

# Extensions of the kinship model

## An introduction to the analysis of population-level kinship structures

Diego Alburez-Gutiérrez<sup>†</sup>

<sup>†</sup>Kinship Inequalities Research Group,  
Max Planck Institute for Demographic Research

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# Agenda

1. Time-variance
2. Two-sex models
3. Multistate models
4. Example: migration of kin

# Recap

- ① What is the general form of the (time-invariant) kinship models?
- ② What are the different 'model specifications' that we discussed yesterday?

# Typology of kinship models

No	time	sex	state	reference
1	invariant	female	age	
2	variant	female	age	
3	invariant	two	age	
4	invariant	female	multiple	
5	variant	two	multiple	

## Time-variance

# Typology of kinship models

No	time	sex	state	reference
1	invariant	female	age	
2	<b>variant</b>	<b>female</b>	<b>age</b>	1
3	invariant	two	age	
4	invariant	female	multiple	
5	variant	two	multiple	

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<sup>1</sup>Caswell, H., & Song, X. (2021). The formal demography of kinship. III. kinship dynamics with time-varying demographic rates. *Demographic Research*, 45, 517–546

# Time-variant kinship models

- ① Demographic rates change over time
- ② Past demographic change → contemporary kinship structures
- ③ E.g., mortality crises, baby booms
- ④ Estimates by age, period, and cohort

## Recap: Time-invariant, one-sex model

The models are of the general form:

$$\underbrace{\mathbf{k}(x+1)}_{\text{age structure of kin at Focal's age } x+1} = \underbrace{\mathbf{U} \mathbf{k}(x)}_{\text{ageing and survival of existing kin}} + \underbrace{\begin{cases} \mathbf{0} \\ \mathbf{F} \mathbf{k}^*(x) \end{cases}}_{\text{new kin members added to the population}}.$$

where:

- ▶ **U** a matrix with survival probabilities in the subdiagonal
- ▶ **F** a matrix with fertility rates in the first row

## Time-variant, one-sex model

The models are of the general form:

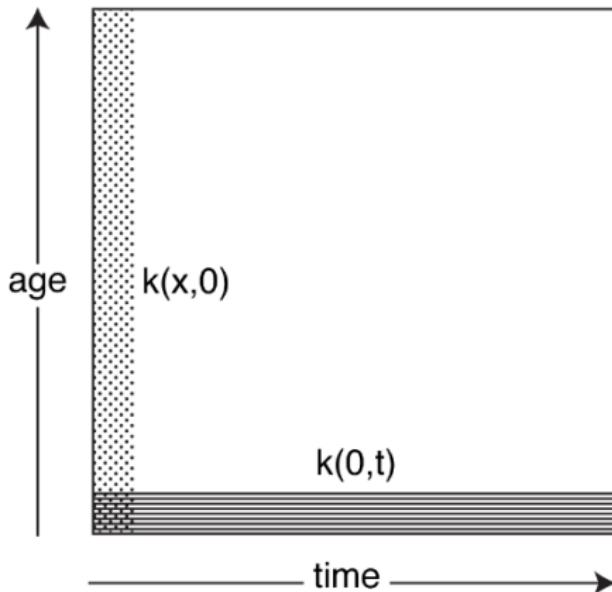
$$\underbrace{\mathbf{k}(x+1, t+1)}_{\substack{\text{age structure of kin} \\ \text{at Focal's age } x+1 \\ \text{and time } t+1}} = \underbrace{\mathbf{U}_t \mathbf{k}(x, t)}_{\substack{\text{ageing and survival} \\ \text{of existing kin}}} + \underbrace{\begin{cases} \mathbf{0} \\ \mathbf{F}_t \mathbf{k}^*(x, t) \end{cases}}_{\substack{\text{new kin members} \\ \text{added to the population}}}.$$

where:

- ▶  $\mathbf{U}_t$  a matrix with time-variant survival probabilities in the subdiagonal
- ▶  $\mathbf{F}_t$  a matrix with time-variant fertility rates in the first row

## Boundary conditions

**Boundary conditions.** The figure contains ages from 0 to  $\omega$  and times from 0 to  $T$ . The boundary conditions correspond to  $k(x, 0)$  for all  $x$  from 0 to  $\omega$  and  $k(0, t)$  for all  $t$  from 0 to  $T$



## Boundary conditions

- ▶ specify the complete age vector at time  $t = 0$

$$\mathbf{k}(x, 0) \quad x = 0, \dots, \omega.$$

- ▶ Specify the initial vector at each time

$$\mathbf{k}(0, t) \quad t = 0, \dots, \omega.$$

# Daughters

Daughters (**a**) are the result of the reproduction of Focal:

$$\underbrace{\mathbf{a}(x+1, t+1)}_{\text{age structure of daughters at Focal's age } x+1} = \underbrace{\mathbf{U}_t \mathbf{a}(x, t)}_{\text{ageing and survival of existing daughters}} + \underbrace{\mathbf{F}_t \mathbf{e}_x}_{\text{new daughters (subsidy)}}. \quad (1)$$

$$a(0) = \mathbf{0}.$$

where:

- ▶  $\mathbf{U}_t$  is a matrix with time-variant survival probabilities in the subdiagonal
- ▶  $\mathbf{F}_t$  is a matrix with time-variant fertility rates in the first row
- ▶  $\mathbf{F}_t \mathbf{e}_x$  is the subsidy vector
- ▶  $\mathbf{e}_x$  is the unit vector for age  $x$
- ▶  $a(0)$  is the distribution of daughters at Focal's birth

# Mothers

The population of mothers (**d**) of Focal consists of at most a single individual:

$$\underbrace{\mathbf{d}(x+1, t+1)}_{\text{age structure of mothers at Focal's age } x+1} = \underbrace{\mathbf{U}_t \mathbf{d}(x, t)}_{\text{ageing and survival of existing mothers}} + \underbrace{0}_{\substack{\text{new mothers} \\ (\text{subsidy})}} \quad (2)$$

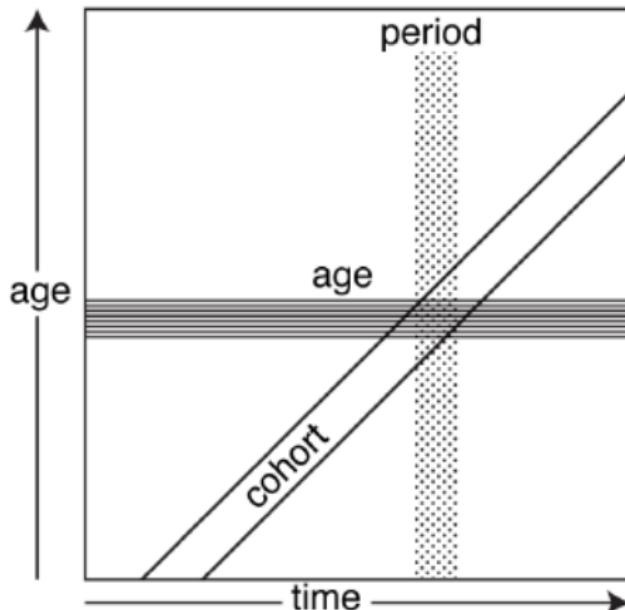
$$d(0) = \pi(t).$$

where:

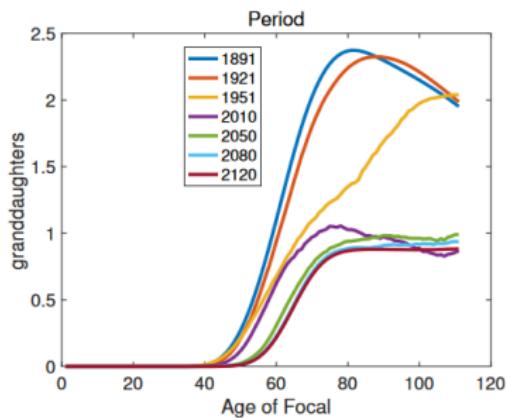
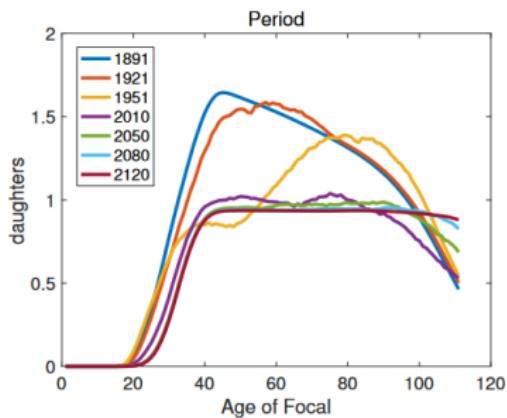
- ▶  $b(0)$  is the distribution of mothers at Focal's birth
- ▶  $\pi(t)$  is the distribution of ages of mothers in the population

# Age, period, and cohort in kinship models

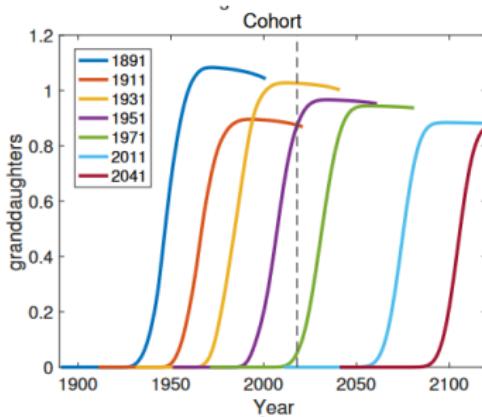
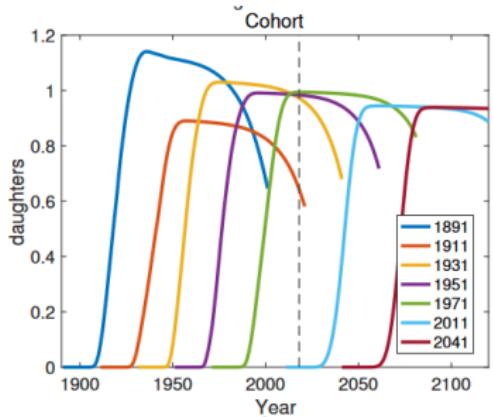
The period, cohort, and age dimensions of kinship development, within the age $\times$ time domain shown in Figure 2



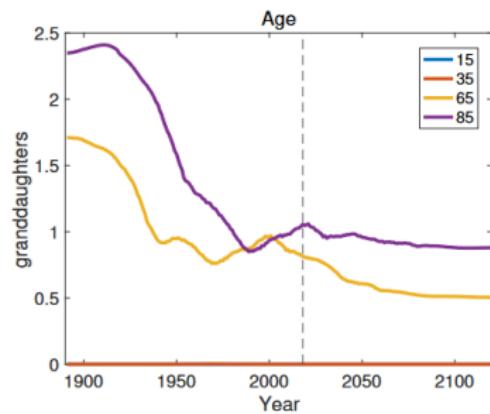
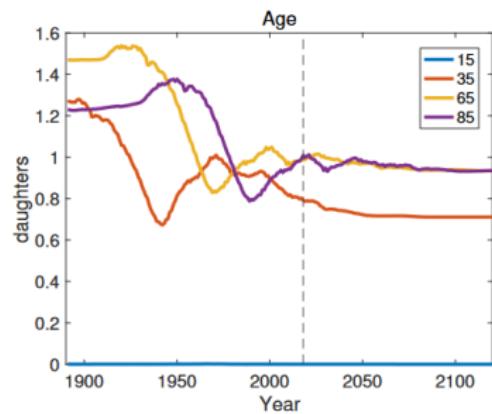
# Period results for numbers of daughters and granddaughters in Sweden



# Cohort results for numbers of daughters and granddaughters in Sweden



# Age results for numbers of daughters and granddaughters in Sweden



## Discuss

- ① What is the difference between the expected number of daughters calculated using (i) a time-invariant model, and (ii) the period dimension of the time-variant model?
- ② What is the difference between the period and cohort results of the time-variant model?
- ③ How do the time-variant models deal with missing demographic data before a certain year (e.g., the UN only reports data starting in 1950)?

# Break

## Two-sex models

# Typology of kinship models

No	time	sex	state	reference
1	invariant	female	age	
2	variant	female	age	
<b>3</b>	<b>invariant</b>	<b>two</b>	<b>age</b>	<sup>2</sup>
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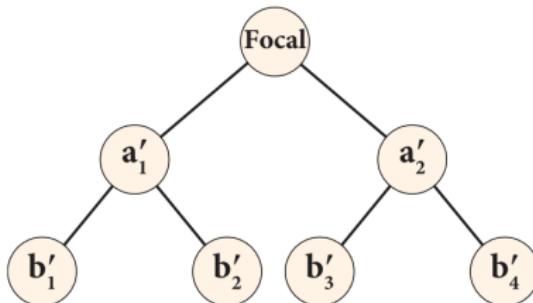
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<sup>2</sup>Caswell, H. (2022). The formal demography of kinship IV: Two-sex models and their approximations. *Demographic Research*, 47, 359–396.

## Why do we need two-sex models?

- ① Differential survival and reproduction for women and men
- ② These differences are not stable: change over time
- ③ More pronounced in some settings
- ④ Estimate male and female kin for male and female Focals

## Two-sex model (descendants)



$$\tilde{\mathbf{a}} = \begin{pmatrix} \mathbf{a}'_1 \\ \mathbf{a}'_2 \end{pmatrix}$$

where

- ▶  $\tilde{\mathbf{a}}$  is a block-structured matrix of the expected number of living offspring
- ▶  $\mathbf{a}'_1$  is the expected number of living sons
- ▶  $\mathbf{a}'_2$  is the expected number of living daughters

## Offspring (sons and daughters)

Children ( $\tilde{a}$ ) are the result of the reproduction of Focal:

$$\underbrace{\tilde{a}(x+1)}_{\text{age structure of offspring at Focal's age } x+1} = \underbrace{\tilde{U}\tilde{a}(x)}_{\text{ageing and survival of existing offspring}} + \underbrace{\tilde{F}\tilde{\phi}(x)}_{\text{new offspring (subsidy)}}. \quad (3)$$

$$\tilde{a}(0) = \mathbf{0}.$$

where:

- ▶  $\tilde{U}$  is a block-structured matrix of survival probabilities
- ▶  $\tilde{F}$  is a block-structured matrix of fertility rates
- ▶  $\tilde{F}\tilde{\phi}(x)$  is the subsidy vector
- ▶  $\tilde{\phi}(x)$  is the state vector of a Focal of specified sex
- ▶  $\tilde{a}(0)$  is the distribution of offspring at Focal's birth

## Blocks-structured input matrices

For mortality:

$$\tilde{\mathbf{U}} = \begin{pmatrix} \mathbf{U}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{U}_m \end{pmatrix}$$

For fertility:

$$\tilde{\mathbf{F}} = \begin{pmatrix} \bar{\alpha} \mathbf{F}_f & \bar{\alpha} \mathbf{F}_m \\ \alpha \mathbf{F}_f & \bar{\alpha} \mathbf{F}_m \end{pmatrix}$$

where

- ▶  $\mathbf{U}_f$  is a matrix with female survival probabilities in the subdiagonal
- ▶  $\mathbf{F}_f$  is a matrix with female fertility rates in the first row
- ▶  $\alpha$  is the proportion males among offspring
- ▶  $\bar{\alpha}$  is  $1 - \alpha$

## Parents

The population of parents ( $\tilde{\mathbf{d}}$ ) of Focal consists of at most a single individual:

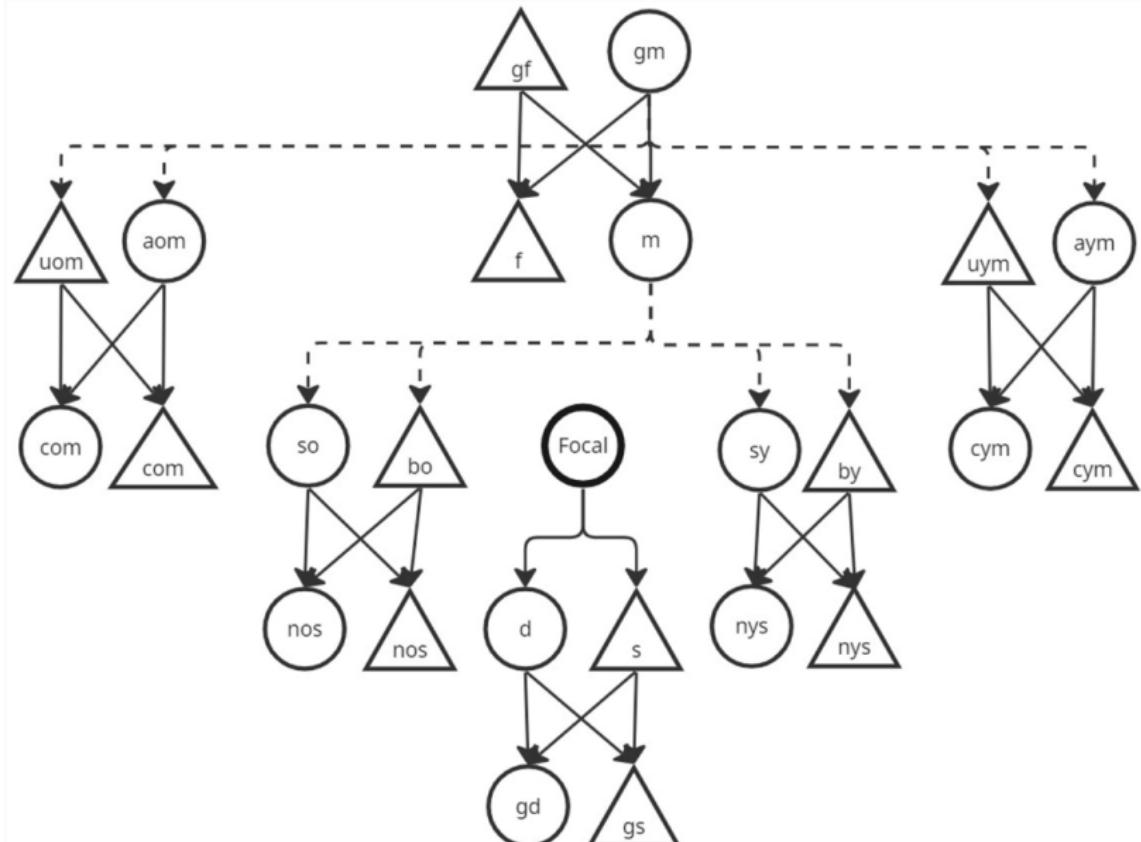
$$\underbrace{\tilde{\mathbf{d}}(x+1)}_{\text{age structure of parents at Focal's age } x+1} = \underbrace{\tilde{\mathbf{U}} \tilde{\mathbf{d}}(x)}_{\text{ageing and survival of existing parents}} + \underbrace{0.}_{\text{new parents (subsidy)}} \quad (4)$$

$$\tilde{d}(0) = \tilde{\pi}.$$

where:

- ▶  $\tilde{b}(0)$  is the distribution of parents at Focal's birth
- ▶  $\tilde{\pi}$  is the distribution of ages of parents in the population

# Two-sex kin estimation



## Data requirements

$\mathbf{U}_f, \mathbf{U}_m$  = female and male survival matrices

$\mathbf{F}_f, \mathbf{F}_m$  = female and male fertility matrices

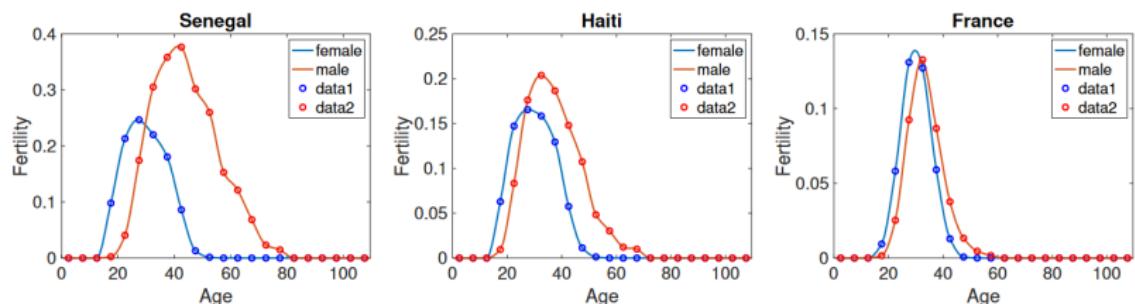
$\pi_f, \pi_m$  = distribution of ages at maternity and paternity

$\alpha$  = proportion males among offspring

$\bar{\alpha} = 1 - \alpha$

# Male and female fertility

**Figure 5:** The observed (circles) and interpolated (lines) age-specific fertility rates for Senegal (2013), Haiti (2010), and France (2012). Based on data from Schoumaker (2019).



# Approximations for two-sex kinship models

## ① Androgynous fertility

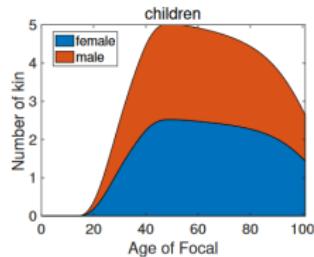
- ▶ Assume that  $\mathbf{F}_m = \mathbf{F}_f$

## ② GKP factors

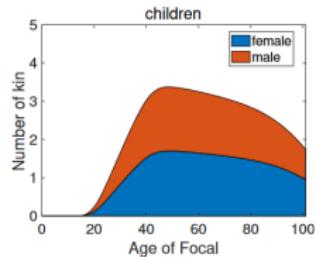
- ▶ Run one-sex model and multiply resulting kinship structure by a 'GKP factor'
- ▶ daughters  $\times 2$ , granddaughters  $\times 4$ , great-granddaughters  $\times 8$ , mothers  $\times 2$ , grandmothers  $\times 4$ , great-grandmothers  $\times 8$ , sisters  $\times 2$ , nieces  $\times 4$ , aunts  $\times 4$ , and cousins  $\times 8$

# Expected number of female and male kin in three countries

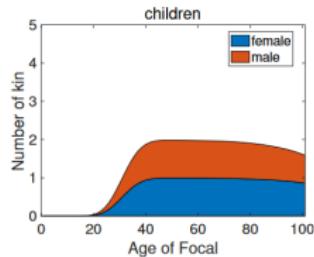
**Senegal**



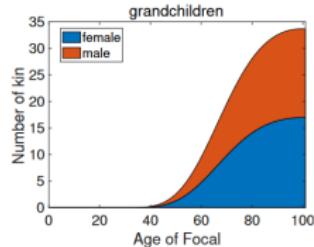
**Haiti**



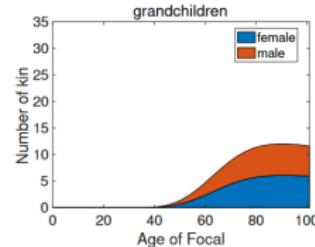
**France**



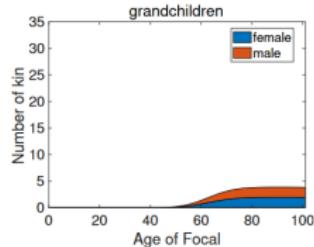
**grandchildren**



**grandchildren**



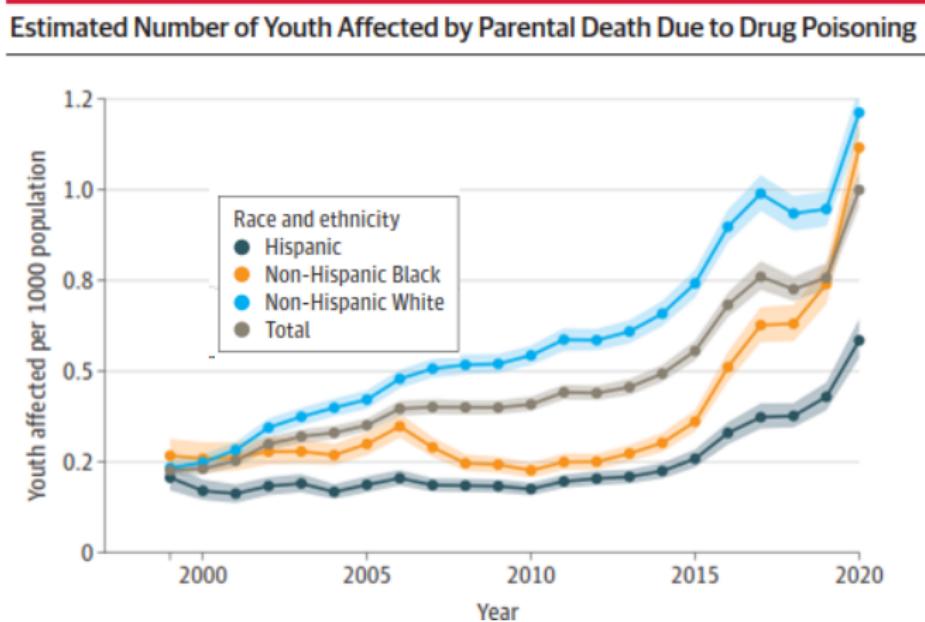
**grandchildren**



## Discuss

- ① Why do we need the ‘androgynous’ and ‘GKP factor’ approximations for two-sex kinship models?
- ② Which of the two do you think is better? Can you think of other possible ‘approximations’?

## Example: Kin loss by cause of death<sup>3</sup>



<sup>3</sup>Schlüter, B.-S., Alburez-Gutierrez, D., Bibbins-Domingo, K., Alexander, M. J., & Kiang, M. V. (2024). Youth Experiencing Parental Death Due to Drug Poisoning and Firearm Violence in the US, 1999-2020. *JAMA*. <https://doi.org/10.1001/jama.2024.8391>

## Multistate models

# Typology of kinship models

No	time	sex	state	reference
1	invariant	female	age	
2	variant	female	age	
3	invariant	two	age	
4	<b>invariant</b>	<b>female</b>	<b>multiple</b>	<sup>4</sup>
5	variant	two	multiple	

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<sup>4</sup>Caswell, H. (2020). The formal demography of kinship II: Multistate models, parity, and sibship. *Demographic Research*, 42, 1097–1146.

## Why multistate models?

- ▶ Extend kinship models beyond age-only classification.
- ▶ Jointly classify kin by age *and* another “stage” (e.g., location, education).
- ▶ Capture demographic processes (survival, fertility, migration, transitions) in a single unified framework.
- ▶ Particularly useful when kinship structures depend on heterogeneous life-course pathways.

## Core idea

- ▶ Each kin type has an age–stage distribution collected in a block-structured vector:

$$\tilde{\mathbf{k}} = \begin{pmatrix} \mathbf{k}_{11} \\ \vdots \\ \mathbf{k}_{s1} \\ \hline \vdots \\ \mathbf{k}_{1w} \\ \vdots \\ \mathbf{k}_{sw} \end{pmatrix}$$

- ▶ Each block  $\mathbf{k}_{ij}$  counts kin in age class  $i$  and stage  $j$ .
- ▶ Population projection follows standard matrix population logic extended via vec-permutation tools.

## Input matrices

The multistate kinship model requires:

$\mathbf{U}_i$  : stage transition probabilities within age class  $i$

$\mathbf{D}_j$  : survival/age-advancement for stage  $j$

$\mathbf{F}_i$  : fertility rates for age class  $i$

$\mathbf{H}_j$  : offspring assignment matrix (e.g. assigning children to mother's stage)

These matrices encode movement across stages, ageing, reproduction, and the stage at which each new kin enters the system.

## Projection equation

The multistate update is:

$$\tilde{\mathbf{k}}(x+1) = \tilde{\mathbf{U}} \tilde{\mathbf{k}}(x) + \tilde{\beta}(x),$$

where:

- ▶  $\tilde{\mathbf{U}}$  combines all  $\mathbf{U}_i$  and  $\mathbf{D}_j$  into one block-structured transition matrix.
- ▶  $\tilde{\beta}(x)$  represents new kin produced by a kin type that reproduces between ages  $x$  and  $x+1$ .
- ▶ Initial condition  $\tilde{\mathbf{k}}_0$  encodes plausible age–stage distribution of mothers at Focal's birth and zeros for impossible kin types.

Example: migration of kin

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JOURNAL ARTICLE

Kinship Structures for Left Behind Older Adults in High  
Outmigration Contexts: Evidence From Puerto Rico [Get access >](#)

Amílcar Matos-Moreno, PhD, MPH , Diego Alburez-Gutierrez, PhD, Iván Williams, MS, Ashton M Verdery, PhD,  
Mariana Fernández Soto, PhD, Alexis Santos-Lozada, PhD

*The Journals of Gerontology: Series B*, Volume 80, Issue 6, June 2025, gbaf052, <https://doi.org/10.1093/geronb/gbaf052>

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## Case study: Puerto Rico as a high-outmigration context

- ▶ Puerto Rico has experienced substantial outmigration of working-age adults since the 2000s.
- ▶ Older adults increasingly age in place with fewer co-resident or nearby kin.
- ▶ We use a time-invariant, one-sex, multistate kinship model to quantify the **location of close kin** for older adults.
- ▶ States: (1) residing in Puerto Rico, (2) migrant in the US, (3) return migrant.

## Why a multistate model is required

- ▶ Classical (age-only) kinship models capture mortality and fertility but **not kin location**.
- ▶ Outmigration redistributes kin across geographic states, altering:
  - ▶ availability of instrumental support,
  - ▶ caregiving potential,
  - ▶ transnational structure of families.
- ▶ The multistate framework embeds the migration process directly in the kinship projection matrices, allowing kin to move between PR and the US across the life course.

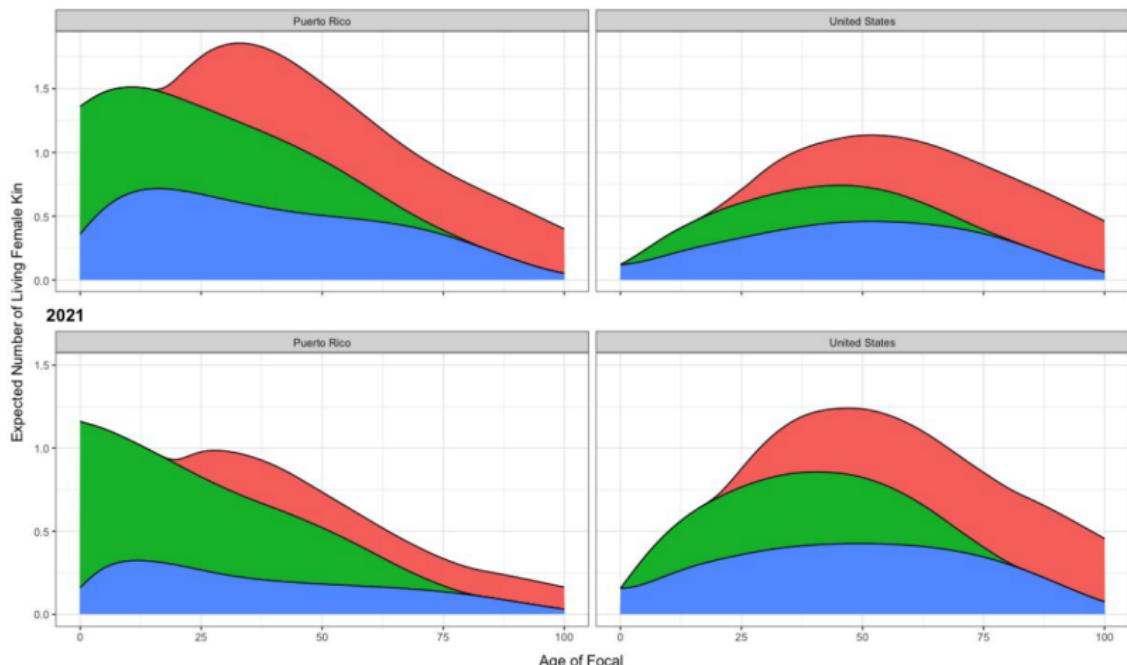
## Model implementation

- ▶ Fertility and mortality: UN WPP (2000 and 2021).
- ▶ Migration transitions: estimated female outmigration and return migration probabilities from Census 2000 and ACS 2022.
- ▶ Multistate projection gives expected kin counts by:
  - ▶ kin type (daughters, sisters, mothers),
  - ▶ focal age,
  - ▶ location (PR vs US).
- ▶ Resulting kin distributions interpret like period life tables: expected kin given demographic rates in a single year.

# Number of kin of Focal by location of kin

2000

kin Daughter Mother Siblings



## Discuss

- ① Do you see any application of the kinship models to your own work?
- ② Which model specification would be more appropriate for this?

# Lab session today

No	time	sex	state	reference
1	invariant	female	age	
2	variant	female	age	
3	invariant	two	age	
4	invariant	female	multiple	
5	<b>variant</b>	two	<b>multiple</b>	<sup>5</sup>

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<sup>5</sup>Williams, I., Alburez-Gutierrez, D., & DemoKin Team. (2023). *DemoKin*: 1.0.3. <https://CRAN.R-project.org/package=DemoKin>