Statistics of inter-individual variation in lifetime fertility: a Markov chain approach*[†]

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Abstract

Lifetime fertility is the total number of children (or sometimes of female children) to which a woman gives birth over her lifetime. The net reproductive rate R_0 is the expectation of lifetime fertility. The total fertility rate (TFR) is the expectation conditional on the woman surviving through her childbearing years. Both R_0 and TFR can be calculated from age- or stage-classified demographic models. Because it is an expectation, R_0 provides no information on variability. Here, I present and apply a new approach, based on the theory of Markov chains with rewards, that provides all the moments of the distribution of lifetime reproduction. The approach applies to age- or stage-classified models, to constant, periodic, or stochastic environments, and to any kind of reproductive schedule. As examples, I calculate and compare these statistics for models in which fertility depends on age, or on age and parity, using data from Sweden in 1970 and the Czech Republic in 1950.

1 Introduction

1.1 Lifetime fertility

Lifetime fertility is the total number of children, or sometimes the number of female children, a woman has over her lifetime. The net reproductive rate R_0 measures the expectation of lifetime fertility. As is well known (Cushing and Zhou, 1994; Caswell, 2001, 2009), R_0 expressed as female offspring per female is also the population growth rate per generation (not per unit of time), and is an indicator function for population growth, in that population growth is positive if and only if $R_0 > 1$. It is calculated from age-classified models as

$$R_0 = \int_0^\infty \ell(x) m(x) dx, \tag{1}$$

where $\ell(x)$ is surivorship to age x and $m(x)$ is fertility at age x (Rhodes, 1940), and from stage classified models as

$$R_0 = \max \operatorname{eig} \left[\mathbf{F} \left(\mathbf{I} - \mathbf{U} \right)^{-1} \right], \tag{2}$$

where $\mathbf{F}$ is a matrix of stage-specific fertilities and $\mathbf{U}$ is a matrix giving transition probabilities of individuals among stages (Cushing and Zhou, 1994; Caswell, 2001, 2009; de Camino-Beck and Lewis, 2007). In evolutionary demography, R_0 is sometimes used as a measure of fitness, although this works only under certain circumstances (Metz, 2008). In epidemiology, R_0 gives the expected number of secondary infections following the introduction of a single infectious individual into a susceptible population (Heesterbeek, 2002). The infection can spread and produce an outbreak if and only if $R_0 > 1$.

Because it is an expectation, R_0 provides no information on that baseline level of variability. My goal here is to present a general and tractable calculation of all the moments of lifetime fertility, applicable to stage- or age-classified populations, for arbitrary distributions of stage-specific reproduction. Although I will not address it here, it applies to constant, periodic, and stochastic environments (Caswell, 2011). The calculations use a mathematical framework (Markov chains with rewards) that has many potential applications to questions in addition to lifetime reproductive output.

Notation. Matrices are denoted by upper-case bold symbols (e.g., $\mathbf{P}$), vectors by lower-case bold symbols (e.g., $\boldsymbol{\rho}$). Some block-structured matrices are denoted by, e.g., $\mathbb{P}$. Vectors are column vectors by default. The transpose of $\mathbf{P}$ is $\mathbf{P}^{\mathsf{T}}$. The vector $\mathbf{1}$ is a vector of ones. The diagonal matrix with the vector $\mathbf{x}$ on the diagonal and zeros elsewhere is denoted $\mathcal{D}(\mathbf{x})$. The expected value is denoted by $E(\cdot)$, the variance by $V(\cdot)$, the coefficient of variation by $CV(\cdot)$ and the skewness by $Sk(\cdot)$. The Hadamard, or element-by-element, product of matrices $\mathbf{A}$ and $\mathbf{B}$ is denoted by $\mathbf{A} \circ \mathbf{B}$. Transition matrices of Markov chains are written in column-to-row orientation, and hence are column-stochastic.

1.2 The approach: Markov chains with rewards

The method used here was introduced in Caswell (2011) and applied there to a variety of species. We use an absorbing Markov chain to describe the life cycle, and associate a "reward" with each possible transition among the states of the Markov chain. Death appears in the model as an absorbing state, or possibly multiple absorbing states (e.g., representing causes of death). The transition matrix of this absorbing chain can be written

$$\mathbf{P} = \left(\begin{array}{c|c} \mathbf{U} & 0 \\ \hline \mathbf{M} & \mathbf{I} \end{array} \right) \tag{3}$$

where $\mathbf{U}$ is the transient matrix (dimension $s \times s$) and $\mathbf{M}$ is a matrix of mortality rates. I will assume throughout that the dominant eigenvalue of $\mathbf{U}$ is less than 1, so that an individual beginning in any transient state will eventually be absorbed (i.e., will eventually die) with probability 1.

In a Markov chain with rewards, an individual moving from state j to state i collects a reward r_{ij}. In the present application, the reward corresponds to reproduction. Markov chains with rewards were introduced by Howard (1960) to analyze Markov decision processes. In his development, the reward r_{ij} was a fixed quantity. Here, however, I will consider the r_{ij} to be random variables with specified statistical properties (Benito, 1982). Fixed rewards follow as a special case.

1.3 Reproduction as a reward

In age-classified demographic models, reproduction between t and $t+1$ is a function of the age at time t, independent of the transition made by the individual between t and $t+1$. If this is so, the r_{ij} will depend only on j. In an age-parity model, reproduction is associated with the transition from one parity state to the next. In this case, r_{ij} will depend explicitly on both i and j. The analysis here also assumes that the dead do not reproduce, so $r_{ij} = 0$, for all j that represent absorbing states.

2 Analytical methods

As an individual moves through the stages of the life cycle, it accumulates reproductive rewards. The goal of our analysis is to calculate the statistical properties (mean, variance, skewness) of the accumulated lifetime reward. The solution to this problem is provided by an simple set of recurrence relations (Caswell, 2011).

Define $\boldsymbol{\rho}$ as the vector (dimension $(s+1) \times 1$) of accumulated rewards as a function of the initial stage of the individual. The vector of kth moments of the entries of $\boldsymbol{\rho}$ is denoted $\boldsymbol{\rho}_k$, where

$$\boldsymbol{\rho}_k = \left(\; E\left[\rho_i^k\right] \; \right). \tag{4}$$

The rewards r_{ij} are random variables. The matrix of the kth moments of the r_{ij} is denoted $\mathbf{R}_k$:

$$\mathbf{R}_k = \left(\; E\left[r_{ij}^k \right] \; \right). \tag{5}$$

Caswell (2011) proved that the moment vectors $\boldsymbol{\rho}_i$ can be calculated recursively as follows. Let $\mathbf{P}$ be the transition matrix of the Markov chain, let $\mathbf{R}_k$ be the matrix of kth moments of the transition-specific rewards. Calculations are referenced to a terminal time T. The first three moments of the accumulated reward satisfy

$$\begin{aligned}
\boldsymbol{\rho}_1(t+1) &= (\mathbf{P} \circ \mathbf{R}_1)^{\mathsf{T}} \mathbf{1} + \mathbf{P}^{\mathsf{T}} \boldsymbol{\rho}_1(t) && (6)\\
\boldsymbol{\rho}_2(t+1) &= (\mathbf{P} \circ \mathbf{R}_2)^{\mathsf{T}} \mathbf{1} + 2\,(\mathbf{P} \circ \mathbf{R}_1)^{\mathsf{T}} \boldsymbol{\rho}_1(t) + \mathbf{P}^{\mathsf{T}} \boldsymbol{\rho}_2(t) && (7)\\
\boldsymbol{\rho}_3(t+1) &= (\mathbf{P} \circ \mathbf{R}_3)^{\mathsf{T}} \mathbf{1} + 3\,(\mathbf{P} \circ \mathbf{R}_2)^{\mathsf{T}} \boldsymbol{\rho}_1(t) + 3\,(\mathbf{P} \circ \mathbf{R}_1)^{\mathsf{T}} \boldsymbol{\rho}_2(t) + \mathbf{P}^{\mathsf{T}} \boldsymbol{\rho}_3(t) && (8)
\end{aligned}$$

for $t = 0, \ldots, T-1$, with $\boldsymbol{\rho}_1(0) = \boldsymbol{\rho}_2(0) = \boldsymbol{\rho}_3(0) = 0$. In general, the mth moments of accumulated rewards are given by

$$\boldsymbol{\rho}_m(t+1) = \sum_{k=0}^{m} \binom{m}{k} (\mathbf{P} \circ \mathbf{R}_{m-k})^{\mathsf{T}} \boldsymbol{\rho}_k(t) \tag{9}$$

with $\boldsymbol{\rho}_m(0) = 0$. The combination of the assumptions that $\mathbf{P}$ has the structure (3) and that $r_{ij} = 0$ for all absorbing states j means that every individual will eventually be absorbed in a state in which future rewards are zero; thus $\boldsymbol{\rho}_1(t)$ will converge to a limit as $T \to \infty$; this limit is the expectation of lifetime rewards calculated over the entire lifetime of every individual. See Caswell (2011) for proofs and further references.

The first moment $\boldsymbol{\rho}_1$ gives the mean lifetime reproductive output. The variance, standard deviation, coefficient of variation, and skewness of lifetime reproductive output are calculated from the moment vectors

$$\begin{aligned}
V(\boldsymbol{\rho}) &= \boldsymbol{\rho}_2 - \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_2 && (10)\\
SD(\boldsymbol{\rho}) &= \sqrt{V(\boldsymbol{\rho})} && (11)\\
CV(\boldsymbol{\rho}) &= \mathcal{D}(\boldsymbol{\rho}_1)^{-1}\, SD(\boldsymbol{\rho}) && (12)\\
Sk(\boldsymbol{\rho}) &= \mathcal{D}\left[V(\boldsymbol{\rho})\right]^{-3/2} \left(\rho_3 - 3\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_2 + 2\boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1 \circ \boldsymbol{\rho}_1\right). && (13)
\end{aligned}$$

The variance is useful because it can be partitioned additively among sources. The standard deviation cannot be partitioned in this way, but it has the advantage of appearing in the same units as $\boldsymbol{\rho}$. The CV scales the standard deviation relative to the mean, and hence is dimensionless. The CV is also the square root of Crow's (1958) index of the opportunity for selection; this provides a upper bound on the rate of increase of mean fitness, if fitness is measured by lifetime reproduction and all the variance in reproduction is genetic. Finally, the skewness, which is dimensionless, measures the symmetry of the distribution of rewards. Positive skewness implies a long tail of positive values, and vice versa.

The ith element of the vector $\boldsymbol{\rho}$ gives the lifetime reproductive output of an individual of age i; this can be referred to as the *remaining lifetime* accumulation.

Several authors in the widely scattered literature on Markov chains with rewards have addressed the variance, but not the complete set of moments, of accumulated rewards. (e.g., Sladkỳ and van Dijk, 2005; Benito, 1982).

3 Analysis of age-dependent fertility

Age-dependent fertility is parameterized by the vector $\mathbf{p}$ of age-specific survival probabilities and the vector $\mathbf{f}$ of age-specific fertilities. The model follows the standard structure of an age-classified Leslie matrix. A surviving individual moves to the next age class, hence the transition matrix $\mathbf{U}$ contains survival probabilities on the subdiagonal and zeros elsewhere (Figure 1a):

$$\mathbf{U} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ p_1 & 0 & 0 & 0 \\ 0 & p_2 & 0 & 0 \\ 0 & 0 & p_3 & 0 \end{pmatrix} \tag{14}$$

(here written for 4 age classes).

The reward matrices are defined from the vector $\mathbf{f}$ of age-specific fertilities. Ignoring multiple births, the number of offspring at age j is a Bernoulli random variable with moments

$$E[r_{ij}] = f_j \tag{15}$$

$$E\left[r_{ij}^2\right] = f_j \tag{16}$$

$$E\left[r_{ij}^3\right] = f_j. \tag{17}$$

Thus the reward matrices containing the moments of offspring production are

$$\mathbf{R}_k = \left(\begin{array}{cccc|c} f_1^k & f_2^k & f_3^k & f_4^k & 0 \\ f_1^k & f_2^k & f_3^k & f_4^k & 0 \\ f_1^k & f_2^k & f_3^k & f_4^k & 0 \\ f_1^k & f_2^k & f_3^k & f_4^k & 0 \\ \hline f_1^k & f_2^k & f_3^k & f_4^k & 0 \end{array}\right) \qquad k = 1, 2, 3 \tag{18}$$

(again, for the case with four age classes).

As an example, I analyze a historical sequence of mortality and fertility for the human population of Sweden from 1891 to 2007 (Human Mortality Database, 2013; Human Fertility Database, 2013). This period included two world wars, the 1916 flu epidemic, and a health transition sufficient to raise female life expectancy at birth from 53 to 83 years.

4 Analysis of fertility dependent on age and parity

The life cycle graph for a population in which individuals are classified by age and parity is shown in Figure 1b. The Markov chain matrix appropriate to this classification is derived using the vec-permutation methodology (Hunter and Caswell, 2005; Caswell, 2011).

We begin by defining age classes $1, \ldots, \omega$ and parity states $1, \ldots, s$. Transitions among parity states for age class i are described by a $s \times s$ matrix given by

$$\mathbf{B}(i) = \begin{pmatrix} 1 - q_1(i) & 0 & 0 & 0 \\ q_1(i) & 1 - q_2(i) & 0 & 0 \\ 0 & q_2(i) & 1 - q_3(i) & 0 \\ 0 & 0 & q_3(i) & 1 \end{pmatrix} \qquad i = 1, \ldots, \omega \tag{19}$$

(shown here for $s = 4$ parity classes). The quantity $q_j(i)$ is the probability of transition from parity class j to $j+1$ for an individual in age class i.

For ages less than the age at first reproduction, $\mathbf{B}(i) = \mathbf{I}_s$, and it is impossible to advance to the next parity class. The entry in the bottom right corner corresponds to an open final parity class. The parity transition probabilities q_i are available for parity 0, 1, 2, 3, 4, and 5+ from the age-parity fertility tables in the Human Fertility Database Human Fertility Database (2013).

Transitions from one age class to the next for parity state j are given by a $\omega \times \omega$ matrix

$$\mathbf{M}(j) = \begin{pmatrix} 0 & 0 & 0 & 0 \\ p_1(i) & 0 & 0 & 0 \\ 0 & p_2(i) & 0 & 0 \\ 0 & 0 & p_3(i) & 0 \end{pmatrix} \qquad i = 1, \ldots, s \tag{20}$$

(shown here for $\omega = 4$ age classes). The matrix entry $p_i(j)$ is the surival probability of an individual in age class i and parity class j. In the absence of parity-specific mortality data, all the $\mathbf{M}(j)$ will be equal.

The Markov chain describing the joint dynamics of age and parity is created from the block diagonal matrices

$$\mathbb{B} = \begin{pmatrix} \mathbf{B}(1) & & \\ & \ddots & \\ & & \mathbf{B}(\omega) \end{pmatrix} \qquad \text{parity state transitions} \tag{21}$$

$$\mathbb{M} = \begin{pmatrix} \mathbf{M}(1) & & \\ & \ddots & \\ & & \mathbf{M}(s) \end{pmatrix} \qquad \text{age transitions} \tag{22}$$

The transient matrix $\tilde{\mathbf{U}}$ and the transition matrix $\tilde{\mathbf{P}}$ are then

$$\tilde{\mathbf{U}} = \mathbf{K}^{\mathsf{T}}\, \mathbb{M}\, \mathbf{K}\, \mathbb{B} \tag{23}$$

$$\tilde{\mathbf{P}} = \left(\begin{array}{c|c} \tilde{\mathbf{U}} & 0 \\ \hline \mathbf{1}^{\mathsf{T}} - \mathbf{1}^{\mathsf{T}}\tilde{\mathbf{U}} & 1 \end{array}\right) \tag{24}$$

Where the row vector $\mathbf{1}^{\mathsf{T}} - \mathbf{1}^{\mathsf{T}}\tilde{\mathbf{U}}$ contains the age- and parity-specific probabilities of death. The matrix $\mathbf{K}$ is the vec-permutation matrix (also called the commutation matrix) of order (s, ω) (Henderson and Searle, 1981; Magnus and Neudecker, 1979; Hunter and Caswell, 2005).

Rewards, in the form of reproduction, are obtained when an individual advances from one parity state to the next (Figure 1b). The reward matrices corresponding to the parity transition matrix (19) are

$$\mathbf{R}_j(i) = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & q_s(i) \end{pmatrix} \qquad \begin{array}{l} i = 1, \ldots, \omega \\ j = 1, 2, 3 \end{array} \tag{25}$$

The entry $q_s(i)$ in the lower right corner is the reward obtained by treating reproduction in the open parity interval as a Bernoulli random variable.

The reward matrix corresponding to age-parity transition matrix $\tilde{\mathbf{P}}$ is a block-structured matrix constructed from the $\mathbf{R}_j(i)$:

$$\tilde{\mathbf{R}}_j = \left(\begin{array}{ccc|c} \mathbf{R}_j(1) & \cdots & \mathbf{R}_j(\omega) & 0 \\ \vdots & & \vdots & \vdots \\ \mathbf{R}_j(1) & \cdots & \mathbf{R}_j(\omega) & 0 \\ \hline \mathbf{0}_{s\times 1} & \cdots & \mathbf{0}_{s\times 1} & 0 \end{array} \right) \tag{26}$$

The analysis of lifetime reproduction now proceeds using (6)–(13), using the Markov chain matrix $\tilde{\mathbf{P}}$ and the reward matrices $\tilde{\mathbf{R}}_1$, $\tilde{\mathbf{R}}_2$, and $\tilde{\mathbf{R}}_3$.

The result is a set of moment vectors $\boldsymbol{\rho}_i$, of dimension $(s\omega + 1) \times 1$, that give the moments of lifetime reproduction as a function of current age and parity.

5 Applications: Sweden and Czech Republic

The results of the age-specific and the age-parity-specific fertility models can be examined in seveal different ways. One of these, the analysis of temporal trends, will be presented elsewhere (van Daalen and Caswell in prep.). Here, I examine the age patterns of the mean and variation in lifetime fertility, for two countries, selected (more or less arbitrarily) to represent two different mortality and fertility situations. Sweden in 1970 had a period female life expectancy at birth of 77.2 years, and a TFR of 1.9. The Czech Republic in 1950 had a life expectancy of 66.8 years and a TFR of 2.8. The results may hint at patterns to be expecte comparing countries in the earlier and the later stages of a fertility transition. Period life tables were obtained from the Human Mortality Database (2013), and age-parity fertility tables from the Human Fertility Database (2013).

The results are shown in a series of figures, organized as follows:

1. Age trajectories of the mean, standard deviation, coefficient of variation, and skewness of lifetime reproduction for Sweden 1970 (Figure 2).
2. Age trajectories of the mean, standard deviation, coefficient of variation, and skewness of lifetime reproduction for Czech Republic 1950 (Figure 3).
3. Bar plots showing the interaction of age and parity in determining the statistics of lifetime reproduction for selected ages, for Sweden 1970 (Figures 4 and 6).
4. Bar plots showing the interaction of age and parity in determining the statistics of lifetime reproduction for selected ages, for Czech Republic 1950 (Figures 5 and 8).

A few patterns are obvious from these comparisons. In both Sweden and Czech Republic, the mean and standard deviation of remaining lifetime reproduction decline with age (no surprise in the former; the latter is not as easily predictable). When variation is measured relative to the mean, there is a dramatic increase in the CV with age. The skewness follows the same pattern. In both countries, then, remaining lifetime reproduction becomes more uncertain and highly positively skewed at ages breater than about 35 (Figures 2 and 3).

The age-parity-specific model shows similar patterns, but there is a striking difference between Sweden and Czech Republic. For Sweden, the mean, standard deviation, CV, and skewness in lifetime reproduction are highest for parity 0, and lower for higher parity states. The pattern is the opposite in the Czech Republic; higher parity women have a higher expectation and standard deviation of lifetime reproduction.

The effects of parity are far from trivial. At the same age, differences in parity may change the mean, standard deviation, and CV of lifetime reproduction by a factor of 3 or more, and the skewness by a factor of 5.

6 Discussion

6.1 Variability and heterogeneity are not the same thing

Empirical measurements of lifetime fertility (in any species) typically reveal variation — often large amounts of variation — among individuals. The distribution is often positively skewed, with a long tail of rare individuals producing more than the average number of offspring; e.g., many examples in Clutton-Brock (1988) and Newton (1989). The observed variability and skewness of lifetime fertility is sometimes interpreted as evidence of heterogeneity among individuals. However, variability in lifetime fertility is to be expected even in the absence of heterogeneity.

Demographic variation in lifetime fertility arises from three sources. One source is individual stochasticity: stochastic variation among individuals in the pathways they take through the life cycle (Caswell, 2009). A cohort of identical individuals, experiencing identical vital rates at every stage, will differ in how long they live and how long they spend in each stage (Caswell, 2009). A second source of variation is within-stage variation in reproduction. A cohort of identical individuals, in the same stage, experiencing the same probability distribution of stage-specific reproduction, will differ in how many offspring they produce. The analysis here includes both sources. These stochastic processes are collectively called *individual stochasticity* Caswell (2009, 2011). They produce variation even if all individuals are absolutely identical, experiencing the same vital rates at every age or stage. The results presented here obtained in exactly this way; every individual experiences the same probabilities as captured in $\mathbf{P}$ and the $\mathbf{R}_i$. Thus these results provide cannot be used to infer differences among women due to heterogeneity.

Of course, *unobserved heterogeneity* does exist; individuals are genuinely different from each other in ways not captured by age, or by age and parity. If individuals are different, they will experience different transition probabilities ($\mathbf{P}$) and/or rewards ($\mathbf{R}_i$). Heterogeneity may reflect fixed differences (e.g., genetic differences, or differences in local environment among individuals of sessile species), or differences that develop over time (e.g., accumulated damage caused by environmental factors). In order to compare the contributions of heteregenity and individual stochasticity, the heterogeneity must be incorporated into the Markov chain model. This has been done for mortality models based on heterogeneous frailty (Caswell, 2014), and will be pursued for fertility in a future paper.

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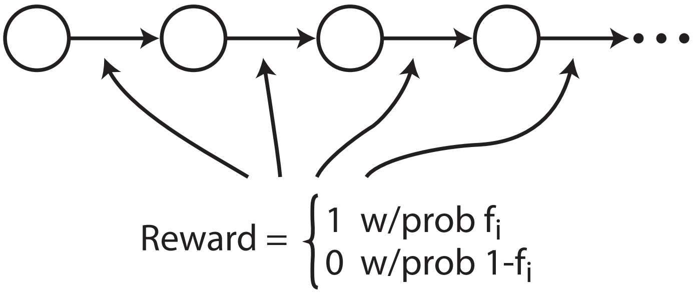
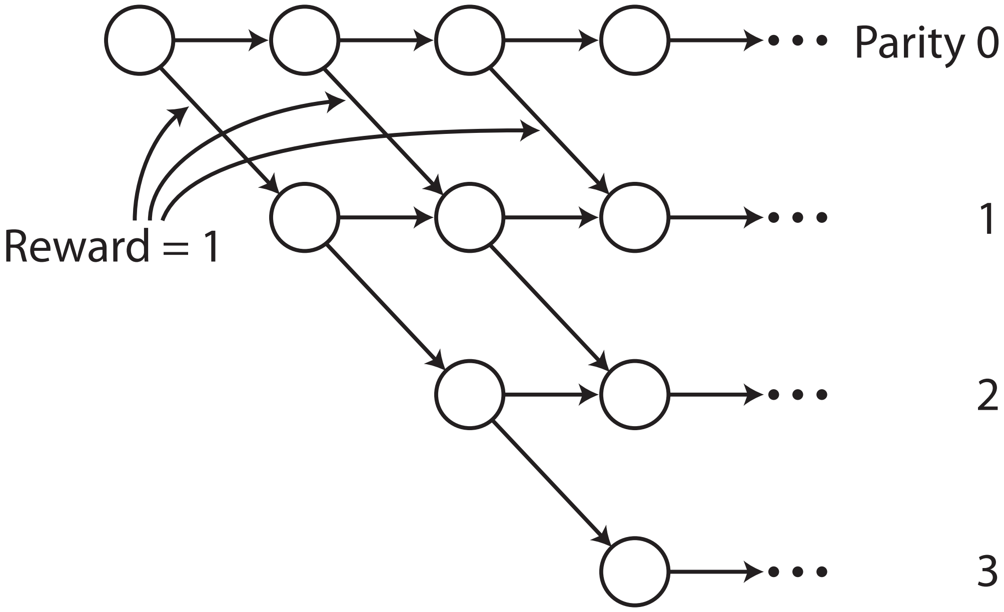
8 Figures

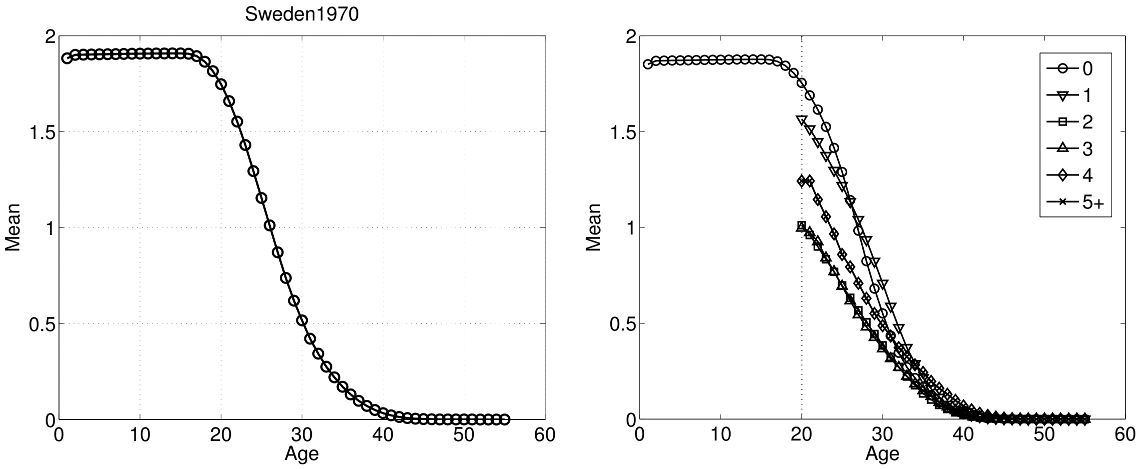


(a) Age-dependent fertility



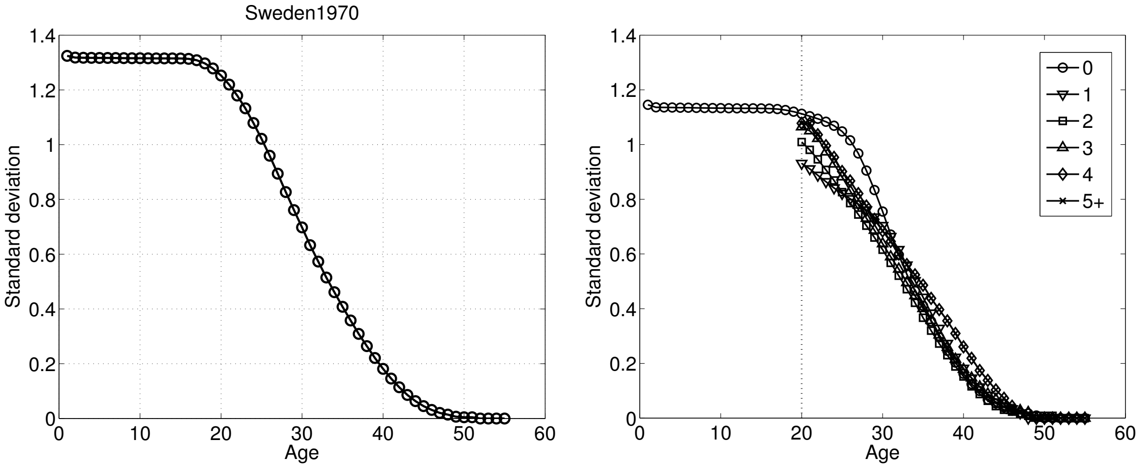
(b) Age-parity-dependent fertility

Figure 1: Life cycle structures for (a) age-dependent fertility and (b) age-parity-dependent fertility, showing the rewards dependent on stages (for the first case) and on transitions (for the second case).



(a) Age-dependent

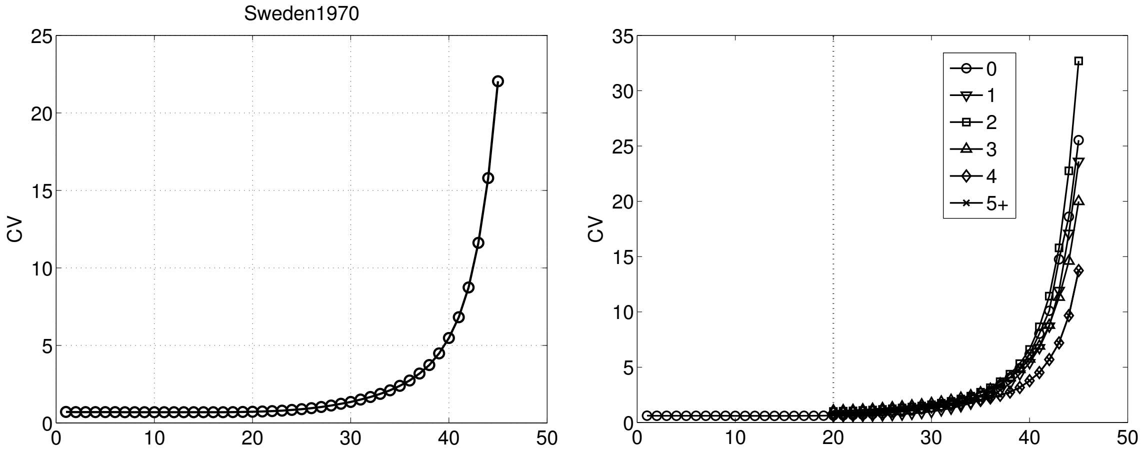
(b) Parity-dependent



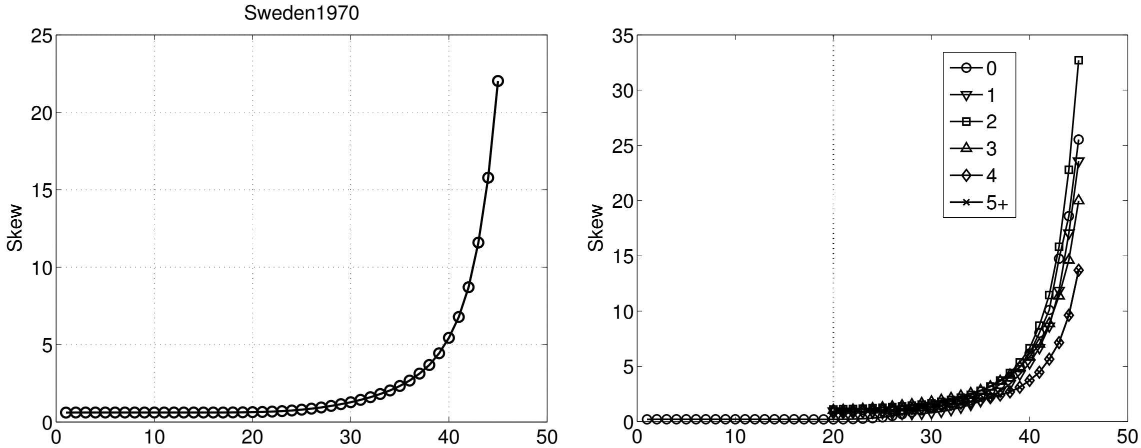
(c) Age-dependent

(d) Parity-dependent

Figure 2: The mean (above) and standard deviation (below) of lifetime reproductive out put for Sweden in 1970. Graphs in the left column show statistics of *age-specific* lifetime reproduction. The right column shows *age-parity-specific* lifetime reproduction. Values for parity states greater than 0 are shown from age 20 onwards. Continued on next figure.

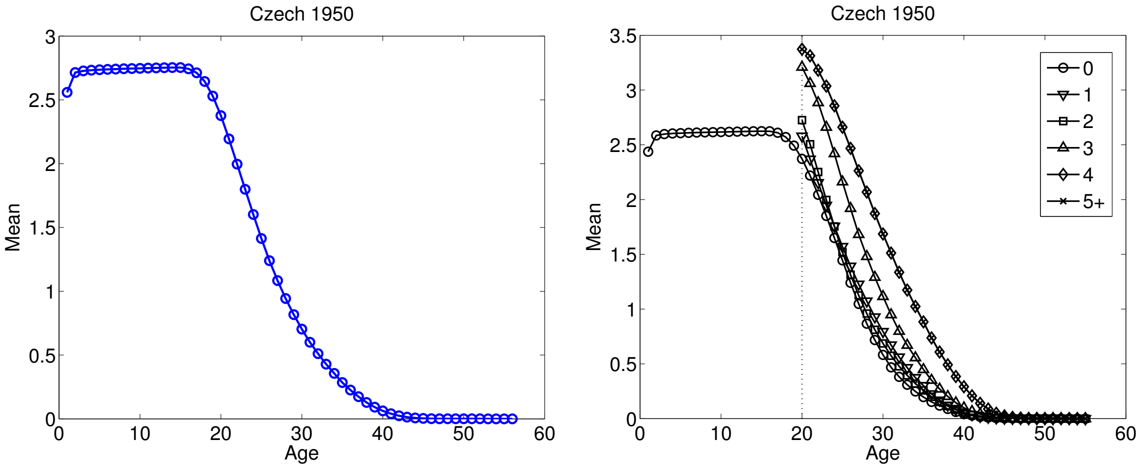


(a) Age-dependent **(b)** Parity-dependent

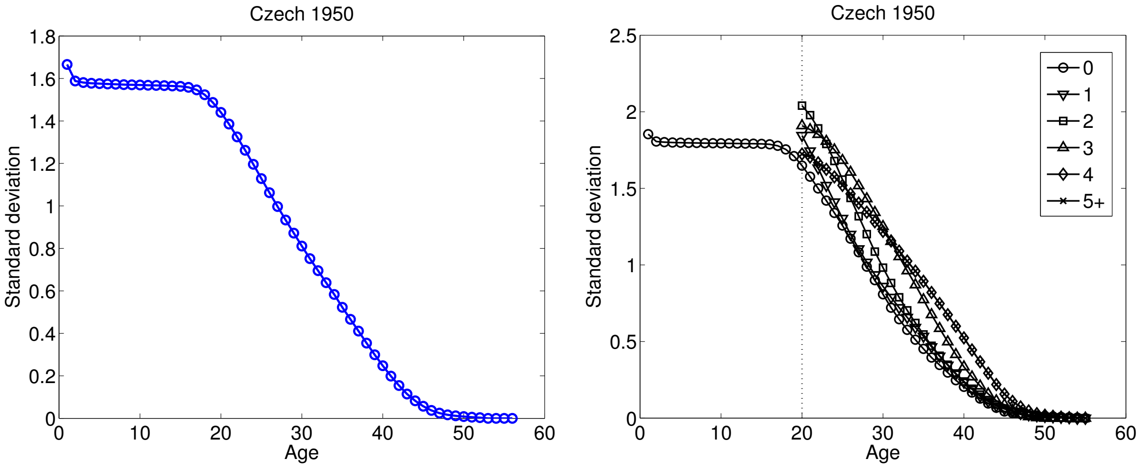


(c) Age-dependent **(d)** Parity-dependent

Figure 2: (continued) The coefficient of variation (above) and skewness (below) of lifetime reproductive out put for Sweden in 1970. Graphs in the left column show statistics of *age-specific* lifetime reproduction. The right column shows *age-parity-specific* lifetime reproduction. Values for parity states greater than 0 are shown from age 20 onwards.

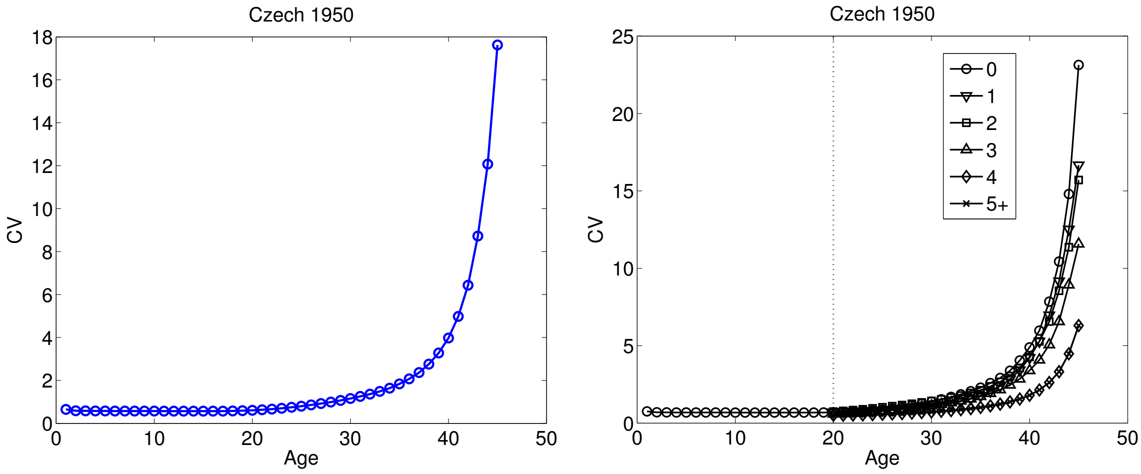


(a) Age-dependent **(b)** Parity-dependent

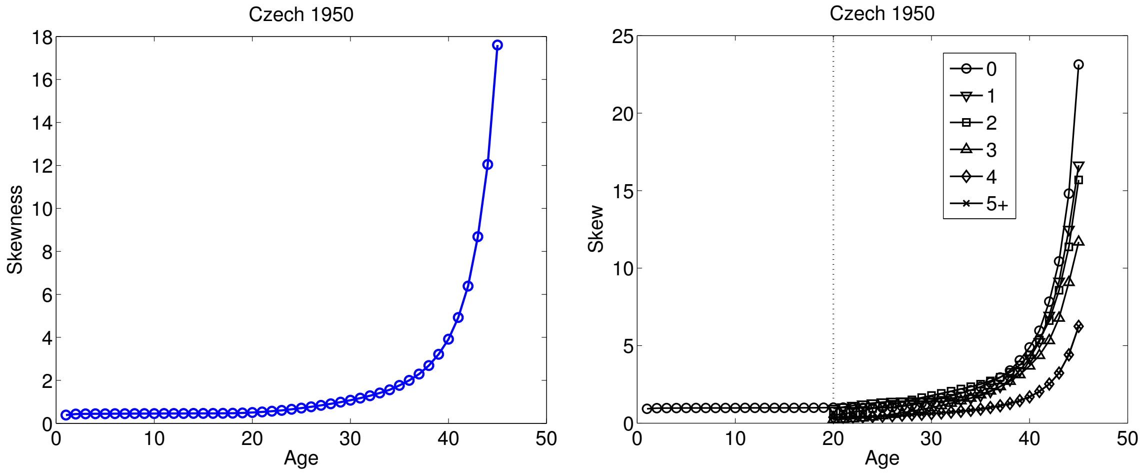


(c) Age-dependent **(d)** Parity-dependent

Figure 3: The mean (above) and standard deviation (below) of lifetime reproductive out put for Czech Republic in 1950. Graphs in the left column show statistics of *age-specific* lifetime reproduction. The right column shows *age-parity-specific* lifetime reproduction. Values for parity states greater than 0 are shown from age 20 onwards. Continued on next figure.

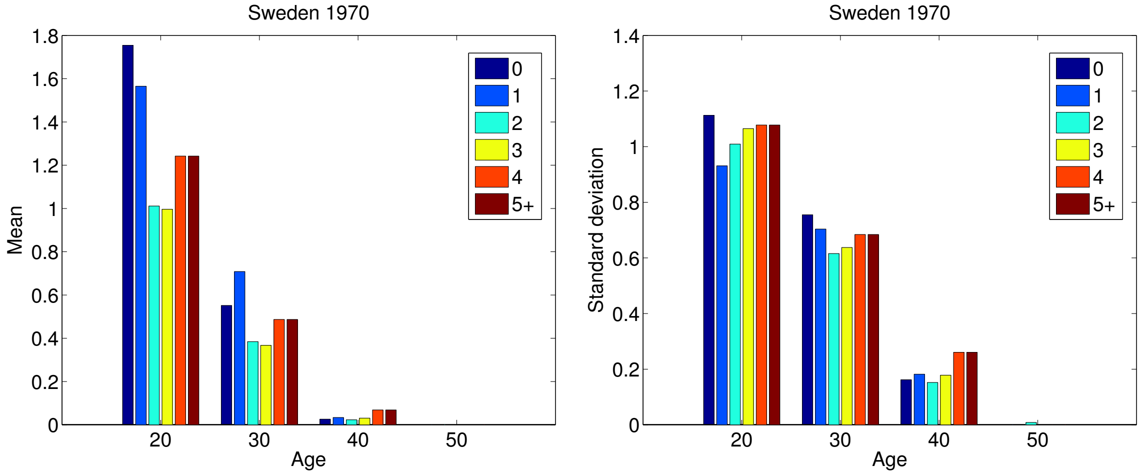


(a) Age-dependent **(b)** Parity-dependent

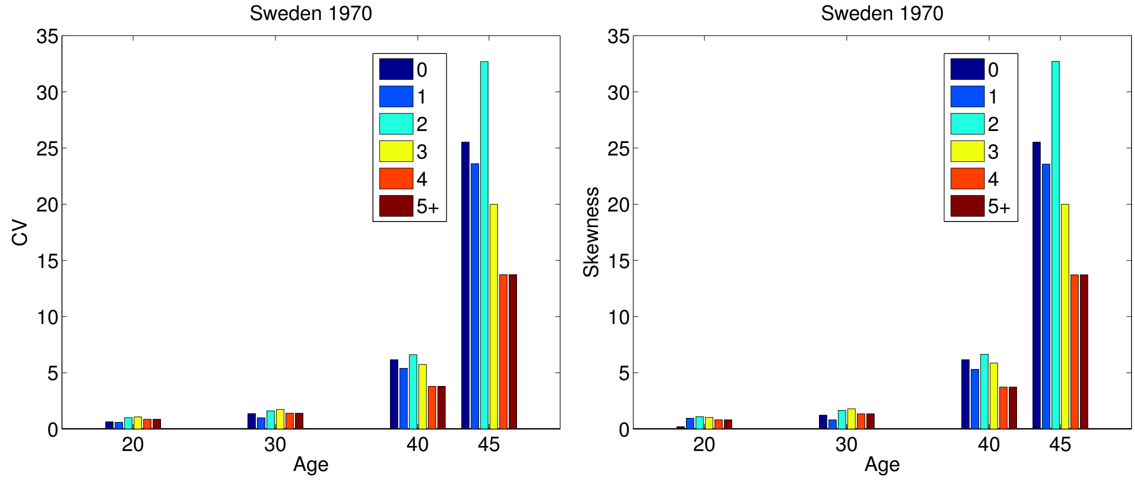


(c) Age-dependent **(d)** Parity-dependent

Figure 3: (continued) The coefficient of variation (above) and skewness (below) of lifetime reproductive out put for Czech Republic in 1950. Graphs in the left column show statistics of *age-specific* lifetime reproduction. The right column shows *age-parity-specific* lifetime reproduction. Values for parity states greater than 0 are shown from age 20 onwards.

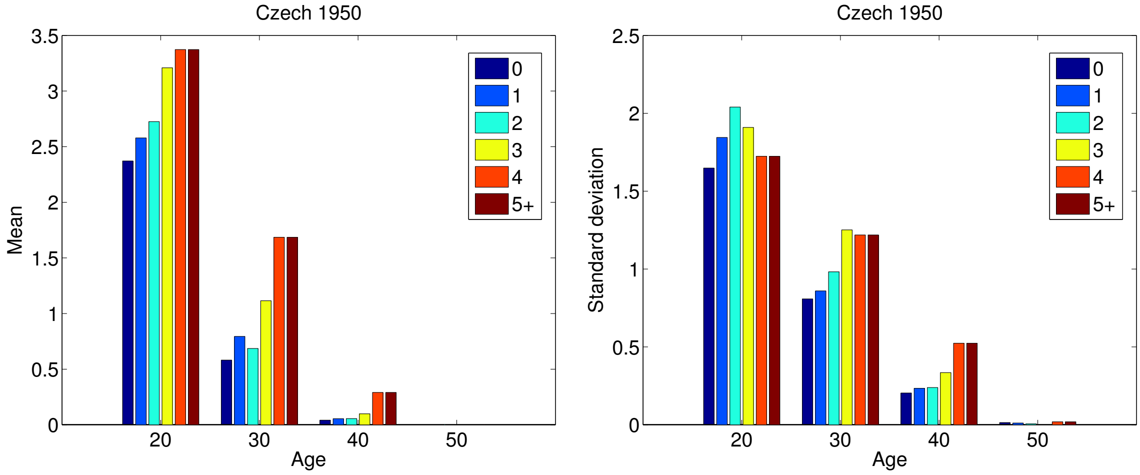


(a) Mean **(b)** Standard deviation

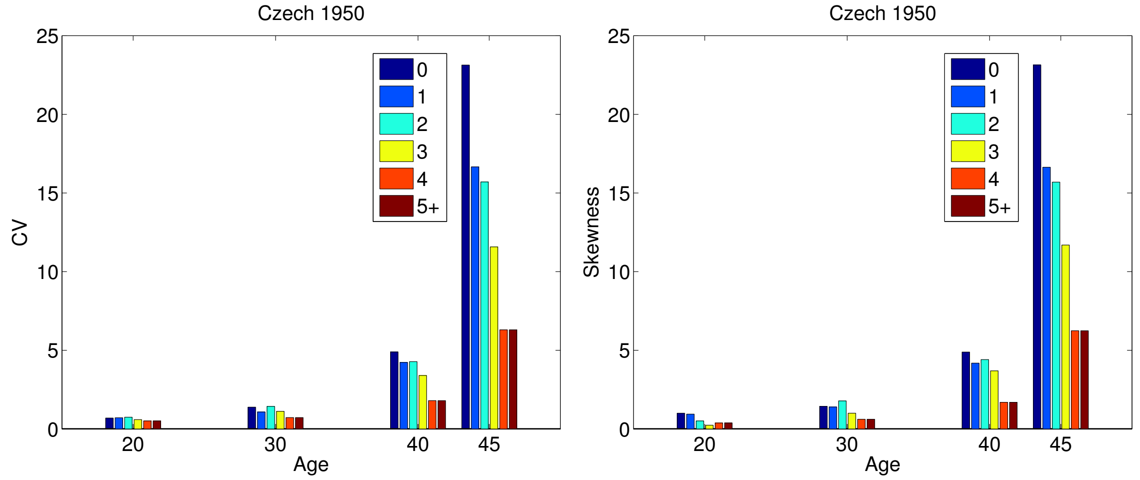


(c) CV **(d)** Skewness

Figure 4: Statistics of lifetime reproduction as a function of age and parity for Sweden in 1970.

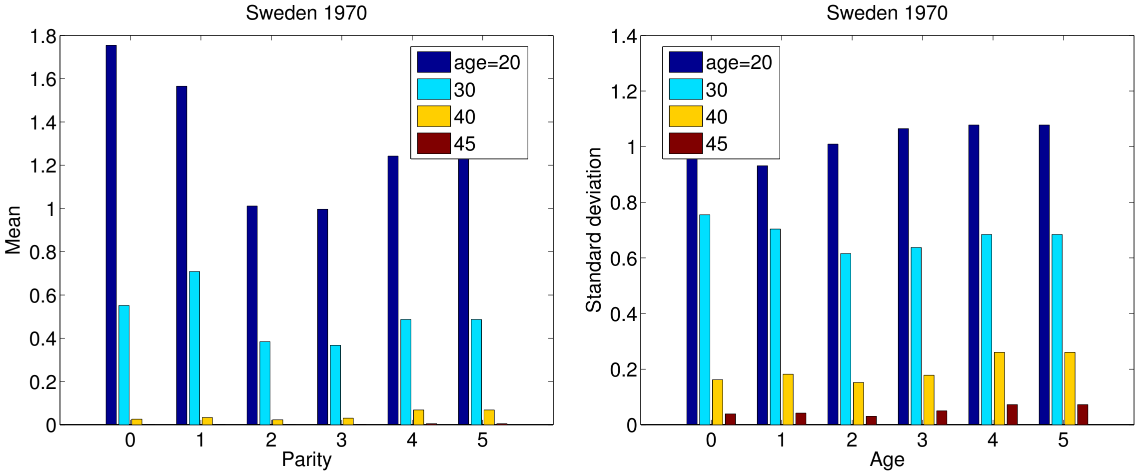


(a) Mean **(b)** Standard deviation

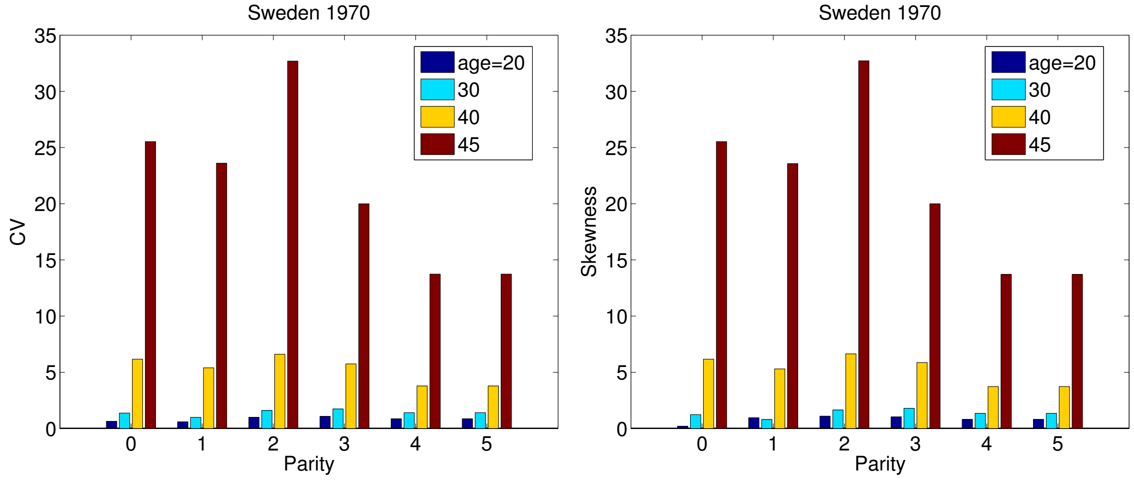


(c) CV **(d)** Skewness

Figure 5: Statistics of lifetime reproduction as a function of parity and age for Czech Republic in 1950.

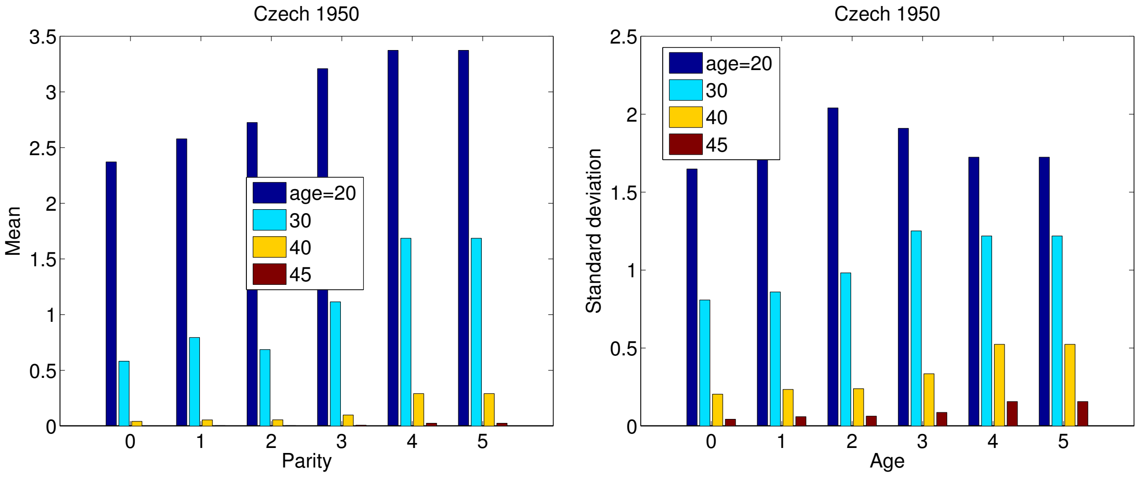


(a) Mean **(b)** Standard deviation

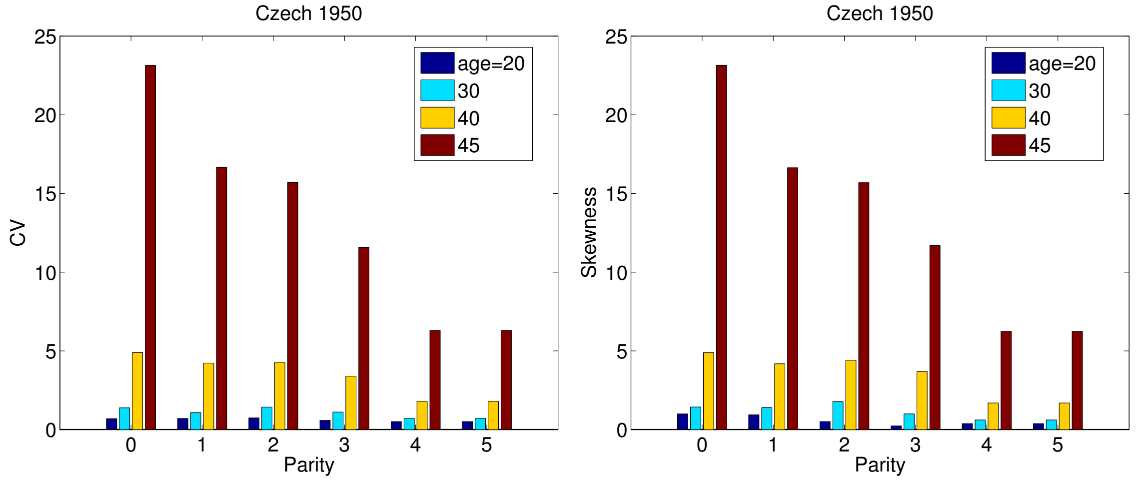


(c) CV **(d)** Skewness

Figure 6: Statistics of lifetime reproduction as a function of parity and age for Sweden in 1970.



(a) Mean **(b)** Standard deviation



(c) CV **(d)** Skewness

Figure 7: Czech Republic 1950

Figure 8: Statistics of lifetime reproduction as a function of parity and age for Czech Republic in 1950.