 2100$ to projections and for years > 2100 vital rates correspond to their 2100 value; (a) expected number of sisters of *ego*, as a function of *ego*'s age, for various years; (b) probability that *ego*'s grandmother is alive, as a function of *ego*'s age, for various years; (c) evolution over time of the number of a few close kin, for *ego* taken at random in the population and (d) evolution over time of the number of individuals in *ego*'s *g*-kinship network, for various genealogical depths *g*, for *ego* taken at random in the population; in (d), social units indicate the genealogical depth *g* they evoke; as the model is one-sex, kin are female kin related through female lines

The expected number of sisters shows two main patterns (Fig. 5a,c): an initial increase followed by decline, and a progressive shift of the age at which sibship is maximal from 20 years in 1950 to 60 years in 2050. These patterns reflect cohort effects generated by the demographic transition: individuals born during high-fertility periods retain larger sibships at older ages owing to improved survival. The probability that *ego*'s grandmother is alive at birth increases from 1950 to 2100 due to improved survival (Fig. 5b). However, the pattern reverses later in life: a 40-year-old in 2050 is more likely to have a living grandmother than one in 2100. This counter-intuitive result arises because delayed fertility increases generation time (Fig. 4b, the grandmother of a 40-year-old in 2050 is, on average, much younger than that of a 40-year-old in 2100) faster than survival improves longevity.

When averaged across the population (i.e. for *ego* taken at random), the expected numbers of close kin

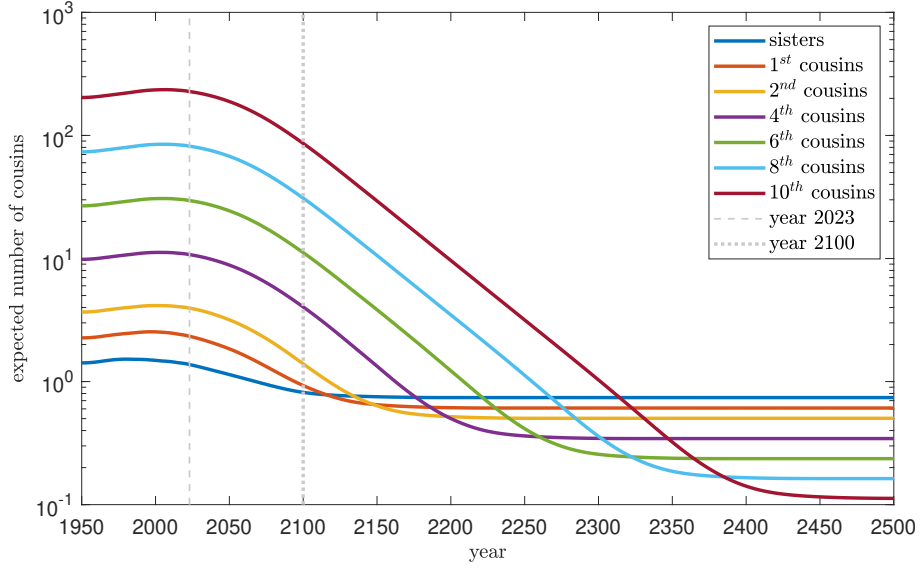


Figure 6: variation of the number of k^{th} -cousins of Indian *ego* taken at random in the population, over time, for $k = 0$ (corresponding to sisters) to $k = 10$; for years < 2023 , vital rates correspond to observation, for $2023 < \text{years} < 2100$ to estimations and for years > 2100 vital rates correspond to their 2100 value.

initially increase before declining after 2005 (Fig. 5c). These quantities are obtained from the unstructured kinship matrix (eq.23) which is symmetrical: the number of daughters is equal to that of mothers (i.e. to the probability that the mother is alive), grand-daughters to grandmothers, and nieces to aunts. These kin, together with sisters and first cousins, make up the 3-kinship network of *ego*, which increases initially before declining transiently towards its equilibrium (corresponding to projected vital rates for 2100). This can be observed on Fig. 5d which shows that kinship networks of all depths decline substantially under the demographic transition: the female 8-kinship network (about 200 female kin related through female lines in 2021) is projected to halve by 2100 and shrink to a few dozen individuals by 2300 despite constant vital rates after 2100.

More distant kin exhibit markedly slower convergence, as predicted by the transient analysis (section 5). For a^{th} cousins (i.e., the $[a + 2, a + 2]$ -kin, Fig. 6), the demographic transition reverses over time the ranking of abundances: distant cousins initially outnumber closer relatives, but this ordering is inverted by 2500. The expected number of 10th cousins requires 372 years (from 2100 to 2472) to approach equilibrium (with a less than 1% difference). These results illustrate the long demographic memory of deep genealogical kin-relationships, whereby environmental changes, such as demographic transitions, leave persistent signatures in kinship networks long after population structure and growth rate have stabilised.

7 Discussion and Conclusion

This study develops a general projection framework for kinship networks in structured populations experiencing environmental variation. By embedding kinship within the same mathematical machinery used

to project population abundances, we show that the dynamics of relatedness can be analysed with a level of generality, flexibility, and analytical tractability previously reserved for abundances alone (Caswell, 2001; Tuljapurkar and Caswell, 1997; Keyfitz, 1977). The central result—the kinship projection equation, eq.10—demonstrates that the expected kinship structure of a population is fully determined by its demographic processes, including survival, reproduction, and their temporal variation, in direct analogy with classical matrix population models. This study provides three main advances over previous work on kinship demography.

First, unlike existing varying-environment approaches (Jiang et al., 2023; Caswell and Song, 2021; Butterick et al., 2025) and their constant-environment counterparts (Caswell, 2019; Coste et al., 2021), the kinship projection equation yields the exact expectation of the number of any kin for *any one-sex population projection model*, irrespective of population structure or reproductive mechanism. The framework is not restricted to age-structured populations but applies equally to models structured by stage, size, location, genotype, etc. or combinations thereof, including demographic-genetic and integral projection models (Rees and Ellner, 2009; Metcalf et al., 2013; Simmonds et al., 2020; Coulson et al., 2017; de Vries and Caswell, 2019). It accommodates arbitrary reproductive processes (e.g. Bernoulli, Poisson, or more general forms) and extends the constant-environment formulation of (Coste, 2025) by explicitly allowing covariation between survival and reproduction.

Second, as in (Coste, 2025) but in contrast with much of the kinship demography literature originating with (Goodman et al., 1974), kinship is treated explicitly as a *network* rather than as a collection of kin categories analysed separately. Classical and recent approaches typically derive distinct equations for individual kin types (e.g. mothers, daughters, sisters), limiting analysis of their joint dynamics (Caswell, 2019; Caswell and Song, 2021; Butterick et al., 2025; Coste et al., 2021). Here, all kin categories up to an arbitrary genealogical depth (g) are embedded within a single integrated g -kinship network. This representation aligns kinship demography with broader work on social networks, where the structure of relationships — not merely their marginal counts — shapes ecological and evolutionary outcomes (Croft et al., 2016; Farine and Whitehead, 2015; Silk, 2007; Silk and Hodgson, 2021), and allows the joint study of *kinship and social dynamics* (Croft et al., 2021).

Third, the framework explicitly links individual kinship demography — the expected number of kin of a focal individual — to the number of kin pairs in the population through the relationship between the individual and population kinship matrices. This bridge unifies perspectives historically treated separately in population ecology and allows kinship dynamics to be analysed using the full machinery of structured population theory while retaining direct access to individual-level quantities relevant to social behaviour, inclusive fitness, and life-history evolution, which is crucial for the integration of kin selection within a broader demographic perspective (Hamilton, 1964; Taylor and Frank, 1996; Ronce et al., 2000).

Because the kinship projection equation mirrors the classical population projection equation, it inherits many of its analytical properties. In particular, extending transient analyses from structured population theory (Keyfitz, 1971; Tuljapurkar, 1983) shows that, in general, the *kinship stable state* is reached later than the classical *demographic stable state* and that convergence depends on genealogical depth, with distant kin responding more slowly to changes in vital rates. A population will therefore approach its stable age or stage distribution while its kinship structure remains far from equilibrium, implying that kinship retains a longer memory of past demographic conditions than population abundance or structure alone. The illustration based on India’s demographic transition highlights the empirical relevance of this result: long after fertility and mortality stabilise, the abundance of several kin categories—especially distant relatives—continues to change. Demographic transitions thus reshape social and familial environments over timescales far exceeding those typically considered in demographic analyses (Alburez-Gutierrez et al., 2023). Because kin availability feeds back into individual fitness (Koster et al., 2019; Hooper et al., 2015), demographic events in the distant past may continue to influence present population dynamics.

The same formal analogy allows established results from structured population theory to be extended to kinship dynamics. We show here that, in periodic environments, kinship stable states are, like demographic stable states (Tuljapurkar, 1985; Bacaër, 2009), themselves periodic and phase-dependent. Further, results on environmental stochasticity (Tuljapurkar, 1990, 1984) can be translated to kinship networks, noting that because both members of a kin pair experience the same environment, averaging over environmental realisations requires $\mathbb{E}[\mathbb{M}_t \otimes \mathbb{M}_t]$ rather than $\mathbb{E}[\mathbb{M}_t] \otimes \mathbb{E}[\mathbb{M}_t]$. This would enable systematic analysis of how environmental variability shapes the availability and composition of kinship networks.

Just as the classical abundance projection equation allows vital rates to depend on population abundance or structure—thereby capturing density and frequency dependence (Engen et al., 2020; May, 1976; Gamelon et al., 2016, 2024)—the kinship projection equation allows vital rates to depend explicitly on *kinship structure*. Survival, reproduction, or dispersal can thus be modelled as functions of the presence or abundance of specific kin categories, embedding kinship-dependent processes directly within demographic models. When vital rates depend non-linearly on the kin of each individual, computing them from expected kinship is a mean-field approximation, exactly as in classical models of density dependence, in which vital rates depend on the expected (deterministic) abundance (May, 1974, 1976; Caswell, 2001); an exact treatment requires the distribution of kin numbers among individuals (see below). This framework opens new avenues for analysing the demographic and evolutionary consequences of social interactions, including competition among relatives, cooperation, parental care, cooperative breeding, and altriciality.

By allowing kinship to feed back onto vital rates within a general projection equation, the framework

provides a systematic approach to eco-evolutionary dynamics driven by kin interactions, rather than treating kinship as a passive outcome of demography (Croll and Caswell, 2024; Johnstone and Cant, 2010; Pavard and Branger, 2012). In essence, the kinship projection equation embeds both sides of *kinship demography* (Pavard and Coste, 2020) within a single unified framework: the effect of demography on kinship and the feedback of kinship on demography.

The present manuscript focuses on expectations of kinship networks. Natural extensions include computation of *higher moments*. Existing stochastic kinship models proceed kin category by kin category, and therefore give the variance within each category (Caswell, 2024; Butterick et al., 2026); the network formulation gives direct access to covariances among kin categories, which would allow the stochastic structure of kinship networks to be analysed explicitly and provide direct access to variation in inclusive fitness among individuals (Taylor and Maciejewski, 2014; Hooper et al., 2015; Rousset and Ronce, 2004). A second important extension concerns *two-sex models*, enabling explicit incorporation of mating functions, sex-specific demography, and sex ratios (Miller and Inouye, 2011; Cachelou et al., 2024; Jenouvrier et al., 2010). Such models would distinguish full kin (sharing both parents) from half kin (sharing a single parent) and, more generally, allow direct computation of population inbreeding levels. Although technically more complex, these developments will benefit from the natural foundation established here.

Kinship networks are dynamic structures governed by the demographic processes that shape population growth and composition. By deriving a general projection equation for kinship under variable environments, we place kinship demography on the same theoretical footing as structured population dynamics. The framework shows that kinship often responds more slowly than demography to environmental change, generating long-lasting transients with important social, demographic, and evolutionary consequences. By unifying individual- and population-level perspectives and treating kinship as an integrated network rather than isolated categories, the kinship projection equation provides a flexible foundation for future work on kinship dynamics, social evolution, population viability of social species, and the kin-mediated demographic and evolutionary consequences of environmental change.

8 Appendices

8.1 Properties and conditions of population kinship matrices

We provide here the mathematical formulation of the properties and conditions of population kinship matrices corresponding to section 2.2:

$$\left\{ \begin{array}{l} \text{(a) } ego \text{ is not a kin of } ego: \quad \mathbb{K}_t^{(p)}[1,1](i,j) = 0 \\ \text{(b) symmetry of population kinship : } \quad \mathbb{K}_t^{(p)}[a,b](i,j) = \mathbb{K}_t^{(p)}[b,a](j,i) \\ \text{(c) kin pairs are pairs : } \quad \sum_{a,b} \mathbb{K}_t^{(p)}[a,b](i,j) \leq P_t(i,j) \\ \text{(d) } ego \text{ has at most one } b\text{-ancestor: } \quad \sum_i \mathbb{K}_t^{(p)}[1,b](i,j) \leq n_t(j) \end{array} \right., \quad (22)$$

where $\mathbf{P}_t$ corresponds to the structured number of pairs in the population, given in SI eq.S28. From equation 3, we provide the corresponding conditions on the individual Kinship Matrix in SI S5.

8.2 Unstructured kinship

We call $\mathbb{K}_t^{(u)}$, the unstructured kinship matrix, of size $g \times g$, where $\mathbb{K}_t^{(u)}(a,b)$ is the expected number of $[a,b]$ -kin of an individual taken at random in the population and $\mathbf{k}_t^{(u)}$ its vectorised version. Then (see SI S9.4 and table 1)

$$\mathbb{K}_t^{(u)} = \frac{1}{n_t} \mathbb{J}_y \mathbb{K}_t^{(p)} \mathbb{J}_y^T \quad \text{or, equivalently,} \quad \mathbf{k}_t^{(u)} = \frac{1}{n_t} (\mathbb{J}_y \otimes \mathbb{J}_y) \mathbf{k}_t \quad (23)$$

8.3 Non-contemporary kin

While the main focus of kinship demography is to consider how many kin an individual has at a given time, the approach developed in this paper also allows one to consider the number of non-contemporary kin. Denoting $\mathbb{K}_{t,t_e}$, the expected number of kin alive at time t for ego alive at time t_e , and $\mathbb{K}_{t,t_e}^{(p)}$ the corresponding number of kin-pairs, we obtain (see SI S9.1, where we also provide formulas for constant environment):

$$\left\{ \begin{array}{l} \mathbb{K}_{t,t_e} = \mathbb{K}_{t,t_e}^{(p)} \mathbb{D}_{\mathbf{n}_{t_e}}^{-1} \quad \text{with} \\ \text{for } t_e \leq t, \quad \mathbb{K}_{t,t_e}^{(p)} = \mathbb{K}_{t,t_e} \mathbb{D}_{\mathbf{n}_{t_e}} = \mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} (\mathbb{K}_{t_e}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) - \mathbb{S}_{t-1} \dots \mathbb{S}_{t_e+1} \mathbb{S}_{t_e} \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}} \\ \text{for } t_e \geq t, \quad \mathbb{K}_{t,t_e}^{(p)} = (\mathbb{K}_{t_e,t}^{(p)})^T \end{array} \right., \quad (24)$$

where $\mathbb{J} = (\mathbf{e}_1^{(g)} \mathbf{e}_1^{(g)T}) \otimes \mathbf{I}_s$. We note that $(\mathbb{K}_{t_e} + \mathbb{J})$ is the (individual) kinship network of ego that counts ego as a kin of ego (SI S9.1).

8.4 Periodic environments

An environment has period T when, for any t , $\mathbf{F}_{t+T} = \mathbf{F}_t$ and $\mathbf{S}_{t+T} = \mathbf{S}_t$. Periodic environments are particularly important for population ecology as they lie at the core of pre- and post-breeding models, where survival and reproduction occur at various "seasons" within the year. The study of periodic projection models (Bacaër, 2009; Cushing and Henson, 2018; Caswell et al., 1994) has shown that, at the stable state, the vector of relative abundances is also periodic, with the same period. We show in SI S9.2, that this result extends to the kinship network: at the kinship and demographic stable state, the individual kinship matrix is periodic, with the same periodicity as the environment. We further show, in this SI, how to compute these periodic IKMs.

9 Bibliography

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Supplementary Information

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S1 Navigating multi-trait models

Many instruments used in this manuscript are multi-trait vectors and related matrices. This is the case of the kinship matrices, $\mathbb{K}_t$ and $\mathbb{K}_t^{(P)}$ which are structured by states and kin type, of the generation structured projection model $\mathbb{M}_t$ structured by states and generation, of the variance-covariance of fertility $\mathbf{V}_t$ and the cross-covariance of fertility and survival $\mathbf{C}_t$ structured, for their inputs/columns by states, but for their outputs/rows by states twice, etc. For these reasons, we provide here simple rules allowing to navigate such matrices

S1.1 classic properties of the kronecker product and vec operator

For three matrices (or vectors) $\mathbf{A}$, $\mathbf{B}$ and $\mathbf{C}$ of dimensions such that the product $\mathbf{ABC}$ can be formed, we have (Henderson and Searle, 1981; Henderson et al., 1983)

$$\text{vec}(\mathbf{ABC}) = (\mathbf{C}^T \otimes \mathbf{A})\text{vec}(\mathbf{B}) \quad (\text{S1})$$

For four matrices (or vectors) $\mathbf{A}$, $\mathbf{B}$, $\mathbf{C}$ and $\mathbf{D}$ of dimensions such that the products $\mathbf{ABC}$ can be formed, we have

$$(\mathbf{A} \otimes \mathbf{B})(\mathbf{C} \otimes \mathbf{D}) = (\mathbf{AC}) \otimes (\mathbf{BD}) \quad (\text{S2})$$

S1.2 navigating multi-trait vectors and matrices

A matrix $\mathbf{A}$ of dimension $a \times b$, can be decomposed into its components via:

$$\begin{cases} \mathbf{A} = \sum_{i=1}^a \sum_{j=1}^b A(i, j) \mathbf{e}_i^{(a)} \mathbf{e}_j^{(b)T} \\ A(i, j) = \mathbf{e}_i^{(a)T} \mathbf{A} \mathbf{e}_j^{(b)} \end{cases}, \quad (\text{S3})$$

where $\mathbf{e}_a^{(b)}$ is the vector of length b which is zero everywhere but for entry a which is equal to 1.

A multi-dimensional (or multi-trait) vector, is called a tensor. If it contains 2 traits, it can be fathomed as a matrix: If trait 1, containing a_1 categories is considered "within" trait 2, containing a_2 categories of dimension, this vector-matrix is $\mathbf{A}$, of dimension $a_1 \times a_2$, with $A(i_1, i_2)$ corresponding to the value i_1 (with $1 \leq i_1 \leq a_1$) of trait 1 and i_2 (with $1 \leq i_2 \leq a_2$) of trait 2. We could equivalently consider trait 1 "within" trait 2, which would yield the transposed vector-matrix. In order to be projected over time, the vector-matrix has to be vectorised: $\mathbf{a} = \text{vec}(\mathbf{A})$ which corresponds to, from eq. S1:

$$A(i_1, i_2) = \text{vec}(A(i_1, i_2)) = \text{vec}(\mathbf{e}_{i_1}^{(a_1)T} \mathbf{A} \mathbf{e}_{i_2}^{(a_2)}) = (\mathbf{e}_{i_2}^{(a_2)T} \otimes \mathbf{e}_{i_1}^{(a_1)T}) \text{vec}(\mathbf{A}) = (\mathbf{e}_{i_2}^{(a_2)T} \otimes \mathbf{e}_{i_1}^{(a_1)T}) \mathbf{a}, \quad (\text{S4})$$

where $\otimes$ is the Kronecker (aka direct) product. In other words, the $1 \leq i \leq a_1 a_2$ entry of vector $\mathbf{a}$, corresponds to $A(i_1, i_2)$ when $i = i_1 + a_1(i_2 - 1)$. Similarly, if $\mathbf{B}$ is a multitrait matrix projection a population structured by these two traits, then denoting $B[i_1, j_1](i_2, j_2)$ the entry of the matrix corresponding to state (i_1, i_2) for the row and state (j_1, j_2) for the column, so that $B[i_1, j_1](i_2, j_2) = B((i_1, i_2), (j_1, j_2))$, we have

$$\begin{cases} B((i_1, i_2), (j_1, j_2)) = (\mathbf{e}_{i_2}^{(a_2)T} \otimes \mathbf{e}_{i_1}^{(a_1)T}) \mathbf{B} (\mathbf{e}_{j_2}^{(a_2)} \otimes \mathbf{e}_{j_1}^{(a_1)}) \quad \text{or equivalently} \\ \mathbf{B} = \sum_{i_1, i_2, j_1, j_2} B((i_1, i_2), (j_1, j_2)) (\mathbf{e}_{i_2}^{(a_2)} \otimes \mathbf{e}_{i_1}^{(a_1)}) (\mathbf{e}_{j_2}^{(a_2)} \otimes \mathbf{e}_{j_1}^{(a_1)})^T \end{cases} \quad (\text{S5})$$

S1.3 navigating the kinship matrices

Multitrait matrices, such as $\mathbb{K}_t$ can also be navigated via the Kronecker product:

$$\mathbb{K}_t[a, b](i, j) = (\mathbf{e}_a^{(g)} \otimes \mathbf{e}_i^{(s)})^T \mathbb{K}_t (\mathbf{e}_b^{(g)} \otimes \mathbf{e}_j^{(s)}), \quad (\text{S6})$$

For the population kinship matrix, we can therefore directly write:

$$\begin{aligned} \mathbb{K}^{(p)}[a, b](i, j) &= \text{vec}(\mathbf{e}_a^{(g)} \otimes \mathbf{e}_i^{(s)})^T \mathbb{K}_t^{(p)} (\mathbf{e}_b^{(g)} \otimes \mathbf{e}_j^{(s)}) \\ &= \left((\mathbf{e}_b^{(g)} \otimes \mathbf{e}_j^{(s)})^T \otimes (\mathbf{e}_a^{(g)} \otimes \mathbf{e}_i^{(s)})^T \right) \text{vec}(\mathbb{K}_t^{(p)}) = (\mathbf{e}_b^{(g)} \otimes \mathbf{e}_j^{(s)} \otimes \mathbf{e}_a^{(g)} \otimes \mathbf{e}_i^{(s)})^T \mathbf{k}_t \end{aligned} \quad (\text{S7})$$

This implies, from eq. 4, that the expected number of [a,b]-kin in state i of *ego* in state j at time t can also be read directly from the kinship vector and the abundance vector:

$$\mathbb{K}_t[a,b](i,j) = \frac{\mathbb{K}_t^{(p)}[a,b](i,j)}{n_t(j)} = \frac{(\mathbf{e}_b^{(g)} \otimes \mathbf{e}_j^{(s)} \otimes \mathbf{e}_a^{(g)} \otimes \mathbf{e}_i^{(s)})^T \mathbf{k}_t}{\mathbf{e}_j^{(s)T} \mathbf{n}_t} \text{ if } n_t(j) \neq 0 \text{ and } 0 \text{ otherwise.}$$

We note that it is possible to navigate between the kinship vector and the IKM in vector form (eq.3) via the Hadamard or termwise product $\bullet$:

$$\begin{cases} \text{vec}(\mathbb{K}_t) = \mathbf{q}_t \bullet \mathbf{k}_t & \text{with} \\ \mathbf{q}_t = \mathbf{1}_g \otimes \left(\sum_i \frac{\mathbf{e}_i^{(s)}}{n_t(i)} \right) \otimes \mathbf{1}_g \otimes \mathbf{1}_s \end{cases} \quad (\text{S8})$$

S2 Inputs: vital rates (expectation and variance) and their scope

S2.1 Expectation of vital rates: the matrix population model

In equation 1, the vector of expected abundances at time t , $\mathbf{n}_t$, has length s , the number of states used to categorise the population. The population projection matrix at time t , $\mathbf{M}_t$, of dimension $s \times s$, can be decomposed into survival and fertility components (eq.2), so that

$$\mathbf{n}_{t+1} = (\mathbf{S}_t + \mathbf{F}_t) \mathbf{n}_t = \mathbf{M}_t \mathbf{n}_t, \quad (1)$$

where $\mathbf{F}_t$ and $\mathbf{S}_t$ contain the expectations of vital rates at time t . The population projection equation (eq. 1) corresponds to the classic discrete-time, discrete-state, one-sex structured population model of population ecology and demography, commonly known as a Matrix Population Model ((Caswell, 2001)).

S2.2 Variance-covariance of vital rates

S2.2.1 demographic stochastic (branching) process

The population projection (eq. 1) projects over time $\mathbf{n}_t$ the vector of expected population abundance (structured by the s classes of the population). The entries of this vector are real and non-negative, as they are expectations of a stochastic process: at a given time-step t , the structured abundances correspond to a given realisation $\tilde{\mathbf{n}}_t$, which is a vector of (non-negative) integers. We denote $\tilde{F}_t(i,j)$ the random variable of the number of i offspring produced by a j individual and $\tilde{S}_t(i,j)$ the survival r.v., which is equal to 1, for a j individual, if it survives the time-step and transitions to state i and 0 otherwise. The elements of $\mathbf{F}_t$ and $\mathbf{S}_t$ correspond to the expectation across individuals of these random variables: $F_t(i,j) = E(\tilde{F}_t(i,j))$ and $S_t(i,j) = E(\tilde{S}_t(i,j))$. We denote $\tilde{M}_t(i,j) = \tilde{F}_t(i,j) + \tilde{S}_t(i,j)$, the r.v. of the number of individuals "produced" via survival and/or reproduction in state i by an individual in state j , at time t . These elements are grouped into matrices of random variables $\tilde{\mathbf{M}}_t = \tilde{\mathbf{F}}_t + \tilde{\mathbf{S}}_t$. Using the

notations and conventions in (Coste, 2025b),

$$\tilde{\mathbf{n}}_{t+1} = \tilde{\mathbf{M}}_t \diamond \tilde{\mathbf{n}}_t = (\tilde{\mathbf{F}} + \tilde{\mathbf{S}}) \diamond \tilde{\mathbf{n}}_t \quad (\text{S9})$$

describes a multi-type state-dependent branching process, where $\tilde{F}(i, j)$ and $\tilde{S}(i, j)$ represent, respectively, for an individual in j , the number of offspring in j produced and its state at the next time-step. The $\diamond$ notation in eq.S9 reads: $\tilde{\mathbf{n}}_{t+1}$ corresponds to the demographic stochastic and multivariate process $\tilde{\mathbf{M}}_t$ applied independently to each individual in $\tilde{\mathbf{n}}_t$ (for an individual in state i , the process applied, specifically, corresponds to the stochastic vector that is the i^{th} column of $\tilde{\mathbf{M}}_t$). Taking the expectation on both sides of equation S9 leads back to eq.1. Summing the entries of $\tilde{\mathbf{n}}_t$ (respectively of expectation $\mathbf{n}_t = \mathbf{E}(\tilde{\mathbf{n}}_t)$), yields the total abundances $\tilde{n}_t$ (respectively its expectation n_t):

$$\tilde{n}_t = \sum_i \tilde{n}_t(i) = \mathbf{1}^T \tilde{\mathbf{n}}_t \quad \text{and} \quad n_t = \sum_i n_t(i) = \mathbf{1}^T \mathbf{n}_t = \mathbf{E}(\tilde{n}_t) \quad (\text{S10})$$

S2.2.2 variance-covariance of abundance vector

The vector $\tilde{\mathbf{n}}_t$ being random (or stochastic), it has a certain distribution, a certain expectation ($\mathbf{n}_t$) and a certain variance-covariance, $\mathbf{var}(\tilde{\mathbf{n}}_t)$:

$$\mathbf{var}(\tilde{\mathbf{n}}_t) = \mathbf{E}(\tilde{\mathbf{n}}_t \tilde{\mathbf{n}}_t^T) - (\mathbf{E}(\tilde{\mathbf{n}}_t) \mathbf{E}(\tilde{\mathbf{n}}_t)^T) = \mathbf{E}(\tilde{\mathbf{n}}_t \tilde{\mathbf{n}}_t^T) - \mathbf{n}_t \mathbf{n}_t^T \quad (\text{S11})$$

where T denotes matrix transposition. $\mathbf{var}(\tilde{\mathbf{n}}_t)$ is a variance-covariance matrix, that is symmetrical and which i, j entry correspond to $[\mathbf{var}(\tilde{\mathbf{n}}_t)](i, j) = \text{cov}(\tilde{n}_t(i), \tilde{n}_t(j))$. This variance-covariance matrix can be vectorised; $\mathbf{V}(\tilde{\mathbf{n}}_t)$ is a vector of length s^2 such that

$$\mathbf{V}(\tilde{\mathbf{n}}_t) = \mathbf{vec}(\mathbf{var}(\tilde{\mathbf{n}}_t)) \quad (\text{S12})$$

where $\mathbf{vec}$, the vec operator (Henderson et al., 1983; Henderson and Searle, 1981). Taking the variance on both sides of equation S9 leads to (Coste, 2025b; Pollard, 1966; Harris, 1963)

$$\mathbf{V}(\tilde{\mathbf{n}}_{t+1}) = (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{V}(\tilde{\mathbf{n}}_t) + \mathbf{V}(\tilde{\mathbf{M}}_t) \mathbf{n}_t, \quad (\text{S13})$$

where $\mathbf{V}(\tilde{\mathbf{M}})$, by extension of the $\mathbf{V}$ notation, as per Coste (2025b) is a $s^2 \times s$ matrix whose j^{th} column is the vectorised version of the variance-covariance matrix of $\tilde{\mathbf{M}}_j$ the stochastic vector representing the demography (reproduction and survival) of individuals in state j . Classic tensor computations of SI S1 allow to relate $\mathbf{V}(\tilde{\mathbf{M}}_t)$ with its entries, the variance-covariance of the various matrix entries of $\tilde{\mathbf{M}}_t$ (see, e.g., eqs 14 and 13).

S2.2.3 variance-covariance of demography as a function of survival and reproduction

The variance-covariance $\mathbf{V}(\tilde{\mathbf{M}}_t)$ of time-step demography $\tilde{\mathbf{M}}_t = \tilde{\mathbf{F}}_t + \tilde{\mathbf{S}}_t$ can be decomposed according to

survival and fertility:

$$\text{cov}(\tilde{M}_t(i, j), \tilde{M}_t(l, j)) = \text{cov}(\tilde{F}_t(i, j), \tilde{F}_t(l, j)) + \text{cov}(\tilde{S}_t(i, j), \tilde{S}_t(l, j)) + \text{cov}(\tilde{S}_t(i, j), \tilde{F}_t(l, j)) + \text{cov}(\tilde{F}_t(i, j), \tilde{S}_t(l, j)),$$

that is, in matrix form:

$$\mathbf{V}(\tilde{\mathbf{M}}_t) = \mathbf{V}(\tilde{\mathbf{F}}_t + \tilde{\mathbf{S}}_t) = \mathbf{V}(\tilde{\mathbf{F}}_t) + \mathbf{V}(\tilde{\mathbf{S}}_t) + \mathbf{C}_t + \mathbf{C}_t^*, \quad (\text{S14})$$

with $\mathbf{C}_t$, the cross-covariance between reproduction and demography defined as

$$\begin{cases} \mathbf{C}_t = \sum_{i,j,k} \text{Cov}(\tilde{S}_t(j, k), \tilde{F}_t(i, k)) (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_k^{(s)T} & \text{or equivalently} \\ (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)})^T \mathbf{C}_t \mathbf{e}_k^{(s)} = \text{cov}(\tilde{S}_t(j, j), \tilde{F}_t(i, k)) \end{cases} \quad (14)$$

$\mathbf{C}_t^*$ contains the same information than $\mathbf{C}_t$:

$$\mathbf{C}_t^* = \sum_{i,j,k} \text{Cov}(\tilde{F}_t(j, k), \tilde{S}_t(i, k)) (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_k^{(s)T} \quad (\text{S15})$$

and can obtained from the latter directly via

$$\begin{cases} \mathbf{C}_t^* = \mathbf{J}_e \mathbf{C}_t & \text{with} \\ \mathbf{J}_e = \sum_{i,j} (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) (\mathbf{e}_i^{(s)T} \otimes \mathbf{e}_j^{(s)T}) \end{cases} \quad (18)$$

$$\text{proof: } (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)})^T \mathbf{J}_e \mathbf{C}_t \mathbf{e}_k^{(s)} = (\mathbf{e}_i^{(s)} \otimes \mathbf{e}_j^{(s)})^T \sum_{a,b} \text{Cov}(\tilde{F}_t(a, k), \tilde{S}_t(b, k)) (\mathbf{e}_b^{(s)} \otimes \mathbf{e}_a^{(s)}) = \text{Cov}(\tilde{F}_t(j, k), \tilde{S}_t(i, k)).$$

In this study $\mathbf{V}(\tilde{\mathbf{F}}_t)$ is denoted $\mathbf{V}_t = \mathbf{V}(\tilde{\mathbf{F}}_t)$:

$$\begin{cases} \mathbf{V}_t = \sum_{i,j,k} \text{Cov}(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_k^{(s)T} & \text{or equivalently} \\ (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)})^T \mathbf{V}_t \mathbf{e}_k^{(s)} = \text{cov}(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) \end{cases} \quad (13)$$

This implies that (see SI S1)

$$\text{for } a = i + s(j - 1), \quad V_t(a, k) = \text{Cov}(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) \quad (\text{S16})$$

As survival is Bernoulli, we can in general express its variance-covariance as a function of its expectation.
From (Coste, 2025b):

$$\mathbf{V}(\tilde{\mathbf{S}}_t) = \mathbf{J}_d \mathbf{S}_t - (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d \quad (\text{S17})$$

with

$$\mathbf{J}_d = \sum_{k=1}^s (\mathbf{e}_k^{(s)} \otimes \mathbf{e}_k^{(s)}) \mathbf{e}_k^{(s)T} \quad (16)$$

Dummy matrix $\mathbf{J}_d$ allows to simplify the computation of the vectorisation of a diagonal matrix:

$$\text{vec}(\mathbf{D}_a) = \mathbf{J}_d \mathbf{a} \quad (\text{S18})$$

proof: $\text{vec}(\mathbf{D}_a) = \text{vec}(\sum_i a(i) \mathbf{e}_i^{(s)} \mathbf{e}_i^{(s)T})$. From equation S1, this is $\text{vec}(\mathbf{D}_a) = \sum_i (\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) a(i) = \sum_i (\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_i^{(s)T} \mathbf{a} = \mathbf{J}_d \mathbf{a}$.

Overall, eq.S14 can be rewritten as:

$$\mathbf{V}(\tilde{\mathbf{M}}_t) = \mathbf{V}_t + \mathbf{J}_d \mathbf{S}_t - (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d + \mathbf{C}_t + \mathbf{J}_e \mathbf{C}_t \quad (\text{S19})$$

We illustrate these points in SI S8.

S2.3 Variance of vital rates and kinship

The numbers of the various kin of an individual, like population abundances, are direct functions of past vital rates. The kinship projection equation derived in the result section (eq. 10), which is analogous to the population projection equation (eq. 1), therefore also depends on $\mathbf{S}_t$ and $\mathbf{F}_t$. The information stored in $\mathbf{S}_t$ and $\mathbf{F}_t$ is sufficient to deduce the consequences of the kinship network at time t on the kinship network at time $t+1$. However, the kinship network at time $t+1$ contains also newly formed kin relationship, that do not stem from kin relationships at time t , namely (a) newborn sister-newborn sister and (b) mother-newborn daughter kin relationships, which requires knowledge, beyond the expectations of $\mathbf{F}_t$ and $\mathbf{S}_t$, of the variance of the demographic processes. Specifically, the kinship projection equation requires knowledge of

- (a) $\mathbf{V}_t$, the variance(-covariance) of the reproductive process (eq.13) (of which $\mathbf{F}_t$ represents the expectation). As per the pioneering work of Goodman et al. (1974) in the context of non-overlapping generations, this variance determines the number of new (same-litter) sister-sister pairs entering the population; SI S6.4; its formulation is particularly simple for common reproductive models such as

- for Bernoulli reproduction (Coste, 2025b; Pollard, 1966):

$$\text{Bernoulli reproduction: } \mathbf{V}_t = \mathbf{J}_d \mathbf{F}_t - (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d \quad (\text{S20})$$

- for independent Poisson reproduction, $\text{Cov}(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) = \delta(i, j) F_t(i, k)$, that is, in matrix form:

$$\text{Independent Poisson reproduction: } \mathbf{V}_t = \mathbf{J}_d \mathbf{F}_t \quad (\text{S21})$$

- one newborn state: if there is only one newborn state (state 1) and $\mathbf{v}$ is the vector such that

$v(i) = \text{var}(\tilde{F}(1, i))$ then

$$\text{One newborn state: } \mathbf{V}_t = \mathbf{e}_1^{s \times s} \mathbf{v}^T \quad (\text{S22})$$

We also have $\mathbf{F}_t = \mathbf{e}_1^{(s)} \mathbf{f}^T$, where $f_t(i) = F_t(1, i)$.

(b) $\mathbf{C}_t$, the (cross-)covariance between reproduction and survival (eq.14). this covariance affects the number of new daughter-mother kin relationships which require than an individual reproduces *and* survives. We show how to integrate $\mathbf{C}_t$ in the kinship projection equation, in SI S6.5. A common particular case is

- if survival and fertility of an individual in a given state at a given time:

$$\text{Fertility and Reproduction are independent: } \mathbf{C}_t = \mathbf{0} \quad (\text{S23})$$

These concepts and formulas are illustrated in SI section S8

S2.4 Scope of the projection models for this method and comparison to other approaches

The method in this manuscript is valid for any one-sex population projection model: there is no restriction on the structure of these matrices, apart from basic biological constraints:

- a. all entries of $\mathbf{F}_t$ and $\mathbf{S}_t$ must be non-negative
- b. survival probabilities cannot exceed one (i.e. $\forall j, t, \sum_i S_t(i, j) \leq 1$)
- c. all individuals eventually die (formally $\forall t, \lim_{a \rightarrow \infty} \mathbf{S}_{t+a} \cdots \mathbf{S}_{t+1} \mathbf{S}_t = \mathbf{0}$).

Further, thanks to our integration of $\mathbf{V}_t$ and $\mathbf{C}_t$, it applies to models

- A. with any reproductive process: Bernoulli, Poisson, etc. or any non-standard reproductive process
- B. where reproduction and survival covary. This allows to model the effect of cost of reproduction on kinship

It therefore applies, in particular,

- in contrast to (Caswell, 2019, 2020) and follow-up studies to models with multiple offspring states (i.e. types, where $\mathbf{F}_t$ has several non-zero rows), including quantitative-genetic models (de Vries and Caswell, 2019; Coulson et al., 2017) and quantitative-trait models (e.g. IPMs; Rees et al., 2014; Metcalf et al., 2013), which are central to understanding the evolution of structured populations (Steiner and Tuljapurkar, 2012; Hamel et al., 2018).
- in contrast to (Caswell, 2019, 2020; Coste et al., 2021; Butterick et al., 2025; Goodman et al., 1974) and follow-up papers, to models where age is not a trait of the model, such as many IPMs and stage-structured models. The approach in (Coste et al., 2021; Butterick et al., 2025) allows one to consider such models but only provides an approximation of the number of kin in that case.

- in contrast to (Caswell, 2019, 2020; Jiang et al., 2023) and follow-up studies to models where reproduction is not Bernoulli
- in contrast to these papers and (Coste, 2025a), to models where reproduction and survival covary

The kinship projection equation is therefore applicable to a wide range of structured population projection models commonly used in population ecology, epidemiology, and genetics, including models without age as a state variable, with multiple types, with non-Bernoulli reproduction, and where survival and reproduction are not independent.

S3 Expectation and Variance of the number of pairs in the population

S3.1 From structured abundances to number of pairs

The random variable of the directional number of pairs at time t between individuals in states i and j is

$$\tilde{P}_t(i, j) = \tilde{n}_t(i)\tilde{n}_t(j) - \delta(i, j)\tilde{n}_t(j) \quad (\text{S24})$$

where $\delta(i, j) = 1$ if $i = j$ and $= 0$ otherwise. Indeed, if $i \neq j$, the directional number of pairs is simply $\tilde{n}_t(i)\tilde{n}_t(j)$: for each individual in i there are $\tilde{n}_t(j)$ directional pairs. If $i = j$, then for each individual in i there are $\tilde{n}_t(i) - 1$ directional pairs (as the individual is part of that group). In matrix form:

$$\tilde{\mathbf{P}}_t = \tilde{\mathbf{n}}_t \tilde{\mathbf{n}}_t^T - \mathbf{D}_{\tilde{\mathbf{n}}_t} \quad (\text{S25})$$

where $\mathbf{D}_{\mathbf{a}}$, for a vector $\mathbf{a}$ of length a , is the $a \times a$ diagonal matrix with vector $\mathbf{a}$ as its diagonal.

We have that that $\tilde{P}_t(i, j) = \tilde{P}_t(j, i)$ that is, $\tilde{\mathbf{P}}_t$ is symmetrical; $\tilde{\mathbf{P}}_t = \tilde{\mathbf{P}}_t^T$. We also have that the total number of directional pairs in the population is

$$\tilde{p}_t = \sum_{i,j} \tilde{P}_t(i, j) = \mathbf{1}^T \tilde{\mathbf{P}}_t \mathbf{1} = \mathbf{1}^T \tilde{\mathbf{n}}_t \tilde{\mathbf{n}}_t^T \mathbf{1} - \mathbf{1}^T \mathbf{D}_{\tilde{\mathbf{n}}_t} \mathbf{1} = \tilde{n}_t^2 - \mathbf{1}^T \tilde{\mathbf{n}}_t = \tilde{n}_t^2 - \tilde{n}_t = \tilde{n}_t(\tilde{n}_t - 1), \quad (\text{S26})$$

S3.1.1 non-directional pairs

The number of directional pairs counts twice every single non-directional pair in the population. Let us denote $P^*(i, j)$ the number of non-directional pairs between individuals in i and j in the population, where for $i > j$, $P^*(i, j) = 0$. For $i \neq j$, $\tilde{P}_t^*(\min(i, j), \max(i, j)) = \tilde{P}_t(j, i) = \tilde{P}_t(i, j) = \tilde{n}_t(i)\tilde{n}_t(j)$ and $\tilde{P}_t^*(i, i) = \frac{1}{2}\tilde{P}_t(i, i) = \frac{\tilde{n}_t(i)(\tilde{n}_t(i)-1)}{2}$. $\tilde{\mathbf{P}}_t^*$ is then an upper triangular matrix such that

$$\tilde{\mathbf{P}}_t = \tilde{\mathbf{P}}_t^* + \tilde{\mathbf{P}}_t^{*T}$$

We note that $\tilde{P}_t^*(i, i)$ is indeed, always an integer, as $\tilde{n}_t(i)(\tilde{n}_t(i) - 1)$ is always even.

These concepts and formulas are illustrated in SI section S8

S3.2 expected number of pairs

From these, we can compute the expectation of the number of pairs $P_t(i, j) = E(\tilde{P}_t(i, j))$, or in matrix form:

$$\mathbf{P}_t = \mathbf{E}(\tilde{\mathbf{P}}_t) \quad (\text{S27})$$

From the definition of the variance-covariance of a random vector (eq.S11) and as $\mathbf{E}(\mathbf{D}_{\tilde{\mathbf{a}}}) = \mathbf{D}_{\mathbf{E}(\tilde{\mathbf{a}})}$, we obtain, from eq. S25, that $\mathbf{P}_t = \mathbf{E}(\tilde{\mathbf{n}}_t \tilde{\mathbf{n}}_t^T) - \mathbf{E}(\mathbf{D}_{\tilde{\mathbf{n}}_t}) = \mathbf{var}(\tilde{\mathbf{n}}_t) + \mathbf{E}(\tilde{\mathbf{n}}_t) \mathbf{E}(\tilde{\mathbf{n}}_t)^T - \mathbf{D}_{\mathbf{n}_t}$, that is

$$\mathbf{P}_t = \mathbf{var}(\tilde{\mathbf{n}}_t) + \mathbf{n}_t \mathbf{n}_t^T - \mathbf{D}_{\mathbf{n}_t} \quad (\text{S28})$$

This is important, as it implies for instance that

$$p_t = E(\tilde{p}_t) = \mathbf{1}^T \mathbf{P}_t \mathbf{1} = \mathbf{var}(\tilde{n}_t) + n_t^2 - n_t \quad (\text{S29})$$

i.e. the expected number of pairs is *not* equal to the expected abundance multiplied by the expected abundance minus one (as per eq.S26): $p_t \neq n_t^2 - n_t$, unless $\mathbf{var}(\tilde{n}_t) = 0$, that is, unless all possible realisations of $\tilde{n}_t$ have the same abundance.

These concepts and formulas are illustrated in SI section S8

S4 Kinship matrices in a stochastic context

As we did for the vector of abundances (eq.S9) and the structured number of pairs (eq.S25), we consider the number of kin of *ego* (individual kinship) and the number of kin-pairs (population kinship) in a stochastic context. We denote the demographic stochastic kinship matrices, $\tilde{\mathbb{K}}_t^{(p)}$ and $\tilde{\mathbb{K}}_t$ of which the kinship matrices proper ($\mathbb{K}_t^{(p)}$ and $\mathbb{K}_t$) are the expectations.

S4.1 population kinship matrix as a sub-set of all pairs

For the population kinship matrix, this expectation is easy to fathom, now that we have considered the number of pairs (eq.S27), and corresponds to the expectation across all realisations of the stochastic process $\tilde{\mathbf{n}}_t$:

$$\mathbb{K}_t^{(p)} = \mathbf{E}(\tilde{\mathbb{K}}_t^{(p)}) \quad (\text{S30})$$

a kin-pair is a pair Indeed, the population kinship matrix is a subset of all directional pairs in the population: a kin-pair is a pair. Therefore $\sum_{a,b} \tilde{\mathbb{K}}_t^{(p)}[a, b] \leq \tilde{\mathbf{P}}_t$, which translates for the expectations into

$\sum_{a,b} \mathbb{K}_t^{(p)}[a,b] \leq \mathbf{P}_t$, that is, from equation S28

$$\text{a kin-pair is a pair: } \sum_{a,b} \mathbb{K}_t^{(p)}[a,b] \leq \mathbf{var}(\tilde{\mathbf{n}}_t) + \mathbf{n}_t \mathbf{n}_t^T - \mathbf{D}_{\mathbf{n}_t} \quad (\text{S31})$$

S4.2 what is the individual kinship matrix the expectation of?

For the stochastic individual kinship matrix, we have that the number of [a,b]-kin in i of ego in j is the number of directional pairs of such kin in the population, divided by the number of individuals in j :

$$\tilde{\mathbb{K}}_t[a,b](i,j) = \frac{\tilde{\mathbb{K}}_t^{(p)}[a,b](i,j)}{\tilde{n}_t(j)} \quad (\text{S32})$$

The individual kinship matrix being an individual metric, the expectation has to be taken both on the realisations of the population stochastic process and on the individuals. The expected number of number of [a,b]-kin in i of ego in j corresponds to the mean across realisation of $\tilde{\mathbb{K}}_t[a,b](i,j)$ weighted by $\tilde{n}_t(j)$ and the result has to be scaled by the expectation of these weights $E(\tilde{n}_t(j)) = n_t(j)$:

$$\mathbb{K}_t[a,b](i,j) = \frac{E(\tilde{n}_t(j) \tilde{\mathbb{K}}_t[a,b](i,j))}{n_t(j)} \quad (\text{S33})$$

From equations S32 and S30, this is

$$\mathbb{K}_t[a,b](i,j) = \frac{E(\tilde{\mathbb{K}}_t^{(p)}[a,b](i,j))}{n_t(j)} = \frac{\mathbb{K}_t^{(p)}[a,b](i,j)}{n_t(j)} \quad (3)$$

which, in matrix form, corresponds to

$$\mathbb{K}_t = \mathbb{K}_t^{(p)} \mathbb{D}_{\mathbf{n}_t}^{-1} \quad (3)$$

These concepts and formulas are illustrated in SI section S8

S5 Properties and conditions of kinship networks

The kinship matrix of a given population is not random. Contrary to the expected abundance vector, $\mathbf{n}_t$, which only property is to be a vector of non-negative real numbers, $\mathbb{K}_t$ and $\mathbb{K}_t^{(p)}$ have certain properties:

- (a) ego is not a kin of ego
- (b) the population Kinship Matrix is symmetrical
- (c) the number of kin-pairs is at most equal to the number of pairs
- (d) ego has at most one b -ancestor

explanation of the conditions and corresponding formulas for the kinship matrices

- (a) Property (a) is a convention; other choices are possible (see eg section ...); as ego corresponds to the [1,1]-block of $\mathbb{K}_t$, this implies that $\forall i,j \quad \mathbb{K}_t[1,1](i,j) = 0$ and therefore $\forall i,j \quad \mathbb{K}_t^{(p)}[1,1](i,j) = 0$.

- (b) Property (b), already shown by (Coste, 2025a), stems from the fact that, as $\mathbb{K}_t^{(p)}$ contains the number of direction pairs, it counts twice every non-directional kin pair: for every niece in i of an aunt in j , there is an aunt in j of a sister in i (non-diagonal blocks) and for every sister in i of a sister j , there is a sister in j of a sister in i (diagonal blocks). In other words $\forall a, b, i, j \quad \mathbb{K}_t^{(p)}[a, b](i, j) = \mathbb{K}_t^{(p)}[b, a](j, i)$, that is $\mathbb{K}_t^{(p)} = \mathbb{K}_t^{(p)T}$.
- (c) Property (c), already encountered stems from the obvious: a kin-pair is a pair; there cannot be more kin pairs than pairs in a population. The formula for $\mathbb{K}^{(p)}$ is equation S31: $\sum_{a,b} \mathbb{K}_t^{(p)}[a, b] \leq \mathbf{P}_t$. Note that if the population is initiated at $t = 0$ with a single individual, then for g large enough (e.g. $g \geq t$), the sum of all elements in $\mathbb{K}_t^{(p)}$ is the expected number of directional pairs in the population: $\sum_{a,b} \mathbb{K}_t^{(p)}[a, b] = \mathbf{P}_t$
- (d) Finally, property (d) comes from the fact that we study here one-sex lineages. In such a lineage, an individual has at most one mother, one grandmother, one great-grandmother, etc. This implies that $\forall b, j \quad \sum_i \mathbb{K}_t[1, b](i, j) \leq 1$. From eq.3, this is $\forall b, j \quad \sum_i \mathbb{K}_t^{(p)}[1, b](i, j) \leq n_t(j)$

These formulas are aggregated in appendix 8.1 of the main text. From eq.3, we obtain the corresponding conditions on the Individual Kinship Matrix: We provide the properties and conditions of the population kinship matrix as eq.22. Via eq. 3, we provide here the corresponding properties and conditions on the individual Kinship Matrix:

$$\left\{ \begin{array}{l} \text{(a) } ego \text{ is not a kin of } ego: \quad \mathbb{K}_t[1, 1](i, j) = 0 \\ \text{(b) symmetry of population kinship : } \quad n_t(j) \mathbb{K}_t[a, b](i, j) = n_t(i) \mathbb{K}_t[b, a](j, i) \\ \text{(c) kin pairs are pairs: } \quad \sum_{a,b} \mathbb{K}_t[a, b](i, j) \leq \frac{P_t(i, j)}{n_t(j)} \\ \text{(d) } ego \text{ has at most one } b\text{-ancestor: } \quad \sum_i \mathbb{K}_t[1, b](i, j) \leq 1 \end{array} \right. \quad (\text{S34})$$

These concepts and formulas are illustrated in SI section S8

S6 Method: Proof of the kinship projection equation

As per the main text and figure S1, we decompose the elements of $\mathbb{K}_{t+1}^{(p)}$, that is, the kin-pairs (structured by kin type and states) in the population at time $t + 1$ according to whether they stem from a kin-pair at time t , $\mathbb{A}_{t+1}^{(p)}$, or whether they are new, "immigrant" pairs, $\mathbb{B}_{t+1}^{(p)}$:

$$\mathbb{K}_{t+1}^{(p)} = \underbrace{\mathbb{A}_{t+1}^{(p)}}_{\text{descendants of existing pairs}} + \underbrace{\mathbb{B}_{t+1}^{(p)}}_{\text{"immigrant" kin pairs}}. \quad (5)$$

We will consider directly the vectorised version of these kinship matrices:

$$\mathbf{k}_{t+1} = \text{vec}\left(\mathbb{K}_{t+1}^{(p)}\right) = \text{vec}\left(\mathbb{A}_{t+1}^{(p)}\right) + \text{vec}\left(\mathbb{B}_{t+1}^{(p)}\right) \quad (\text{S35})$$

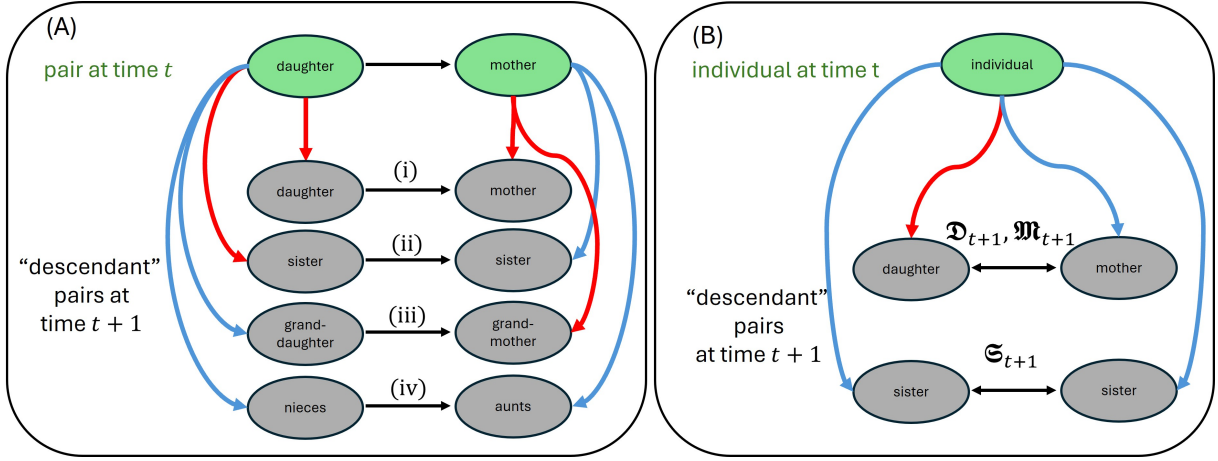


Figure S1: Diagram illustrating the method corresponding to the figure of the main text with additional notations. The kin pairs in the population at time $t + 1$ arise from (A) existing pairs at time t (left side) and (B) from new pairs. (A) an existing kin pair at time t yields kin pairs at time $t + 1$ via (i) survival of both members, (ii)-(iii), survival of one member and reproduction of the other and (iv) reproduction of both members. (B) an individual at time t can generate $\mathfrak{D}_{t+1}$ (resp. $\mathfrak{M}_{t+1}$) new daughter-mother (resp. mother-daughter) kin pairs if it survives *and* reproduces and $\mathfrak{S}_{t+1}$ new sister-sister kin pairs if it produces two daughters or more.

S6.1 descendants of existing pairs

We decompose $\mathbb{A}_{t+1}^{(p)}$ according to four components:

- **Q**: surviving kin pairs (i.e., kin pairs at time $t + 1$ stemming from kin pairs at time t , where both individuals survived)
- **W**: kin pairs at time $t + 1$ stemming from the daughters of individuals in a kin pair at time t (providing both individuals reproduced)
- **Y**: kin pairs at time $t + 1$ stemming from the daughter of one element of a kin pair at time t (providing it reproduced) and the other element itself (providing it survived)

The component **Q** of $\mathbb{A}_{t+1}^{(p)}[a, b]$ that is made of surviving kin pairs at time t is such that

$$Q(i, j) = \sum_{k, l} S_t(i, k) S_t(j, l) \mathbb{K}_t^{(p)}[a, b](k, l) \quad (\text{S36})$$

Indeed $\mathbb{K}_t^{(p)}[a, b](k, l)$ counts all $[a, b]$ directional kin pairs relating an individual in k and an individual in l at time t ; if both individuals survive, the kin pair will survive (as an $[a, b]$ -pair) at the next time-step.

Populating the matrix (see SI.S1.2) from its elements (eq.S36), we have

$$\begin{aligned} \mathbf{Q} &= \sum_{i, j} \mathbf{e}_i^{(s)} Q(i, j) \mathbf{e}_j^{(s)T} = \sum_{i, j, k, l} \mathbf{e}_i^{(s)} \left(\mathbf{e}_i^{(s)T} \mathbf{S}_t \mathbf{e}_k^{(s)} \right) \left(\mathbf{e}_k^{(s)T} (\mathbb{K}_t^{(p)}[a, b]) \mathbf{e}_l^{(s)} \right) \left(\mathbf{e}_j^{(s)T} \mathbf{S}_t \mathbf{e}_l^{(s)} \right) \mathbf{e}_j^{(s)T} \\ &= \sum_{i, j, k, l} \mathbf{e}_i^{(s)} \left(\mathbf{e}_i^{(s)T} \mathbf{S}_t \mathbf{e}_k^{(s)} \right) \left(\mathbf{e}_k^{(s)T} (\mathbb{K}_t^{(p)}[a, b]) \mathbf{e}_l^{(s)} \right) \left(\mathbf{e}_l^{(s)T} \mathbf{S}_t^T \mathbf{e}_j^{(s)} \right) \mathbf{e}_j^{(s)T} \end{aligned}$$

Since $\sum_i \mathbf{e}_i^{(s)} \mathbf{e}_i^{(s)T} = \mathbf{I}_s$, this leads to

$$\mathbf{Q} = \mathbf{S}_t (\mathbb{K}_t^{(p)}[a, b]) \mathbf{S}_t^T \quad (\text{S37})$$

The component $\mathbf{W}$ of $\mathbb{E}_{t+1}^{(p)}[a, b]$ that is made of the offspring of kin pairs at time t is such that

$$W(i, j) = \sum_{k, l} F_t(i, k) F_t(j, l) \mathbb{K}_t^{(p)}[a-1, b-1](k, l)$$

Indeed the daughter of the $[a-1, b-1]$ -kin of ego, is an $[a, b-1]$ -kin of ego and therefore and $[a, b-1]$ -kin of the daughter of ego. With the same computational steps than above, we obtain

$$\mathbf{W} = \mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b-1])\mathbf{F}_t^T \quad (\text{S38})$$

Finally, with the same reasoning and computational steps when considering the kin-pairs at $t+1$ formed by the survivor of one of the individual and the daughter of the other, and vice versa, we have

$$\mathbf{Y} = \mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b-1])\mathbf{F}_t^T + \mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b])\mathbf{S}_t^T \quad (\text{S39})$$

From equations S37, S38 and S39, we obtain

$$\begin{aligned} \mathbb{A}_{t+1}^{(p)}[a, b] &= \mathbf{Q} + \mathbf{Y} + \mathbf{W} \\ &= \underbrace{\mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b])\mathbf{S}_t^T}_{\text{surviving kin-pairs}} + \underbrace{\mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b-1])\mathbf{F}_t^T}_{\text{survivor/daughter kin-pairs}} + \underbrace{\mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b])\mathbf{S}_t^T}_{\text{daughter/survivor kin-pairs}} + \underbrace{\mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b-1])\mathbf{F}_t^T}_{\text{daughters of kin-pairs}} \end{aligned} \quad (\text{S40})$$

We now populate $\mathbb{A}_{t+1}^{(p)}$ with its blocks (see SI S1):

$$\begin{aligned} \mathbb{A}_{t+1}^{(p)} &= \sum_{a, b \leq g} \sum_{i, j} \mathbb{A}_{t+1}^{(p)}[a, b](i, j) (e_a^{(g)} \otimes e_i^{(s)}) (e_b^{(g)T} \otimes e_j^{(s)T}) \\ &= \sum_{a, b \leq g} \sum_{i, j} (e_a^{(g)} \otimes e_i^{(s)}) e_i^{(s)T} (\mathbb{A}_{t+1}^{(p)}[a, b]) e_j^{(s)} (e_b^{(g)T} \otimes e_j^{(s)T}) \\ &= \sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) (\mathbb{A}_{t+1}^{(p)}[a, b]) (e_b^{(g)T} \otimes \mathbf{I}_s) \end{aligned} \quad (\text{S41})$$

From equations S40 and S41, we get

$$\begin{aligned} \mathbb{A}_{t+1}^{(p)} &= \sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) \left(\mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b])\mathbf{S}_t^T + \mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b-1])\mathbf{F}_t^T + \right. \\ &\quad \left. \mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b])\mathbf{S}_t^T + \mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b-1])\mathbf{F}_t^T (e_b^{(g)T} \otimes \mathbf{I}_s) \right) \\ &= \underbrace{\sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) \left(\mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b])\mathbf{S}_t^T \right) (e_b^{(g)T} \otimes \mathbf{I}_s)}_{\mathbb{A}_1} + \underbrace{\sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) \left(\mathbf{S}_t(\mathbb{K}_t^{(p)}[a, b-1])\mathbf{F}_t^T \right) (e_b^{(g)T} \otimes \mathbf{I}_s)}_{\mathbb{A}_1} + \\ &\quad \underbrace{\sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) \left(\mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b])\mathbf{S}_t^T \right) (e_b^{(g)T} \otimes \mathbf{I}_s)}_{\mathbb{A}_3} + \underbrace{\sum_{a, b \leq g} (e_a^{(g)} \otimes \mathbf{I}_s) \left(\mathbf{F}_t(\mathbb{K}_t^{(p)}[a-1, b-1])\mathbf{F}_t^T \right) (e_b^{(g)T} \otimes \mathbf{I}_s)}_{\mathbb{A}_4} \end{aligned} \quad (\text{S42})$$

Denoting $\mathbf{J}_1 = \sum_{c < g} \mathbf{e}_{c+1}^{(g)} \mathbf{e}_c^{(g)T}$ and

$$\mathbf{S}_t = \mathbf{I}_g \otimes \mathbf{S}_t, \quad \mathbf{F}_t = \mathbf{J}_g \otimes \mathbf{F}_t, \quad \mathbf{M}_t = \mathbf{F}_t + \mathbf{S}_t, \quad (7)$$

we obtain

$$\begin{aligned} \mathbb{A}_1 &= \sum_{a, b \leq g} (\mathbf{e}_a^{(g)} \otimes \mathbf{I}_s) \mathbf{S}_t (\mathbf{e}_a^{(g)T} \otimes \mathbf{I}_s) \mathbb{K}_t^{(p)} (\mathbf{e}_b^{(g)} \otimes \mathbf{I}_s) \mathbf{S}_t^T (\mathbf{e}_b^{(g)T} \otimes \mathbf{I}_s) \\ &= \sum_{a, b \leq g} (\mathbf{e}_a^{(g)} \mathbf{e}_a^{(g)T} \otimes \mathbf{S}_t) \mathbb{K}_t^{(p)} (\mathbf{e}_b^{(g)} \mathbf{e}_b^{(g)T} \otimes \mathbf{S}_t^T) = (\mathbf{I}_g \otimes \mathbf{S}_t) \mathbb{K}_t^{(p)} (\mathbf{I}_g \otimes \mathbf{S}_t^T) = \mathbf{S}_t \mathbb{K}_t^{(p)} \mathbf{S}_t^T \end{aligned} \quad (\text{S43})$$

For the second element, we have

$$\begin{aligned} \mathbb{A}_2 &= \sum_{a, b \leq g} (\mathbf{e}_a^{(g)} \otimes \mathbf{I}_s) \mathbf{S}_t (\mathbf{e}_a^{(g)T} \otimes \mathbf{I}_s) \mathbb{K}_t^{(p)} (\mathbf{e}_{b-1}^{(g)} \otimes \mathbf{I}_s) \mathbf{F}_t^T (\mathbf{e}_b^{(g)T} \otimes \mathbf{I}_s) \\ &= \sum_{a, b \leq g} (\mathbf{e}_a^{(g)} \mathbf{e}_a^{(g)T} \otimes \mathbf{S}_t) \mathbb{K}_t^{(p)} (\mathbf{e}_{b-1}^{(g)} \mathbf{e}_b^{(g)T} \otimes \mathbf{F}_t^T) = (\mathbf{I}_g \otimes \mathbf{S}_t) \mathbb{K}_t^{(p)} (\mathbf{J}_g^T \otimes \mathbf{F}_t^T) = \mathbf{S}_t \mathbb{K}_t^{(p)} \mathbf{F}_t^T \end{aligned} \quad (\text{S44})$$

With the same steps for the third and fourth elements, we obtain:

$$\begin{cases} \mathbb{A}_3 = \mathbf{F}_t \mathbb{K}_t^{(p)} \mathbf{S}_t^T \\ \mathbb{A}_4 = \mathbf{F}_t \mathbb{K}_t^{(p)} \mathbf{F}_t^T \end{cases} \quad (\text{S45})$$

Overall, from equations S43, S44 and S45 applied to equation S42, we obtain

$$\begin{aligned} \mathbb{A}_{t+1}^{(p)} &= \mathbf{S}_t \mathbb{K}_t^{(p)} \mathbf{S}_t^T + \mathbf{S}_t \mathbb{K}_t^{(p)} \mathbf{F}_t^T + \mathbf{F}_t \mathbb{K}_t^{(p)} \mathbf{S}_t^T + \mathbf{F}_t \mathbb{K}_t^{(p)} \mathbf{F}_t^T = \mathbf{S}_t \mathbb{K}_t^{(p)} (\mathbf{S}_t^T + \mathbf{F}_t^T) + \mathbf{F}_t \mathbb{K}_t^{(p)} (\mathbf{S}_t^T + \mathbf{F}_t^T) \\ &= \mathbf{M}_t \mathbb{K}_t^{(p)} \mathbf{M}_t^T \end{aligned} \quad (\text{S46})$$

Vectorising equation S46 leads to (see eq.S1):

$$\text{vec}(\mathbb{A}_{t+1}^{(p)}) = (\mathbf{M}_t \otimes \mathbf{M}_t) \text{vec}(\mathbb{K}_t^{(p)}) = (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{k}_t \quad (6)$$

S6.2 "immigrant" kin pairs

Some of the kin pairs at time $t + 1$ do not stem from existing pairs at t . These "immigrant" pairs in the kinship network are caused by the reproduction of individuals. Contrary to $\mathbb{A}_{t+1}^{(p)}$ which is solely a function of the expectations of survival and reproduction at time t (i.e., $\mathbf{F}_t$ and $\mathbf{S}_t$, organised in $\mathbf{M}_t$, see equations 6 and 7), $\mathbb{B}_{t+1}^{(p)}$ depends also, in the general case, on the variance of the reproductive process, $\mathbf{V}_t$, and the covariance of reproduction and survival $\mathbf{C}_t$.

If an individual produces one or more daughters and survives, this generates new daughter-mother and mother-daughter directional pairs, which in vectorised form (and structured by the states of individuals)

correspond to $\mathfrak{D}_t$ and $\mathfrak{M}_t$ detailed in app.S6.5. If an individual produces more than one daughter, this generates new sister-sister kin-pairs (same-litter sisters), which in vectorised form (and structured by the states of individuals) correspond to $\mathfrak{S}_t$ detailed in app.S6.4.

Denoting $\mathbf{J}_{2,1} = \mathbf{e}_1^g \otimes \mathbf{I}_s \otimes \mathbf{e}_2^g \otimes \mathbf{I}_s$, $\mathbf{J}_{1,2} = \mathbf{e}_2^g \otimes \mathbf{I}_s \otimes \mathbf{e}_1^g \otimes \mathbf{I}_s$ and $\mathbf{J}_{2,2} = \mathbf{e}_2^g \otimes \mathbf{I}_s \otimes \mathbf{e}_2^g \otimes \mathbf{I}_s$, we can place these elements in the corresponding blocks of $\mathbb{B}_{t+1}$:

$$\text{vec}(\mathbb{B}_{t+1}) = \mathbf{J}_{2,1} \text{vec}(\mathfrak{D}_t) + \mathbf{J}_{1,2} \text{vec}(\mathfrak{M}_t) + \mathbf{J}_{2,2} \text{vec}(\mathfrak{S}_t) \quad (\text{S47})$$

From equations S54 and S58, we can develop eq. S47:

$$\text{vec}(\mathbb{B}_{t+1}) = (\mathbf{J}_{2,1} (\mathbf{C}_t + (\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J}_d) + \mathbf{J}_{1,2} (\mathbf{J}_e \mathbf{C}_t + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d) + \mathbf{J}_{2,2} (\mathbf{V}_t + (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t)) \mathbf{n}_t \quad (\text{S48})$$

that is

$$\text{vec}(\mathbb{B}_{t+1}) = \mathbb{N}_t \mathbf{n}_t \quad (8)$$

with

$$\mathbb{N}_t = (\mathbf{J}_{2,1} (\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2} (\mathbf{F}_t \otimes \mathbf{S}_t) + \mathbf{J}_{2,2} (\mathbf{F}_t \otimes \mathbf{F}_t)) \mathbf{J} - \mathbf{J}_{2,2} \mathbf{J} \mathbf{F}_t + \mathbf{J}_{2,2} \mathbf{V}_t + (\mathbf{J}_{2,1} + \mathbf{J}_{1,2} \mathbf{J}_e) \mathbf{C}_t \quad (8)$$

S6.3 overall

Overall, vectorising equation 5, we obtain, from equations 6 and 8

$$\mathbf{k}_{t+1} = \text{vec}(\mathbb{K}_{t+1}^{(p)}) = \text{vec}(\mathbb{A}_{t+1}^{(p)}) + \text{vec}(\mathbb{B}_{t+1}^{(p)}) = (\mathbb{M}_t \otimes \mathbb{M}_t) \mathbf{k}_t + \mathbb{N}_t \mathbf{n}_t \quad (9)$$

S6.4 Same-litter sisters and reproductive variance

At any time t , the individuals in the population vector $\mathbf{n}_t$ can produce daughters and therefore (when there are more than one daughter produced) sisters, that we call same-litter sisters. Each individual in state k in that population has a reproduction according to the k^{th} column vector of matrix of random variables $\tilde{\mathbf{F}}_t$, which i, k entry, $\tilde{F}_t(i, k)$, represents the number of offspring in i produced by an individual in k at time t and which expectation is $\mathbf{F}_t = \mathbf{E}(\tilde{\mathbf{F}}_t)$. We remind the reader that we denote the variance of the reproductive process at time t , $\mathbf{V}_t$. It is a $s^2 \times s$ matrix which k^{th} column represents, in vectorised form, the variance-covariance matrix of the offspring produced by an individual in k :

$$\mathbf{V}_t = \sum_{i,j,k} \text{Cov}(\tilde{F}_t(i, k), \tilde{F}_t(j, k)) (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_k^{(s)T} \quad (13)$$

number of newborn sister kin pairs We denote $\mathfrak{S}_t$ the expected number of new sister-sister directional pairs (structured by their states) produced at time t (and appearing in the population at time

$t + 1$) by individuals producing more than one offspring. Let us call $\mathfrak{S}_t^{(i)}$ the expected number of new sister-sister directional pairs (structured by their states) produced at time t by an individual in state i :

$$\mathfrak{S}_t = \sum_i \mathfrak{S}_t^{(i)} n_t(i) \quad (\text{S49})$$

Let us denote $\tilde{\mathbf{F}}_t^{(i)}$ the stochastic vector of the production of offspring by an individual in i . Then following the reasoning of equations S25 and S27, we have

$$\mathfrak{S}_t^{(i)} = \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T} - \mathbf{D}_{\tilde{\mathbf{F}}_t^{(i)}}) = \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T}) - \mathbf{D}_{\mathbf{E}(\tilde{\mathbf{F}}_t^{(i)})} \quad (\text{S50})$$

We can rewrite, from the definition of the variance of a random vector $\mathbf{E}(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T}) = \mathbf{var}(\tilde{\mathbf{F}}_t^{(i)}) + \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)}) \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)})^T$, which in vectorised form is (from eq.S1):

$$\mathbf{vec}(\mathbf{E}(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T})) = \mathbf{V}(\tilde{\mathbf{F}}_t^{(i)}) + \mathbf{vec}(\mathbf{F}_t \mathbf{e}_i^{(s)} \mathbf{e}_i^{(s)T} \mathbf{F}_t^T) = \mathbf{V}(\tilde{\mathbf{F}}_t) \mathbf{e}_i^{(s)} + (\mathbf{F}_t \otimes \mathbf{F}_t)(\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) \quad (\text{S51})$$

From eq.S18, we get

$$\mathbf{vec}(\mathbf{D}_{\mathbf{E}(\tilde{\mathbf{F}}_t^{(i)})}) = \mathbf{J}_d \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)}) = \mathbf{J}_d \mathbf{F}_t \mathbf{e}_i^{(s)} \quad (\text{S52})$$

so that overall, from equations S50,S51 and S52:

$$\mathbf{vec}(\mathfrak{S}_t^{(i)}) = \mathbf{V}_t \mathbf{e}_i^{(s)} + (\mathbf{F}_t \otimes \mathbf{F}_t)(\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) - \mathbf{J}_d \mathbf{F}_t \mathbf{e}_i^{(s)} \quad (\text{S53})$$

From equations S49 and S53, we get:

$$\begin{aligned} \mathbf{vec}(\mathfrak{S}_t) &= \sum_i \mathbf{vec}(\mathfrak{S}_t^{(i)}) n_t(i) = \sum_i \left(\mathbf{V}_t \mathbf{e}_i^{(s)} + (\mathbf{F}_t \otimes \mathbf{F}_t)(\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) - \mathbf{J}_d \mathbf{F}_t \mathbf{e}_i^{(s)} \right) \mathbf{e}_i^{(s)T} n_t \\ &\quad \left(\mathbf{V}_t \sum_i \mathbf{e}_i^{(s)} \mathbf{e}_i^{(s)T} + (\mathbf{F}_t \otimes \mathbf{F}_t) \sum_i (\mathbf{e}_i^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_i^{(s)T} - \mathbf{J}_d \mathbf{F}_t \sum_i \mathbf{e}_i^{(s)} \mathbf{e}_i^{(s)T} \right) n_t \\ &= (\mathbf{V}_t + (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t) \mathbf{n}_t \quad (\text{S54}) \end{aligned}$$

S6.5 New daughter-mother kin pairs and covarying reproduction and survival

At any time t , the individuals in the population vector $\mathbf{n}_t$ can both survive and produce one daughter or more, therefore generating new mother-daughter (and daughter-mother) kin pairs in the population. Each individual in state k in that population has a reproduction and survival according to the k^{th} column vector of matrices $\tilde{\mathbf{F}}_t$ and $\tilde{\mathbf{S}}_t$. We remind the reader that denote the covariance of the reproductive and survival processes at time t , $\mathbf{C}_t$. It is a $s^2 \times s$ matrix which k^{th} column represents, in vectorised form for an individual in k , the cross-covariance matrix of the offspring produced and survival:

$$\mathbf{C}_t = \sum_{i,j,k} \text{Cov}(\tilde{F}_t(i,k), \tilde{S}_t(j,k)) (\mathbf{e}_j^{(s)} \otimes \mathbf{e}_i^{(s)}) \mathbf{e}_k^{(s)T} \quad (14)$$

number of new daughter-mother kin pairs We follow here the same reasoning that above denoting $\mathfrak{D}_t$ and $\mathfrak{M}_t$ the expected number of new daughter-mother and mother-daughter directional pairs (structured by their states) produced at time t (and appearing in the population at time $t + 1$) by individuals reproducing *and* surviving and calling $\mathfrak{D}_t^{(i)}$ and $\mathfrak{M}_t^{(i)}$ the expected number of new daughter-mother and mother-daughter directional pairs (structured by their states) produced at time t by an individual in state i .

$$\begin{cases} \mathfrak{D}_t = \sum_i \mathfrak{D}_t^{(i)} n_t(i) \\ \mathfrak{M}_t = \sum_i \mathfrak{M}_t^{(i)} n_t(i) \end{cases} \quad (\text{S55})$$

where the individual expectations are equal to

$$\begin{cases} \mathfrak{D}_t^{(i)} = E(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{S}}_t^{(i)T}) \\ \mathfrak{M}_t^{(i)} = E(\tilde{\mathbf{S}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T}) = \mathfrak{D}_t^{(i)T} \end{cases} \quad (\text{S56})$$

which leads to

$$\begin{cases} \text{vec}(\mathfrak{D}_t^{(i)}) = \text{vec}(E(\tilde{\mathbf{F}}_t^{(i)} \tilde{\mathbf{S}}_t^{(i)T})) = C_t e_i^{(s)} + \text{vec}(\mathbf{F}_t e_i^{(s)} e_i^{(s)T} \mathbf{S}_t^T) = C_t e_i^{(s)} + (\mathbf{S}_t \otimes \mathbf{F}_t)(e_i^{(s)} \otimes e_i^{(s)}) \\ \text{vec}(\mathfrak{D}_t^{(i)}) = C_t^* e_i^{(s)} + (\mathbf{F}_t \otimes \mathbf{S}_t)(e_i^{(s)} \otimes e_i^{(s)}) = \mathbf{J}_e C_t e_i^{(s)} + (\mathbf{F}_t \otimes \mathbf{S}_t)(e_i^{(s)} \otimes e_i^{(s)}) \end{cases} \quad (\text{S57})$$

From equations S55 and S57, we get:

$$\begin{cases} \text{vec}(\mathfrak{D}_t) = \sum_i \text{vec}(\mathfrak{D}_t^{(i)}) n_t(i) = (C_t + (\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J}_d) \mathbf{n}_t \\ \text{vec}(\mathfrak{M}_t) = (C_t^* + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d) \mathbf{n}_t = (\mathbf{J}_e C_t + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d) \mathbf{n}_t \end{cases} \quad (\text{S58})$$

S7 Propagation of properties/conditions via the projection equations

We prove here, that projected by the kinship projection equation, the four conditions on kinship networks ((a): *ego* is not a kin of *ego*, (b) the PKM is symmetrical, (c) kin pairs are pairs and (d) *ego* has, at most, one *b*-ancestor), introduced in section 2.2, made explicit for PKMs in appendix 8.1 and detailed in SI S5, are propagated via the kinship projection equation.

S7.1 preliminary derivations

We will use here the PKMs (conditions in appendix 8.1) and its projection equation, written as eq 5.

From eq S46, we have an explicit development of $\mathbb{A}_{t+1}$; we obtain one for $\mathbb{B}_{t+1}$ from eq.S47

$$\mathbb{B}_{t+1} = ((e_2^{(s)} e_1^{(s)T}) \otimes \mathfrak{D}_t) + ((e_1^{(s)} e_2^{(s)T}) \otimes \mathfrak{M}_t) + ((e_2^{(s)} e_2^{(s)T}) \otimes \mathfrak{S}_t) \quad (\text{S59})$$

proof: $\mathbb{B}_{t+1} = \sum_{a,b} \sum_{i,j} \mathbb{B}_{t+1}[a,b](i,j) (e_a^{(g)} \otimes e_i^{(s)}) (e_b^{(g)T} \otimes e_j^{(s)T}) = \sum_{a,b} \sum_{i,j} \mathbb{B}_{t+1}[a,b](i,j) (e_a^{(g)} e_b^{(g)T}) \otimes (e_i^{(s)} e_j^{(s)T}) = \sum_{a,b} (e_a^{(g)} e_b^{(g)T}) \otimes \left(\sum_{i,j} \mathbb{B}_{t+1}[a,b](i,j) (e_i^{(s)} e_j^{(s)T}) \right) = \sum_{a,b} (e_a^{(g)} e_b^{(g)T}) \otimes \mathbb{B}_{t+1}[a,b]$.

Therefore from equations 5, S46 and S59, we have

$$\mathbb{K}_{t+1}^{(p)} = \underbrace{\mathbb{M}_t \mathbb{K}_t^{(p)} \mathbb{M}_t^T}_{\mathbb{A}_{t+1}} + \underbrace{((e_2^{(s)} e_1^{(s)T}) \otimes \mathfrak{D}_t) + ((e_1^{(s)} e_2^{(s)T}) \otimes \mathfrak{M}_t) + ((e_2^{(s)} e_2^{(s)T}) \otimes \mathfrak{S}_t)}_{\mathbb{B}_{t+1}} \quad (\text{S60})$$

From this we obtain that

$$\left\{ \begin{array}{l} \mathbb{B}_{t+1}[a, b] = \mathbf{0} \quad \text{for all } a, b, \text{ but for } \mathbb{B}_{t+1}[2, 1] = \mathfrak{D}_t, \quad \mathbb{B}_{t+1}[1, 2] = \mathfrak{M}_t \quad \mathbb{B}_{t+1}[2, 2] = \mathfrak{S}_t \\ \mathbb{A}_{t+1}[1, 1] = \mathbf{S}_t \mathbb{K}_t^{(p)}[1, 1] \mathbf{S}_t^T \\ \forall a > 1, \mathbb{A}_{t+1}[a, 1] = \mathbf{S}_t \mathbb{K}_t^{(p)}[a, 1] \mathbf{S}_t^T + \mathbf{F}_t \mathbb{K}_t^{(p)}[a-1, 1] \mathbf{S}_t^T \\ \forall b > 1, \mathbb{A}_{t+1}[1, b] = \mathbf{S}_t \mathbb{K}_t^{(p)}[1, b] \mathbf{S}_t^T + \mathbf{S}_t \mathbb{K}_t^{(p)}[1, b-1] \mathbf{F}_t^T \\ \forall a, b > 1 \quad \mathbb{A}_{t+1}[a, b] = \mathbf{S}_t \mathbb{K}_t^{(p)}[a, b] \mathbf{S}_t^T + \mathbf{S}_t \mathbb{K}_t^{(p)}[a, b-1] \mathbf{F}_t^T + \mathbf{F}_t \mathbb{K}_t^{(p)}[a-1, b] \mathbf{S}_t^T + \mathbf{F}_t \mathbb{K}_t^{(p)}[a-1, b-1] \mathbf{F}_t^T \end{array} \right. \quad (\text{S61})$$

S7.2 proofs by induction of the propagation of properties

We now prove, for each of the four conditions, that it is propagated by the kinship projection equation

ego is not a kin of ego

We assume that $\mathbb{K}_t^{(p)}[1, 1] = \mathbf{0}$. From eqs S60 and S61, we have $\mathbb{K}_{t+1}^{(p)}[1, 1] = \mathbf{S}_t \mathbb{K}_t^{(p)}[1, 1] \mathbf{S}_t^T = \mathbf{S}_t \mathbf{0} \mathbf{S}_t^T = \mathbf{0}$, which completes the proof by induction.

symmetry of population kinship matrix

We assume that $\mathbb{K}_t^{(p)} = \mathbb{K}_t^{(p)T}$. From eq.S60, we have $\mathbb{K}_{t+1}^{(p)T} = \mathbb{M}_t \mathbb{K}_t^{(p)T} \mathbb{M}_t^T + ((e_1^{(s)} e_2^{(s)T}) \otimes \mathfrak{D}_t^T) + ((e_2^{(s)} e_1^{(s)T}) \otimes \mathfrak{M}_t^T) + ((e_2^{(s)} e_2^{(s)T}) \otimes \mathfrak{S}_t^T)$. From eq.S50, $\mathfrak{S}_t^{(i)} = \mathfrak{S}_t^{(i)T}$; therefore from eq.S49, $\mathfrak{S}_t = \mathfrak{S}_t^T$. From eq.S56, $\mathfrak{M}_t^{(i)} = \mathfrak{D}_t^{(i)T}$, therefore from eq.S55, $\mathfrak{M}_t^T = \mathfrak{D}_t^T$. This implies, from the assumption that $\mathbb{K}_{t+1}^{(p)T} = \mathbb{M}_t \mathbb{K}_t^{(p)} \mathbb{M}_t^T + ((e_1^{(s)} e_2^{(s)T}) \otimes \mathfrak{M}_t) + ((e_2^{(s)} e_1^{(s)T}) \otimes \mathfrak{D}_t) + ((e_2^{(s)} e_2^{(s)T}) \otimes \mathfrak{S}_t) = \mathbb{K}_{t+1}^{(p)}$, which completes the proof by induction.

ego has at most one b-ancestor

We assume that $\mathbf{1}^T \mathbb{K}_t^{(p)}[1, b] \leq \mathbf{n}_t^T$. From eqs S60 and S61, we have $\mathbb{K}_{t+1}^{(p)}[1, b] = \mathbb{A}_{t+1}[1, b] + \mathbb{B}_{t+1}[1, b] = \mathbf{S}_t \mathbb{K}_t^{(p)}[1, b] \mathbf{S}_t^T + \mathbf{S}_t \mathbb{K}_t^{(p)}[1, b-1] \mathbf{F}_t^T + \delta(b, 2) \mathfrak{M}_t$. We segregate two cases (a) $b = 2$ and (b) $b > 2$. In case (a), $\mathbf{1}^T \mathbb{K}_{t+1}^{(p)}[1, 2] = \mathbf{1}^T \mathbf{S}_t \mathbb{K}_t^{(p)}[1, 2] \mathbf{S}_t^T + \mathbf{1}^T \mathfrak{M}_t$. From eqs. S55 and S56, and as survival is always inferior to 1, $\mathbf{1}^T \mathfrak{M}_t = \sum_i \mathbf{E}(\mathbf{1}^T \tilde{\mathbf{S}}_t^{(i)} \tilde{\mathbf{F}}_t^{(i)T}) n_t(i) \leq \sum_i \mathbf{E}(\tilde{\mathbf{F}}_t^{(i)T}) n_t(i) = \sum_i \mathbf{n}_t^T \mathbf{e}_i \mathbf{F}_t^{(i)T} = \mathbf{n}_t^T \mathbf{F}_t^T$. From this inequality, the assumption, and, again, the fact that survival is always inferior to 1 get $\mathbf{1}^T \mathbb{K}_{t+1}^{(p)}[1, 2] \leq \mathbf{1}^T \mathbf{S}_t \mathbb{K}_t^{(p)}[1, 2] \mathbf{S}_t^T + \mathbf{n}_t^T \mathbf{F}_t^T \leq \mathbf{1}^T \mathbb{K}_t^{(p)}[1, 2] \mathbf{S}_t^T + \mathbf{n}_t^T \mathbf{F}_t^T \leq \mathbf{n}_t^T \mathbf{S}_t^T + \mathbf{n}_t^T \mathbf{F}_t^T = ((\mathbf{S}_t + \mathbf{F}_t) \mathbf{n}_t)^T = \mathbf{n}_{t+1}^T$. In case (b), and with the similar arguments, $\mathbf{1}^T \mathbb{K}_{t+1}^{(p)}[1, b] = \mathbf{1}^T \mathbf{S}_t \left(\mathbb{K}_t^{(p)}[1, b] \mathbf{S}_t^T + \mathbb{K}_t^{(p)}[1, b-1] \mathbf{F}_t^T \right) \leq \mathbf{1}^T \left(\mathbb{K}_t^{(p)}[1, b] \mathbf{S}_t^T + \mathbb{K}_t^{(p)}[1, b-1] \mathbf{F}_t^T \right) = \mathbf{1}^T \mathbb{K}_t^{(p)}[1, b] \mathbf{S}_t^T + \mathbf{1}^T \mathbb{K}_t^{(p)}[1, b-1] \mathbf{F}_t^T \leq \mathbf{n}_t^T \mathbf{S}_t^T + \mathbf{n}_t^T \mathbf{F}_t^T = \mathbf{n}_{t+1}^T$. In all cases, therefore, $\mathbf{1}^T \mathbb{K}_{t+1}^{(p)}[1, b] \leq \mathbf{n}_{t+1}^T$.

which completes the proof by induction.

a kin pair is a pair

Here we provide the proof, via the infinite kinship matrices of SI S7.3. In an infinite kinship matrix, $g = +\infty$ and one considers that at some (possibly very remote) point in the past, the population was made of one individual only. Therefore all individuals are related (albeit at very large genealogical distances) and these relationships are all represented in the infinite kinship matrix (as $g = +\infty$. therefore for any t ,

$$\sum_{a,b} \mathbb{K}_t^{(p)}[a,b] \leq \sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b] \quad (\text{S62})$$

We prove here, by induction, that, for all t , $\sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b] \leq \mathbf{P}_t$ which, from eq.S62, then guarantees that for all t , $\sum_{a,b} \mathbb{K}_t^{(p)}[a,b] \leq \mathbf{P}_t$.

We assume that $\sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b] = \mathbf{P}_t = \mathbf{var}(\tilde{\mathbf{n}}_t) + \mathbf{n}_t \mathbf{n}_t^T - \mathbf{D}_{\mathbf{n}_t}$, which in vectorised form is $\mathbf{vec}(\sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b]) = \mathbf{vec}(\mathbf{P}_t) = \mathbf{V}(\tilde{\mathbf{n}}_t) + (\mathbf{n}_t \otimes \mathbf{n}_t) - \mathbf{J}_d \mathbf{n}_t$.

We have, from eq. S60 that $\sum_{a,b} \mathbb{K}_{t+1}^{(p)\infty}[a,b] = \sum_{a,b} (\mathbb{M}_t^\infty \mathbb{K}_t^{(p)\infty} \mathbb{M}_t^{\infty T})[a,b] + \mathfrak{D}_t + \mathfrak{M}_t + \mathfrak{S}_t$, where $\mathbb{M}_t^\infty$ is the generation structured projection matrix for $g = \infty$ which contains, in each block-column, one $\mathbf{F}_t$ and one $\mathbf{S}_t$. Therefore, from eq. S61, $\sum_{a,b} (\mathbb{M}_t^\infty \mathbb{K}_t^{(p)\infty} \mathbb{M}_t^{\infty T})[a,b] \leq (\mathbf{S}_t + \mathbf{F}_t) \left(\sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b] \right) (\mathbf{S}_t + \mathbf{F}_t)^T = \mathbf{M}_t \left(\sum_{a,b} \mathbb{K}_t^{(p)\infty}[a,b] \right) \mathbf{M}_t^T$, which from the assumption, and in vectorised form, yields: $\mathbf{vec} \left(\sum_{a,b} \mathbb{K}_{t+1}^{(p)\infty}[a,b] \right) \leq (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{vec}(\mathbf{P}_t) + \mathbf{vec}(\mathfrak{D}_t) + \mathbf{vec}(\mathfrak{M}_t) + \mathbf{vec}(\mathfrak{S}_t) = (\mathbf{M}_t \otimes \mathbf{M}_t) (\mathbf{V}(\tilde{\mathbf{n}}_t) + (\mathbf{n}_t \otimes \mathbf{n}_t) - \mathbf{J}_d \mathbf{n}_t) + \mathbf{vec}(\mathfrak{D}_t) + \mathbf{vec}(\mathfrak{M}_t) + \mathbf{vec}(\mathfrak{S}_t) = \mathbf{Q}$.

From equations S13 , we can rewrite $\mathbf{Q} = (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{V}(\tilde{\mathbf{n}}_t) + (\mathbf{M}_t \otimes \mathbf{M}_t) (\mathbf{n}_t \otimes \mathbf{n}_t) - (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{J}_d \mathbf{n}_t + \mathbf{vec}(\mathfrak{D}_t) + \mathbf{vec}(\mathfrak{M}_t) + \mathbf{vec}(\mathfrak{S}_t) = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) - \mathbf{V}(\tilde{\mathbf{M}}_t) \mathbf{n}_t + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{J}_d \mathbf{n}_t + \mathbf{vec}(\mathfrak{D}_t) + \mathbf{vec}(\mathfrak{M}_t) + \mathbf{vec}(\mathfrak{S}_t)$ From eq. S19, this becomes $\mathbf{Q} = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) - (\mathbf{V}_t + \mathbf{J}_d \mathbf{S}_t - (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d + \mathbf{C}_t + \mathbf{J}_e \mathbf{C}_t) \mathbf{n}_t + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{J}_d \mathbf{n}_t + \mathbf{vec}(\mathfrak{D}_t) + \mathbf{vec}(\mathfrak{M}_t) + \mathbf{vec}(\mathfrak{S}_t)$. From equations S54 and S58, we obtain $\mathbf{Q} = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) - (\mathbf{V}_t + \mathbf{J}_d \mathbf{S}_t - (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d + \mathbf{C}_t + \mathbf{J}_e \mathbf{C}_t) \mathbf{n}_t + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{J}_d \mathbf{n}_t + (\mathbf{C}_t + (\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J}_d) \mathbf{n}_t + (\mathbf{J}_e \mathbf{C}_t + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d) \mathbf{n}_t + (\mathbf{V}_t + (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t) \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) + (-\mathbf{V}_t - \mathbf{J}_d \mathbf{S}_t + (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d - \mathbf{C}_t - \mathbf{J}_e \mathbf{C}_t - (\mathbf{J}_e \mathbf{C}_t + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d) \mathbf{n}_t + (\mathbf{V}_t + (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t) \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) + (-\mathbf{J}_d \mathbf{S}_t + (\mathbf{S}_t \otimes \mathbf{S}_t) \mathbf{J}_d - (\mathbf{M}_t \otimes \mathbf{M}_t) \mathbf{J}_d + (\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J}_d + (\mathbf{F}_t \otimes \mathbf{S}_t) \mathbf{J}_d + (\mathbf{F}_t \otimes \mathbf{F}_t) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}_t) \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) + (-\mathbf{J}_d \mathbf{S}_t - \mathbf{J}_d \mathbf{F}_t) \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - \mathbf{J}_d (\mathbf{S}_t + \mathbf{F}_t) \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - \mathbf{J}_d (\mathbf{M}_t \mathbf{n}_t = \mathbf{V}(\tilde{\mathbf{n}}_{t+1}) + (\mathbf{n}_{t+1} \otimes \mathbf{n}_{t+1}) - \mathbf{J}_d \mathbf{n}_{t+1}$, which completes the proof by induction.

S7.3 infinite kinship matrices

we consider $\mathbb{K}_t^\infty$ and $\mathbb{K}_t^{(p)\infty}$, matrices of infinite size, that encompass all kin (whatever g) in the population at time t . We further consider that, for a given realisation of the kinship network all pairs are kin pairs (be

it at a great distance): $\sum_{a,b} \tilde{\mathbb{K}}_t^{(p)\infty}[a,b](i,j) = n_t(j)(n_t(i) - \delta(i,j))$ and $\sum_{a,b} \tilde{\mathbb{K}}_t^\infty[a,b](i,j) = n_t(i) - \delta(i,j)$.

$$\begin{cases} \sum_{a,b} \tilde{\mathbb{K}}_t^{(p)\infty}[a,b](i,j) = \tilde{n}_t(j)(\tilde{n}_t(i) - \delta(i,j)) \\ \sum_{a,b} \tilde{\mathbb{K}}_t^\infty[a,b](i,j) = \tilde{n}_t(i) - \delta(i,j) \end{cases} \quad (\text{S63})$$

We note that this leads to $\sum_{a,b,i,j} \tilde{\mathbb{K}}_t^{(p)\infty}[a,b](i,j) = \sum_{i,j} \tilde{n}_t(j)(\tilde{n}_t(i) - \delta(i,j)) = \sum_{i,j} \tilde{n}_t(j)\tilde{n}_t(i) - \sum_{i,j} \tilde{n}_t(j)\delta(i,j) = (\tilde{n}_t)^2 - \sum_j \tilde{n}_t(j) \sum_i \delta(i,j) = (\tilde{n}_t)^2 - \sum_j \tilde{n}_t(j) = (\tilde{n}_t)^2 - \tilde{n}_t$ which indeed represents all directional pairs in a population of size $\tilde{n}_t$. Similarly, $\sum_{a,b,i,j} \tilde{\mathbb{K}}_t^\infty[a,b](i,j) = \sum_{i,j} \tilde{n}_t(i) - \delta(i,j) = \sum_i \tilde{n}_t(i) - 1 = \tilde{n}_t - 1$.

$$\begin{cases} \sum_{a,b,i,j} \tilde{\mathbb{K}}_t^{(p)\infty}[a,b](i,j) = \tilde{n}_t(\tilde{n}_t - 1) \\ \sum_{a,b,i,j} \tilde{\mathbb{K}}_t^\infty[a,b](i,j) = \tilde{n}_t - 1 \end{cases} \quad (\text{S64})$$

S8 Simple stochastic illustration

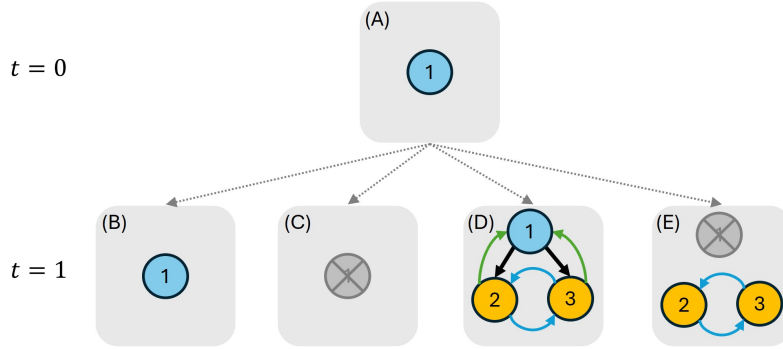


Figure S2: In a model with $s = 2$ states (juveniles, in orange, and adults, in blue), where adults produce either 0 or 2 offspring, a population of 1 adult (top row) at time $t = 0$ can produce 4 different realisations of the kinship structure at time $t = 1$ (bottom row). Directional pairs are denoted by arrows (mother-daughter in black, daughter-mother in green and sister-sister in blue).

Consider a population structured by $s = 2$ states, juveniles (state 1) and adults (state 2), where, at time $t = 0$, adults survive with a probability $S_0(2, 2) = 0.5$ and all juveniles become adult ($S_0(2, 1) = 1$). Adults either produce, with equal probabilities, 0 offspring or 2 offspring, so that, the expectation of fertility is $F_0(1, 2) = 1$ and its variance $V_0(1, 2) = \frac{1}{2}0^2 + \frac{1}{2}2^2 - F_0(1, 2)^2 = 1$. We consider that survival and reproduction are independent. This yields the following demographic inputs:

$$\mathbf{S}_0 = \begin{bmatrix} 0 & 0 \\ 1 & 0.5 \end{bmatrix}, \quad \mathbf{F}_0 = \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}, \quad \mathbf{V}_0 = \begin{bmatrix} 0 & 1 \\ 0 & 0 \\ 0 & 0 \end{bmatrix} \text{ and } \mathbf{C}_0 = \mathbf{0} \quad (\text{a})$$

We consider that at time $t = 0$ the population corresponds to realisation (A) of Figure S2 (top row) with one adult individual only: $\mathbf{n}_0 = \mathbf{n}^{(A)} = \begin{bmatrix} 0 \\ 1 \end{bmatrix}$ and therefore $\mathbb{K}_0 = \mathbb{K}^{(A)} = \mathbb{K}_0^{(p)} = \mathbb{K}^{(p)(A)} = \mathbf{0}$: there is no pair in this population, therefore there is no kin-pair.

From the demographic process described above, there are four possible realisation of the stochastic

process at time $t = 1$:

- (B) the individual survives and does not reproduce: $\mathbf{n}^{(B)} = \begin{bmatrix} 0 \\ 1 \end{bmatrix}$,
- (C) the individual dies and does not reproduce: $\mathbf{n}^{(C)} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$,
- (D) the individual survives and reproduces: $\mathbf{n}^{(D)} = \begin{bmatrix} 2 \\ 1 \end{bmatrix}$ and
- (E) the individual dies and reproduces: $\mathbf{n}^{(E)} = \begin{bmatrix} 2 \\ 0 \end{bmatrix}$, and each of these realisations has the same probability to occur $p_B = p_C = p_D = p_E = 0.25$ to occur.

Similarly we can count the number of kin pairs (PKM) in each realisations, there are none in (B) and (C). In realisations (D) and (E) there are respectively 3 and 2 individuals, all related to one another; there are therefore, respectively, $3 \times 2 = 6$ and $2 \times 1 = 2$ directional kin pairs: organised, in the 2-kinship network, as

$$\mathbb{K}^{(p)(B)} = \mathbf{0} \quad , \quad \mathbb{K}^{(p)(C)} = \mathbf{0} \quad , \quad \mathbb{K}^{(p)(D)} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 2 & 0 \\ 0 & 2 & 2 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \text{and} \quad \mathbb{K}^{(p)(E)} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 2 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

where the [2,2]-kin (sisters) are denoted in blue, the [2,1]-kin (mother) in black and the [1,2]-kin (daughters) in green as per the colours of Fig. S2.

We can also count the number of kin of *ego* (IKM) for each realisation (or deduce directly, for each realisation (H), $\mathbb{K}^{(H)}$ from $\mathbb{K}^{(p)(H)}$ and $\mathbf{n}^{(H)}$ via equation 3). There is no individual in (C) , therefore no *ego*, and for the other realisations we get:

$$\mathbb{K}^{(B)} = \mathbf{0} \quad , \quad \mathbb{K}^{(D)} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 2 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \text{and} \quad \mathbb{K}^{(E)} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$\mathbb{K}^{(D)}$ informs us that, in realisation (D), and as per Fig. S2, a juvenile always has its mother alive (as an adult) and one sister (as a juvenile) and that an adult has 2 daughters.

To generate the expected abundances and the population Kinship Matrix from these realisations, one takes the average quantities weighted by the probability of the realisations of the stochastic process (B to E). Because the Individual Kinship Matrix is an individual metric, its computation from the various realisations is different: one can either use eq. 3 or consider directly the various realisations weighted by the number of individuals as per equation S33. Overall, this is:

$$\begin{cases} \mathbf{n}_1 = p_B \mathbf{n}^{(B)} + p_C \mathbf{n}^{(C)} + p_D \mathbf{n}^{(D)} + p_E \mathbf{n}^{(E)} = \begin{bmatrix} 1 \\ 0.5 \end{bmatrix} \\ \mathbb{K}_1^{(p)} = p_B \mathbb{K}^{(p)(B)} + p_C \mathbb{K}^{(p)(C)} + p_D \mathbb{K}^{(p)(D)} + p_E \mathbb{K}^{(p)(E)} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0 \\ 0 & 0.5 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \\ \mathbb{K}_1 = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \end{cases} \quad (b)$$

We can verify that all conditions (eq.22 or eq.S34) are respected and in particular here, in this population where all pairs are kin pairs, $\sum_{a,b} \mathbb{K}_1^{(p)}[a,b] = \begin{bmatrix} 1 & 0.5 \\ 0.5 & 0 \end{bmatrix} = \mathbf{P}_1$ (see SI. S3), noting that $\mathbf{P}_1 \neq \mathbf{n}_1 \mathbf{n}_1^T - \mathbf{D}_{\mathbf{n}_1}$.

In practice, one does not compute the expectations of abundances by browsing through all possible realisations (i.e., via simulations) as per equation b1, but via the population projection equation (eq.1):

$$\mathbf{n}_1 = (\mathbf{S}_0 + \mathbf{F}_0) \mathbf{n}_0 = \begin{bmatrix} 0 & 1 \\ 1 & 0.5 \end{bmatrix} \begin{bmatrix} 0 \\ 1 \end{bmatrix} = \begin{bmatrix} 1 \\ 0.5 \end{bmatrix} \quad (\text{d})$$

kinship projection equation for the simple stochastic illustration

The kinship projection equation of this manuscript provides a similar way to compute $\mathbb{K}_1$ and $\mathbb{K}_1^{(p)}$ without having to consider the full range of possible realisations of the stochastic process (equations b2 and b3). In that population, the demography at time $t = 0$ is given by eq.a and the initial conditions given by $\mathbf{k}_0 = \mathbf{0}$ (no kin-pair in the population) and $\mathbf{n}_0 = \begin{bmatrix} 0 \\ 1 \end{bmatrix}$. We consider $g = 2$ (we limit ourselves to mothers, daughters and sisters).

From $\mathbf{S}_0$ and $\mathbf{F}_0$ (eq.a), we can produce $\mathbf{M}_0 = \begin{bmatrix} 0 & 1 \\ 1 & 0.5 \end{bmatrix}$ and $\mathbb{M}_0 = \begin{bmatrix} \mathbf{S}_0 & \mathbf{0} \\ \mathbf{F}_0 & \mathbf{S}_0 \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 1 & 0.5 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0.5 \end{bmatrix}$. Accounting further for $\mathbf{V}_0$ and $\mathbf{C}_0$ (eq.a), we obtain $\mathbb{N}_0$, which is equal to zero everywhere but for $\mathbb{N}(7,2) = 0.5, \mathbb{N}(10,2) = 0.5, \mathbb{N}(11,2) = 1$. Put together as $\mathcal{M}_0 = \begin{bmatrix} \mathbb{M}_0 \otimes \mathbb{M}_0 & \mathbb{N}_0 \\ \mathbf{0} & \mathbf{M}_0 \end{bmatrix}$ a matrix of dimension 18×18 , this allows to obtain $\begin{bmatrix} \mathbf{k}_1 \\ \mathbf{n}_1 \end{bmatrix} = \mathcal{M}_0 \begin{bmatrix} \mathbf{k}_0 \\ \mathbf{n}_0 \end{bmatrix}$. This yields $(\mathbf{n}_1 = \begin{bmatrix} 1 \\ 0.5 \end{bmatrix})$ as per eq.b1), and $\mathbb{K}_1^{(p)} = \mathbf{v} \mathbf{e} \mathbf{c}^{-1}(\mathbf{k}_1) = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0 \\ 0 & 0.5 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$ as per eq.b2.

From eq.4, this generates directly the (individual) kinship matrix of equation eq.b3 and from eq.23 we obtain the unstructured kinship matrix at $t = 1$: $\mathbb{K}_1^{(u)} = \begin{bmatrix} 0 & \frac{1}{3} \\ \frac{1}{3} & \frac{2}{3} \end{bmatrix}$, which says that an individual at random in the population has a probability $p_1 = \frac{1}{3}$ to have its mother alive, and is expected to have $p_2 = \frac{1}{3}$ daughters and $p_3 = \frac{2}{3}$ sisters. Indeed, when considering the $t = 1$ populations of figure S2, where realisations (B)-(E) have the same probabilities therefore all 6 individuals the same probability to exist, we see that one individual only has daughters, and has 2 of them therefore $p_2 = \frac{1}{6} \times 2 = \frac{1}{3}$, that two individuals have a mother; $p_1 = \frac{2}{6} \times 1 = \frac{1}{3}$ and four individuals have one sister: $p_3 = \frac{4}{6} \times 1 = \frac{2}{3}$. In SI S12, we provide the code (R) implementing the kinship projection equation for any one-sex projection model.

S9 Supplementary information for results and extensions

S9.1 Non-contemporary kin derivations

While the main focus of kinship demography is to consider how many kin an individual has at a given time, the approach developed in this paper also allows one to consider the number of non-contemporary kin. We denote $\mathbb{K}_{t,t_e}$, the expected number of kin alive at time t for *ego* alive at time t_e . $\mathbb{K}_{t,t_e}$ has same dimension that $\mathbb{K}_t$ and is structured by kin categories and the state of the kin (at t) and of *ego* (at t_e); we have $\mathbb{K}_{t_e,t_e} = \mathbb{K}_{t_e}$. We also consider the population equivalent of this metric, that we denote

$\mathbb{K}_{t,t_e}^{(p)} = \mathbb{K}_{t,t_e} \mathbb{D}_{\mathbf{n}_{t_e}}$ and which counts the number of kin-pairs across times t and t_e .

S9.1.1 kin in the future If $t \geq t_e$ (we consider the future kin of *ego*): $\mathbb{K}_{t,t_e}[a,b](i,j)$ is the expected number of $[a,b]$ -kin in state i that *ego*, alive and in state j at time t_e , is expected to have at future time $t \geq t_e$. The "descendants" at time t (via survival and reproduction) of the kinship-network of *ego* at time t_e correspond to $\mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} \mathbb{K}_{t_e}$. We also need to account for the "descendants" of *ego* itself (which is not part of its kinship network, condition (a)) counted in $\mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} \mathbb{J}$ where $\mathbb{J} = (\mathbf{e}_1^{(g)} \mathbf{e}_1^{(g)T}) \otimes \mathbf{I}_s$. Further, we need to ensure that *ego* itself is not accounted: the probability that it is still alive at t appears in $\mathbb{S}_{t-1} \dots \mathbb{S}_{t_e+1} \mathbb{S}_{t_e} \mathbb{J}$. Overall, we have therefore

$$\text{for } t_e \leq t, \quad \mathbb{K}_{t,t_e} = \mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} (\mathbb{K}_{t_e} + \mathbb{J}) - \mathbb{S}_{t-1} \dots \mathbb{S}_{t_e+1} \mathbb{S}_{t_e} \mathbb{J} \quad (\text{S65})$$

We now consider the population equivalent of this metric:

$$\text{for } t_e \leq t, \quad \mathbb{K}_{t,t_e}^{(p)} = \mathbb{K}_{t,t_e} \mathbb{D}_{\mathbf{n}_{t_e}} = \mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} (\mathbb{K}_{t_e}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) - \mathbb{S}_{t-1} \dots \mathbb{S}_{t_e+1} \mathbb{S}_{t_e} \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}} \quad (\text{S66})$$

If $t = t_e$, this is, simply, $\mathbb{K}_{t_e,t_e}^{(p)} = (\mathbb{K}_{t_e}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) - \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}} = \mathbb{K}_{t_e}^{(p)}$. We note that $(\mathbb{K}_{t_e} + \mathbb{J})$ is the (individual) kinship network of *ego* that counts *ego* as a kin of *ego* (see below).

S9.1.2 kin in the past We use the same notation, $\mathbb{K}_{t,t_e}$, for the case $t_e \geq t$, where it then designates the number of kin of *ego* (alive at time t_e) that were alive at a past time-step, t . The corresponding number of kin-pairs, $\mathbb{K}_{t,t_e}^p$, correspond to the same kin-pairs than in $\mathbb{K}_{t_e,t}^p$ but considered from the opposite direction: '

$$\text{for } t_e \geq t, \quad (\mathbb{K}_{t,t_e}^{(p)})^T = \mathbb{K}_{t_e,t}^{(p)} \quad (\text{S67})$$

S9.1.3 in the general case , we have therefore

$$\left\{ \begin{array}{l} \mathbb{K}_{t,t_e} = \mathbb{K}_{t,t_e}^{(p)} \mathbb{D}_{\mathbf{n}_{t_e}}^{-1} \quad \text{with} \\ \text{for } t_e \leq t, \quad \mathbb{K}_{t,t_e}^{(p)} = \mathbb{K}_{t,t_e} \mathbb{D}_{\mathbf{n}_{t_e}} = \mathbb{M}_{t-1} \dots \mathbb{M}_{t_e+1} \mathbb{M}_{t_e} (\mathbb{K}_{t_e}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) - \mathbb{S}_{t-1} \dots \mathbb{S}_{t_e+1} \mathbb{S}_{t_e} \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}} \\ \text{for } t_e \geq t, \quad \mathbb{K}_{t,t_e}^{(p)} = (\mathbb{K}_{t_e,t}^{(p)})^T \end{array} \right. \quad (\text{S68})$$

S9.1.4 constant environment in a constant environment, calling $\Delta t = t - t_e$, this is simply, for $\Delta t \geq 0$, $\mathbb{K}_{\Delta t}^{(p)} = \mathbb{M}^{\Delta t} (\mathbb{K}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) - \mathbb{S}^{\Delta t} \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}$ and for $\Delta t \leq 0$, $\mathbb{K}_{\Delta t}^{(p)} = (\mathbb{K}_{-\Delta t}^{(p)})^T = (\mathbb{K}^{(p)} + \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}}) (\mathbb{M}^T)^{-\Delta t} - \mathbb{J} \mathbb{D}_{\mathbf{n}_{t_e}} (\mathbb{S}^T)^{-\Delta t}$, which yield, for individual kinship, rather simple formulas:

$$\left\{ \begin{array}{l} \text{for } \Delta t \geq 0, \quad \mathbb{K}_{\Delta t} = \mathbb{M}^{\Delta t} (\mathbb{K} + \mathbb{J}) - \mathbb{S}^{\Delta t} \mathbb{J} \\ \text{for } \Delta t \leq 0, \quad \mathbb{K}_{\Delta t} = \mathbb{D}_{\mathbf{w}} ((\mathbb{K}^T + \mathbb{J}) \mathbb{M}^{T-\Delta t} - \mathbb{J} \mathbb{S}^{T-\Delta t}) \mathbb{D}_{\mathbf{w}}^{-1} \end{array} \right. \quad (\text{S69})$$

The second equation comes from for $\Delta t \leq 0$, $\mathbb{K}_{\Delta t} = \mathbb{K}_{\Delta t}^{(p)} \mathbb{D}_{\mathbf{n}_{t_e}}^{-1} = (\mathbb{K}_{-\Delta t}^{(p)})^T \mathbb{D}_{\mathbf{n}_{t_e}}^{-1} = (\mathbb{K}_{-\Delta t} \mathbb{D}_{\mathbf{n}_{t_e}})^T \mathbb{D}_{\mathbf{n}_{t_e}}^{-1} = (\mathbb{K}_{-\Delta t} \mathbb{D}_{\mathbf{w}})^T \mathbb{D}_{\mathbf{w}}^{-1} = \mathbb{D}_{\mathbf{w}} (\mathbb{K}_{-\Delta t})^T \mathbb{D}_{\mathbf{w}}^{-1} = \mathbb{D}_{\mathbf{w}} (\mathbb{M}^{-\Delta t} (\mathbb{K} + \mathbb{J}) - \mathbb{S}^{-\Delta t} \mathbb{J})^T \mathbb{D}_{\mathbf{w}}^{-1} = \mathbb{D}_{\mathbf{w}} ((\mathbb{K}^T + \mathbb{J}) \mathbb{M}^{T-\Delta t} - \mathbb{J} \mathbb{S}^{T-\Delta t}) \mathbb{D}_{\mathbf{w}}^{-1}$

Kinship matrices where *ego* is a kin of *ego* We mark with an asterisk (*), an alternative version of the kinship matrices that count *ego* within the kinship network: $\mathbb{K}_t^* = \mathbb{K}_t + \mathbb{J}$ and therefore $\mathbb{K}_t^{(p)*} = \mathbb{K}_t^{(p)} + \mathbb{J} \mathbb{D}_n$

$$\begin{cases} \mathbb{K}_t^* = \mathbb{K}_t + \mathbb{J} \\ \mathbb{K}_t^{(p)*} = \mathbb{K}_t^{(p)} + \mathbb{J} \mathbb{D}_n \end{cases} \quad (\text{S70})$$

S9.2 Periodic environments: algebraic derivations

Let us now consider that the environment is periodic, that is, that is constant at the level of a certain time-step, itself split into various "seasons" corresponding to different demographic rates. Let's us consider 3 seasons $i = a, b$ or c , occurring in that order within a year, where for season i , the demography is given by $\mathbf{M}_i = \mathbf{F}_i + \mathbf{S}_i$. If one considers that the year starts before season a , one can project the population vector over a year via $\mathbf{A} = \mathbf{M}_c \mathbf{M}_b \mathbf{M}_a$, which is constant. From the eigen-analysis of $\mathbf{A}$, one obtains its asymptotic vector of relative abundances $\hat{\mathbf{w}}_A$ as the right-eigenvector associated to its maximum eigenvalue λ . From $\mathcal{M}_a, \mathcal{M}_b$ and $\mathcal{M}_c$ (equation 10), one can construct $\mathcal{M}_A = \mathcal{M}_c \mathcal{M}_b \mathcal{M}_a$ which allows to compute, from $\hat{\mathbf{w}}_A$ the asymptotic kinship vector $\hat{\mathbf{k}}_A^w$ as (eqs. 10 and S76):

$$\lambda \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix} = \mathcal{M}_A \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix} = \mathcal{M}_c \mathcal{M}_b \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix} \quad (\text{S71})$$

Consider now that the year starts before season b ; the annual projection matrix of abundances becomes $\mathbf{B} = \mathbf{M}_a \mathbf{M}_c \mathbf{M}_b$ and that of kinship $\mathcal{M}_B = \mathcal{M}_a \mathcal{M}_c \mathcal{M}_b$. We get

$$\mathcal{M}_B \left(\mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix} \right) = \mathcal{M}_a \left(\mathcal{M}_c \mathcal{M}_b \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix} \right) = \lambda \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix}$$

Therefore λ is also the maximum value of $\mathcal{M}_B$ (and $\mathbf{B}$) and its related right-eigen vector is

$$\begin{bmatrix} \hat{\mathbf{k}}_B^{(w)} \\ \hat{\mathbf{w}}_B \end{bmatrix} = \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix}$$

This implies that at the (kinship and demographic) stable state, the (individual) kinship vector is also periodic and can obtained via $\begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix}, \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix}$ and $\mathcal{M}_b \mathcal{M}_a \begin{bmatrix} \hat{\mathbf{k}}_A^{(w)} \\ \hat{\mathbf{w}}_A \end{bmatrix}$.

This allows to relax the assumption of independence of survival and reproduction in the case of pre-, post-breeding models. In such "pulse-breeding" projection models the "annual" projection either considers that reproduction (via $\mathbf{F}^*$) occurs first, followed by survival (pre-breeding) $\mathbf{M}_{pre} = \mathbf{S}(\mathbf{I} + \mathbf{F}^*) = \mathbf{S} + \mathbf{S}\mathbf{F}^* = \mathbf{S} + \mathbf{F}_{pre}$, with $\mathbf{F}_{pre} = \mathbf{S}\mathbf{F}^*$ or that survival occurs first (post-breeding): $\mathbf{M}_{post} = (\mathbf{I} + \mathbf{F}^*)\mathbf{S} = \mathbf{S} + \mathbf{F}^*\mathbf{S} = \mathbf{S} + \mathbf{F}_{post}$, with $\mathbf{F}_{post} = \mathbf{F}^*\mathbf{S}$. In both cases, at the annual level, reproduction ($\mathbf{F}_{pre}$ or $\mathbf{F}_{post}$) is a function

of survival and therefore these are not independent. Still one can compute the kinship of this population by considering equation 10 for each of the two seasons. At that level reproduction and survival are independent (as each season considers one of the two processes).

S9.3 Particular reproductive cases

For the vast majority of projection models in the literature, survival and reproduction are considered independent (for all t , $\mathbf{C}_t = \mathbf{0}$), and reproduction follows either Bernoulli (no more than one offspring produced per time-step) or Poisson (each $\tilde{F}_t(i, j)$ is a Poisson independent from the other reproductive rate) process. Then, $\mathbb{N}_t$ simplifies to, from eq.8 and SI S2.3:

$$\begin{cases} \text{Bernoulli:} & \mathbb{N}_t = (\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t)) \mathbf{J} \\ \text{Poisson:} & \mathbb{N}_t = (\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) + \mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t) + \mathbf{J}_{2,2}(\mathbf{F}_t \otimes \mathbf{F}_t)) \mathbf{J} \end{cases} \quad (\text{S72})$$

S9.4 Unstructured kinship

We call $\mathbb{K}_t^{(u)}$, the unstructured kinship matrix, of size $g \times g$, where $\mathbb{K}_t^{(u)}(a, b)$ is the expected number of $[a, b]$ -kin of an individual taken at random in the population. We define $\mathbf{k}_t^{(u)} = \text{vec}(\mathbb{K}_t^{(u)})$ and $n_t = \mathbf{1}^T \mathbf{n}_t$ the total population abundance at time t . The probability that an individual at random in the population at time t is in state j is $\frac{n_t(j)}{n_t}$. Then $\mathbb{K}_t^{(u)}(a, b) = \sum_{i,j} \mathbb{K}_t[a, b](i, j) \frac{n_t(j)}{n_t} = \frac{1}{n_t} \sum_{i,j} \mathbb{K}_t^{(p)}[a, b](i, j)$, therefore

$$\mathbb{K}_t^{(u)} = \frac{1}{n_t} \mathbb{J}_y \mathbb{K}_t^{(p)} \mathbb{J}_y^T \quad \text{or, equivalently,} \quad \mathbf{k}_t^{(u)} = \frac{1}{n_t} (\mathbb{J}_y \otimes \mathbb{J}_y) \mathbf{k}_t \quad (23)$$

with $\mathbb{J}_y = (\mathbf{I}_g \otimes \mathbf{1}_s^T)$ and $\mathbf{1}_s$ the vector (of size s) of ones. From the structured or unstructured kinship, one can obtain further obtain measures of relatedness, and inclusive fitness by computing the number of kin at a certain genealogical distance and weighting these number by the relatedness distance as per (Coste, 2025a).

S10 Computational steps for section Asymptotic and Transient dynamics of kinship networks

If one lets the environment fluctuate for, say, $t \leq 0$, but force it to be constant for $t \geq 0$ (that is $\forall t \geq 0, \mathbf{F}_t = \mathbf{F}$ and $\mathbf{S}_t = \mathbf{S}$), then the theory of population projection matrices (Caswell, 2001) applied to eq.1, tells us that

$$\text{as } t \rightarrow \infty \quad \frac{\mathbf{n}_t}{n_t} \rightarrow \hat{\mathbf{w}}, \quad \frac{n_{t+1}}{n_t} \rightarrow \hat{\lambda} \quad \text{and} \quad \frac{\mathbf{n}_t}{\hat{\lambda}^t} \rightarrow (\hat{\mathbf{v}}^T \mathbf{n}_0) \hat{\mathbf{w}}, \quad (\text{S73})$$

where $\hat{\lambda} = \rho(\mathbf{M})$ is the maximum eigenvalue of $\mathbf{M} = \mathbf{F} + \mathbf{S}$ and $\hat{\mathbf{w}}$ and $\hat{\mathbf{v}}$, its associated right and left eigenvectors (scaled so $\mathbf{1}^T \hat{\mathbf{w}} = \hat{\mathbf{v}}^T \hat{\mathbf{w}} = 1$), corresponding, respectively, to the asymptotic relative abundances and the reproductive values. We can apply the same considerations to eq.10. We first note that $\rho(\mathbf{M} \otimes \mathbf{M}) < \hat{\lambda}$ ($\lim_{t \rightarrow \infty} \mathbf{M}^t = \mathbf{0}$, therefore $\rho(\mathbf{M}) < 1$, which leads to $\rho(\mathbf{M} \otimes \mathbf{M}) = \rho(\mathbf{M})^2 < \rho(\mathbf{M}) < \rho(\mathbf{M})$),

so that it is the bottom right block of $\mathcal{M}$ that contains its maximum eigenvalue $\rho(\mathcal{M}) = \hat{\lambda}$. This implies that the left-eigenvector of $\mathcal{M}$ related to $\hat{\lambda}$ is $[\frac{\mathbf{0}}{\hat{\mathbf{v}}}]$ and that the right-eigenvector can be written as $[\frac{\hat{\mathbf{k}}^{(w)}}{\hat{\mathbf{w}}}]$. The asymptotic properties of equation 10, mirror and include those of equation 1 described in equation S73 and therefore correspond also to

$$\text{as } t \rightarrow \infty, \quad \frac{\mathbf{k}_t}{n_t} \rightarrow \hat{\mathbf{k}}^{(w)}, \quad \frac{\mathbf{1}^T \mathbf{k}_{t+1}}{\mathbf{1}^T \mathbf{k}_t} \quad \text{and} \quad \frac{\mathbf{k}_t}{\hat{\lambda}^t} \rightarrow (\hat{\mathbf{v}}^T \mathbf{n}_0) \hat{\mathbf{k}}^{(w)} \quad (\text{S74})$$

From eq.4, this implies therefore that

$$\text{as } t \rightarrow \infty, \quad \mathbb{K}_t \rightarrow \hat{\mathbb{K}} = \text{vec}^{(-1)}(\hat{\mathbf{k}}^{(w)}) \mathbb{D}_{\hat{\mathbf{w}}}^{-1} \quad (\text{S75})$$

In other words, the number of kin pairs (within a given g-kinship network) in the population increases or decreases asymptotically exponentially according to $\hat{\lambda}$ (population-level kinship), and the expected number of kin of *ego* tends toward a constant individual kinship matrix $\hat{\mathbb{K}}$ (individual-level kinship).

One can explicitly compute $\hat{\mathbb{K}}$ by first generating $\hat{\mathbf{k}}^{(w)}$, which obeys $\hat{\lambda}[\frac{\hat{\mathbf{k}}^{(w)}}{\hat{\mathbf{w}}}] = \mathcal{M}[\frac{\hat{\mathbf{k}}^{(w)}}{\hat{\mathbf{w}}}]$, that is, $\hat{\lambda} \hat{\mathbf{k}}^{(w)} = (\mathbb{M} \otimes \mathbb{M}) \hat{\mathbf{k}}^{(w)} + \mathbb{N} \hat{\mathbf{w}}$, which leads to

$$\hat{\mathbf{k}}^{(w)} = (\hat{\lambda} \mathbb{I}_{s^2 g_m^2} - (\mathbb{M} \otimes \mathbb{M}))^{-1} \mathbb{N} \hat{\mathbf{w}}, \quad (\text{S76})$$

and therefore

$$\hat{\mathbb{K}} = \text{vec}^{(-1)} \left((\hat{\lambda} \mathbb{I}_{s^2 g_m^2} - (\mathbb{M} \otimes \mathbb{M}))^{-1} \mathbb{N} \hat{\mathbf{w}} \right) \mathbb{D}_{\hat{\mathbf{w}}}^{-1} \quad (\text{S77})$$

which extends the main result of (Coste, 2025a) (eq.7) to the general case where reproduction and survival may not be independent, as we show in SI S10.4.

S10.1 dynamics of the number of kin-pairs

In general (accounting for all kin, not limiting oneself to a g-network), the number of (kin) pairs either grows as $\hat{\lambda}^2$ or decreases as $\hat{\lambda}$.

Proof: When considering all kin-pairs in the population at time t , in $\mathbf{K}_t$, structured by the states of individuals but not the kin-category, we have $\mathbf{K}_{t+1} = \mathbf{M} \mathbf{K}_t \mathbf{M}^T + \mathfrak{D} + \mathfrak{M} + \mathfrak{S}$, which leads to $\text{vec}(\mathbf{K}_{t+1}) = (\mathbf{M} \otimes \mathbf{M}) \text{vec}(\mathbf{K}_t) + \mathbf{Q} \mathbf{n}_t$, with $\mathbf{Q}$ a constant matrix that does not need expliciting. Then

$$\begin{bmatrix} \text{vec}(\mathbf{K}_{t+1}) \\ \mathbf{n}_{t+1} \end{bmatrix} = \begin{bmatrix} \mathbf{M} \otimes \mathbf{M} & \mathbf{Q} \\ \mathbf{0} & \mathbf{M} \end{bmatrix} \begin{bmatrix} \text{vec}(\mathbf{K}_t) \\ \mathbf{n}_t \end{bmatrix}$$

the dominant eigenvalue of this matrix, which drives the asymptotic dynamic of $\mathbf{K}_t$, is $\rho \left(\begin{bmatrix} \mathbf{M} \otimes \mathbf{M} & \mathbf{Q} \\ \mathbf{0} & \mathbf{M} \end{bmatrix} \right) = \max(\rho(\mathbf{M}), \rho(\mathbf{M} \otimes \mathbf{M})) = \max(\rho(\mathbf{M}), \rho(\mathbf{M})^2) = \max(\hat{\lambda}, \hat{\lambda}^2)$

S10.2 kinship transient

Consider, in the general case of structured populations, that one is at the *demographic stable state* $\frac{\mathbf{n}_0}{n_0} = \hat{\mathbf{w}}$, but not at the *kinship stable state* $\frac{\mathbf{k}_0}{n_0} \neq \hat{\mathbf{k}}^{(w)}$ then, from equation 10, we have

$$\begin{aligned} \frac{\mathbf{k}_{t+1}}{n_{t+1}} &= \frac{1}{n_{t+1}} ((\mathbb{M} \otimes \mathbb{M})\mathbf{k}_t + \mathbb{N}(n_t \hat{\mathbf{w}})) = \frac{1}{n_{t+1}} ((\mathbb{M} \otimes \mathbb{M})\mathbf{k}_t + n_t (\hat{\lambda} \mathbf{I} - \mathbb{M} \otimes \mathbb{M}) \hat{\mathbf{k}}^{(w)}) \\ &= \frac{1}{n_{t+1}} ((\mathbb{M} \otimes \mathbb{M})(\mathbf{k}_t - n_t \hat{\mathbf{k}}^{(w)}) + n_t \hat{\lambda} \hat{\mathbf{k}}^{(w)}) = \frac{n_t}{n_{t+1}} \left((\mathbb{M} \otimes \mathbb{M}) \left(\frac{\mathbf{k}_t}{n_t} - \hat{\mathbf{k}}^{(w)} \right) + \hat{\lambda} \hat{\mathbf{k}}^{(w)} \right) \\ &= \left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \left(\frac{\mathbf{k}_t}{n_t} - \hat{\mathbf{k}}^{(w)} \right) + \hat{\mathbf{k}}^{(w)} \right) \end{aligned}$$

Therefore $\frac{\mathbf{k}_{t+1}}{n_{t+1}} - \hat{\mathbf{k}}^{(w)} = \frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \left(\frac{\mathbf{k}_t}{n_t} - \hat{\mathbf{k}}^{(w)} \right)$ which leads to

$$\frac{\mathbf{k}_t}{n_t} - \hat{\mathbf{k}}^{(w)} = \left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^t \left(\frac{\mathbf{k}_0}{n_0} - \hat{\mathbf{k}}^{(w)} \right), \quad (21b)$$

which converges towards $\mathbf{0}$, as $\lim_{t \rightarrow \infty} \left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^t = \mathbf{0}$. Indeed, we saw that $\rho(\mathbb{M}) < 1$ and $\rho(\mathbb{M}) < \rho(\mathbf{M})$, therefore $\rho(\mathbb{M} \otimes \mathbb{M}) = \rho(\mathbf{M})\rho(\mathbf{M}) < 1 \times \rho(\mathbf{M}) = \hat{\lambda}$, therefore $\rho\left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}}\right) < 1$.

When age is a trait of the model, there exists a maximum age ω for individuals in the population. Then

$$\left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^{g\omega} = \mathbf{0} \quad (S78)$$

Indeed $\left(\frac{\mathbb{M} \otimes \mathbb{M}}{\hat{\lambda}} \right)^{g\omega} = \frac{1}{\hat{\lambda}^{2g\omega}} (\mathbb{M}^{g\omega} \otimes \mathbb{M}^{g\omega}) = \mathbf{0}$ as $\mathbb{M}^{g\omega} = \mathbf{0}$.

Proof: we have $\mathbb{S}^\omega = (\mathbf{I} \otimes \mathbf{S})^\omega = (\mathbf{I}^\omega \otimes \mathbf{S}^\omega) = (\mathbf{I} \otimes \mathbf{0}) = \mathbf{0}$, $\mathbb{F}^g = (\mathbf{J}_1 \otimes \mathbf{F})^g = (\mathbf{J}_1^g \otimes \mathbf{F}^g) = (\mathbf{0} \otimes \mathbf{F}^g) = \mathbf{0}$ and, more generally

$$\begin{aligned} \mathbb{M}^{g\omega} &= (\mathbf{I} \otimes \mathbf{S} + \mathbf{J}_1 \otimes \mathbf{F})^{g\omega} = \sum_{\alpha \in [0,1]^{g\omega}} (\mathbf{I} \otimes \mathbf{S})^{a(1)} (\mathbf{J}_1 \otimes \mathbf{F})^{1-a(1)} (\mathbf{I} \otimes \mathbf{S})^{a(2)} (\mathbf{J}_1 \otimes \mathbf{F})^{1-a(2)} \dots (\mathbf{I} \otimes \mathbf{S})^{a(g\omega)} (\mathbf{J}_1 \otimes \mathbf{F})^{1-a(g\omega)} \\ &= \sum_{\alpha \in [0,1]^{g\omega}} [(\mathbf{I}^{a(1)} \mathbf{J}_1^{1-a(1)} \mathbf{I}^{a(2)} \mathbf{J}_1^{1-a(2)} \dots \mathbf{I}^{a(g\omega)} \mathbf{J}_1^{1-a(g\omega)}) \otimes (\mathbf{S}^{a(1)} \mathbf{F}^{1-a(1)} \mathbf{S}^{a(2)} \mathbf{F}^{1-a(2)} \dots \mathbf{S}^{a(g\omega)} \mathbf{F}^{1-a(g\omega)})] = \sum_{\alpha \in [0,1]^{g\omega}} \mathbf{B}_\alpha \end{aligned}$$

with $\mathbf{B}_\alpha = (\mathbf{J}_1^{g\omega - \sum a(k)}) \otimes (\mathbf{S}^{a(1)} \mathbf{F}^{1-a(1)} \mathbf{S}^{a(2)} \mathbf{F}^{1-a(2)} \dots \mathbf{S}^{a(g\omega)} \mathbf{F}^{1-a(g\omega)})$.

If $g\omega - \sum a(k) \geq g$, $\mathbf{J}_1^{g\omega - \sum a(k)} = \mathbf{0}$, and therefore $\mathbf{B}_\alpha = \mathbf{0}$.

If $g\omega - \sum a(k) < g$, $\mathbf{S}^{a(1)} \mathbf{F}^{1-a(1)} \mathbf{S}^{a(2)} \mathbf{F}^{1-a(2)} \dots \mathbf{S}^{a(g\omega)} \mathbf{F}^{1-a(g\omega)}$ corresponds to R times matrix $\mathbf{F}$, with $R < g$, each preceded by $\mathbf{S}^{\alpha_r}$ with $\sum_{1 \leq r \leq R} \alpha_r = g\omega - R$. If $\forall r, \alpha_r \leq \omega - 1$, then $\sum_{1 \leq r \leq R} \alpha_r \leq R(\omega - 1)$, that is $g\omega - R \leq R(\omega - 1)$ or $g \leq R$ which contradicts the above. Therefore $\exists r, \alpha_r \geq \omega$, for which $\mathbf{S}^{\alpha_r} = \mathbf{0}$, and therefore $\mathbf{B}_\alpha = \mathbf{0}$.

Therefore $\forall \alpha \in [0,1]^{g\omega}$, $\mathbf{B}_\alpha = \mathbf{0}$ which leads to $\mathbb{M}^{g\omega} = \mathbf{0}$, which completes the proof and implies that, for models with maximum age ω :

$$\text{duration of kinship transient of } g\text{-kinship network: } T = g\omega \quad (21c)$$

S10.3 Convergence of kinship and damping ratios

S10.3.1 ineffectiveness of damping ratio The speed of convergence of the g -kinship network, following a specific perturbation of the kinship network (leaving the relative abundances unchanged), can be computed numerically via equation 21b. In general, because of the nested structure of kinship, the damping ratio and other related eigenvalue tools are not suited for such an analysis. Indeed the damping ratio associated with $\frac{\mathbf{M} \otimes \mathbf{M}}{\hat{\lambda}}$ and its dominant eigenvalue $\rho\left(\frac{\mathbf{M} \otimes \mathbf{M}}{\hat{\lambda}}\right) = \frac{\rho(\mathbf{S})^2}{\rho(\mathbf{M})}$ are independent from g . The $\rho\left(\frac{\mathbf{M} \otimes \mathbf{M}}{\hat{\lambda}}\right)$ eigen-value provide the eventual speed of convergence of all kin pairs towards their equilibrium, but does not differentiate between kin categories. This is because of the block-triangular shape of this matrix (i.e. its nestedness) which can be studied via, e.g., Jordan form approaches.

S10.3.2 speed of convergence of specific kin categories For particular kin categories, the general study of the behaviour of the transient dynamics of specific kin categories towards their equilibrium, is relatively easy for very close kin. For example, as the number of daughter-mother pairs in the population at time $t + 1$, depends on the number of daughter-mother pairs at time t and no other kin pairs, its transient behaviour is relatively simple to compute:

$$\left(\mathbb{K}_t^{(p)}[2, 1] - \hat{\mathbb{K}}^{(p)}[2, 1]\right) = \left(\frac{\mathbf{S}}{\sqrt{\lambda}}\right)^t \left(\mathbb{K}_0^{(p)}[2, 1] - \hat{\mathbb{K}}^{(p)}[2, 1]\right) \left(\frac{\mathbf{S}^T}{\sqrt{\lambda}}\right)^t \quad (\text{S79})$$

This implies that, eventually, the expected number of daughters (and the probability for the mother of *ego* to be alive) reaches its equilibrium, either in finite time if there is ω , $\mathbf{S}^\omega = \mathbf{0}$ or exponentially at a negative rate equal to $\frac{\rho(\mathbf{S})^2}{\lambda}$.

Developing exact expressions for the transient of more remote kin categories for a unstructured population, shows that the speed of convergence of the number of [a,b]-kin contains a term in $c^t t^{a+b-3}$. This implies indeed that the speed of convergence of all [a,b]-kin numbers is eventually c^t but that this speed is, at first, and only when $a + b > 3$, reduced by the t^{a+b-3} term: the higher $a + b$, the longer it takes for the number of [a,b]-kin to reach their equilibrium.

proof: For an unstructured population in a constant environment, for which the kinship projection equation is:

$$\begin{bmatrix} \mathbf{k}_{t+1} \\ n_{t+1} \end{bmatrix} = \begin{bmatrix} \mathbf{M} \otimes \mathbf{M} & \mathbf{N} \\ \mathbf{0} & f+s \end{bmatrix} \begin{bmatrix} \mathbf{k}_t \\ n_t \end{bmatrix} \quad (\text{S80})$$

that is

$$\begin{cases} (f+s)\mathbb{K}_{t+1} = \mathbb{M}\mathbb{K}_t\mathbb{M}^T + \mathbb{A} \\ (f+s)\hat{\mathbb{K}} = \mathbb{M}\hat{\mathbb{K}}\mathbb{M}^T + \mathbb{A} \quad \text{with} \\ \mathbb{A} = \begin{bmatrix} 0 & sf & 0 & \dots & 0 \\ sf & z & 0 & \dots & 0 \\ 0 & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & 0 \end{bmatrix} \end{cases} \quad (\text{S81})$$

Therefore

$$\mathbb{K}_{t+1} - \hat{\mathbb{K}} = \frac{1}{f+s} \mathbb{M}(\mathbb{K}_t - \hat{\mathbb{K}})\mathbb{M}^T \quad (\text{S82})$$

We can decompose this according to the various kin categories:

$$\begin{aligned} (f+s)(\mathbb{K}_{t+1}[a,b] - \hat{\mathbb{K}}[a,b]) &= \sum_{c,d \leq g} \mathbb{M}[a,c] (\mathbb{K}_t[c,d] - \hat{\mathbb{K}}[c,d]) \mathbb{M}^T[d,b] = \sum_{c,d \leq g} \mathbb{M}[a,c] (\mathbb{K}_t[c,d] - \hat{\mathbb{K}}[c,d]) \mathbb{M}[b,d] \\ &= \mathbb{M}[a,a] (\mathbb{K}_t[a,b] - \hat{\mathbb{K}}[a,b]) \mathbb{M}[b,b] + \underbrace{\mathbb{M}[a,a] (\mathbb{K}_t[a,b-1] - \hat{\mathbb{K}}[a,b-1]) \mathbb{M}[b,b-1]}_{\text{only for } b \geq 2} \\ &+ \underbrace{\mathbb{M}[a,a-1] (\mathbb{K}_t[a-1,b] - \hat{\mathbb{K}}[a-1,b]) \mathbb{M}[b,b]}_{\text{only for } a \geq 2} + \underbrace{\mathbb{M}[a,a-1] (\mathbb{K}_t[a-1,b-1] - \hat{\mathbb{K}}[a-1,b-1]) \mathbb{M}[b,b-1]}_{\text{only for } a,b \geq 2} \\ &= s^2 (\mathbb{K}_t[a,b] - \hat{\mathbb{K}}[a,b]) + \underbrace{sf (\mathbb{K}_t[a,b-1] - \hat{\mathbb{K}}[a,b-1])}_{\text{only for } b \geq 2} + \underbrace{sf (\mathbb{K}_t[a-1,b] - \hat{\mathbb{K}}[a-1,b])}_{\text{only for } a \geq 2} \\ &\quad + \underbrace{f^2 (\mathbb{K}_t[a-1,b-1] - \hat{\mathbb{K}}[a-1,b-1])}_{\text{only for } a,b \geq 2} \quad (\text{S83}) \end{aligned}$$

simplifying notations, this is:

$$(f+s)d_{t+1}[a,b] = s^2 d_t[a,b] + sf d_t[a,b-1] + sf d_t[a-1,b] + f^2 d_t[a-1,b-1] \quad (\text{S84})$$

therefore:

$$\left\{ \begin{aligned} (f+s)d_{t+1}[2,1] &= s^2 d_t[2,1] \\ (f+s)d_{t+1}[2,2] &= s^2 d_t[2,2] + 2sf d_t[2,1] \\ (f+s)d_{t+1}[3,1] &= s^2 d_t[3,1] + sf d_t[2,1] \\ (f+s)d_{t+1}[3,2] &= s^2 d_t[3,2] + sf d_t[3,1] + sf d_t[2,2] + f^2 d_t[2,1] \\ (f+s)d_{t+1}[3,3] &= s^2 d_t[3,3] + 2sf d_t[3,2] + f^2 d_t[2,2] \\ (f+s)d_{t+1}[4,1] &= s^2 d_t[4,1] + sf d_t[3,1] \\ (f+s)d_{t+1}[4,2] &= s^2 d_t[4,2] + sf d_t[4,1] + sf d_t[3,2] + f^2 d_t[3,1] \\ (f+s)d_{t+1}[4,3] &= s^2 d_t[4,3] + sf d_t[4,2] + sf d_t[3,3] + f^2 d_t[3,2] \\ (f+s)d_{t+1}[4,4] &= s^2 d_t[4,4] + 2sf d_t[4,3] + f^2 d_t[3,3] \end{aligned} \right. \quad (\text{S85})$$

organising this as a vectorised tensor:

$$(f+s)\mathbf{d}_{t+1} = (f+s) \begin{bmatrix} d_{t+1}[2,1] \\ d_{t+1}[2,2] \\ d_{t+1}[3,1] \\ d_{t+1}[3,2] \\ d_{t+1}[3,3] \\ d_{t+1}[4,1] \\ d_{t+1}[4,2] \\ d_{t+1}[4,3] \\ d_{t+1}[4,4] \end{bmatrix} = \begin{bmatrix} s^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 2sf & s^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ sf & 0 & s^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ f^2 & sf & sf & s^2 & 0 & 0 & 0 & 0 & 0 \\ 0 & f^2 & 0 & 2sf & s^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & sf & 0 & 0 & s^2 & 0 & 0 & 0 \\ 0 & 0 & f^2 & sf & 0 & sf & s^2 & 0 & 0 \\ 0 & 0 & 0 & f^2 & sf & 0 & sf & s^2 & 0 \\ 0 & 0 & 0 & 0 & f^2 & 0 & 0 & 2sf & s^2 \end{bmatrix} \mathbf{d}_t \quad (\text{S86})$$

We get $\mathbf{d}_{t+1} = \mathbf{A}_g \mathbf{d}_t$. Considering $g = 2$, we get $\mathbf{A}_g = \mathbf{V} \mathbf{J} \mathbf{V}^{-1}$, with $\mathbf{J} = \begin{bmatrix} \frac{s^2}{f+s} & 0 \\ 1 & \frac{s^2}{f+s} \end{bmatrix}$ and $\mathbf{V} = \begin{bmatrix} \frac{2fs}{f+s} & 0 \\ 0 & 1 \end{bmatrix}$ which implies that

$$d_t[2, 1] = \left(\frac{s^2}{f+s} \right)^t d_0[2, 1]$$

and

$$d_t[2, 2] = \left(\frac{s^2}{f+s} \right)^t d_0[2, 2] + t \frac{2sf}{s+f} \left(\frac{s^2}{f+s} \right)^{t-1} d_0[2, 1]$$

Considering $g = 3$, this is

$$\begin{cases} d_t[2, 1] = \left(\frac{s^2}{f+s} \right)^t d_0[2, 1] \\ d_t[2, 2] = \left(\frac{s^2}{f+s} \right)^t d_0[2, 2] + t \frac{2sf}{s+f} \left(\frac{s^2}{f+s} \right)^{t-1} d_0[2, 1] = \left(\frac{s^2}{f+s} \right)^t (d_0[2, 2] + t \frac{2f}{s} d_0[2, 1]) \\ d_t[3, 1] = \left(\frac{s^2}{f+s} \right)^t d_0[3, 1] + t \frac{sf}{s+f} \left(\frac{s^2}{f+s} \right)^{t-1} d_0[2, 1] = \left(\frac{s^2}{f+s} \right)^t (d_0[2, 2] + t \frac{f}{s} d_0[2, 1]) \\ d_t[3, 2] = \left(\frac{s^2}{f+s} \right)^t (d_0[3, 2] + t \frac{f}{s} (d_0[3, 1] + d_0[2, 1]) + t^2 \frac{3f^2}{2s^2} d_0[2, 1]) - t \frac{f^2}{2s^2} d_0[2, 1]) \\ d_t[3, 3] = \left(\frac{s^2}{f+s} \right)^t (d_0[3, 3] + t \frac{2f}{s+f} d_0[3, 2] + t^2 \frac{f^2}{s^2} d_0[3, 1] - t \frac{f^2}{s^2} d_0[3, 1] + t^2 \frac{f^2}{s^2} d_0[2, 2] + t^3 \frac{f^3}{s^3} d_0[2, 1] - t^2 \frac{f^3}{s^3} d_0[2, 1]) \end{cases} \quad (\text{S87})$$

so that the maximum coefficient of t for $d_t[a, b]$ is $a + b - 3$

S10.4 proof correspondence with result of (Coste, 2025a)

Proof: As per (Coste, 2025a), let us consider that survival and reproduction are independent, i.e. $\mathbf{C} = \mathbf{0}$, then, in equation S77, $\mathbb{N}\hat{\mathbf{w}}$ is

$$\begin{cases} \mathbb{N}\hat{\mathbf{w}} = \mathbf{G} + \mathbf{H} \quad \text{with} \\ \mathbf{G} = \underbrace{\mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t)\mathbf{J}\hat{\mathbf{w}}}_{\mathbf{G}_1} + \underbrace{\mathbf{J}_{1,2}(\mathbf{F}_t \otimes \mathbf{S}_t)\mathbf{J}\hat{\mathbf{w}}}_{\mathbf{G}_2} \\ \mathbf{H} = \mathbf{J}_{2,2}((\mathbf{F} \otimes \mathbf{F})\mathbf{J} - \mathbf{J}\mathbf{F} + \mathbf{V})\hat{\mathbf{w}} \end{cases} \quad (\text{S88})$$

$$\begin{aligned}
\mathbf{G}_1 &= \mathbf{J}_{2,1}(\mathbf{S}_t \otimes \mathbf{F}_t) \mathbf{J} \hat{\mathbf{w}} = \underbrace{(e_1^{(g)} \otimes \mathbf{I}_s \otimes e_2^{(g)} \otimes \mathbf{I}_s)}_{\mathbf{J}_{2,1}} (\mathbf{S}_t \otimes \mathbf{F}_t) \underbrace{\text{vec}(\mathbf{D}_{\hat{\mathbf{w}}})}_{\mathbf{J} \hat{\mathbf{w}}} = (e_1^{(g)} \otimes \mathbf{S}_t \otimes e_2^{(g)} \otimes \mathbf{F}_t) \text{vec}(\mathbf{D}_{\hat{\mathbf{w}}}) = \\
&= \text{vec} \left((e_2^{(g)} \otimes \mathbf{F}_t) \mathbf{D}_{\hat{\mathbf{w}}} (e_1^{(g)T} \otimes \mathbf{S}_t^T) \right) = \text{vec} \left((e_2^{(g)} e_1^{(g)T}) \otimes (\mathbf{F}_t \mathbf{D}_{\hat{\mathbf{w}}} \mathbf{S}_t^T) \right) = \text{vec} \left(\underbrace{(\mathbf{J}_1 e_1^{(g)} e_1^{(g)T})}_{e_2^{(g)}} \otimes (\mathbf{F} \mathbf{D}_{\hat{\mathbf{w}}} \mathbf{S}^T) \right) \\
&= \text{vec} \left((\mathbf{J}_1 \otimes \mathbf{F}) \underbrace{((e_1 e_1^T) \otimes \mathbf{I}_s)}_{\mathbf{J}} \underbrace{(\mathbf{I}_g \otimes \mathbf{D}_{\hat{\mathbf{w}}})}_{\mathbf{D}_{\hat{\mathbf{w}}}} (\mathbf{I}_g \otimes \mathbf{S})^T \right) = \underbrace{((\mathbf{I}_g \otimes \mathbf{S}))}_{\mathbf{S}} \otimes \underbrace{(\mathbf{J}_1 \otimes \mathbf{F})}_{\mathbf{F}} \text{vec}(\mathbb{J} \mathbf{D}_{\hat{\mathbf{w}}}) = (\mathbf{S} \otimes \mathbf{F}) \text{vec}(\mathbb{J} \mathbf{D}_{\hat{\mathbf{w}}})
\end{aligned}$$

Similarly, $\mathbf{G}_2 = (\mathbf{F} \otimes \mathbf{S}) \text{vec}(\mathbb{J} \mathbf{D}_{\hat{\mathbf{w}}})$

$$\begin{aligned}
\text{vec}(\mathbf{Z}^\dagger) &= \text{vec}(\underbrace{(e_2^{(g)} e_2^{(g)T})}_{\mathbf{Z}^\dagger} \otimes \mathbf{Z}^\dagger) = \text{vec}((e_2^{(g)} 1 e_2^{(g)T}) \otimes (\mathbf{I}_s \mathbf{Z}^\dagger \mathbf{I}_s)) = \text{vec}((e_2^{(g)} \otimes \mathbf{I}_s) (1 \otimes \mathbf{Z}^\dagger) (e_2^{(g)T} \otimes \mathbf{I}_s)) \\
&= \underbrace{(e_2^{(g)} \otimes \mathbf{I}_s \otimes e_2^{(g)} \otimes \mathbf{I}_s)}_{\mathbf{J}_{2,2}} \text{vec}(\underbrace{1 \otimes \mathbf{Z}^\dagger}_{\mathbf{Z}^\dagger}) = \mathbf{J}_{2,2} \text{vec}(\mathbf{Z}^\dagger)
\end{aligned}$$

with $Z^\dagger(i, j) = \sum_k \hat{w}(k) (Cov(\tilde{F}(i, k), \tilde{F}(j, k)) + F(i, k)F(j, k) - \delta(i, j)F(j, k))$ that is

$$\mathbf{Z}^\dagger = \sum_{a,b} Z^\dagger(a, b) e_a^{(s)} e_b^{(s)T} = \sum_{a,b,k} \hat{w}(k) (Cov(\tilde{F}(a, k), \tilde{F}(b, k)) + F(a, k)F(b, k) - \delta(a, b)F(b, k)) e_a^{(s)} e_b^{(s)T}$$

$$\begin{aligned}
\text{vec}(\mathbf{Z}^\dagger) &= \sum_{a,b,k} (e_b^{(s)} \otimes e_a^{(s)}) \left(\underbrace{(e_b^{(s)} \otimes e_a^{(s)})^T \mathbf{V} e_k^{(s)}}_{Cov(\tilde{F}(a,k), \tilde{F}(b,k))} + \underbrace{e_a^{(s)T} \mathbf{F} e_k^{(s)}}_{F(a,k)} \underbrace{e_b^{(s)T} \mathbf{F} e_k^{(s)}}_{F(b,k)} - \underbrace{e_a^{(s)T} e_b^{(s)}}_{\delta(a,b)} e_b^{(s)T} \mathbf{F} e_k^{(s)} \right) \underbrace{e_k^{(s)T} \hat{\mathbf{w}}}_{\hat{w}(k)} \\
&= \underbrace{\sum_{a,b,k} (e_b^{(s)} \otimes e_a^{(s)}) (e_b^{(s)} \otimes e_a^{(s)})^T \mathbf{V} e_k^{(s)} e_k^{(s)T} \hat{\mathbf{w}}}_{\mathbf{V} \hat{\mathbf{w}}} + \sum_{a,b,k} (e_b^{(s)} \otimes e_a^{(s)}) \left(e_a^{(s)T} \mathbf{F} e_k^{(s)} e_b^{(s)T} \mathbf{F} e_k^{(s)} e_k^{(s)T} \hat{\mathbf{w}} \right) \\
&\quad - \sum_{a,b,k} (e_b^{(s)} \otimes e_a^{(s)}) \left(\underbrace{e_a^{(s)T} e_b^{(s)}}_{=0, \text{ unless } a=b} e_b^{(s)T} \mathbf{F} \underbrace{e_k^{(s)} e_k^{(s)T}}_{\sum_k e_k^{(s)} e_k^{(s)T} = \mathbf{I}_s} \hat{\mathbf{w}} \right) \\
&= \mathbf{V} \hat{\mathbf{w}} + \sum_{a,b,k} (e_b^{(s)} \otimes e_a^{(s)}) \left(e_a^{(s)T} \mathbf{F} e_k^{(s)} (e_k^{(s)T} \hat{\mathbf{w}}) e_k^{(s)T} \mathbf{F}^T e_b^{(s)} \right) - \underbrace{\sum_a (e_a^{(s)} \otimes e_a^{(s)}) e_a^{(s)T} \mathbf{F} \hat{\mathbf{w}}}_{\mathbf{J}_d \hat{\mathbf{w}}} \\
&= \mathbf{V} \hat{\mathbf{w}} + \sum_{a,b} (e_b^{(s)} \otimes e_a^{(s)}) \left(e_a^{(s)T} \mathbf{F} \underbrace{\left(\sum_k e_k^{(s)} e_k^{(s)T} \hat{\mathbf{w}} e_k^{(s)T} \right)}_{\mathbf{D}_{\hat{\mathbf{w}}}} \mathbf{F}^T e_b^{(s)} \right) - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}} \\
&= \mathbf{V} \hat{\mathbf{w}} + \sum_{a,b} (e_b^{(s)} \otimes e_a^{(s)}) \left(e_a^{(s)T} \mathbf{F} \mathbf{D}_{\hat{\mathbf{w}}} \mathbf{F}^T e_b^{(s)} \right) - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}}
\end{aligned}$$

$$\begin{aligned}
&= \mathbf{V}\hat{\mathbf{w}} + \sum_{a,b} (e_b^{(s)} \otimes e_a^{(s)}) \text{vec} \left(e_a^{(s)T} \mathbf{F} \mathbf{D}_{\hat{\mathbf{w}}} \mathbf{F}^T e_b^{(s)} \right) - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}} \\
&= \mathbf{V}\hat{\mathbf{w}} + \underbrace{\sum_{a,b} (e_b^{(s)} \otimes e_a^{(s)}) (e_b^{(s)} \otimes e_a^{(s)})^T}_{=\mathbf{I}_{s^2}} \underbrace{\text{vec}(\mathbf{F} \mathbf{D}_{\hat{\mathbf{w}}} \mathbf{F}^T)}_{=(\mathbf{F} \otimes \mathbf{F}) \text{vec}(\mathbf{D}_{\hat{\mathbf{w}}})} - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}} \\
&= \mathbf{V}\hat{\mathbf{w}} + (\mathbf{F} \otimes \mathbf{F}) \underbrace{\text{vec}(\mathbf{D}_{\hat{\mathbf{w}}})}_{=\mathbf{J}_d \hat{\mathbf{w}}} - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}} = \mathbf{V}\hat{\mathbf{w}} + (\mathbf{F} \otimes \mathbf{F}) \mathbf{J}_d \hat{\mathbf{w}} - \mathbf{J}_d \mathbf{F} \hat{\mathbf{w}} \\
&= (\mathbf{V} + (\mathbf{F} \otimes \mathbf{F}) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}) \hat{\mathbf{w}}
\end{aligned}$$

Therefore

$$\text{vec}(\mathbb{Z}^\dagger) = \mathbf{J}_{2,2} (\mathbf{V} + (\mathbf{F} \otimes \mathbf{F}) \mathbf{J}_d - \mathbf{J}_d \mathbf{F}) \hat{\mathbf{w}} = \mathbf{H}$$

and overall;

$$\begin{aligned}
\hat{\mathbb{K}} &= \text{vec}^{(-1)} \left(\left(\hat{\lambda} \mathbf{I}_{s^2 g_m^2} - (\mathbb{M} \otimes \mathbb{M}) \right)^{-1} (\mathbf{G}_1 + \mathbf{G}_2 + \mathbf{H}) \right) \mathbb{D}_{\hat{\mathbf{w}}}^{-1} \\
&= \text{vec}^{(-1)} \left(\left(\hat{\lambda} \mathbf{I}_{s^2 g_m^2} - (\mathbb{M} \otimes \mathbb{M}) \right)^{-1} ((\mathbf{S} \otimes \mathbf{F}) \text{vec}(\mathbb{J} \mathbb{D}_{\hat{\mathbf{w}}}) + (\mathbf{F} \otimes \mathbf{S}) \text{vec}(\mathbb{J} \mathbb{D}_{\hat{\mathbf{w}}}) + \text{vec}(\mathbb{Z}^\dagger)) \right) \mathbb{D}_{\hat{\mathbf{w}}}^{-1}
\end{aligned}$$

as per equation 7 in (Coste, 2025a), which completes the proof.

S11 Steps for section Illustration: India's demographic transition

Data is obtained from the data of the World Population Prospects of the United Nations (<https://population.un.org/wpp/>). Specifically, we use historical annual survival and fertility rates of Indian women, from 1950 to 2024 and medium-variant projections for these rates for 2024–2100. We consider that vital rates before 1950 were constant at the level of 1950 and after 2100 constant at the level of 2100.

These vital rates are grouped into annual Leslie matrices (age structured matrix projection models), $\mathbf{F}_t$ and $\mathbf{S}_t$, which content is depicted in Fig.4a and b. Assuming that reproduction is Poisson, this provides $\mathbf{V}_t = \mathbf{J}_d \mathbf{F}_t$ (table 1), and assuming that survival and fertility rates are independent, $\mathbf{C}_t$. For each year, we can therefore generate $\mathbf{M}_t$ (eq.2), $\mathbb{M}_t$ (eq.7) and $\mathbb{N}_t$ (eq.8), and thus $\mathcal{M}_t$ (eq.10), to project both abundance and kinship vectors over time. From the vector of structured abundances, we obtain the annual population birth rate $b_t = \frac{\mathbf{1}^T \mathbf{F}_t \mathbf{n}_t}{\mathbf{1}^T t \mathbf{n}_t}$ and the annual population (mean) survival rate $s_t = \frac{\mathbf{1}^T \mathbf{S}_t \mathbf{n}_t}{\mathbf{1}^T t \mathbf{n}_t}$, shown on Fig.4c. Their sum is the annual population growth rate $\lambda_t = b_t + s_t = \frac{\mathbf{1}^T \mathbf{M}_t \mathbf{n}_t}{\mathbf{1}^T t \mathbf{n}_t} = \frac{\mathbf{1}^T \mathbf{n}_{t+1}}{\mathbf{1}^T t \mathbf{n}_t}$ shown on Fig.4d together with the population's mean age $m_t = \frac{1}{n_t} \sum_a a n_t(a)$.

From the abundance and kinship vectors, and via the correspondence of eq.4, we, in turn, obtain the time-series for the PKM $\mathbb{K}_t^{(p)}$ and the IKM $\mathbb{K}_t$. We depict specifically $\sum_i \mathbb{K}_t[1,2](i,j)$ (the probability, for *ego* of age j that its mother is alive) and $\sum_i \mathbb{K}_t[2,2](i,j)$ (the expected number of sisters, for *ego* of age j) on Figures 5a and b. From the abundance and kinship vectors, and via eq.23, we obtain the time-

series for the unstructured Kinship Matrix $\mathbb{K}_t^{(u)}$, which provides at each time-step the expected number of (any) kin (whatever their state) of *ego* taken at random in the population. We depict these time-series for specific kin categories on Figures 5c and 6. We sum these values up to various $g - \sum_{a,b \leq g} \mathbb{K}_t^{(u)}(a,b)$ which yields Figure 5d.

S11.1 Convergence of India's kinship networks towards equilibrium

For a population at the demographic stable state, and for an age-structured population such as the model used in this section, one can compute the (finite) time, it takes for the kinship network to reach its equilibrium via eq. 21c. However, this population is never at the demographic stable state exactly; we therefore compute the time of convergence of various kin categories for the unstructured kinship via

$$\begin{cases} T(a,b) = \min_t \left(\frac{\|\mathbb{K}_t^{(u)}(a,b) - \bar{\mathbb{K}}_t^{(u)}(a,b)\|}{\|\bar{\mathbb{K}}_t^{(u)}(a,b)\|} < \epsilon \right) & \text{with} \\ \epsilon = 0.01 \end{cases} \quad (\text{S89})$$

This yields:

$$\mathbf{T} = \begin{bmatrix} 42 & 51 & 65 & 74 & 73 \\ 42 & 62 & 74 & 83 & 97 & 110 & 118 & 123 & 111 \\ 51 & 74 & 93 & 105 & 115 & 128 & 143 & 154 & 163 & 170 & 172 & 156 \\ 65 & 83 & 105 & 124 & 136 & 146 & 160 & 175 & 188 & 199 & 209 & 216 \\ 74 & 97 & 115 & 136 & 155 & 168 & 178 & 191 & 206 & 221 & 233 & 245 \\ 73 & 110 & 128 & 146 & 168 & 186 & 199 & 209 & 223 & 238 & 253 & 266 \\ 118 & 143 & 160 & 178 & 199 & 217 & 230 & 241 & 254 & 269 & 284 \\ 123 & 154 & 175 & 191 & 209 & 230 & 249 & 262 & 273 & 286 & 301 \\ 111 & 163 & 188 & 206 & 223 & 241 & 262 & 280 & 293 & 304 & 317 \\ 170 & 199 & 221 & 238 & 254 & 273 & 293 & 311 & 324 & 336 \\ 172 & 209 & 233 & 253 & 269 & 286 & 304 & 324 & 342 & 355 \\ 156 & 216 & 245 & 266 & 284 & 301 & 317 & 336 & 355 & 372 \end{bmatrix}$$

which indicates that the number of 10^{th} cousins converges with *epsilon* = 1% of the equilibrium over $T(12, 12) = 372$ years.

S12 Code

The R code below implements the kinship projection equation (eq. 10) for any one-sex projection model, here applied to the ground squirrel population of Coste (2025a). With the constant rates used here, the projected kinship converges to the stable kinship given by the Kinship Formula (Coste, 2025a).

```
# =====
# KINSHIP PROJECTION EQUATION (one-sex model)
# Projects the population kinship vector k_t jointly with the
# abundance vector n_t (eq 10), up to genealogical depth g, for a
# population with s states.
# The demography below is the 3-stage female life cycle of the
# Daurian ground squirrel (Spermophilus dauricus) used in Coste (2025,
# PNAS, https://doi.org/10.1073/pnas.2411888122), built from the life
# table in Luo & Fox (1990, J. Mammal. 71: 364-370), but any one-sex
# projection model can be used by replacing Ft, St (and Vt, Ct) in the
# projection loop;
# the example uses constant rates; for time-varying rates, make the matrices depend on t.
# Kronecker products are built explicitly, as in the equations; for
# large models, use sparse matrices (R package 'Matrix').
# =====

# =====
# PARAMETERS
# =====
```

```

g <- 3 # depth of the kinship network investigated (arbitrary, g >= 2)
s <- 3 # number of states of the projection model, i.e. the number of
      # rows and columns of Ft and St

# =====
# DUMMY MATRICES (Table 1)
# =====

# J1: subdiagonal of 1s (g x g), eq 15
J1 <- matrix(0, nrow = g, ncol = g)
if (g > 1) J1[cbind(2:g, 1:(g-1))] <- 1

# Jd: (s^2 x s), eq 16
Jd <- matrix(0, nrow = s^2, ncol = s)
for (i in 1:s) {
  ei <- rep(0, s); ei[i] <- 1
  Jd <- Jd + (kronecker(ei, ei) %*% t(ei)) # (s^2 x 1) %*% (1 x s) => (s^2 x s)
}

# J12, J21, J22: J_{a,b} (s^2 g^2 x s^2), eq 17
e1 <- rep(0, g); e1[1] <- 1
e2 <- rep(0, g); e2[2] <- 1
J12 <- kronecker(kronecker(e2, diag(s)), kronecker(e1, diag(s)))
J21 <- kronecker(kronecker(e1, diag(s)), kronecker(e2, diag(s)))
J22 <- kronecker(kronecker(e2, diag(s)), kronecker(e2, diag(s)))

# Je: (s^2 x s^2), eq 18
Je <- matrix(0, nrow = s^2, ncol = s^2)
for (i in 1:s) {
  for (j in 1:s) {
    ei <- rep(0, s); ei[i] <- 1
    ej <- rep(0, s); ej[j] <- 1
    v1 <- kronecker(ej, ei) # length s^2
    v2 <- kronecker(ei, ej) # length s^2
    Je <- Je + (v1 %*% t(v2))
  }
}

# Jy = kron(I_g, ones(1,s)): sums over states (g x gs), eq 19
Jy <- kronecker(diag(g), matrix(1, nrow = 1, ncol = s))

# =====
# INITIAL CONDITIONS
# =====
n0 <- rep(0, s)
n0[1] <- 1 # initiate with one individual in the first state

k0 <- rep(0, s^2 * g^2) # empty kinship vector
kn0 <- c(k0, n0) # stacked state

# =====
# PROJECTION
# =====
tmax <- 200

knt <- matrix(0, nrow = (s^2 * g^2 + s), ncol = (tmax + 1))
knt[, 1] <- kn0

for (t in 1:tmax) {
  # -----
  # USER INPUT: demographic matrices for time step t
  # Enter here the possibly time-varying, density- or kinship-dependent
  # fertility matrix Ft and survival matrix St of the projection model
  # at time t (dependence can use the current abundance and kinship
  # vectors, i.e. knt[, t]; with nonlinear dependence, the projection
  # is a mean-field approximation, as classically done for density-
  # dependence, see Discussion), as well as Vt and
  # Ct. For simplicity, constant matrices are used here as placeholders
  # (squirrel example).
  # -----
  Ft <- matrix(c(
    0.2300, 0.5100, 0.8400,
    0.0000, 0.0000, 0.0000,
    0.0000, 0.0000, 0.0000
  ), nrow = s, byrow = TRUE)

```

```

St <- matrix(c(
  0.0000, 0.0000, 0.0000,
  0.5700, 0.0000, 0.0000,
  0.0000, 0.5400, 0.4600
), nrow = s, byrow = TRUE)

Vt <- Jd %*% Ft                                # fertility variances-covariances (eq 13); here
                                                # independent Poisson reproduction, Vt = Jd Ft (Table 1)
Ct <- matrix(0, nrow = s^2, ncol = s)          # survival-fertility covariances (eq 14); here
                                                # independent survival and reproduction, Ct = 0 (Table 1)
# ----- end of user input -----

# check that the matrices entered match the number of states s
if (!all(dim(Ft) == c(s, s), dim(St) == c(s, s),
        dim(Vt) == c(s^2, s), dim(Ct) == c(s^2, s)))
  stop("Ft and St must be s x s, and Vt and Ct s^2 x s (time step ", t, ")")

# intermediary computations
Mt <- Ft + St                                # abundance projection matrix (eq 2)
MMt <- kronecker(diag(g), St) + kronecker(J1, Ft) # eq 7

NNt <- J21 %*% (kronecker(St, Ft) %*% Jd + Ct) + # eq 8
      J12 %*% (kronecker(Ft, St) %*% Jd + Je %*% Ct) +
      J22 %*% (kronecker(Ft, Ft) %*% Jd - Jd %*% Ft + Vt)

# big projection matrix (eq 10b)
bigMt <- rbind(
  cbind(kronecker(MMt, MMt), NNt),
  cbind(matrix(0, nrow = s, ncol = s^2 * g^2), Mt)
)

# projection proper
knt[, t + 1] <- bigMt %*% knt[, t]
}

# =====
# OUTPUTS
# =====
kt <- knt[1:(s^2 * g^2), , drop = FALSE]      # kinship vector
nt <- knt[(s^2 * g^2 + 1):(s^2 * g^2 + s), , drop = FALSE] # abundance vector
totnt <- colSums(nt)                          # total abundance, length (tmax+1)
kt_norm <- sweep(kt, 2, totnt, "/")           # kt ./ totnt (column-wise)
kut <- kronecker(Jy, Jy) %*% kt_norm          # unstructured kinship vector, eq 23
Kpt <- array(as.vector(kt), dim = c(s * g, s * g, tmax + 1)) # Population Kinship Matrix (eq 4)

# Individual Kinship Matrix: K^(p) divided by the abundance of ego's state
temp <- 1 / nt                                # nt.^(-1)
scale1 <- kronecker(temp, matrix(1, nrow = g, ncol = 1)) # (s*g) x T
scale2 <- kronecker(scale1, matrix(1, nrow = s, ncol = 1)) # (s^2*g) x T
scale3 <- kronecker(matrix(1, nrow = g, ncol = 1), scale2) # (s^2*g^2) x T
kit <- scale3 * kt                             # vectorised Individual Kinship Matrix, eq S8
Kt <- array(as.vector(kit), dim = c(s * g, s * g, tmax + 1)) # Individual Kinship Matrix
Kut <- array(as.vector(kut), dim = c(g, g, tmax + 1))        # unstructured kinship matrix

# kinship matrices at the final time step
Kpt[, , tmax + 1]
Kt[, , tmax + 1]
Kut[, , tmax + 1]

```

S13 SI References

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