Alignment, clocking, and macro patterns of episodes in the life course

Tim Riffe*[1], Angelo Lorenti[1], and Andrés Castro[1]

[1]Max-Planck-Institute for Demographic Research

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Abstract

Background Individuals are often observed passing through a sequence of discrete states in trajectory data. These are usually either simplified into transition probabilities to derive asymptotic values of aggregate statistics using Markov assumptions, or else retained for pattern and group detection using sequence analysis. Markov-derived aggregate statistics are of limited scope, and sequence analysis appears aimed at inferring typologies than generating aggregates.

Objective We broaden the scope of aggregate patterns and summary indices that may be calculated from trajectory data, including trajectories generated from Markov models by proposing a simple grammar of operations for trajectory data.

Methods We introduce the concepts of clocking and alignment as a new framework for generating novel statistics from trajectories.

Data We use different data to demonstrate concepts and give example applications. We use published transition probabilities to simulate discrete trajectories of employment states to demonstrate concepts. We use retrospective fertility and union trajectories from Colombian Demographic and Health Surveys data and disability trajectories simulated from European Statistics on Income and Living Conditions for Italy (EU-SILC) for example applications.

Results We demonstrate several new demographic aggregate patterns in the areas of disability inequalities and birth intervals.

Conclusions We demonstrate the flexibility of this framework and the ease of generating macro patterns. An R package is provided to facilitate experimentation with these operations.

1 Introduction

We propose a measurement framework consisting in a two-element grammar. These two elements serve to extract macro patterns hidden within trajectory data. Such patterns might be age-like patterns of novel prevalence, state-episode-occupancy time measures, or time left to next event. Using this framework, we aim to zoom in on demographic patterns that emerge at various stages of the life course, and so describe a given demographic phenomenon (state) from a variety of perspectives.

We first define *clock* measures, a way to inscribe time, order, prevalence, or other measures into individual life trajectories. This step is analogous to defining a rewards matrix in multistate Markov models (see e.g. Caswell and Zarulli 2018), and the ends are not entirely dissimilar. As an example of a concrete Markov analogy, Dudel and Myrskylä (2017a) defines an algebraic expression to estimate the

*riffe@demogr.mpg.de

expected number of episodes of a given state that individuals experience in a given multistate world. Taken together with the total expected state occupancy time, one can infer an average episode duration. And there are both clunky and elegant approaches close at hand to derive an age pattern of expected episode duration. Such measures (only reported once before to our knowledge (Laditka and Wolf 1998)) would already add insight to demographic processes and outcomes. Clock measures are much more flexible than this, and enable the researcher to decompose expected episode durations into expected time spent and left within episodes, or even by episode length. To illustrate the flexibility of *clocks*, we propose several other variants that go beyond this case.

Second we define *alignment* operations, which shift trajectories to have synchronous timing with respect to the entry to or exit from a given episode of a specified state. Researchers already do similar things: for example Iacobelli and Carstensen (2013) propose a flexible use of time-since-event scales, and Riffe et al. (2017) define flexible Lexis spaces in which life lines are aligned both on birth and on death, and this has been used to reveal hidden health patterns (Riffe et al. 2016) and pathways (Potente and Monden 2018, Raab et al. 2018). We propose more flexible alignment procedures, which allow trajectory synchronization on the start or end of a conditionally specified episode (e.g., first, last, longest).

In isolation or in combination, clock and alignment operations open a large space for the derivation of demographic macro patterns. In the following sections we give concrete examples to illustrate concepts on using a toy example of simulated employment old-age trajectories. We give two abbreviated example applications for the cases of disability inequalities in Italy and birth interval differentials in Colombia. Disability trajectories are simulated from transition probabilities estimated from Italian SILC data. Birth and union histories are recorded histories from the Colombian Demographic and Health surveys. We subject both the simulated and recorded trajectories to a few simple analyses based on our framework, therein defining novel and interpretable comparisons. Though superficial, these examples demonstrate the flexibility of the clocks and alignment framework for aggregations of trajectory data. Work shown here is fully reproducible, and we also offer an `R` package, `Spells`, which enables readers to experiment with flexible clock and alignment operations.

2 Concepts

To demonstrate concepts, we simulate trajectories from a published transition matrix (Dudel and Myrskylä 2017b). This matrix refers to black females aged 50-100 in 1994, and it contains age-structured transition probabilities for movements between employment, inactivity, and retirement, as well as mortality from these three states. Simulation is done using the `rmarkovchain()` function from the `R` package `markovchain` (Spedicato 2017). A glimpse of the first 10 randomly generated individuals is shown in Figure 1. These ten individuals will be recycled in all of the following data manipulations used to demonstrate concepts. All aggregate calculations of age patterns (and so on) are based on a simulated population of 10000 trajectories starting in employment at age 50.

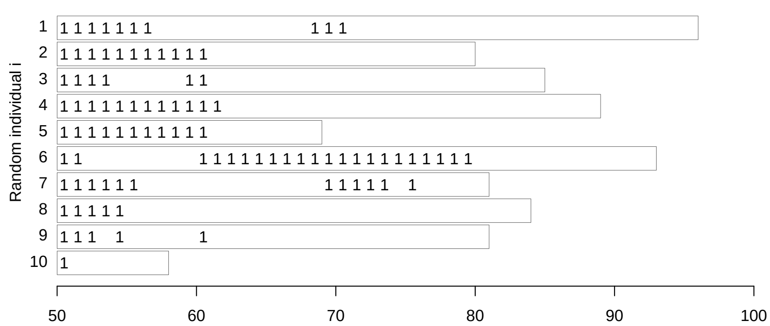
Figure 1: Ten randomly generated state sequences from the 1994 transition matrix of black females (Dudel and Myrskylä 2017b)

3 Clocks

3.1 A binary trajectory matrix gives prevalence

Standard calculations of prevalence typically proceed by imputing reference states with 1s (with 0s elsewhere) and taking column means over survivors in each age. Figure 2 shows such a data construct, where the state sequence matrix has been converted to a binary matrix, with 1s for employment episodes, 0s for other living states (shown blank). Typically one might impute `NA` values in dead states for this sort of calculation. Operations on objects such as this can yield age patterns of prevalence or expectancies, for example. This is not what we call a clock, but this data construct illustrates the setup. As the number of simulated trajectories increases, the resulting age pattern of prevalence will approach the values in the respective column of the so-called fundamental matrix in a Markov approach.

Figure 2: Binary imputation of employment spells



3.2 Duration, step, and order clocks

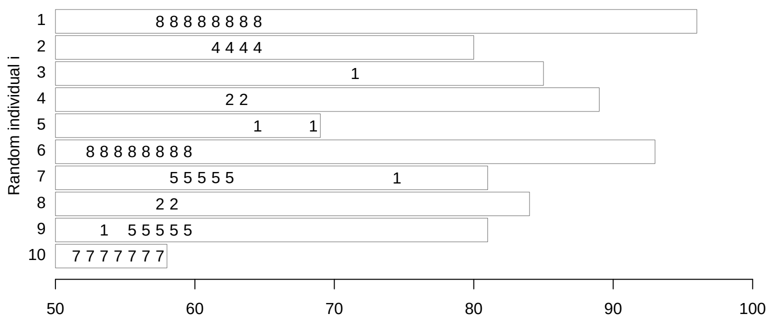
To derive measures other than prevalence, we simply change the 1s to other values. For example, to calculate an age-pattern of spell duration, instead impute time steps with episodes with values equal to the total episode length (Fig. 3a). Column means of the resulting object would give the average episode duration conditional on being in any point of an episode. If instead one wanted to condition on episodes starting (ending) in each age then impute the same values in only the first (last) time step within each episode (not shown). One may also wish to calculate time spent or left in the state episode, per Fig. 3b or 3c [1]. Episodes can also be imputed with other markers, such as episode order, as in Fig. 4 for the case of employment spells, or episode fractions.

There is room for creativity in defining clock measures such as these, and we encourage experimentation along these lines. Clock measures are then aggregated in some way. In these examples, *value* alignment is with respect to episodes, but *aggregation* alignment is still structured by age, such that statistics across individuals in an array produce age patterns. However, one may wish to synchronize trajectories in ways other than time since birth.

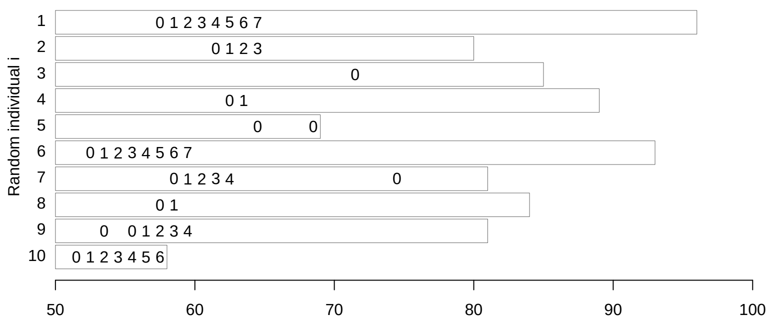
[1] In practice we increment values by $\frac{1}{2}$ for mid-state clocking.

Figure 3: Inactivity spells from Figure 1 are imputed with different duration count variables. It's probably better to add $\frac{1}{2}$ to the displayed *running* values.

(a) Static; Total episode duration of inactivity.



(b) Step; Time spent in episode of inactivity.



(c) Step; Time left in episode of inactivity

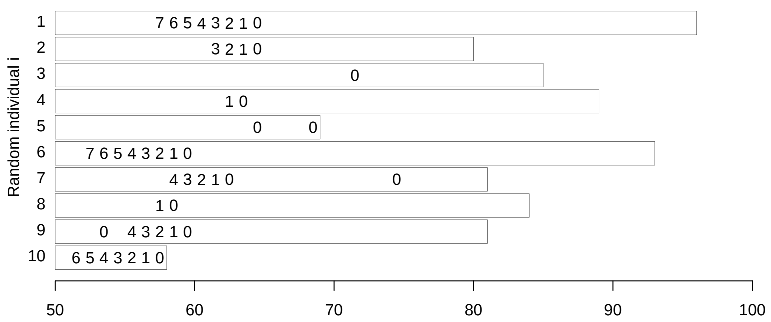
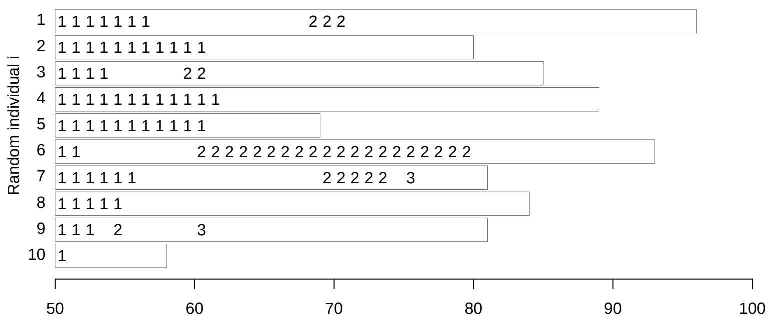
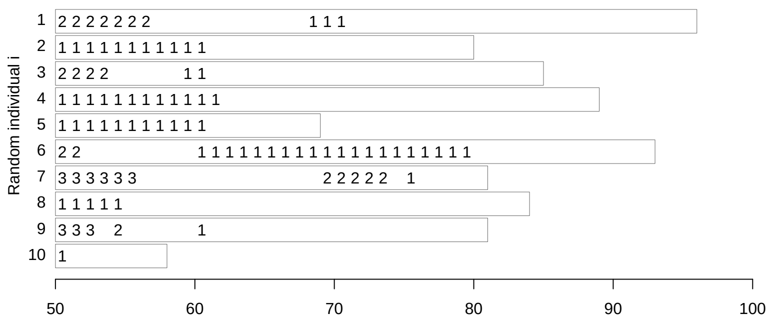


Figure 4: Employment episodes from Figure 1 are imputed with order count variables.

(a) Employment episode order, increasing.



(b) Employment episode order, decreasing.



3.3 Alignment

Episodic *clock* values are aggregated according to some structuring criteria. In all previous figures, the structuring criteria was chronological age, which is how data were generated in the first instance. To introduce a term, the sequences in these figures are *left-aligned* on the event of birth. This is the most common default alignment in social and medical sciences, but other choices may be more compelling for particular questions.

For late-life processes, birth is usually decades away from the events and states of interest, and sharper empirical regularity may be be found with respect to other alignment criteria. Aligning lifelines requires two choices: 1) a reference moment or anchoring *event* must be selected, and 2) the alignment direction must be chosen. A reference event could be any instance of entry, exit, or other compelling anchor point, such as a spell midpoint– ergo such events may relate to episodes themselves. For repeated events, the choice of anchoring episode could itself follow a regular criterion, such as first, last, or longest episode. The *direction* of alignment could be left, right, center, or perhaps something else.

Fig. 5 shows a set of four alignment selections out of the many possible choices. Fig. 5b left-aligns on entry to *first* retirement (if any). One could also choose last, longest, or some other episode of retirement, or of course right-align on exit. Fig. 5c left-aligns on entry into each individual's longest spell of inactivity, whereas Fig. 5d right-aligns on exit from the same spell.

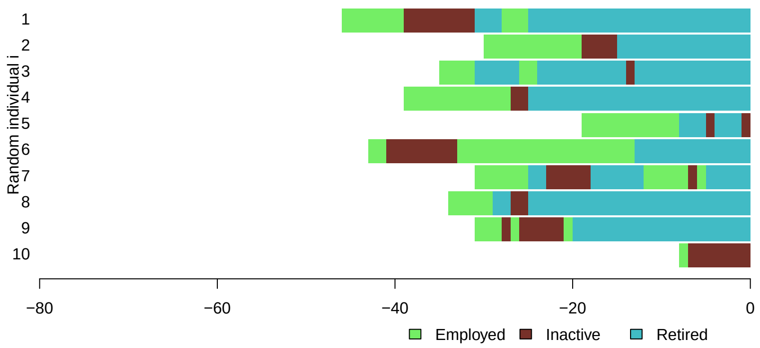
These examples are subset of many possible alignments, in this case column shifting within rows of a matrix. Alignment as shown here is probably insufficient to reveal patterns if one is visualizing raw trajectories, as in these demonstrative figures. One would probably want to define *sort* operations (row-swapping) for this, and that is not something we have ventured to do at this point. In the present, we instead aggregate up to macro patterns.

Two caveats to the use of alignments and clocks are worth noting. First, aggregate measures based on clocks and alignment operations can be biased due to the left- or right-censoring of trajectories, i.e., when the observation window of sequences does not cover the full period over which events (change in states) can be observed. In the previous section, we discussed an example that may be affected by left censoring because we do not know the employment status of individuals before age 50. To partially correct this, the data were simulated so that all individuals are employed by age 50, making all mean calculations based on step clocks conditional on being employed at this age. Right censoring can be a problem for descending clocks (e.g., mean remaining time in a spell), especially at ages that are close to the end of the observation window (e.g. age 80 in our disability example below). Hence, researchers should be careful about the potential bias of the aggregate measures and make clear the conditional nature of them when necessary.

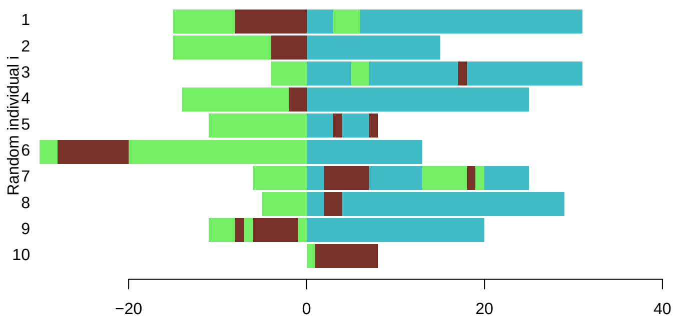
Second, care should be taken when conducting alignment operations as some observations will not be included in the aggregate measures if they do not experience the reference event for alignment. For

Figure 5: The sequences from Figure 1 under a variety of alignment types.

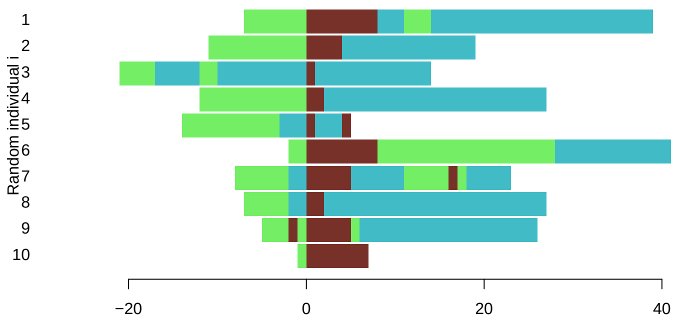
(a) Right-aligned on death.



(b) Left-aligned on *first* retirement.



(c) Left-aligned on entrance to *longest* spell of inactivity



(d) Right-aligned on exit from *longest* spell of inactivity

example, individuals without spells of unemployment will not be included in the calculation of the mean time to next employment after a first job loss. Although these examples seem trivial, we encourage careful thinking when defining alignments, clocks, and aggregate measures.

The following section presents two examples where clocks and alignment operations are used to examine trajectory data. In the first example we rely on an ascending step clock measures and the standard age alignment to produce a disability spell pattern. In the second example we use three clocks and one alignment operation to study the mean duration of birth intervals according to the age of the mother at first birth, and the sex of the first child.

4 Trajectory aggregation

Age-like macro-patterns can be derived in trajectory data by aggregating clocks within discrete intervals. Aggregated clocks could assume any of the varied forms discussed here, or else new variants. Discrete time intervals may draw from the original time scale, often age or similar, or the result of an alignment operation. The aggregation function itself can be freely defined by the user. In our examples, we calculate means, but generally one may measure aspects of a distribution

5 Applications

5.1 Health inequalities

Population level studies of disability typically report values such as mean time spent disabled, either derived from a multistate model of disability (Crimmins et al. 2009) or derived using the Sullivan method (Sullivan 1971, Crimmins et al. 1997). It is rare to see other model statistics reported for health disparities (Laditka and Wolf 1998), even for results based on simulated disability trajectories. Especially for the case of understanding group inequalities, it is valuable to measure quantities beyond health expectancies, such as the age pattern of disability spell length, or the extent to which disability is spread throughout life or concentrated at the end of life. Do new bouts of disability tend to get longer or shorter with age? Who has longer spells of disability, the rich or the poor? We demonstrate some basic clock and alignment operations that enable the calculation of age patterns for i) disability spell duration, ii) disability spell order, and iii) the prevalence of disability specifically in the final years of life.

Long term disability trajectories over the life course of individuals are typically not recorded, except in rare cohort studies, or in long-running health registers. To produce our base set of trajectories, we first estimate transition probabilities, then we simulate over a wide age range. Each of our three measures demonstrates the results of a particular combination of clock and/or alignment operations.

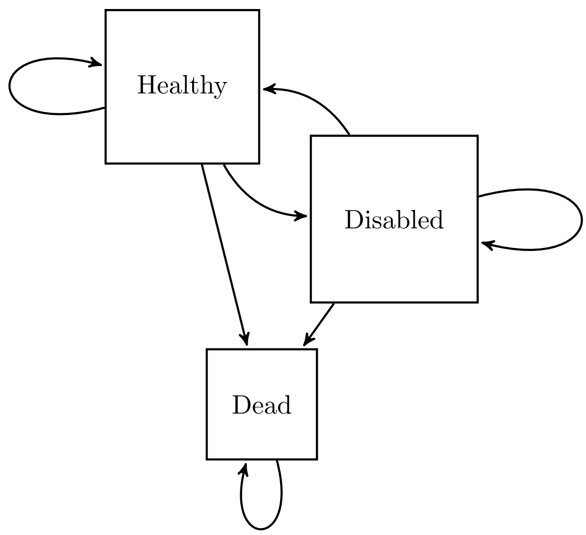


Figure 6: A state space diagram depicting states and transitions for a single age step. States are in boxes and valid transitions are shown as arrows.

5.1.1 Data

We use the Italian survey of the EU-SILC (European Statistics on Income and Living Condition), 2012-2015. The EU-SILC is the European Union (EU) reference source for comparative statistics on income and living conditions for all the countries in the EU. Member States conduct the survey annually, collecting nationally representative household and personal data. There is a cross-sectional and a longitudinal component. The longitudinal Italian EU-SILC is based on the rotational design proposed by Eurostat; each year, a new sample representative of the whole Italian population enters the study, and it is followed for four years. In the initial year, the sample is representative of the population 14 years old and over; for individuals aged over 80, the exact age is not made available in the data.

We use data for individuals who were first interviewed in 2012, 2013, and 2014 and re-interviewed in subsequent years. Thus, in our data, we have 16,872 individuals, 7,919 men and 8,687 women, followed over two, three, or four consecutive years.

To estimate the transition probabilities between healthy and disabled states, we use the general question about how a person perceives his/her general health. Possibles' answers are: "Very good", "Good", "Fair", "Bad", and "Very Bad". We aggregate Bad and Very Bad into Disabled and the remaining options into Healthy. For those lost to the follow-up, information about death are provided by other household members.

Individuals aged 15 can be healthy or disabled, and those who survive up to age 16 can stay healthy or move to the disabled state; the process continues at each successive age, up to 79. The state space and valid transitions for this model is depicted in Fig. 6.

We estimate the transition probabilities using multinomial regression (Allison 1982). We model the probability of being in state i (Healthy, Disabled, Dead) at time $t+1$ as a function of the state j at time

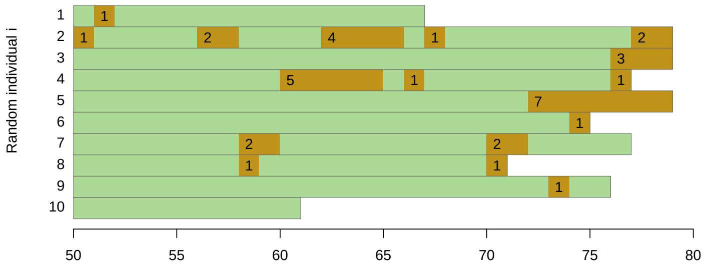
t (Healthy, Disabled) and age and income quintiles, separately by sex. In each of the regressions, age is modelled as a cubic spline. This approach accounts for non-linearity in the relationship between age and the probability of being in a state i. For each sex and income quintile, we produce transition probabilities $p_{i,j}$ for 65 age groups (single ages 15 to 79), and 6 possible transitions.

The following exercise is done for females only. We arrange transition probabilities into standard Markov transition matrices, and then simulate 50,000 trajectories using the `rmarkovchain` package (Spedicato 2017) and assuming that everyone starts healthy at age 15. Each trajectory consists in 65 age steps.

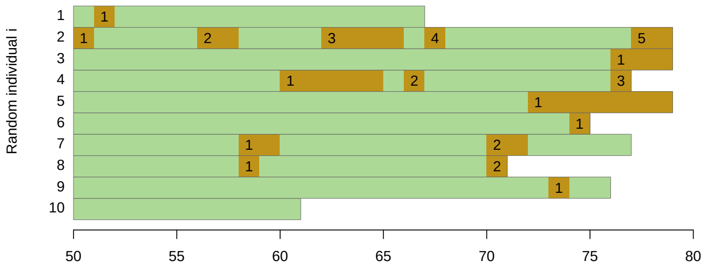
5.1.2 Grammatical operations

We report three kinds of results for this application, which aim to illustrate some of the leverage that can be obtained from isolated clock or alignment operations. These include two clocks (spell duration and order), and one alignment (end of life). We illustrate the meaning of these operations using ten randomly generated trajectories left truncated at age 50 and conditioned on death before age 80. In order to calculate the mean duration of spells starting in age x, we impute the spell duration in the first time step of each disability spell, following the pattern in Fig. 7b. This first analysis requires only a single clock step because we retain the default age alignment. Calculation of the mean conditional spell order (Fig. 7b) is based on a similar setup, with an order indicator imputed in the first time step. These first two clocks are to be aggregated as conditional means (conditional on entering the spell in a given age), so all other values (healthy, dead, later time steps in the same spell) are discarded. The third analysis aims to compare disability prevalence patterns in the final years of life (Fig. 7c). This is based on i) an *identity* clock, which places 1s in each time step within disability spells and 0s in time steps spent healthy, and ii) alignment on the end of life.

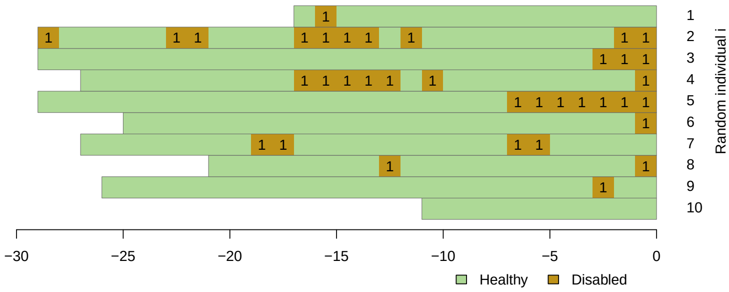
To aggregate macro patterns from the spell duration and order clocks (Figs. 7a and 7b, we calculate conditional means within each age, throwing out any values that are not the first time step in a disability spell. In the time-to-death prevalence we calculate conditional means within the time scale produced by death-alignment. In these examples, only individuals deceased before age 80 are shown, but in the full simulated sample some individuals reach age 80 in a state of disability, which may continue into higher ages if we had the transition probabilities to simulate so far. This introduces a downward bias in spell duration that grows in magnitude with the approach to age 80. For this reason, we right truncate results for spell duration aggregates at age 70.



(a) The first time step in each disability spell is imputed with the spell length, all other values are thrown out.



(b) The first time step in each disability spell is imputed with an ascending spell order clock, all other values are thrown out.



(c) A prevalence clock, with trajectories aligned on the year of death. Healthy years are interpreted as 0s.

Figure 7: Ten example disability trajectories. Figs. a) and b) indicate clock operations, and Fig. c) shows an alignment operation with a binary prevalence clock. Ages below 50 are ignored in these illustrations.

5.1.3 Results

For each of the three variants, we calculate two age patterns, one for the highest and one for the lowest income quintile. One could potentially live 64 years between age 16 and 79, and survival for both income quintiles is close to complete. However, the higher income quintile spends on average 4 years disabled, whereas the lower income quintile spends 8.4 years disabled. Is this due to longer or more frequent bouts of disability? Are these bouts spread over life randomly, or concentrated toward the end?

Fig. 8 shows the results of aggregating trajectories coded as in Fig 7a by taking conditional means within single year age intervals. New disability spells are expected to be of longer duration as age increases. Disability spells are considerably longer on average for women in the lowest income quintile. From such an aggregate picture, a researcher could make various kinds of summary statements: at age 60, new disability spells for the poor are expected to be 40% longer than for the rich. Or one could make statements on the age scale: new disability spells among the poor hit an average of two years duration by age 53, a level only hit by the rich around age 67.

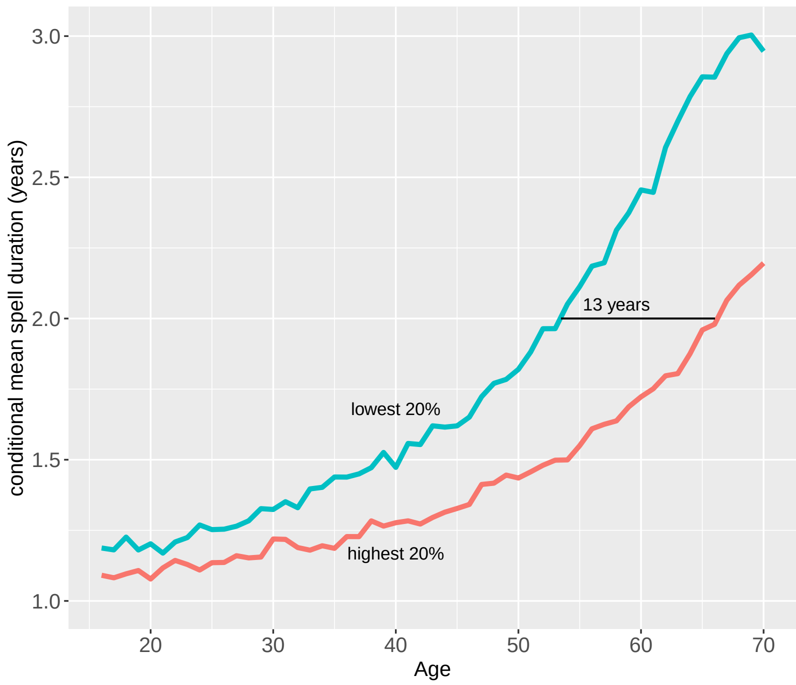


Figure 8: Spells of disability get longer on average with age until at least age 70, and they are considerably longer on average for the lowest income quintile than for the highest. Mean duration of new spells passes two years at age 53 for the poor and age 67 for the rich.

Fig. 9 shows the results of aggregating trajectories coded as in Fig 7b by taking conditional means within single year age intervals. We assume that everyone starts off having never been disabled before age 16, so anyone become disabled at age 16 is a first-timer. Some people recover and become disabled again at a later age, and for this reason new disability spells in higher ages are a mix of first and higher order bouts. In all ages after 20, individuals becoming disabled in the lowest income quintile have been disabled more often in their lives than those from the highest income quintile.

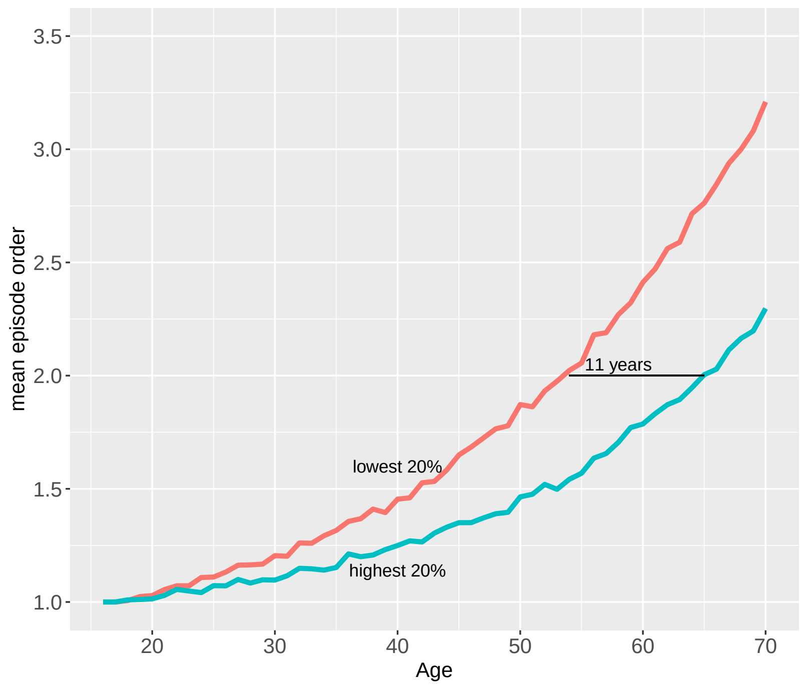


Figure 9: The mean number of disability bouts of those experiencing disability increases with age faster for the lowest income quintile than for the highest.

Fig. 10 shows the results of aggregating trajectories coded as in Fig 7c, where healthy years are coded as 0s and disabled years as 1s. We stratify the sample on 5-year groups by age of death to further demonstrate how the end-of-life pattern has a persistent shape. Lower ages at death are much noisier in this visualization because there are relatively few early deaths. This picture reveals two features of inequality: i) disability is more concentrated at the end of life for the highest income quintile, and ii) disability prevalence is consistently higher in all ages in the final third of life.

This stylized exercise evokes a number of follow-up questions that we do not here pursue: Are these pattern differences caused by onset, recovery, or mortality differences? Is this income gradient really a geographic gradient? How does this age pattern close out in ages higher than 80? Surely disability spell duration must start decreasing in higher ages when the force of mortality starts to dominate. In general, what fraction of disabled life expectancy is spent in short or long spells? What if we invert the analysis to examine healthy spells? Other clocks and alignments may reveal still other features of the health gradient in this domain of research.

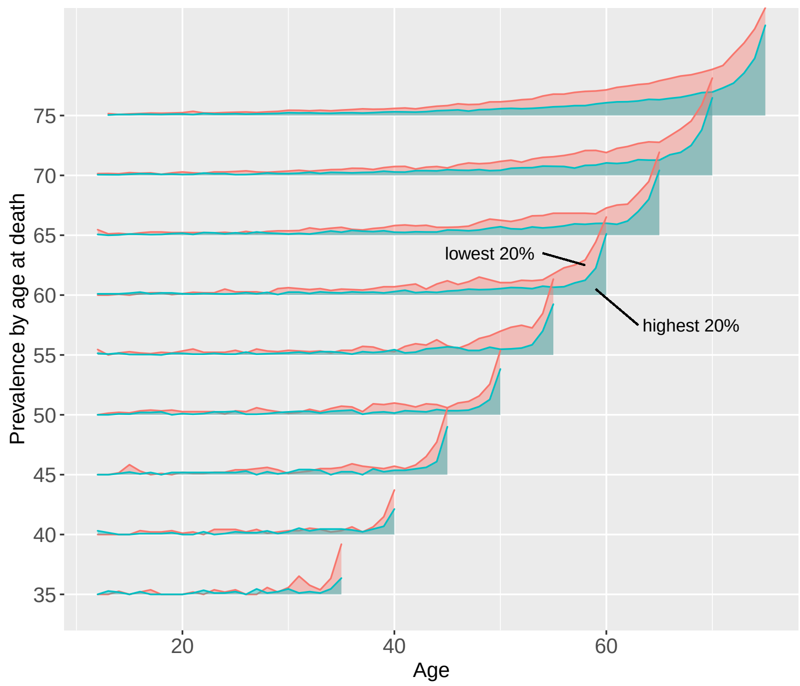


Figure 10: The age pattern of disability prevalence is concentrated at the end of life.

5.2 Birth interval differentials

We use clock and alignment operations to examine the mean time to the second birth over the 15 years following the first birth. We compare these mean times according to the age at first birth (five-year age groups) and the sex of the first child. These comparisons help us answer the question of whether or not the sex of the first child increases the risk (i.e., reduces the mean waiting time) of the second birth.

In addition, we explore the mean times to the next girl and to the next boy separately. Conditioning on the sex of the next birth allows us to examine, for example, if having a first girl imply a faster next girl, or, if having a first boy imply a faster next boy.

All together, these comparisons show how birth interval differentials vary substantially by age at first birth and also according to the sex of the first and second child.

5.2.1 Data

We draw our data from seven waves of the Colombian Demographic and Health Survey (CDHS) collected between 1985 and 2015. The CDHS are nationally representative surveys of women in reproductive ages (15 to 49). All these surveys are publicly available upon registration at: `https://www.dhsprogram.com/data/`.

We use full birth histories to reconstruct the reproductive trajectory of women with at least two children ever born. We are interested in the patterns of the mean time to second birth, mean time to next boy, and mean time to next girl. The starting point of our observation is, naturally, the year of the first birth. Using clocks and alignments, we are able to calculate the conditional mean time to second births diminishing the influence of right censoring, because all women in our sample had at least two children. However, the bias of right censoring affects more the mean times to next boy and next girl. We do not know the mean time to next boy or girl for women whose children are all of the same sex at the survey moment. Moreover, we do not know, for example, if a woman of age 20 with two girls would eventually have a boy in the future. The younger the women, the more likely our calculations will be biased. To avoid this bias, our calculations of mean time to next boy and next girl are based on the sub-sample of women ages 39 and above (53% of the sample). This sub-sample of women are more likely to have finished their reproductive periods, which reduces the influence of right censoring.

Table 1 shows the total number of women by groups of age at first birth. According to this table, most of the first births occur between ages 15 and 24, while a very small proportion are to women age 35 to 39 (0.23%).

Table 1: Total number of women with at least two children ever born by age at first birth and children ever born - Colombian Demographic and Health Surveys, 1985 - 2015

Age at first birth	Children ever born: Two	Three	Four+	Total
10-14	616	791	1754	3161
15-19	12842	10880	15001	38723
20-24	12013	7689	6476	26178
25-29	4408	1831	835	7074
30-34	1206	258	50	1514
35-39	162	14	4	180
Total	31247	21463	24120	76830

Note that calculations of the mean time to next boy and girl are based on two different sub-samples, one for boys and one for girls. These two samples only include women ages 39 and above at the survey moment (around 30% of the total sample). In addition, the sample for boys only include women who had boys at parities above one (second, third, etc.), and the sample for girls only include women with girls at parities above one.

5.2.2 Grammatical operations

We use one alignment operation and three different clocks to get at the aggregate-patterns of mean time to second birth and mean time to next boy and girl. We align women's reproductive trajectory on the age at first birth. Consider a women interviewed at age 39 who had three children at ages 25, 28, and 33. The first two were girls and the last one a boy. The following illustration represents her reproductive trajectory.

Age	15	...	25	26	27	28	29	30	31	32	33	...	39
Sex	-	...	girl	-	-	girl	-	-	-	-	boy	...	-

After alignment, the time zero for this woman is age 25, i.e, the age of her first birth. Using this age as a reference, the first clock counts the number of years to the second birth. The aligned-clocked sub-sequence for ages 25 to 28 for this woman looks like this: 3-2-1-0. This sub-sequence means that when the first birth occur (at age 25) this women had three years left before the second birth. At age 26, she had two years left, etc. By age 28, she had a second birth, for which the clock equals zero.

We define two analogous clocks to examine differences by the sex of the second birth. In the first case, the clock counts the remaining years to the next boy (a descending step clock); in the second case, the clock counts the remaining years to the next girl.

The following illustration displays the aligned sequence and the three clocks for the woman in our example.

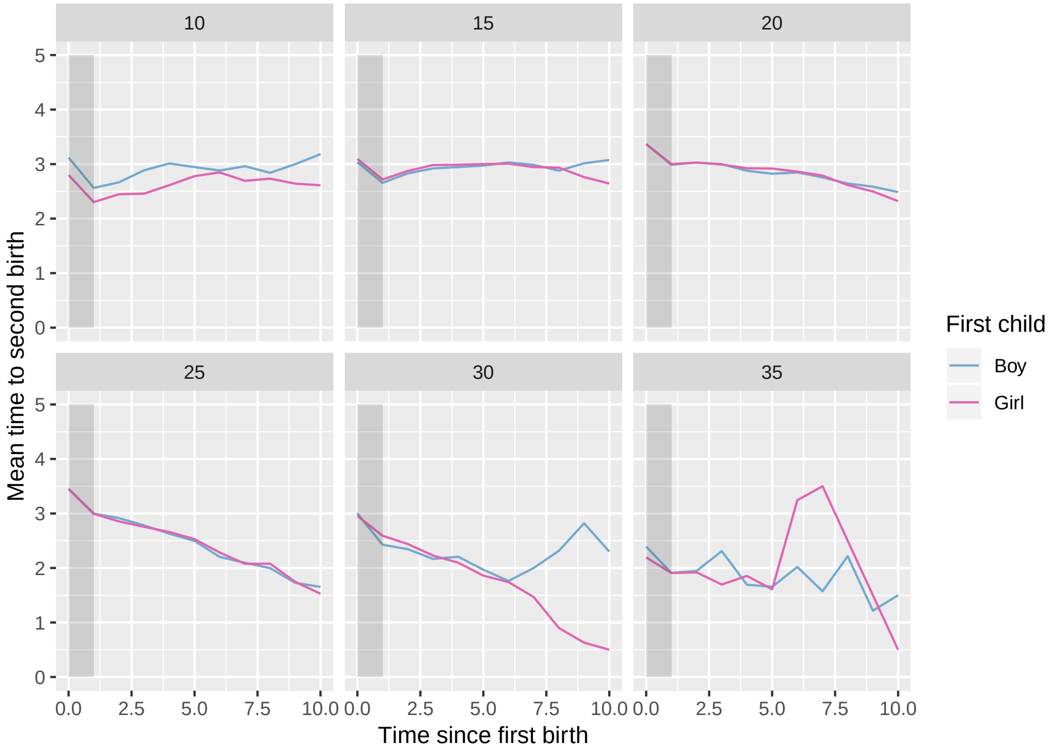
Time since birth	0	1	2	3	4	5	6	7	8	9	10
Age	25	26	27	28	29	30	31	32	33	34	35
Sex	girl	-	-	girl	-	-	-	-	boy	-	-
1st. Clock: To second birth	3	2	1	0	-	-	-	-	-	-	-
2nd. Clock: To next boy	8	7	6	5	4	3	2	1	0	-	-
3rd. Clock: To next girl	3	2	1	0	-	-	-	-	-	-	-

Note that the 2nd. and 3rd. clocks can only be defined if there is at least one boy and one girl after the first birth. This implies that the samples for the mean time to next boy and mean time to next girl are not identical. This difference between the samples is not problematic given the mere illustrative propose of our application. Moreover, clocks and sub-samples can be defined differently so that the two sample became identical, enhancing comparability.

5.2.3 Results

Figure 11 displays the aggregated patterns of the mean time to the second birth over the 10 years after the first child by women's age at first birth, and according to the sex of the first child. Overall, the mean time to the second birth range between 0.5 and slightly more than 3 years. Also, there are significant difference across age at first birth groups, and much more moderate discrepancies according to the sex of the first child.

Figure 11: Mean time to second birth by age at first birth (five-year age groups) and sex of the first child. Colombian DHS 1985-2015



Note: the gray rectangle of one year width indicate the birth of twins, i.e., mean time to next birth less than one year.

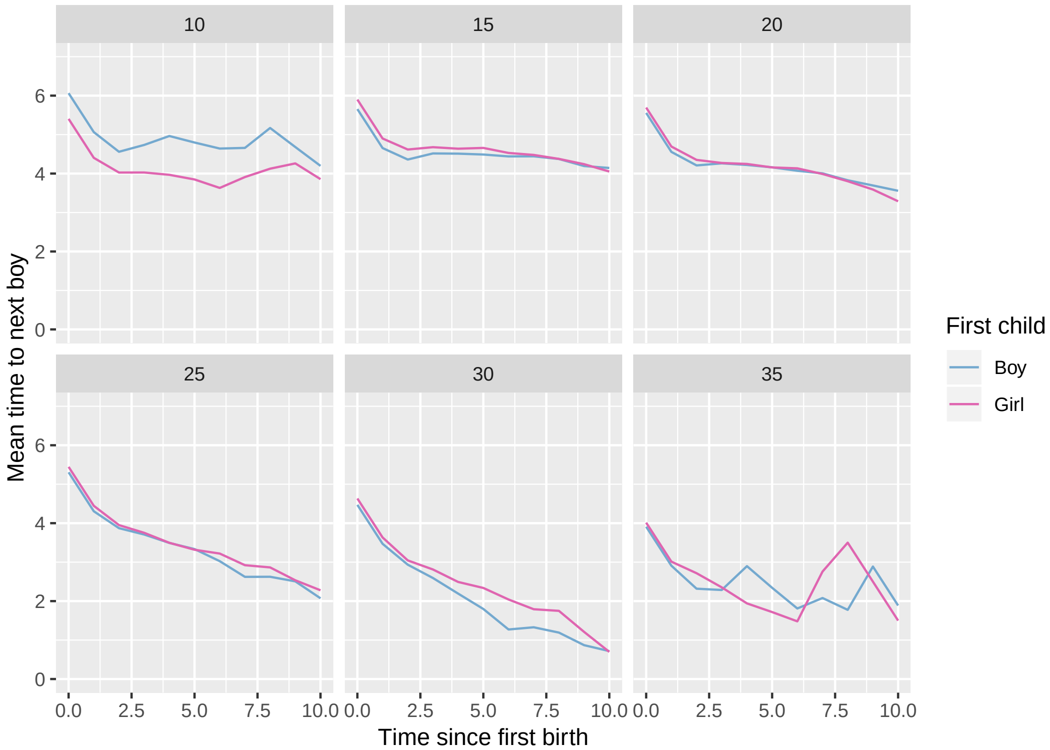
Among the first three age at first birth groups (10-14, 15-19, and 20-24), the mean time to second birth is relatively flat over the 10 years following the first birth meaning that the risk of a second birth is constant over the period after the first child. On average, between 2.5 and 3 years precede the birth of a second child when women become mothers before the age of 25. Additionally, in the first age group, the birth of a boy is associated with higher mean time to second birth during the 10 years after the first birth.

Among the other three age at first birth groups, the mean time to second birth decline over time. This decline is consistent with the fact that our sample include women with at least two children, i.e., we are certain that a second birth would eventually occurs in women's reproductive trajectories. In these three groups, differences by sex of the first birth are very small. Finally, the erratic patterns in the last age groups are due to small sample size.

Figure 12 examine the mean time to next boy, i.e., the mean number of years that precede a male birth, again, by women's age at first birth and the sex of the first child. Because of the way clock are defined, the mean time to next boy are about twice the mean time to second birth (refer to Figure 11). As for the mean time to second birth, differences by age at first birth are substantial, and differences by the sex of the first child are not.

According to Figure 12, early transition to first birth is associated with increasing mean time to next boy. In other words, when the first birth occur before age 15, the risk of having a boy decreases linearly over time. This is an interesting pattern because it is unique to women who had their first birth before age 15, and it does not depend on the sex of the first child. On the contrary, the pattern of the mean time to next boy for women who had their first birth between ages 15 and 24 looks more like an inverted U. By construction, the mean time to next boy among the last three age groups decline linearly.

Figure 12: Mean time to next boy by age at first birth (five-year age groups) and sex of the first child. Colombian DHS 1985-2015

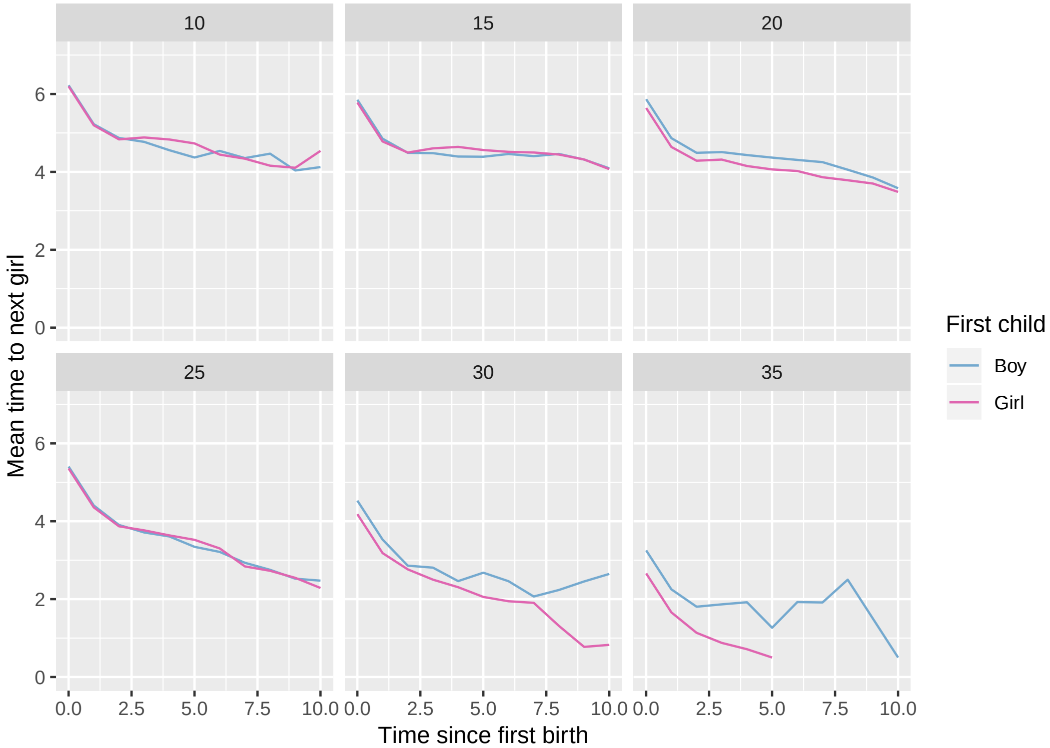


Note: the gray rectangle of one year width indicate the birth of twins, i.e., mean time to next birth less than one year.

Figure 12 also shows that, between ages 15 and 34, having a male first birth is associated with a faster transition to a second male birth at least during the first 10 years after the first birth. Interestingly, these differences are larger among the 25-29 age group, and even more significant in the 30-34 age groups. Consistently with the definitions of the clocks, the sex gap narrows towards the end of the ten-year period because male births eventually occur.

A similar pattern is observed in Figure 13 for the mean time to next girl. The mean time to next girl increases over time for women who had their first child before age 15, and it displays an inverted U-shaped pattern for ages 15 to 24. Consistently, female births are associated with a faster transition to a female birth in these first three age groups.

Figure 13: Mean time to second birth by age at first birth (five-year age groups) and sex of the first child. Colombian DHS 1985-2015



Note: the gray rectangle of one year width indicate the birth of twins, i.e., mean time to next birth less than one year.

Compared to the mean time to the next boy, the mean time to next girl displays larger differences by sex of the first child. In other words, the positive association between the sex of the first birth and the mean time of a birth of the same sex, is stronger for girl than boys.

6 Discussion

We propose a two-part grammar of data operations to facilitate the creative derivation of demographic macro patterns. Our two applications for cases of birth interval differentials and disability inequalities demonstrate some of the flexibility and power of this grammar. The two grammatical elements, clocks and alignment operations, each have several potential variants. These operations may be executed in isolation or together for the same set of trajectories. We demonstrate clocks building from the simplest case of age-structured prevalence, and generalizing to a portfolio of yet-unexplored clock types. Some of these may already be familiar in specific contexts. For example birth parity would be considered an ascending order clock in our framework. Alignment operations are also already familiar in specific contexts, for example time-to-death patterns of morbidity or health expenditure would be considered a right-alignment on the end of life. Indeed, when we do this for the disability example we reproduce stylistic time-to-death patterns that have been directly observed in other populations (Klijs et al. 2010, Riffe et al. 2016). We generalize alignment operations by allowing for conditional alignment, for example on entry or exit from the first, last or longest episode of a given state or merged set of states.

The clocks and alignment framework was developed in order to accelerate experimentation with new macro patterns. Some of these operations might have tractable analogs in using Markov assumptions and matrix algebra approach, but with an extra derivation step, and the solutions will not necessarily be computationally efficient. For the case of patterns derived from observed trajectories, as in our example of retrospective fertility histories, the results of such an exercise would also not be guaranteed to produce identical results as this framework. This is because the Markov approach is based on transition probabilities, which are not guaranteed to generate the same trajectory structure from which they were derived, whereas the clocks and alignment approach builds on this original structure.

The data operations we describe may also be complementary to sequence analysis (SA), or may even be considered a subset of it, or implied by some of its algorithms. We suppose that the operations we describe could also be used within SA as a trajectory pre-processing step. For example, one of the inspirations to design this framework was a sequence analysis of disease states preceding death conducted by peer scientists. This exercise was frustrated and abandoned due to heterogeneity in length of life, but a methods constraint for trajectories to be of equal length. Alignment on end of life, and truncation to the N preceding years would then allow for a variety of sequence clustering algorithms. This is essentially the exercise of Potente and Monden (2018) and Raab et al. (2018). We hope our expanded set of alignment variants facilitates more diverse and flexible pattern detection of this kind.

The purpose of episode clocks and trajectory realignment is to detect important patterns in data (or model results) that are likely to otherwise go unnoticed. Some reasonable priors might include that (i) life course events condition each other; (ii) temporal proximity to life course transitions is likely to be an important predictor of other transitions; (iii) within-episode patterns of other characteristics might be monotonically increasing or decreasing, concave, or convex. Aggregate patterns derived after such operations may be sharper and of more obvious interpretation and consequence than are age patterns. We think that this simple grammar has the potential to stimulate new questions and lead to new discoveries as well as better understandings of seemingly understood phenomena. Its generality is ensured by the provision of grammatical structure, which enables researchers to define new operations and further variants of clocks and alignments.

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References

Paul D. Allison. Discrete-Time Methods for the Analysis of Event Histories. *Sociological Methodology*, 13:61, 1982. ISSN 00811750. doi: 10.2307/270718.

Hal Caswell and Virginia Zarulli. Matrix methods in health demography: a new approach to the stochastic analysis of healthy longevity and dalys. *Population health metrics*, 16(1):8, 2018.

Eileen M Crimmins, Yasuhiko Saito, and Dominique Ingegneri. Trends in disability-free life expectancy in the United States, 1970-90. *Population and Development Review*, pages 555–572, 1997.

Eileen M Crimmins, Mark D Hayward, Aaron Hagedorn, Yasuhiko Saito, and Nicolas Brouard. Change in disability-free life expectancy for americans 70 years old and older. *Demography*, 46(3):627–646, 2009.

C. Dudel and M. Myrskylä. Estimating the expected number and length of episodes using markov chains with rewards. (under review), 2017a.

Christian Dudel and Mikko Myrskylä. Working life expectancy at age 50 in the united states and the impact of the great recession. *Demography*, Oct 2017b. ISSN 1533-7790. doi: 10.1007/s13524-017-0619-6. URL `https://doi.org/10.1007/s13524-017-0619-6`.

Simona Iacobelli and Bendix Carstensen. Multiple time scales in multi-state models. *Statistics in medicine*, 32(30):5315–5327, 2013.

Bart Klijs, Johan P Mackenbach, and Anton E Kunst. Disability occurrence and proximity to death. *Disability and rehabilitation*, 32(21):1733–1741, 2010.

Sarah B Laditka and Douglas A Wolf. New methods for analyzing active life expectancy. *Journal of Aging and Health*, 10(2):214–241, 1998.

Cecilia Potente and Christiaan Monden. Disability pathways preceding death in england by socioeconomic status. *Population studies*, 72(2):175–190, 2018.

Marcel Raab, Anette Fasang, and Moritz Hess. Pathways to death: The co-occurrence of physical and mental health in the last years of life. *Demographic Research*, 38:1619–1634, 2018.

Tim Riffe, Pil H Chung, Jeroen Spijker, and John MacInnes. Time-to-death patterns in markers of age and dependency. *Vienna Yearbook of Population Research*, 14:229–254, 2016.

Tim Riffe, Jonas Schöley, and Francisco Villavicencio. A unified framework of demographic time. *Genus*, 73(1):7, 2017.

Giorgio Alfredo Spedicato. Discrete time markov chains with r. *The R Journal*, 07 2017. URL `https://journal.r-project.org/archive/2017/RJ-2017-036/index.html`. R package version 0.6.9.7.

DF Sullivan. A single index of mortality and morbidity. *HSMHA Health Reports*, 86:347–354, 1971.