Household and Family Dynamics as a Sequential Process

1. Introduction

The level of analysis in demography is generally the aggregate: the size and composition of the population. Much of demographic research addresses issues at the level of population and tries to explain and forecast changes in population size and composition by identifying statistical associations between the behaviour of the population system and other characteristics of the population and the economic and socio-cultural system. An example of this system-level mode of analysis and explanation is the theory of demographic transition. Most demographic models, including the life table and the projection models, study demographic patterns at the system level. Multistate demographic analyses also belong to this mode of analysis. Multistate analysis distinguishes different subpopulations and the level of analysis is the subpopulation.

Another mode of analysis and explanation entails examining processes internal to the system, involving its component parts or units at a level below that of the system of interest. The component parts may be individuals, groups of individuals or institutions. The second approach tries to understand population changes by relating these changes to choices people make, to events that are experienced by individuals, households and families, and to the role played by institutions at various levels. The approach is a variant of methodological individualism. It views the experiences of individuals and the interactions among individuals as the underlying phenomena giving rise to the manifest phenomena at the system level, that is, phenomena that were neither intended nor predicted by the individuals. The system behaviour or macro-level phenomena are outcomes of actions at a lower level (micro and meso). The level of analysis is the individual (or household) and the main objective is to show how individual actions combine to produce systemic behaviour. In other words, the emphasis is on the micro-level underpinning

of macro-level (system level) behaviour. In order to implement this perspective, micro-simulation may be required. Micro-simulation provides an analytical framework to assess the macro-level consequences of individual behaviour.

The need to examine events and experiences at the micro-level in order to understand the structure and changes at the system level is advocated by a growing number of scholars. Examples include Coleman (1990) and Scheff (1990) in sociology and McNicoll (1994) in demography (see also Willekens, 1989, 1992, 1994). Coleman sees several advantages of this approach. First, theories formulated at the system level are difficult to reject or confirm because of the inadequacy of data. Data are generally collected at the level of individuals although they may be made available at aggregate levels only. It is therefore natural to begin the explanation of system behaviour by starting at the level at which observations are made, then "composing", or "synthetizing", the systemic behaviour from the actions of these units (Coleman, 1990, p.3). Second, an explanation in terms of actions of individuals is likely to be more stable and general than an explanation which remains at the system level. A description of system dynamics in terms of the behaviour of the component parts (units) is more fundamental, constituting more nearly a theory of system behaviour, than an explanation which remains at the system level. A good description of the functioning of a system is a theory. Third, interventions in the system are rarely at the level of the system and even if they are, they are implemented at the micro level and that implementation is what determines the consequence for the system. Fourth, a realistic theory should take into account the freedom of individuals to act as they will although the choices are constrained in many ways.

A population consists of individuals who interact with each other and, by interacting, produce relationships some of which are institutionalised. Relations and institutions affect the individual; they enhance or inhibit particular behaviour. Individuals, relationships and institutions have a life of their own, although embedded in a wider context. Each organisation is composed of individuals and the lives of the individuals affect the organisation. Elder (1978, pp. 29-30), for instance, views the family in terms of the interdependent life courses of the family members and stresses that the family life cycle cannot be understood without reference to the life cycle of the individual members, and vice versa. A same perspective is adopted in this paper (see also Willekens, 1988). *The central theme of this paper is how different life courses of individuals give rise to the patterns and changes that we observe at the population level.* For instance how are the empirical regularities in age profiles of marriage and fertility related to behavioural patterns and behavioural changes at the individual level? How does a change in contraceptive behaviour or a postponement of childbearing affect the birth rate? What is the impact on population growth of a preference for a child of

a given sex (e.g. son preference)? Is fertility decline a result of all women having less children or of more women having fewer children (heterogeneity)? Under what conditions will mortality from one cause of death increase as a result of the elimination of another cause of death? These and other questions are the subject of microdemography (Keyfitz, 1985, pp. 303f).

Dynamic models of households and families describe the size and composition of households and families at a given point in time in terms of the size and composition at a previous point in time and the transitions that occurred during the interval. Dynamic models are usually contrasted to headship models, which associate the size and composition of households with the head of household and relate the number of heads of households of various types at a given point in time to the population at the same point in time. Headship models are inherently static and the concept of head of household is ambiguous. The advent of dynamic models and their emphasis on transitions stimulated interest in the number and timing of the transitions that cause the size and composition of households and families to change. A remarkable finding is the empirical regularities in age profiles of such transitions as leaving parental home, marriage, divorce and childbearing. The empirical regularities motivated research aimed at

- a) the identification of 'families' or clusters of age profiles, i.e. age profiles that are very similar, and
- b) the mathematical description of the age profiles.

This way, large amounts of data could be condensed in model profiles or model schedules having a few parameters only. Rogers (1986) presents several of such model schedules. Most of these models are probability distributions. Among the popular functions to parameterise age patterns of demographic events are the double exponential, gamma, beta and Pearson Type I distributions. A major advantage of these distributions is data reduction. A disadvantage is that the behavioural implications are not at all evident and frequently impossible to identify. The distributions describe the empirical regularities but do not provide meaningful explanations. For instance, why is it that the fertility curve can be adequately approximated by a gamma distribution? What underlying processes cause the first-marriage profile to closely follow a double exponential distribution? The distributions are also not well suited to assess the impact of changes in the behaviour of people on the age profiles. For instance, what is the impact of a postponement of marriage on the first-marriage profile? What is the impact of increased living alone and cohabitation on the marriage profile and the proportion marrying? What happens to remarriage when people are less likely to marry and when those who marry, marry later? In order to answer these questions, we must view the event of interest (childbirth, marriage) as the

outcome of a series of past events and *express the observed regularity in terms of type, number and timing of events that give rise to the event of interest*. For instance, marriage is the result of sequence of processes and events involving entry into the marriage market, dating, and formation of a relatively stable relationship. The age at first marriage may change because young adults enter the marriage market later, or prolong the duration of dating, or they may not show the commitment that is required to have a stable relationship. Observed patterns of marriage, divorce, household formation and dissolution are the result of a variety of underlying processes. In order to understand empirical regularities and predict changes, the link between observations and underlying processes must be identified. The processes should incorporate the two major dimensions of any demographic event; namely, chance and choice.

The occurrence of a demographic event in the life of a person is the result of both chance and choice. The occurrence of an event is an outcome of a *stochastic process* and a *choice process*. The influence an individual can exert on the occurrence and timing of events is limited, although the influence is increasing rapidly in an individualised society. The events are to a certain degree beyond the locus of control of the individual. For instance the age at marriage is generally not set in advance. It depends on the availability of adequate partners, on the match, and on other factors such as the presence of an economic base for independent living. An individual may affect the timing by involving actively in a search for a partner. Childbirth and the timing of birth are to a large extent controllable in modern societies. Reliable contraceptives exist and, when they fail, abortion is sometimes relied upon. The individual control over occurrence and timing increases, because (i) the social norms get weaker and (ii) the technology gets better (in case of family planning). Models that describe the timing of demographic events in the lives of people should incorporate the features of chance and choice. Chance is incorporated by viewing the age at which an event occurs as a *random variable*. Choice is incorporated by the formulation of *decision rules*, i.e. rules that describe how people select the event they like to occur and the age at which they like the event to occur.

If we view events as outcomes of sequences of processes, then the age at which the current event (event under study) occurs generally depends on the age at which a prior event occurs. For each event, the age at which it occurs is a random variable and the duration between any two events is also a random variable. Consequently, the age at the current event is a sum of a random variable denoting the age at which a reference event occurs and a set of random variables denoting the durations between events. The sequential process is presented in Figure 1.

The age at which the reference event occurs is denoted by x_0 . It is supposed to be given. In most applications, the reference event is birth and the reference age is 0. The ages at which consecutive events occur are denoted by X_i , where the capital letter is used to denote a random variable. The length of the interval between event $i-1$ and i is denoted by U_i . It is referred to as the waiting time to the i -th event. The number of events that occur by duration x is denoted by $N(x)$; μ_i is the rate at which the i -th event occurs. The age at which an event of interest occurs (e.g. age at which i -th event occurs X_i) is the sum of the reference age and the waiting times to events that occur prior to the event of interest.

In order to explain the timing of the event of interest (current event), the timing must be related to underlying processes and hence to prior events; the age at the current event should therefore be expressed as a sum of random variables denoting the age at the reference event and durations between events. This involves *convolutions*. Convolutions constitute an important model building strategy. They express the age at which life events occur in terms of the timing of events prior in the life course. They provide a way to account for choices made during different stages of the life course and to assess the impact of prior choices on the timing of current events. The mod-

elling strategy may also be worded somewhat differently: the distribution of a random variable that is being sought is the convolution of a number of simple but unknown components. If we are able to identify and characterise the components, we have characterised the distribution of interest. It involves a decomposition of a given (empirical) distribution into unknown components. This problem of decomposition is known as deconvolution.

The organisation of the paper is as follows. Section 2 reviews the earliest convolution in demography; namely, the Lotka model. Section 3 describes the Coale-McNeil model which is the first application of convolutions in family demography and presents applications to first marriage data of the Netherlands and other countries of Europe. Section 4 applies the theory of convolutions to divorce. Section 5 concludes the paper.

2. Early Application of Convolutions in Demography: the Lotka Model

Undoubtedly the best known example in demography of a convolution is the Lotka model. It is the basis of stable population theory. At the beginning of this century, Lotka expressed the number of births at time t (or interval following t) in terms of births in the previous generation. Children born at t are born to women of different ages. Let $m(x)$ be the fertility rate of a women of age x . The probability that a woman x years of age has a child in the infinitesimally small interval from x to $x+dx$ is $m(x)dx$. The interval is considered infinitesimally small if at most one child is born during the interval. Suppose there a $P(x,t)$ women of age x at time t . The value of $P(x,t)$ depends on how many girls are born x years ago and how many of them survived to age x : $P(x,t) = B(t-x)p(x)$, where $B(t-x)$ is the number of girls born at time $t-x$ and $p(x)$ is the probability of survival to age x . The survival probability is assumed to be independent of t . The number of children born to women who are themselves born x years ago is $B(t-x)p(x)m(x)dx$. The total number of children born at t is

$$B(t) = \int_0^t P(x,t) m(x) dx = \int_0^t B(t-x) p(x) m(x) dx = \int_0^t B(t-x) \phi(x) dx \quad (2.1)$$

where $\phi(x) = p(x) m(x)$ is the *net maternity function* and $t \geq \beta$, the highest age of the reproductive period. The integral is known as a convolution of the functions B and ϕ .

If the number of births increases exponentially at a rate r , then

$$B(t) = B(t - x) \exp[rx] \text{ and } B(t - x) = B(t) \exp[-rx].$$

Hence equation (2.1) may be written as

$$B(t) = \int_0^t B(t) \exp[-rx] \phi(x) dx \quad (2.2)$$

and

$$\Psi(r) = \int_{\alpha}^{\beta} \exp[-rx] \phi(x) dx = 1 \quad (2.3)$$

since $m(x)$ is nonzero only in the childbearing ages $\alpha \leq x \leq \beta$ with α the lowest age of childbearing and β the highest age. Equation (2.3) is known as the *characteristic equation* or Lotka equation. It describes the relation between the age-specific fertility rates $m(x)$ and the exponential growth rates of the number of births in case the fertility and mortality profiles are constant. The value of r that satisfies the characteristic equation is the growth rate of the *stable population*. Several values of r may satisfy the equation, but only one is real. The other values are complex numbers. The derivative of the characteristic equation is

$$\Psi'(r) = - \int_{\alpha}^{\beta} x \exp[-rx] \phi(x) dx \quad (2.4)$$

It is minus the mean age of childbearing in the stable population (population growing at a rate r satisfying the characteristic equation).

3 The Coale-McNeil Marriage Model

The first demographic model in which convolutions have been consciously used as a model building strategy and as a technique to give a behavioural underpinning of empirical regularities was the first-marriage model developed by Coale and McNeil (1972). The model has been used relatively often to parameterise first-marriage data, but little was done to exploit the behavioural basis of the model (see also Jun Zhu 1994, p. 157). Parameterisation of age profiles has always been a major subject in demography (for a review, see e.g. Rogers, 1986). But a behavioural basis for parameterisation did not receive much

attention. Coale (1971) observed that the age distributions of first marriage¹ are structurally similar in different populations. The distributions tend to be smooth, unimodal, skewed to the right, and have density close to zero below age fifteen and above age fifty. In Section 3.1, the Coale-McNeil model is reviewed. The formulation of the model as a convolution is presented in Section 3.2. Section 3.3 presents a few applications.

3.1 The Model Schedule

Coale and McNeil expressed the first marriage frequencies recorded in Sweden from 1865 to 1869, which they used as a standard, as a double exponential distribution:

$$g_s(x) = 0.1946 \exp\{-0.174(x - 6.06) - \exp[-2.881(x - 6.06)]\} \quad (3.1)$$

The function is a double-exponential distribution:

$$f(x) = a \exp\{-\alpha(x - \mu) - \exp[-\lambda(x - \mu)]\} \quad (3.2)$$

The parameter a is a scaling parameter. The parameter μ positions the unimodal curve on the time axis (time 0 is the age at which first marriages begin), λ and α reflect the steepness of its ascending and descending sides, respectively (See Rogers, 1986, p. 51). The first marriage frequencies are adjusted such that by the end of life, the proportion ever-married is 100 percent (see Coale, 1971, p. 199). The proportion ever married at age x is

$$G_s(x) = \int_0^x g_s(\xi) d\xi \quad (3.3)$$

The Swedish standard is shown in Figure 2².

1 The distribution of the ratio of first marriages in each age interval to person-years lived in the interval. First marriage frequencies are defined as the number of first marriages in an age interval divided by the number of women (regardless of marital status) in the interval (Coale, 1971, p. 196). The sum of first marriage frequencies is the proportion ever-married.

2 The first marriage density (frequency) is also shown by Coale and McNeil (1972, p. 745); the first marriage rates (risks) are shown by Coale (1971, p. 204).

The first marriage frequencies (densities) increase to a maximum (mode) at 8 years after marriages start. The mean of the empirically-based standard schedule is 11.36 years. The asymptotic value of the empirically calculated hazard (risk) function is 0.174. The first marriage rate is described by the equation (Coale and McNeil, 1972, p. 743).

$$r(x) = 0.174 \exp[-4.411 \exp(-0.309x)] \quad (3.4)$$

Coale related many other observed marriage distributions to the standard. What differs from population to population is the age at which first marriage begins, the rate at which marriage increased and the proportion ever marrying (Coale, 1971, p. 193). The marriage distribution in a given population is related to the Swedish standard by the transform

$$g(x) = \frac{C}{k} g_s(y) \quad (3.5)$$

where $y = \frac{x - x_0}{k}$ with x_0 is the age at which first marriage begins, C is a factor determined by the proportion eventually marrying, and k is a scale factor which may be interpreted as the rate at which marriage occurs (relative to the standard). C influences the level but not the age pattern of the first marriage schedule. According to the standard schedule, half of the female population that will ever marry, experiences first marriage ten years after the earliest age at which a consequential number of first marriages occur. If k is 1.0, first marriages occur at the same pace as in the nineteenth-century Swedish population that served as the basis of the standard; if k is 0.5, first marriages occur at twice the pace of the standard, i.e. one half of the cohort has experienced first marriage five years after x_0 . The parameter k measures the extent to which the time scale is 'compressed'. In a population in which first marriage starts at age x_0 and the horizontal scale is k times the standard, the distance from the origin to age x is k times the distance in the standard (y), hence $y = \frac{x - x_0}{k}$.

The proportion ever married in any cohort x years after first marriages begin is

$$G(x) = C G_s\left(\frac{x - x_0}{k}\right) \quad (3.6)$$

The first marriage frequencies in a population may also be written as follows (Coale and Trussel, 1974, p. 187).

$$g(x) = C \frac{0.1946}{k} \exp\left[-\frac{0.174}{k}(x - x_0 - 6.06k)\right] - \exp\left[-\frac{0.2881}{k}(x - x_0 - 6.06k)\right] \quad (3.7)$$

The schedule is entirely characterised by C , k and x_0 . A change in any of these parameters affect the first marriage schedule in a particular way. In order to determine how the schedule is affected, consider the change in marriage density with age

$$\frac{dg_s(x)}{dx} = 0.1946 \exp[-0.174(x - 6.06)] - \exp[-0.2881(x - 6.06)] \quad (3.8)$$

$$* [0.174 + 0.288 \exp[-0.2881(x - 6.06)]]$$

The first component on the right-hand side is $g_s(x)$. Denote the second component by Z . Differentiation of (3.7) with respect to C , k and x_0 is (Morgan and Chen, 1992, p. 481).

$$\frac{dg(x)}{dC} = \frac{1}{k} g_s(y) \quad (3.9)$$

$$\frac{dg(x)}{dk} = \frac{-C}{k^2} [1 + yZ] \quad (3.10)$$

and

$$\frac{dg(x)}{dx_0} = -\frac{C}{k^2} g_s(y) Z \quad (3.11)$$

$$\text{where } y = \frac{x - x_0}{k}.$$

3.2 The Convolution

Coale and McNeil found that the double exponential can be represented by an infinite convolution of exponential distributions. Let U_j , $j=1,2,\dots,n$ be independent random variables, exponentially distributed with parameter (mean)

$$\xi = \frac{1}{\alpha + (j - 1) \lambda} \quad (3.12)$$

The density of the sum T_j of random variables U_j [$T_j = \sum_{j=1}^n U_j$] is (Coale and McNeil, 1972, p. 747).

$$h_n(x) = \frac{\lambda \Gamma(n + \alpha / \lambda)}{\Gamma(\alpha / \lambda) (n - 1)!} [1 - \exp(-\lambda x)]^{n-1} \exp[-\alpha x] \quad (3.13)$$

where Γ is the gamma function. Note that for $n=1$, the distribution reduces to the density of the exponential distribution:

$$h_1(x) = \alpha \exp(-\alpha x) \quad (3.14)$$

As $n \rightarrow \infty$, the random variable

$$X_n = a + \sum_{j=1}^n \left[U_j - \frac{1}{\alpha + (j - 1) \lambda} \right] \quad (3.15)$$

has density function

$$\bar{g}(x) = \frac{\lambda}{\Gamma(\alpha / \lambda)} \exp[-\alpha(x - \mu) - \exp[-\lambda(x - \mu)]] \quad (3.16)$$

where

$$\mu = \alpha + \frac{1}{\lambda} \frac{\Gamma'(\alpha / \lambda)}{\Gamma(\alpha / \lambda)} \quad (3.17)$$

In case $\alpha = \lambda$, $\bar{g}(x)$ is the density of the extreme value distribution.

$$X_\infty = a + \sum_{j=1}^{\infty} \left[U_j - \frac{1}{\alpha + (j - 1) \lambda} \right] \quad (3.18)$$

An infinite number of exponential random variables where the first term is the sum of m exponentially distributed random variables and Y_m is the residual. When m increases, the residual distribution becomes less and less skewed and approaches the shape of a normal distribution. When m approaches infinity, the residual is a normal distribution with mean zero and variance $1/\lambda^2$. This lead Coale and McNeil to express the first marriage distribution as a convolution of (i) a normal distribution and (ii) a moderate number of exponential components with mean values in harmonic progression. They compared the first marriage frequencies obtained by the double exponential with the convolution of a normal distribution (with appropriate mean and variance) and m exponentially distributed delays, for $m=1, 2$ and 3 . The fit with three delays is quite close. The convolution

may be given a behavioural interpretation. The normally distributed random variable may be regarded as the time to reach a marriageable age, while the exponential random variables may be interpreted as several delays before the marriage is concluded. The Swedish standard may be interpreted as the combination of (i) a normal distribution of attainment of marriageable age with a mean of x_0 (the 'origin' of the standard curve) plus 2.12 years, and a standard deviation of 2.0 years, and (2) three exponentially distributed delays with average durations of 1.33 years, 2.16 years and 5.57 years [$1/(0.174+0.576)$, $1/(0.174+0.288)$, and $1/(0.174)$, respectively]. The mean of the normal distribution is the mean of the standard schedule (11.36 years) less the sum of the three delays (9.24 years) and the variance of the normal curve is the variance of the standard curve less the sum of the variances of the three delays.

The finding that the age at first marriage may be viewed as the sum of four duration variables, the first being normally distributed and the other exponentially distributed, may be given a behavioural interpretation. The first variable may be represented by the age of becoming marriageable or the age at entry into the marriage market. In Western populations, it is the age at which serious dating starts. The first and longest delay is the time between entry into the marriage market and meeting the eventual husband. The two shorter delays may be viewed as the period between beginning to date the future husband and engagement, and between engagement and marriage (Coale and McNeil, 1972, p. 746). The expected (average) duration of the m -th delay is

$$E[U_j] = \frac{1}{\alpha + (j - 1)\lambda} \quad (3.19)$$

In the Swedish standard, $\alpha = 0.1740$ and $\lambda = 0.2881$, and the delays are:

$$E[U_1] = \frac{1}{0.1740} = 5.75 \text{ years}$$

$$E[U_2] = \frac{1}{0.174 + 0.2882} = 2.16 \text{ years} \quad (3.20)$$

$$E[U_3] = \frac{1}{0.174 + 2 * 0.2881} = 1.33 \text{ years}$$

The duration of engagement is exponentially distributed with parameter $(\alpha+2\lambda)=0.7502$. The survival function is

$$\exp[-(\alpha + 2\lambda) x] \quad (3.21)$$

and the density function is

$$(\alpha + 2\lambda) \exp[-(\alpha + 2\lambda) x] \quad (3.22)$$

The duration of acquaintance before engagement is exponentially distributed with parameter $(\alpha + \lambda) = 0.174 + 0.2881 = 0.4621$. The total duration of acquaintance at time of marriage, i.e. the waiting time to marriage provided one has an acquaintance, is a convolution of two exponential distributions. The first distribution characterises the timing of the engagement (first event in this process) and the second distribution characterises the timing of marriage (second event). The probability of being engaged u years after the onset of the acquaintance is identical to the probability of having experienced the first event (engagement) but not the second. It is

$$Pr\{N(u) = 1\} = \int_0^u Pr\{U_1 = \xi\} Pr\{U_2 > (u - \xi)\} d\xi \quad (3.23)$$

where $Pr\{U_1 = \xi\}$ is the probability that the engagement occurs at exact time ξ after the acquaintance, which is equal to the density $v_1 \exp(-v_1 \xi)$ with $v_1 = \alpha + \lambda$, and $Pr\{U_2 > (u - \xi)\}$ is the probability that the second event, marriage, does not occur before u , which is the survival function $\exp[-v_2(u - \xi)]$ with $v_2 = \alpha + 2\lambda$. The probability of being engaged at u is the convolution

$$Pr\{N(u) = 1\} = \int_0^u v_1 \exp[-v_1 \xi] \exp[-v_2(u - \xi)] d\xi \quad (3.24)$$

The convolution has a closed-form solution (see e.g. Willekens, 1991, p. 32):

$$Pr\{N(u) = 1\} = \frac{v_1}{v_1 - v_2} [\exp(-v_2 u) - \exp(-v_1 u)] \quad (3.25)$$

or, in terms of α and λ

$$Pr\{N(u) = 1\} = \frac{\alpha + 2\lambda}{\lambda} \exp[-(\alpha + \lambda)u] - \frac{\alpha + \lambda}{\lambda} \exp[-(\alpha + 2\lambda)u] \quad (3.26)$$

The occurrence of events signifies transitions from one stage of life to a next. In the simple marriage process described by the convolution of two exponential distributions, three stages are distinguished. The first stage is 'being acquainted', the second stage is 'being engaged' and the third stage is 'being married'. The process may be described in terms of the stages or the events of engagement and marriage. Let S_j be the probability of being in stage j ($j=1,2,3$), then

$$\begin{aligned} S_1 &= Pr\{N(u) = 0\} \\ S_2 &= Pr\{N(u) = 1\} \end{aligned} \quad (3.27)$$

$$S_3 = Pr\{N(u) = 2\}$$

The probability of being married u years after the acquaintance is

$$S_3 = 1 - S_1 - S_2 = 1 - \exp[-\nu_1 u] - Pr\{N(u) = 2\} \quad (3.28)$$

where $Pr\{N(u) = 2\}$ is given above (see also Coale and McNeil, 1972, p. 747).

The dynamics of the marriage process may also be written as a Markov process. Let ${}_x S_{ij}(x, y)$ be the probability that an individual in stage (state) i at age x will be in stage (state) j at age y ($y \geq x$). The probability of staying in stage 1 is the survival function $\exp[-\nu_1(y - x)]$. In order to determine the probability of transition from stage 1 (acquaintance) to stage 2 (engaged), suppose that the process is in stage 1 at duration x . The transition probability is the probability that the process is in stage 2 at a later duration y , given that it is currently in stage 1 at duration x . The probability is

$${}_x S_{12}(x, y) = Pr\{N(y) = 2 \mid N(x) = 1\} \quad (3.29)$$

which is equal to

$${}_xS_{12}(x, y) = \frac{\nu_1}{\nu_1 - \nu_2} [\exp[-\nu_2(y - x)] - \exp[-\nu_1(y - x)]] \quad (3.30)$$

The probability that an individual in stage 2 at age x remains in 2 is the survival function $\exp[-\nu_2(y - x)]$. The probability that an individual in stage 2 at age x is in stage 3 at age y is ${}_xS_{23} = 1 - \exp[-\nu_2(y - x)]$. Once an individual reaches stage 3, she remains in that stage. The stage is referred to as an absorbing state. Note that the derivation of transition probabilities assumes at most one transition during the (x, y) -interval.

3.3 Applications

The first marriage patterns in different populations differ in the age at which first marriages begin, the rate at which marriages increase and the proportion ever marrying. The parameter λ is the pace at which first marriage frequencies increase in the standard (Sweden 1865-69) population and α reflects the pace at which first marriage frequencies decline after the maximum is reached. For any first marriage pattern different from the standard, α and λ must be adjusted by a factor expressing the pace at which first marriages occur in a given population relative to the pace in Sweden in the 1860s. Coale and McNeil (1972, p. 747) suggest to obtain the factor as the ratio of the standard deviation of the first marriage schedule in the given population and the standard deviation of the Swedish standard. Consider the first marriage pattern of Dutch women in 1993. The first marriage rates and the densities are shown in Figure 3.

The mean age of first marriage is 28.3 years. Parameterisation of the first marriage schedule (densities) by a double exponential distribution (equation 3.2) gives the following parameters:

$$\begin{aligned} a &= 0.6956 \\ \alpha &= -0.257 \\ \lambda &= -0.273 \\ \mu &= 8.010 \end{aligned}$$

The double-exponential achieves a maximum (mode) at (Rogers, 1986, p. 51)

$$x_h = \mu - \frac{1}{\lambda} \ln \frac{\alpha}{\lambda} \quad (3.31)$$

an expression that does not involve a . The value of the maximum is

$$y_h = a \left(\frac{\alpha}{\lambda} \right)^{\alpha/\lambda} \exp \left(-\frac{\alpha}{\lambda} \right) \quad (3.32)$$

an expression that does not involve μ . If $\lambda > \alpha$, then $x_h > \mu$; but if $\lambda < \alpha$, then $x_h < \mu$.

The lowest age at first marriage is fixed at 18 years. The first marriage densities of the Dutch women and of the Swedish standard are shown in Figure 4.

The Dutch schedule is related to the standard by the transform (3.7) with

$$C = 0.789$$

$$k = 0.857$$

$$x_0 = 18.36$$

The mean and the standard deviation of age at first marriage (for those who ever marry) is estimated using the reformulation of the Coale-McNeil model by Rodriguez and Trussell (1980). These authors expressed the proportion marrying at age x in terms of the mean and the standard deviation of the first marriage profile:

$$g(x) = \frac{E}{\sigma} 1.2813 \exp \left[-1.145 \left(\frac{x - \mu}{\sigma} + 0.805 \right) - \exp \left[-1.896 \left(\frac{x - \mu}{\sigma} + 0.805 \right) \right] \right] \quad (3.33)$$

where E is the proportion ever marrying, μ the mean age at first marriage and σ the standard deviation of age at first marriage. For the Dutch data, the mean age

is 27.93 years, the variance is 5.40 years. In the Swedish standard, the mean age (determined in same way) is 28.4 years and the variance is 6.60 years).

The first marriage model was also applied to female populations of other European countries. Observed first marriage rates for Belgium (B), Germany (D), France (F), Netherlands (NL), Italy (I) and Spain (E) are shown in Figure 5.

All data are for 1990. The double exponential model is fitted to these data. the values of the parameters are given in Table 1.

Parameters of double-exponential model of first marriage rates				
	a	α	μ	λ
Belgium	0.0245	0.4182	23.34	0.3174
Germany	0.0169	0.3185	24.57	0.2359
France	0.0173	0.3107	23.21	0.3254
Netherlands	0.0190	0.2764	23.19	0.3316
Italy	0.0082	0.4105	29.46	0.1643
Spain	0.0006	0.5935	36.28	0.1268

For a selection of countries, the estimated and observed rates are compared in Figure 6.

4 The Divorce Model

The age at divorce depends on the age at marriage and on the duration of marriage at time of divorce. It is sum of two random variables, the age at marriage and the duration of marriage at divorce. Consequently, the age distribution of divorce is a convolution of two (at least two) distributions. The first-marriage distribution was discussed in the previous section. Figure 7 shows the observed rates of divorce by duration of marriage. They were obtained by dividing, for each duration of marriage, the number of women divorcing in 1993 by the number of married women.

The divorce data are from Statistics Netherlands (1994, p. 44). Statistics Netherlands measures the duration of marriage as the duration on 31st December of the year in which the couple divorced. A divorce at duration 0 is therefore a divorce in the year of marriage. This measurement explains the very low level of divorce in the first year of marriage (75 in 1993 on a total of about 30,000

divorces). It is assumed that all divorces pertain to first marriages. The density of divorce is the probability that a marriage is dissolved by divorce at a given duration of marriage. The density is also shown in Figure 7. The density is parameterised using a double exponential distribution (equation 3.2). The estimated parameter values are

$$\begin{aligned}a &= 0.0399 \\ \alpha &= 0.1668 \\ \lambda &= 1.1727 \\ \mu &= 1.2383\end{aligned}$$

We may try to apply to divorce the finding by Coale and McNeil that the double exponential distribution may be written as the sum of a normal distribution and 3 exponential distributions (delays). The mean duration of marriage at time of divorce, given that divorce occurs, is a little more than 7 years. For those who eventually divorce, frictions arise soon after marriage. The first stage in the divorce process takes about 6 years ($1/1.1668$). It is the period during which tensions build up and incompatibilities become manifest, leading to a decision by at least one of the partners that the marriage is damaged beyond repair. The second phase, which takes less than a year [$0.75 \text{ years} = 1/(0.1668+1.1727)$] leads to separation. The third phase, which is shorter than half a year [$0.40 \text{ years} = 1/(0.1668+2*1.1727)$] is the period between separation and divorce. This behavioural interpretation of the divorce model should be subject to empirical study in order to confirm or deny the interpretation.

The double exponential does not provide a very good fit of the divorce pattern. Therefore, the divorce pattern may be approached differently. The pattern of divorce may be caused by several divorce patterns operating simultaneously. The data consist of probabilities of still being married at various durations of marriage. The empirical 'survival function' was obtained as follows. For the first 10 years of marriage, the number of divorces in 1993 by duration of marriage were divided by the number of married women, also classified by duration of marriage. These rates of divorce were used to construct the empirical survival function. Divorce data were available by single years of duration up to 10 years of marriage. The probabilities that a marriage still exists after 15 and 20 years are published as such by Statistics Netherlands (1994, p. 39). The empirical survival function is shown in Figure 8.

The function resembles a logistic function caused by the fact that the risk of divorce increases first and declines afterwards. A logit transformation³ of the survival function reveals a monotonous decline, although not linear nor exponential, of the transformed variable (Figure 9).

Note that an exponential decline of the logit would imply that the odds in favour of marriage being intact would decline following a Gompertz function. The decline is close to exponential at the start, but levels off as duration of marriage increases. This pattern indicates heterogeneity among married couples: couples are not homogenous with respect to the risk of divorce.

³ The logit is the log of the odds in favour of still being married at a given marriage duration. The logit varies between 7 in the first year, when the proportion of marriages dissolved by divorce is very small, to 1.4 after 10 years of marriage, when about 20 percent of the marriages ended in a divorce.

In other words, several divorce patterns may be operational simultaneously. In order to test the heterogeneity assumption, two categories of couples are distinguished. The first category has a high risk of divorce and the other category a low risk. The survival function implied by this model is as follows:

$$\text{logit } S(x) = \ln \frac{S(x)}{1 - S(x)} = K [z * \exp(-v_1 x) + (1 - z) * \exp(-v_2 x)] \quad (4.1)$$

where v_1 is the high risk of divorce, v_2 is the low risk, z is the share of high risk couples and K is a scaling factor. The share of each category, their associated divorce risks and the scaling factor must be estimated from the data. The pattern of change in the log of the odds in favour of marriage is described by the following equation:

$$\text{logit } S(x) = 10.00 [0.86 * \exp(-0.467x) + 0.14 * \exp(-0.001x)] \quad (4.2)$$

The equation shows that 86 percent of the change in the logits is due to couples with a high risk of divorce and divorcing early, and 14 percent is due to couples that have a low risk of divorce. The survival function may be written as follows

$$S(x) = \frac{1}{1 + \exp[-\{10.00 [0.86 \exp(-0.467x) + 0.14 \exp(-0.001x)]\}]} \quad (4.3)$$

The survival function is shown in Figure 8.

A distinction of two categories only does not replicate the observed logit function and the survival function accurately. If three categories are distinguished, the observations are replicated remarkably well. The logit function is

$$\text{logit } S(x) = 13.29 [0.70 \exp(-0.978x) + 0.24 \exp(-0.15x) + 0.06 \exp(+0.03x)] \quad (4.4)$$

and the survival function is

$$S(x) = \frac{1}{1 + \exp[-\text{logit } S(x)]} \quad (4.5)$$

5. Conclusion

Parameterisation techniques are powerful in that they enable the representation of an age profile by a few parameters. A major shortcoming, however, is the frequent absence of a behavioural interpretation of the parameters. By viewing observed age patterns as manifestations of a sequence of underlying processes that have a behavioural interpretation, and by decomposing an observed pattern into these processes, one may contribute to a substantive basis for empirical regularities and statistical models of age patterns. The decomposition, or deconvolution, may show to be a powerful modeling technique in family demography because it decomposes empirical patterns in theoretically sound building blocks and, by doing so, motivates the analyst to develop models that are founded in a theory of demographic behaviour. Using the Coale-McNeil model as an example, this paper demonstrates the direction of research that may contribute to the integration of modelling and theory building in demography.