

# Unequal Years with Kin: Skewed Distributions of Lifetime Kin Overlap

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## Abstract

Lifetime kin overlap (LKO) measures the total years an individual coexists with kin (e.g., parents or children) over the entire life course. This longitudinal measure is a critical proxy for cumulative family support potential, moving beyond the limitations of cross-sectional measures. We recover the full LKO distribution for parent, child, and joint overlaps using U.S. mortality and fertility schedules. This framework, relying only on age-specific demographic rates, is broadly applicable to any population worldwide. We compare results from a novel, efficient Fast Fourier Transform (FFT)-based convolution to those from the moments of the Markov Chain with Rewards (MCWR), a standard tool in formal demography. The FFT method accurately captures the full distributional skewness, particularly the mass at zero, which MCWR-based moment reconstructions smooth out.

Applying this robust FFT method, we show that the LKO distributions in the U.S. are skewed, especially at earlier years, revealing profound inequality in access to family time, with a critical minority experiencing only 0 or 1 year of overlap. Analysis of trends from 1933 to 2021 shows that extremely short overlap ( $LKO < 2$  years) with parents has become rare (e.g., 7% to 1% for males) due to improved survival. Similarly, short overlap with children decreases while remaining a persistent feature (e.g., 12.5% to 2.5% for males), driven structurally by lifetime childlessness. Crucially, the short duration of joint overlap is predominantly determined by the child side. Reporting the full LKO distribution is therefore essential to reveal these hidden inequalities in family support exposure, allowing for the targeting of the most vulnerable subpopulations.

## Introduction

Close family ties structure economic exchanges, caregiving, and emotional support across the life course. The absence of such ties is associated with elevated risks of loneliness, poorer health, and unmet care, particularly at older ages (Margolis and Verdery 2017; Verdery and Margolis 2017; Margolis et al. 2022; Plick et al. 2021; Taylor et al. 2023; Godfrey et al. 2025). Friend networks can buffer some of these risks, yet they are uneven and context dependent (Mair 2019).

Much of the existing literature measures the prevalence of “kinlessness” at specific ages, documenting who does or does not have parents, partners, or children at a point in time (Margolis and Verdery 2017; Verdery and Margolis 2017; Pittavino et al. 2025; Zhou et al. 2019). These cross-sections do not capture how many years individuals actually share with family members over the life course, nor do they describe the full heterogeneity of that exposure.

We use *lifetime kin overlap* (LKO) to recover this longitudinal perspective. In general, LKO is the number of years an individual coexists with kin over the life course. The concept has been formalized within the kinship MCWR framework, which derives analytic expressions for the moments of LKO across kin types (Caswell and de Vries 2025). In this study we focus on the years overlapped with at least one living parent, at least one living child, and the years in which both conditions hold.

Our analysis combines two age-specific ingredients for a given population and period: survival of the individual and the probability of having the relevant kin alive at each age. From these, we obtain the full distribution of LKO using a fast convolution based on the Fast Fourier Transform (FFT) (Tuljapurkar et al. 2020). This distribution provides probabilities for any duration threshold, so we can report the share spending less than two, five, or ten years with kin; the median and other quantiles of overlap duration; the probability mass at or near zero or one; and the share in the upper tail (e.g., the top decile). It

also supports joint statements (e.g., years with both a parent and a child) and contrasts across groups such as sex or period. The FFT approach treats the year-by-year overlap indicators as independent conditional on survival; under that assumption the resulting distribution is exact, and otherwise it serves as a tractable approximation. For comparison, we also reconstruct such a distribution with a *third-order* Gram–Charlier reconstruction whose moments come from a Markov chain with rewards (MCWR) in the formal demography of kinship (Caswell and de Vries 2025; Caswell 2022).

Two substantive features of the LKO distribution emerge. First, the distribution is highly skewed, with visible zero and one masses: many individuals share decades with kin, while a meaningful minority share almost none. Short overlap with parents has become rare with mortality decline, whereas short overlap with children remains a persistent feature, driven by the structural mass at zero created by a nontrivial share of individuals who are childless. Second, moment-based reconstructions based on MCWR smooth over these features, tending to understate the left tail and to overstate the far right tail. Placing the full distribution, rather than the mean, at the center therefore reveals inequalities in access to family support that would otherwise be obscured. Relative to Caswell and de Vries (2025), which formalizes LKO and provides analytic moments via MCWR, our contribution is to characterize the entire distribution via FFT-based convolution and to document zero/one masses and skewness that moment-based reconstructions smooth out.

## Data and methods

### Data and kinship model

Age- and sex-specific mortality rates and populations were obtained from the Human Mortality Database (Human Mortality Database 2024), and age- and sex-specific fertility rates were drawn from the Human Fertility Database (Human Fertility Database 2024).

We applied a two-sex, time-varying kinship model (Caswell 2022) to estimate the expected number and age of living kin that an average individual in the population (the “Focal”) has for a specified type (for example, a parent or a child). The kinship model was implemented in a matrix projection framework, with each kin type represented as a distinct subpopulation, and was stratified by the age and sex of both Focal and their kin. All computations were performed using the `DemoKin` R package (Williams et al. 2021).

The two-sex kinship model requires a complete series of age- and sex-specific fertility rates for both sexes as it tracks the production of children by both mothers and fathers. For the United States, we have complete female fertility rates ( $ASFR_f$ ) from 1933 to 2021, but male fertility rates ( $ASFR_m$ ) are missing before 1969 and after 2015. To address this gap, we imputed the missing  $ASFR_m$  using the relationship between male and female fertility while accounting for observed differences in the age distributions of fertility. Specifically, we estimated a regression model of male fertility on female fertility, age, year, and the time-varying male–female peak age difference, and then used the fitted model to predict missing values. Small negative predictions at very young ( $< 18$ ) and very old ( $> 50$ ) ages were truncated to zero.

### Probability of having at least one living kin

Our kinship model computes the expected number of living kin of a given type, denoted  $k_x$ , for a Focal at age  $x$ . To derive the probability of having at least one living kin from this mean value, we must make an assumption about the underlying distribution of the number of kin. Following Caswell (2024), we apply established distributional assumptions based on kin type.

For descendant kin (e.g., children), where the number can be large, we assume the number of kin follows a Poisson distribution with mean  $k_x$ . The probability of having at least one child is then:

$$p_x = 1 - \Pr(N_x = 0) = 1 - \exp(-k_x). \quad (1)$$

For direct ancestor kin (e.g., parents), where the maximum number is genealogically fixed at  $N = 2$ , we assume the number of kin follows a Binomial distribution with parameters  $(N, k_x/N)$ . The probability of having at least one parent is:

$$p_x = 1 - \Pr(N_x = 0) = 1 - \left(1 - \frac{k_x}{N}\right)^N. \quad (2)$$

For the probability of having at least one living parent and at least one living child, we calculate the joint probability by assuming independence and multiplying the marginal probabilities.

## Methodological framework: Common inputs

Both methods used to analyze lifetime kin overlap (LKO), the FFT-based convolution and the Markov chain with rewards, rely on the same demographic inputs for a given population and period. These inputs are:

1. **Focal’s age-specific survival probabilities**, which determine the likelihood that an individual survives from one age to the next.
2. **The probability of having at least one living kin** at each age of the Focal, obtained from the previous step.

By using an identical set of inputs, we can directly compare the methodological differences between calculating the full LKO distribution versus approximating it from its statistical moments.

## Distribution via FFT-based convolution

To obtain the distribution of LKO, we apply the FFT-based convolution method of Tuljapurkar et al. (2020). The life course of an individual is treated as a sequence of age-specific events. At each age, the “reward” (one unit of overlap at the chosen temporal resolution) is granted only if the Focal is alive and has at least one living kin.

The convolution treats the age-specific overlap indicators as independent Bernoulli trials with success probabilities  $p_x$  conditional on survival. This yields an exact Poisson–binomial sum under independence; otherwise it should be interpreted as a tractable approximation. The FFT implementation is computationally efficient, reducing the complexity from  $O(n^2)$  to  $O(n \log n)$ , making it scalable for distributions with wide supports.

From the full distribution of overlap time, we are able to report: (i) *threshold shares*, defined as the proportion with less than a given threshold of overlap (by default two years in figures); (ii) the mean and other quantities, such as variance and median; (iii) the mass at or near zero and one; and (iv) upper-tail shares (for example, the top decile). Unless noted otherwise, all thresholds use a strict “less than” definition.

## Moments via Markov chain with rewards (MCWR)

We then use the same demographic inputs within the MCWR framework to calculate the moments of the LKO distribution (Caswell and de Vries 2025). The states of the chain are defined by the age of the Focal. The transition probabilities between states are governed by the Focal’s age-specific survival probabilities. Same as the procedure in FFT-based convolution, in each state (i.e., at each age), a reward of 1 is assigned with a probability equal to the conditional probability of having at least one living kin, and a reward of 0 otherwise. This framework analytically yields moments of the LKO distribution for a newborn; in this paper, we use the first three (mean, variance, and skewness).

## Distribution approximation from MCWR moments

As a point of comparison, we construct an approximate LKO distribution using the moments derived from the MCWR method. We use the Gram–Charlier expansion, implemented via `PDQutils::dapx.gca` in R, which reconstructs a probability distribution from its first three moments (mean, variance, and skewness). Because it relies on a limited set of summary statistics, it can fail to capture critical features of the true distribution, such as zero- or one-inflation.

# Results

## Distributional differences

Figure 1 compares the distributions of lifetime kin overlap for females in 1940 and 2020. These years were chosen to represent a historical baseline before major mid-century mortality declines and a contemporary period reflecting modern demographic regimes. The convolution-based distributions (black lines with points) reveal far more heterogeneity than the smooth Gram–Charlier curves (blue lines). For overlap with parents, the distribution exhibits a notable left skew, particularly in 1940. The distribution is “one-inflated”, with a sharp peak at one year of overlap, primarily driven by early-life mortality of Focal

individuals truncating LKO. For overlap with children, the distribution is zero-inflated, representing individuals who remain childless or those who could not survive to reproductive ages.

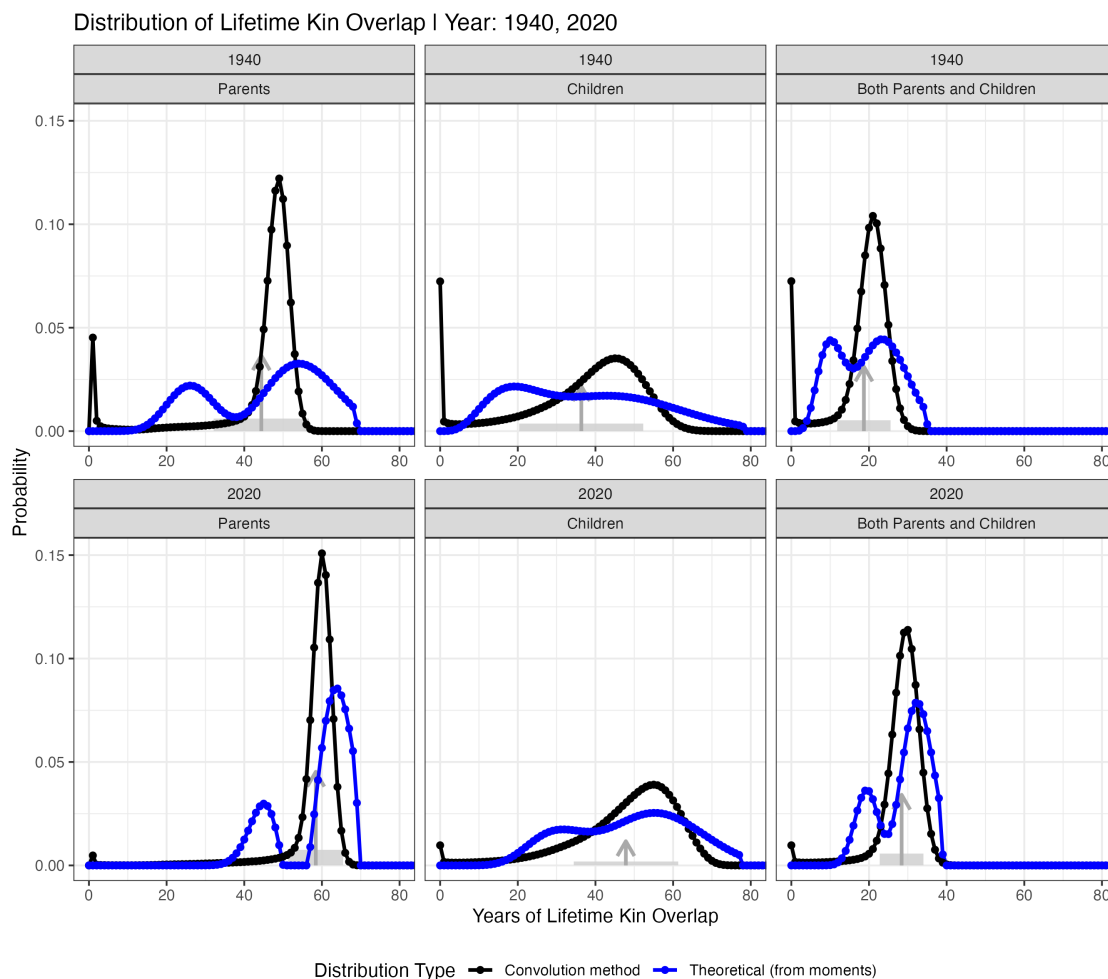


Figure 1: Distribution of lifetime kin overlap for female Focal individuals in the United States, 1940 and 2020. Black lines with points show the convolution distribution; blue lines show the Gram–Charlier approximation. The vertical gray arrow marks the mean, and the horizontal gray bar marks mean  $\pm$  one standard deviation. The convolution method reveals structural features such as zero- or one-inflation; *zero inflation reflects lifetime childlessness, and one inflation reflects infant or early-child mortality truncating overlap*; these are smoothed over by the approximation.

## Trends in extremely short overlap

Figure 2 shows the probability of having fewer than two years (0 or 1 year) of overlap with kin. Across all kin types, the convolution method (solid lines) yields higher estimates than the moment-based reconstruction (dashed lines).

For overlap with at least one parent, the probability of extremely short overlap has fallen markedly over time from 1933 to 2021 (e.g., 7% to 1% for males), reflecting gains in infant and adult survival: parents are increasingly likely to survive into their children’s adulthood, and newborn Focal individuals increasingly survive infancy. As survival improved, the gap between methods narrowed and the true probability approached zero. A persistent sex difference remains, with males showing slightly higher probabilities than females.

For overlap with at least one child, the probability of extremely short overlap is systematically higher than for parents (e.g., 12.5% to 2.5% for males). Three mechanisms contribute: (i) some Focal individuals do not survive to reproductive ages (eliminating any chance of child overlap), (ii) some survive but remain childless (a structural zero), and (iii) among those who have children, some experience very early child deaths that truncate overlap to 0–1 year. Consistent with higher lifetime childlessness among men, males

have higher probabilities than females.

For joint overlap with both a parent and a child, the series for “< 2 years” lies essentially on top of the “child < 2” series. This near identity indicates that once individuals accumulate at least two years of overlap with a child, they almost always have at least one parent alive during those years. In other words, short joint overlap is driven primarily by the child side (especially lifetime childlessness), rather than by parental survival or timing misalignment. Even when the short-overlap probabilities are similar, the full distributions differ.

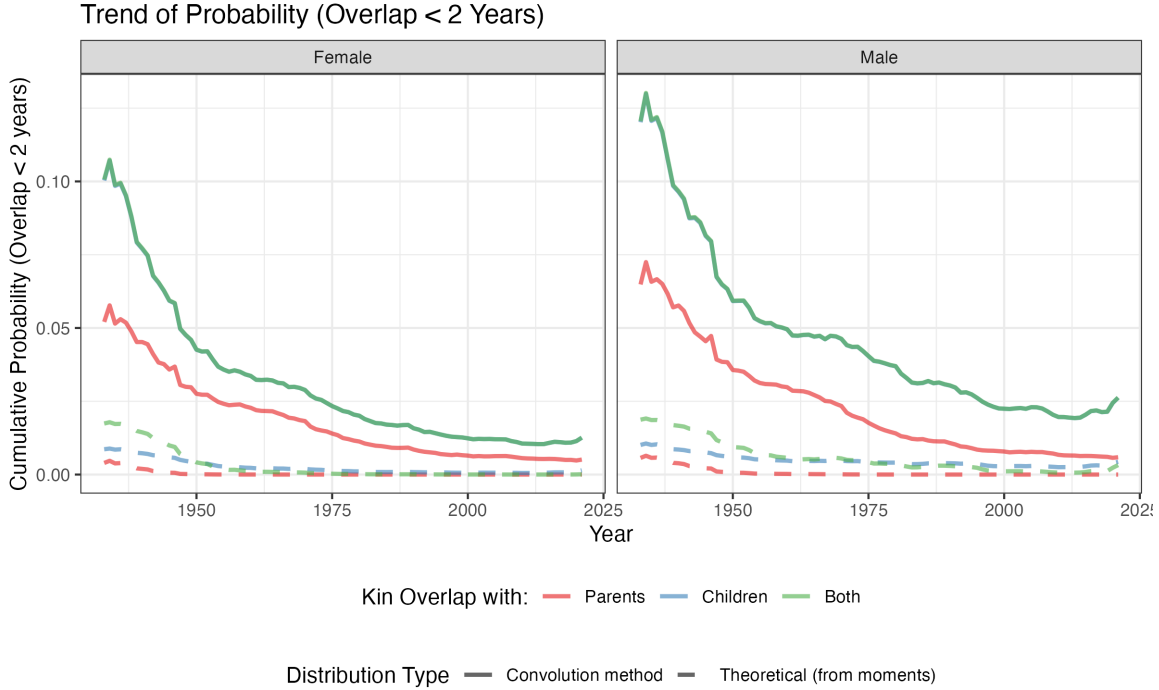


Figure 2: Trends in the probability of having fewer than two years (0 or 1 year) of lifetime overlap with kin in the United States, 1933–2021. Panels show Focal individuals of different sexes. Solid lines show convolution-based estimates; dashed lines show moment-based approximations. The convolution method consistently estimates higher probabilities of extremely short overlap, with differences narrowing for parental overlap but remaining substantial for child overlap.

## Discussion

This analysis demonstrates the value of examining the full distribution of lifetime kin overlap. While moment-based methods provide useful summaries, they miss key structural features. The convolution approach reveals that a non-trivial share of individuals spend zero or one year with close kin, a form of disadvantage that disappears in the mean and variance. It also avoids the tendency of moment-based reconstructions to overstate the probability of very long overlaps. In our setting, the short-overlap probability for joint overlap with both a parent and a child is nearly identical to that for overlap with a child alone, indicating that short joint overlap is driven primarily by the child side (especially lifetime childlessness) rather than by parental survival or timing misalignment.

From a demographic perspective, these findings highlight the mechanisms that create inequality in kinship resources. Short overlaps with parents are largely eliminated by mortality decline, but short overlaps with children persist because fertility decline and childlessness remain significant factors. This divergence underscores how different demographic processes shape overlap with different kin types.

From a methodological perspective, the FFT-based convolution provides a general and efficient way to obtain the full distribution of lifetime outcomes from demographic rates. Zero-inflated parametric models could offer a compact surrogate for the FFT distribution when analytic sensitivity is required, particularly because the zero mass is interpretable (e.g., childlessness), but we do not implement such models here. Two caveats merit attention. First, the convolution is exact under an independence assumption across ages for the overlap indicators; otherwise it should be interpreted as a tractable approximation. Second,

the third-order moment-based reconstruction smooths zero/one masses and under-represents the left tail, so distributional features (e.g., the mass at or near zero) should be taken from the FFT rather than the moment-based curve.

Finally, the substantive implications extend to social policy. LKO is directly related to the potential availability of family support. Our findings reveal a vulnerable subpopulation with minimal or no kin overlap, a group often rendered invisible by analyses focused on averages. Because the mass at zero is substantively interpretable, both the FFT distribution and, in future work, parsimonious zero-inflated specifications can be used to produce targeting metrics for social-care planning.

## Planned extensions

- **Distributional inequality and subgroup decomposition.** We will describe how unequal LKO is in plain terms and show how much of that inequality comes from differences *between* groups (such as sex, race, education) versus differences *within* groups. We will use decomposable measures (e.g., the Theil index, mean log deviation) and report group-specific headcounts at policy-relevant cutoffs (e.g., less than two years) alongside these measures over time.
- **Healthy, unhealthy, and effective LKO.** We will distinguish years of overlap when kin are likely able to provide support (“healthy LKO”) from years when they likely are not (“unhealthy overlap”), for example, overlap with parents in poor health or with severe disability. We will also construct an “effective LKO” that discounts years with limited support potential due to geographic separation, non-coresidence, or incarceration.
- **Thresholds beyond “at least one” and additional kin types.** We will analyze thresholds beyond “at least one” (for example, at least two children or both parents alive) and extend to other kin types (such as siblings, cousins, and grandchildren), and describe how these choices affect the left tail and the upper tail of the distribution.
- **Cumulative kin overlap within critical age ranges.** Beyond the lifetime perspective, we will analyze the cumulative kin overlap during policy-relevant or developmentally critical age windows. For example, overlap with parents during childhood (e.g., ages 0–15) relates to early-life resource security, whereas overlap with children during older ages (e.g., 65+) directly assesses the availability of potential caregiving support in later life. This approach translates the LKO methodology into time- and function-specific metrics essential for social planning and life course analysis.

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