# The Probabilistic Fertility Table and Its Applications

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*A fertility table describes the childbearing process of a hypothetical female cohort that subjects neither to mortality nor migration. This paper first proposes a concise fertility table that could describe family structures such as the proportion families by the number of children, or the proportion of children by the number of siblings. The concise fertility table, however, is deterministic. In the second part of this paper, this approach is extended to reflect the uncertainty of the childbearing process using probabilistic life tables instead of deterministic ones. A probabilistic approach allows to test, for example, whether a change in total fertility is statistically significant or not.*

## Introduction

Period fertility measurement is affected by the compositional structure of the female population in childbearing ages. A female population with more members at the age of maximum fertility will bear more births than other populations. But the age pattern of a population is a result of historical changes of fertility, mortality, and migration, and has nothing to do with current fertility. Following the approach of eliminating the effect of age pattern in the survival process of mortality studies, we can use a hypothetical cohort of women subject to the age-specific fertility rates in a certain period and do not die or migrate. Subsequently, the conventional total fertility, *TF*, is defined as the average number of children that a woman in this cohort would have, and is computed as the sum of the age-specific fertility rates.

In the survival process, the hypothetic cohort is only distributed by age, because death is an unrepeatable event. Delivering birth, however, is a repeatable event; and therefore the childbearing process is more complex than the survival process. In the childbearing process, the hypothetic female cohort is distributed along two dimensions: age and parity. Here, parity refers to having a certain number of children; and parity *i* stands for having *i* children. Using *TF*, however, is insufficient to eliminate the effect of the parity pattern. If the probabilities of delivering birth for women in parity one are bigger than in other parities at all ages, then, a female population with more individuals in parity one will have bigger fertility rate at all ages, and hence a higher *TF*, than that of other populations. Thus, *TF* changes with parity pattern; but the parity pattern is a result of historical events and has nothing to do with current fertility. To deal with the effect of parity pattern, an optional approach is to focus on the parity progression and ignoring the effect of age pattern (e.g., Chiang and Berg, 1982).

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To eliminate the effects of the patterns of both age and parity, individuals at reproductive ages should be assigned into parities according to the age-parity-specific probabilities of delivering birth for the period in question. By doing so, the parity pattern of the hypothetic cohort will no longer be a result of historical events, but determined only by the fertility of the period in question. Along this line, Park (1976) described the lifetime probability of having a certain number of children; and Rallu and Toulemon (1994) indicated both the strength and the age pattern of childbearing process. The childbearing process of such a hypothetical cohort, with specified parities by age, can be called a fertility table, following naming convention used for life tables in mortality studies. A more formal format for the fertility table has been proposed by Jasilioniene and colleagues (2012). These articles are important and reveal the complexity of the childbearing process.

Compared to life tables, less progress has been made in studying fertility tables, partly because data are more difficult to collect and organise. Owing to the effort made by the Human Fertility Database (2013) on collecting, organizing, and estimating data on births and women by age and parity, now fertility tables can be computed for multiple countries and periods. Compared to death, another difficulty remains in that birth is an avoidable and repeatable event, and therefore fertility table is naturally more complex than life table. For this reason, proper attention should be paid to the simplicity of the fertility table.

This paper proposes a concise fertility table, which includes one definition and two assumptions, and describes the childbearing process of the hypothetic cohort in perhaps the simplest way. The definition is about the probability of birth to be discussed next. The first assumption is that a woman can deliver at most one birth within one year; and the second assumption is that births occur evenly within a one-year interval.

The concise fertility table is deterministic, in which, for example, the ratio of childless women at age $a$ to the starting number of the hypothetic cohort is a certain number. When the starting number of the hypothetic cohort is not unrealistically infinite, however, this ratio is uncertain, because the childbearing process is uncertain. Here the situation is the same as that of life tables, where the ratio of survivors at a given age to the starting number of the hypothetic cohort is a certain number, but the survival process is uncertain. To describe the uncertainty of survival process, Li and Tuljapurkar (2013) and Li (2015) proposed the probabilistic life table. In this paper, the same approach as for a probabilistic life table is used to deal with the uncertainty of the childbearing process involving not only age but also parity. As a result, the concise fertility table is extended from deterministic to probabilistic.

**The definition and assumptions of the concise fertility table**

For the hypothetical cohort, let the number of women having *(i-1)* children at age $a$ be $l_{i-1}(a)$, and the number of births delivered by these women at ages *[a,a+1)* be $b_i(a)$.

The probability of delivering the *ith* child in age interval *[a,a+1)* , namely $q_i(a)$ , can be defined as

$$q_i(a) = \frac{b_i(a)}{l_{i-1}(a)}, \qquad (1)$$

 (see Chiang, 1984). The probability for women aged *a* in the open parity *(m-1)+* (having the *(m-1)th* and higher-order births) to deliver the *(m)th* and higher births at ages *[a,a+1)* is defined formally as,

$$q_{m+}(a) = \frac{b_{m+}(a)}{l_{(m-1)+}(a)}. \qquad (2)$$

It should be clarified that, although (2) does not specify the population at the risk of delivering a specific order of birth, it applies now only to the high-order births that are less important. How to compute $q_i(a)$ and $q_{m+}(a)$ using empirical data is indicated in the appendix.

To construct a fertility table, the first assumption is that a woman can deliver only one child within one year. Under this assumption, the childbearing process is modelled as

$$l_{i-1}(a) = \begin{cases} l_{i-1}(a-1) - b_i(a-1), & i = 1, \\ l_{i-1}(a-1) - b_i(a-1) + b_{i-1}(a-1), & 1 < i < m, \end{cases} \qquad (3)$$

$$l_{(m-1)+}(a) = l_{(m-1)+}(a-1) + b_{(m-1)}(a-1). \qquad (4)$$

The first line on the right-hand side of (3) indicates how the number of childless woman declines over age, which is similar to the survival process. The second line of (3) describes how the number of women with *(i-1)* children changes over age; and the change is due only to the *(i-1)th* and *(i)th* births but not any other order of birth, according to the first assumption that a woman can bear at most one birth in a year. Equation (4) indicates the change in the number of women in parity *(m-1)+*. It should be mentioned that, to obtain (3), the age interval must be one year. When the data are organized in 5-year age interval, the first assumption would become helpless, and the second line of (3) would involve more terms of birth in smaller orders, making the dynamics more complicated. It should also be mentioned that, although the age interval must be one year, the period to which a concise fertility table refers can be flexible such as 5 years. This is important for small populations, and will be indicated in the appendix.

According to definition (1) and (2), (3) and (4) can be rewritten using $q_i(a)$ as

$$l_{i-1}(a) = \begin{cases} l_{i-1}(a-1)[1 - q_i(a-1)], & i = 1, \\ l_{i-1}(a-1)[1 - q_i(a-1)] + l_{i-2}(a-1)q_{i-1}(a-1), & 1 < i < m, \end{cases} \qquad (5)$$

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$$l_{(m-1)+}(a) = l_{(m-1)+}(a-1) + l_{(m-2)}(a-1)q_{(m-1)}(a-1). \qquad (6)$$

Equation (5) and (6) describe the childbearing process, of which commonly used measures, such as the total fertility and the mean age of childbearing, can be constructed.

Following the logic of constructing the conventional total fertility, the fertility-table total fertility can also be defined as the average number of children per woman at the maximum reproductive age, namely $a_{max}$. To be distinguished with the conventional total fertility, $TF$, the fertility-table total fertility is denoted as $TF_f$, where the subscript stands for fertility table. According to the definition of $TF_f$, there is,

$$TF_f = \frac{\sum_{a=a_{min}}^{a_{max}} \sum_{i=1}^{m-1} q_i(a)l_{i-1}(a) + \sum_{a=a_{min}}^{a_{max}} q_{m+}(a)l_{(m-1)+}(a)}{l_0(a_{min})}, \qquad (7)$$

where $a_{min}$ represents the minimum reproductive age; and $l_0(a_{min})$ describes the starting number of the hypothetical cohort. The nominator and denominator of (7) are the total number of births and women, respectively. In the nominator of (7), the first term is the number of births summed over age $a$ and parity $i$, and the second term the number of births summed over age $a$ for parity $(m-1)+$. Fertility-table parity-specific total fertility, namely $TF_{f(i)}$ for parity $i$, can be computed similarly using the births to parity $i$ rather than all parities. Using conventional parity-specific total fertility, $TF_{(i)}$, one may encounter the problem of $TF_{(i)} > 1$, especially for $i = 1$, which cannot be interpreted, because on average a woman cannot have more than one first child. This problem will not occur to $TF_{f(i)}$ because of the following reason. Noticing $l_{i-1}(a)/l_0(a_{min})$ is the probability of reaching parity $(i-1)$ at age $a$ from parity $0$ at age $a_{min}$, it is apparent that

$TF_{f(i)} = \sum_{a=a_{min}}^{a_{max}} q_i(a)l_{i-1}(a)/l_0(a_{min})$ is the lifetime probability of having the $ith$ and more

children, and hence cannot be bigger than 1.

To compute the fertility-table mean age of childbearing, namely $MAC_f$, the second assumption, that on average the births to women aged $[a,a+1)$ appear at age $a+0.5$, is needed. Under this assumption, there is

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$$MAC_f = \frac{\sum_{a=a_{\min}}^{a_{\max}} (a+0.5)[b_{m+}(a) + \sum_{i=1}^{m-1} b_i(a)]}{\sum_{a=a_{\min}}^{a_{\max}} [b_{m+}(a) + \sum_{i=1}^{m-1} b_i(a)]}$$
$$= \frac{\sum_{a=a_{\min}}^{a_{\max}} (a+0.5)[l_{(m-1)+}(a)q_{m+}(a) + \sum_{i=1}^{m-1} l_{i-1}(a)q_i(a)]}{\sum_{a=a_{\min}}^{a_{\max}} [l_{(m-1)+}(a)q_{m+}(a) + \sum_{i=1}^{m-1} l_{i-1}(a)q_i(a)]} \quad . \quad (8)$$

For the (*i*)*th* parity, the fertility-table mean age of childbearing, $MAC_{f(i)}$, can be computed similarly, using the births of parity *i* rather than all parities.


**The probabilistic fertility table**

Based on observed values of $q_i(a)$, a fertility table can be computed according to the above formulas, and can be called an observed fertility table. The observed fertility table is deterministic, in which, for example, the ratio of $l_0(a)/l_0(a_{\min})$ is a certain number that does not change when choosing different $l_0(a_{\min})$. For this reason, the value of $l_0(a_{\min})$ is chosen arbitrarily in deterministic fertility tables. On the other hand, denoting the probability of being childless at age *a* as $p_0(a)$, and assuming that childless women deliver their first births independently each other, then, the ratio of $l_0(a)/l_0(a_{\min})$ obeys a binomial distribution. In other words, $l_0(a)/l_0(a_{\min})$ has a variance that is $p_0(a)[1 - p_0(a)]/l_0(a_{\min})$. Therefore, $l_0(a)/l_0(a_{\min})$ is uncertain, unless $l_0(a_{\min})$ is infinitely large.

Why is there a fundamental difference about whether $l_0(a)/l_0(a_{\min})$ is deterministic or probabilistic? The answer is there are two different definitions of probability. The demographic definition of probability is (1) and (2), which is the basis of the concise fertility table. On the other hand, the statistical definition of probability includes not only (1) and (2), but also a condition that the denominators of (1) and (2) are infinitely large (see Agresti and Finlay, 1997), which will lead to the probabilistic fertility table below.

Using the statistical definition to describe the childbearing process, the value of $l_0(a_{\min})$ matters and can no longer be arbitrary. What value should $l_0(a_{\min})$ take? In developing the probabilistic life table, Li and Tuljapurkar (2013) suggested to estimate the stationary-equivalent population, which is a hypothetic cohort with a specific starting number that minimizes the difference between the person-years of the cohort and the observed population. Since the hypothetical cohort is subject neither to mortality nor migration, the number of its population is constant over age, and the value of

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$l_0(a_{min})$ should be this constant. To describe the person-years of the observed female population that changes with age, the value of $l_0(a_{min})$ should be the over-age average of the observed person-years according to Li and Tuljapurkar (2013). Thereafter, $l_0(a_{min})$ is no longer arbitrary but the average of the observed person-years of women in reproductive ages; and the stationary-equivalent population is the hypothetical cohort starting with this $l_0(a_{min})$.

The differences between the age patterns of the hypothetical cohort and the observed population are expected; and they are the reason for introducing the hypothetical cohort. These differences can be viewed as the effects of historical demographic changes, which include fertility, mortality and migration, and have nothing to do with current mortality. Subsequently, the rationale of introducing the hypothetical cohort can be understood as to eliminate the effects of historical demographic changes on the age pattern of the observed population. According to this view, the age pattern of the hypothetical cohort would be the age pattern of the observed population, if there were no effects of historical demographic changes that made the age pattern of the observed population irregular.

Clearly, specifying the stationary-equivalent population is to eliminate the effects of historical demographic events on the age-specific person-years of the observed population. As a result, the person-years of the stationary-equivalent population would be the corresponding person-years of the observed population, if there were no above noted effects. Accordingly, the uncertain childbearing process of the stationary-equivalent population would be the uncertain childbearing process of the observed population, if again there were no above noted effects. Subsequently, using the stationary-equivalent population, the uncertainties of the childbearing process of the observed population can be utilized to produce insights that cannot be understood otherwise. On the other hand, the childbearing process of a cohort with an arbitrary starting number is also uncertain; but its uncertainty is meaningless.

When the value of $l_0(a_{min})$ is obtained, the childbearing process can be modelled under two assumptions. The first assumption is that an individual woman delivers birth independently from others; and the second is that the observed probabilities of delivering birth are unbiased, meaning that they differ from the corresponding true values only randomly. Let $q_i(a,0)$ be the observed probability for a woman aged *a* with *(i-1)* children to deliver the *(i)th* child at ages *[a,a+1)*, where index 0 is reserved for the observed sample. Then, under the first assumption, the childbearing process at age *a* can be described by a random variable $\Delta(1,q_i(a,0))$ that is generated by a Bernoulli distribution with probability $q_i(a,0)$, or a binomial distribution with trail 1 and probability $q_i(a,0)$. More specifically, $\Delta(1,q_i(a,0))$ takes value 1 to represent the event of having the *ith* child at ages *[a, a+1)*, or 0 otherwise. The values of $\Delta(1,q_i(a,0))$ can be generated by almost any computing software. For example, if $q_i(a,0) = 0.1$, then among 100 sample values of $\Delta(1,q_i(a,0))$, 1 would appear approximately 10 times, indicating roughly 10 would have

the (i)th child among the 100 women aged a with (i-1) children. The exact number of $\Delta(1, q_i(a,0)) = 1$, however, is uncertain.

Having the values of $\Delta(1, q_i(a,0))$, the childbearing process of a sample cohort, namely the (j)th sample cohort, can now be modelled. For the (k)th women at age a in the (j)th sample cohort, denoting her number of children by $c(a, j, k)$, then the values of $c(a, j, k)$ can be computed as

$$c(a, j, k) = c(a-1, j, k) + \Delta(1, q_{c(a-1,j,k)-1}(a,0)), \quad c(a-1, j, k) < m-1. \quad (9)$$

Equation (9) indicates that, for the (k)th woman at age (a-1) with the number of children smaller than (m-1), her number of children at age a will be $c(a-1, j, k) + 1$, if $\Delta(1, q_{c(a-1,j,k)-1}(a,0)) = 1$, or remain the same as at age (a-1) if $\Delta(1, q_{c(a-1,j,k)-1}(a,0)) = 0$. On the other hand, when this woman's number of children reaches (m-1) at age (a-1), she enters the parity (m-1)+ and will stay in this parity at older ages. For each woman in the (j)th cohort, her number of children starts with 0 at age $a_{min}$, and at some unpredictable age it may increase to 1, and so on.

Subsequently, the number of women aged a with i children in the (j)th sample cohort is computed as:

$$l_i(a, j) = \sum_{k=1}^{l_0(a_{min})} \delta(c(a, j, k) - i), \quad i < m-1,$$

$$l_{(m-1)+}(a, j) = l_0(a_{min}) - \sum_{i=0}^{m-2} l_i(a, j). \quad (10)$$

In (10), $\delta(y)$ is a function that takes value 1 for y=0 and 0 for other y. The first line of (10) indicates that $l_i(a, j)$ is the total number of $c(a, j, k) = i$; and the second line of (10) is obtained from the absence of mortality and migration.

Since multiple Bernoulli distributions with the same probability can be replaced by a binomial distribution with multiple trails, namely *B(number of trails, probability)*, $l_i(a, j)$ could be generated at the cohort rather than individual level. More specifically,

$l_0(a, j)$ could be obtained as a random sample of $B(l_0(a-1, j), 1-q_1(a-1,0))$;

and $l_i(a, j)$ a random sample of $B(l_i(a-1, j), 1-q_{i+1}(a-1,0)) + B(l_{i-1}(a-1, j), q_i(a-1,0))$.

This way could remarkably reduce computing time, but may be less transparent in describing the childbearing process.

Recalling that $q_i(a,0)$ are observed from a limited population, the *(j)th* sample cohort should have its own sample values of birth probability, namely $q_i(a, j)$, which may differ from $q_i(a,0)$. Given $l_i(a, j)$, $q_i(a, j)$ for $i<m$ can be computed using (5), or the demographic definition of sample probability, as below

$$q_1(a, j) = 1 - \frac{l_0(a, j)}{l_0(a-1, j)},$$

$$q_i(a, j) = 1 - \frac{l_{i-1}(a) - l_{i-2}(a-1)q_{i-1}(a-1)}{l_{i-1}(a-1)}, \quad 1 < i < m. \tag{11}$$

For the *(m-1)+* parity, since $l_{(m-1)+}(a-1, j)$ is obtained from (10), $b_{m+}(a, j)$ can be described by a random sample $\Delta(l_{(m-1)+}(a-1, j), q_{m+}(a-1,0))$, which is generated by a binomial distribution with $l_{(m-1)+}(a-1, j)$ trials and probability $q_{m+}(a-1,0)$. Thus,

$$q_{m+}(a, j) = \frac{\Delta(l_{(m-1)+}(a-1, j), q_{m+}(a-1,0))}{l_{(m-1)+}(a-1, j)}. \tag{12}$$

Having the sample values $q_i(a, j)$, other fertility measures such as $TF_f(j)$ and $MAC_f(j)$ can be computed according to the formulas of the deterministic fertility table. Thus, the *(j)th* sample fertility table is obtained.

Repeating the above process, the *(j)th* sample fertility table for *j=1, 2, ..., $s_n$* are computed, where $s_n$ stands for the number of sample cohorts. Using a large $s_n$, an approximate probability distribution of the fertility table is obtained, which composes a

probabilistic fertility table. According to the second assumption that the values of $q_i(a,0)$ are unbiased, the estimate true values of the probability of delivering birth, which are defined by the statistical definition and cannot be observed exactly when the population size is not infinite, are now described by the approximate probability distributions $q_i(a,j)$.

**An application of the concise fertility table**

Through its use of parity information the concise fertility table can describe the family structures in the stationary-equivalent population. For example, as the lifetime probability of having the (*i*)*th* child, $l_i(a_{max})/l_0(a_{min})$ is obviously the proportion of the women (or families) who have *i* children[2] at age $a_{max}$. For another example, $TF_f \cdot l_0(a_{min})$ and $i \cdot l_i(a_{max})$ are the total number of children and the number of children who have *(i-1)* siblings, respectively. Thus, $i \cdot l_i(a_{max})/[TF_f \cdot l_0(a_{min})]$ is the proportion of children who have *(i-1)* siblings when their mothers aged $a_{max}$.

The above examples refer to the population multiplied by the hypothetic cohort. Using the age-parity-specific probabilities of delivering birth to replace the age-specific fertility rates in the cohort-component model, cohort-component models could be extended to include the above family structures.

**An application of the probabilistic fertility table**

Using probabilistic fertility tables, the statistical significance of a difference, between a fertility-table variable observed in two countries or at two times, can be tested in the way identical to that of probabilistic life tables (Li and Tuljapurkar, 2013).

Denote a fertility-table variable for populations 1 and 2 by $x_1$ and $x_2$, and the corresponding sample values by $x_1(j)$ and $x_2(j)$ for *j=1,2,... $s_n$*. Here populations 1 and

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[2] Here the deaths of children are neglected.

2 could be that of two different countries, or one country at two different times. To test the significance of the difference between the mean values of $x_1$ and $x_2$, the null hypothesis can be set as *Ho: mean($x_1$) = mean($x_2$)*. Under this hypothesis, a test statistic can be constructed as

$$z = \frac{x_1 - x_2 - mean(x_1 - x_2)}{\sqrt{\hat{\sigma}_1^2 + \hat{\sigma}_2^2}}, \qquad (13)$$

where $\hat{\sigma}_1^2$ and $\hat{\sigma}_2^2$ are the estimated variances of $x_1$ and $x_2$, and can be computed from the sample distributions as

$$\hat{\sigma}_h^2 = \sum_{j=1}^{s_n}[x_h(j) - \sum_{k=1}^{s_n} x_h(k)/s_n]^2/s_n, \quad h=1,2. \quad (14)$$

On the other hand, without the null hypothesis, the observed value of the test statistic *z* is

$$z(0) = \frac{x_1(0) - x_2(0)}{\sqrt{\hat{\sigma}_1^2 + \hat{\sigma}_2^2}}, \qquad (15)$$

where the observed values of the fertility-table variable in question, namely $x_1(0)$ and $x_2(0)$, are computed from the corresponding deterministic fertility tables.

In the usual applications of significance test, the analytic distribution of *z* is known as standard normal; and accordingly the 95% confidence interval is [-1.96, 1.96]. If *z(0)* falls outside [-1.96, 1.96], then the *Ho* is rejected at 0.05 level; and the conclusion is that the difference between the mean values of $x_1$ and $x_2$ is statistically significant. Otherwise, the difference between the mean values of $x_1$ and $x_2$ cannot be claimed statistically significant.

Here we do not know the analytic distribution, but we have the approximate probability distribution, of $z$. Since the rank, $j$, are chosen randomly for $x_1(j)$ and $x_2(j)$, the approximate probability distribution of $z$ can be constructed as

$$z(j) = \frac{x_1(j) - x_2(j) - \sum_{j=1}^{s_n}(x_1(j) - x_2(j))/s_n}{\sqrt{\hat{\sigma}_1^2 + \hat{\sigma}_2^2}}, \quad j = 1 \sim s_n. \quad (16)$$

Using the approximate probability distribution of $z$, we can find out the 95% confidence interval, namely $[c_1, c_2]$, numerically and approximately. Subsequently, a significance test can be carried out by looking at whether $z(0)$ falls outside $[c_1, c_2]$, following the same logic as using analytic distributions.

**Examples**

For the purpose of illustration, the examples choose a country with roughly the median population size among the countries of the world, Switzerland[3]. The data on the age-parity-specific fertility rate and female population of year 2008, 2009, and 2010 are downloaded from the Human Fertility Database (2013). The values of $a_{min}$, $a_{max}$, and $s_n$ are taken as 15, 49, and 1000, respectively. The observed age-parity-specific probabilities of delivering birth are then computed according to the formulas in the appendix.
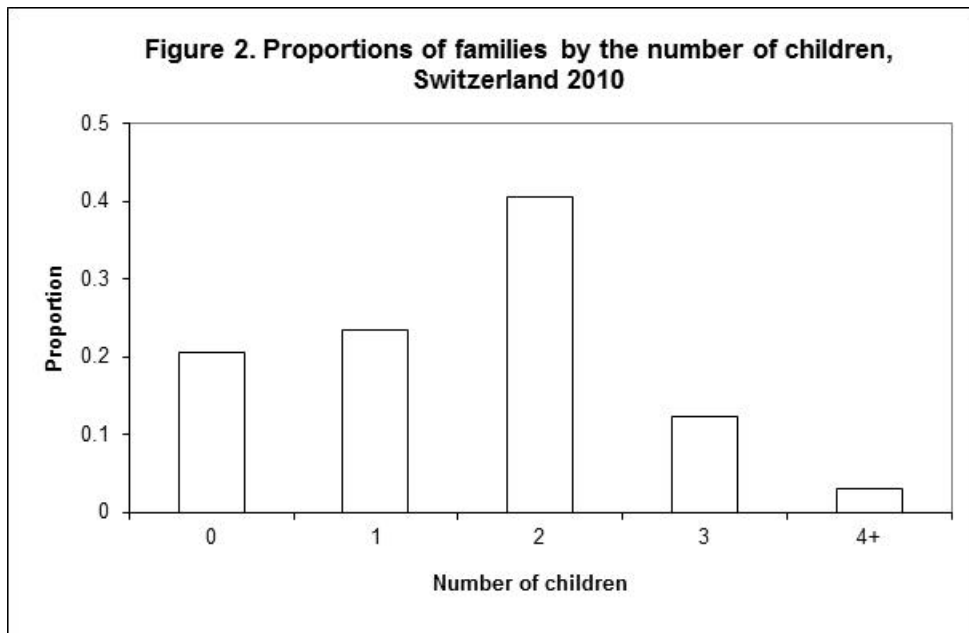
The values of the conventional total fertility ($TF$) and the fertility-table total fertility ($TF_f$) are displayed in Figure 1. First, Figure 1 shows that the values of $TF_f$ are larger than that of $TF$. Second, it can be seen that fertility level increased faster in 2008-2009 than that in 2009-2010 according to $TF_f$; but the $TF$ shows otherwise. Noting that $TF$ suffers the effect of parity change but $TF_f$ does not, and that the significance of a change in $TF$ cannot be tested but for $TF_f$ the test can be done, the recommendation is to use $TF_f$, when it could be computed.

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[3] Among the world's 201 countries and areas with 90 thousand and more residents in mid-2010, the number of countries and areas with population larger than that of Switzerland was 95 (source: United Nations (2013). *World Population Prospects: the 2012 revision*).

Figure 1. Conventional total fertility (TF) and fertility-table total fertility (TF$_f$) of Switzerland
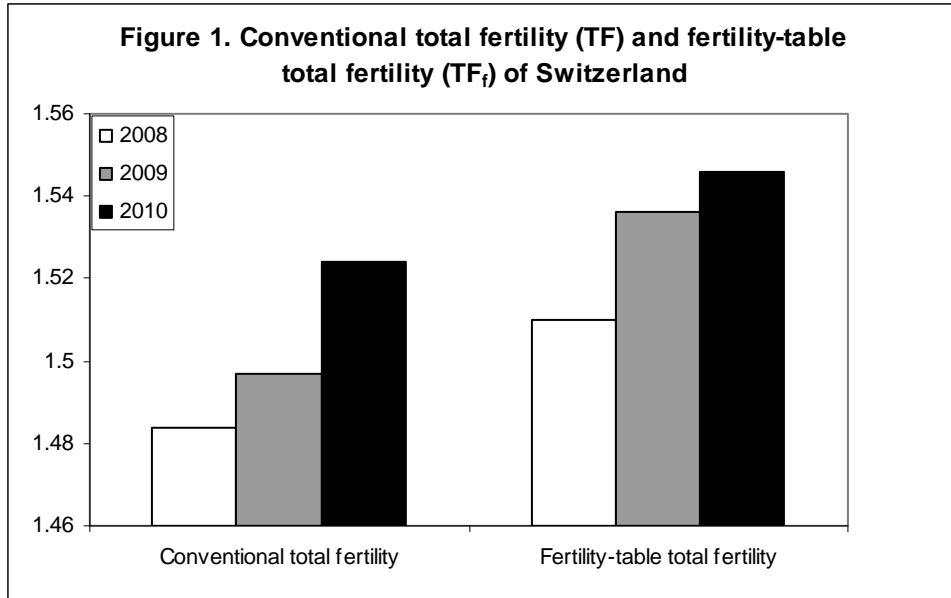
The concise fertility table can also describe family structures and provide informative insights, as are displayed in Figures 2 and 3.



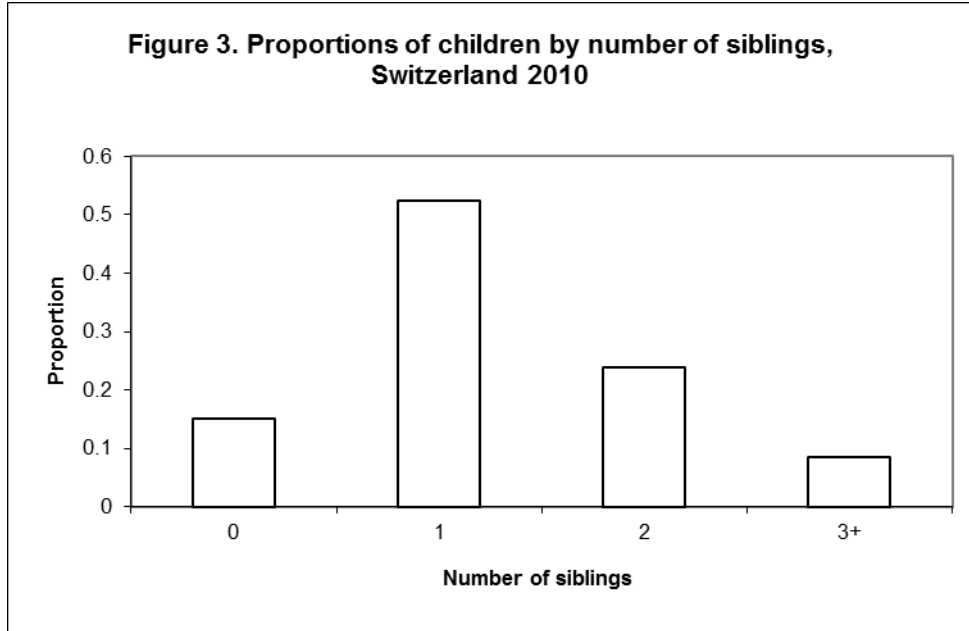Figure 2. Proportions of families by the number of children, Switzerland 2010

Figure 3. Proportions of children by number of siblings, Switzerland 2010

Figure 2 indicates the most common families still have two children, although the $TF_f$ is lower than 1.56 as is shown in Figure 1. Furthermore, Figure 3 shows that the proportion of single child is smaller than that of the children who have two siblings, although one-child families are more than those of three children.

The $TF_f$ in Figure 1 are observed samples and not necessarily the true values, which cannot be exactly observed unless $l_0(a_{min})$ is infinitely large. Nonetheless, the approximate probability distributions, or sample distributions, of the estimate true values are provided by the probabilistic fertility table, in the first and second panels of Figure 4 for 2009 and 2010, in which the vertical axis indicates the number of samples in each bar. Subsequently, although the true values of $TF_f$ cannot be observed exactly, whether the difference between them is, or is not, statistically significant could still be inferred. It can be seen that the sample mean increased from 2009 to 2010, but the increase is not statistically significant, because the observed value of the test statistic, $z(0)$, falls in the 95% confidence interval $[c_1, c_2]$. What conditions could make the difference between the mean values more likely significant? One is a bigger difference between the observed samples, which will push the $z(0)$ far away from zero. And another is a larger $l_0(a_{min})$ that will narrow the probability distributions of $TF_f$ and reduce $[c_1, c_2]$.

Figure 4. Sample distributions and significant test of $TF_f$, 2009 and 2010
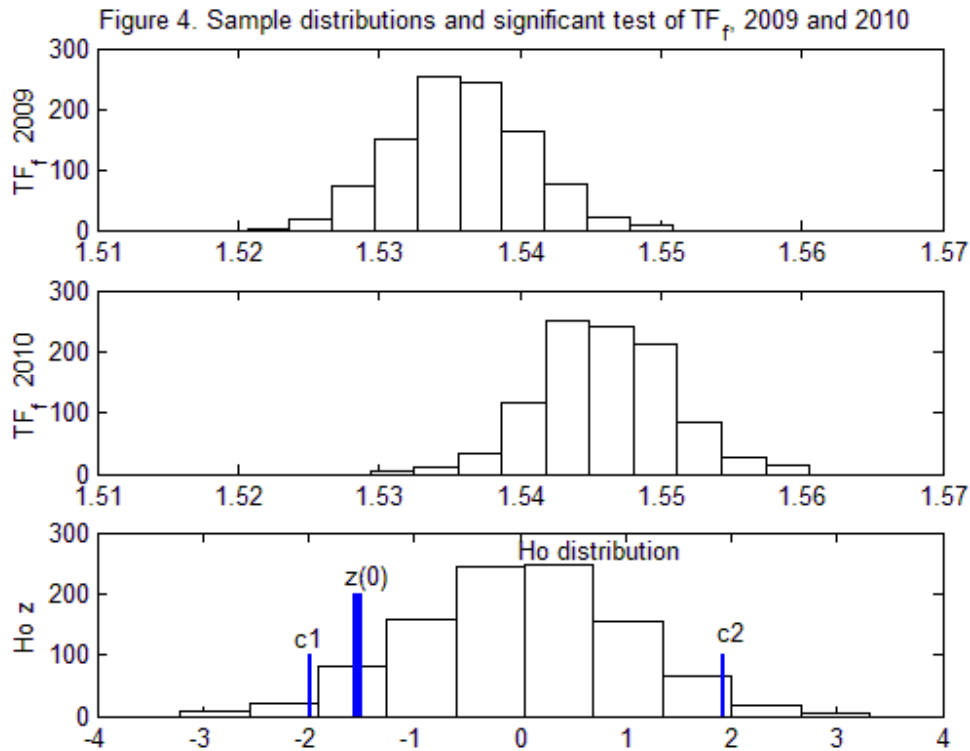
Compared to sample surveys often providing standard error of *TF* such as in the reports of the Demographic and Health Surveys (http://www.dhsprogram.com/), uncertainties can hardly be found for fertility measures derived from vital registration at national level. Explanations to this situation could be summarised into two parts. The first is that national population sizes are large; and therefore the uncertainties must be too trivial to be useful. This explanation is quantitative, and is quantitatively rejected by the example in Figure 4. The second explanation is that, when errors in counting all births and women are negligible, as can be assumed for developed countries, resulted fertility measures are 'population parameters' or the true values. Here we may recall that although tossing a perfect coin subjects no error, the proportion of observed face is not necessarily close to 0.5, unless the number of tossing is infinitely large.

The first and second panels of Figure 5 describe the sample distributions of $MAC_f$ in 2009 and 2010. The sample mean of $MAC_f$ also increased, and again the increase is not statistically significant, as is indicated by the third panel of Figure 5. Since the changes of $TF_f$ and $MAC_f$ are both statistically insignificant, one may conclude that the observed fertility change in 2009-2010 is more likely a random fluctuation.

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Figure 5. Sample distributions and significant test of $MAC_f$, 2009 and 2010
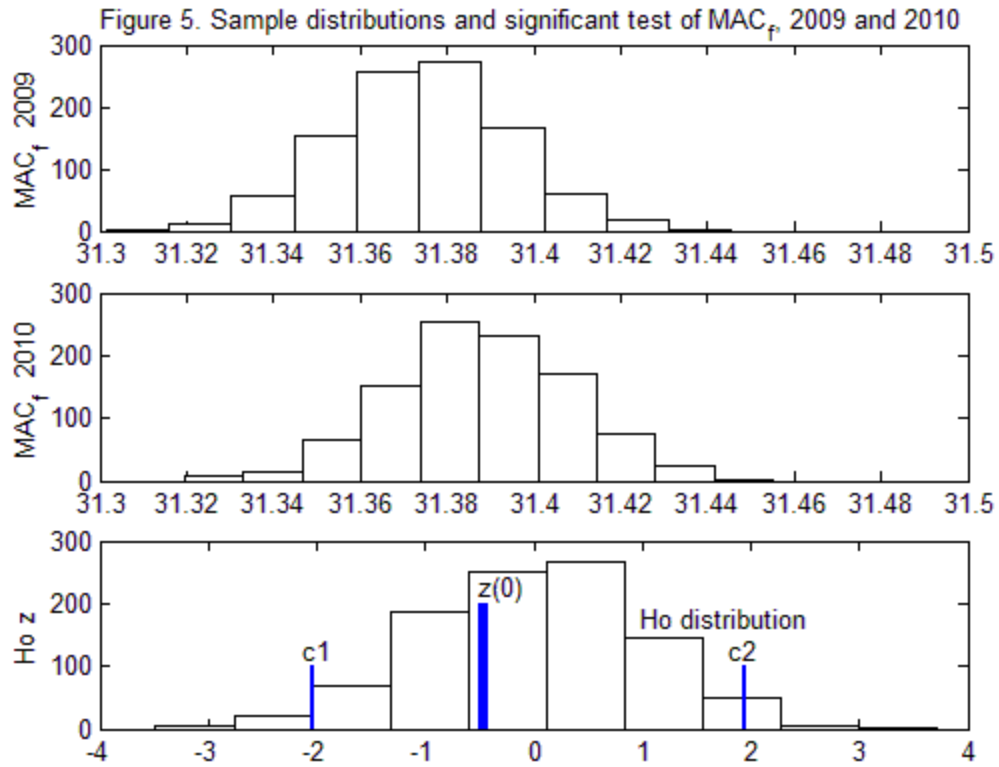
Turning to the fertility change in 2008-2009, however, the situation is different. Figure 1 shows that the change in 2008-2009 is bigger than that of 2009-2010. Further, Figure 6 indicates that the increase of $TF_f$ in 2008-2009 is statistically significant. The sample mean of $MAC_f$ also increased in 2008-2009, and the increase is again statistically significant, as is shown in Figure 7.

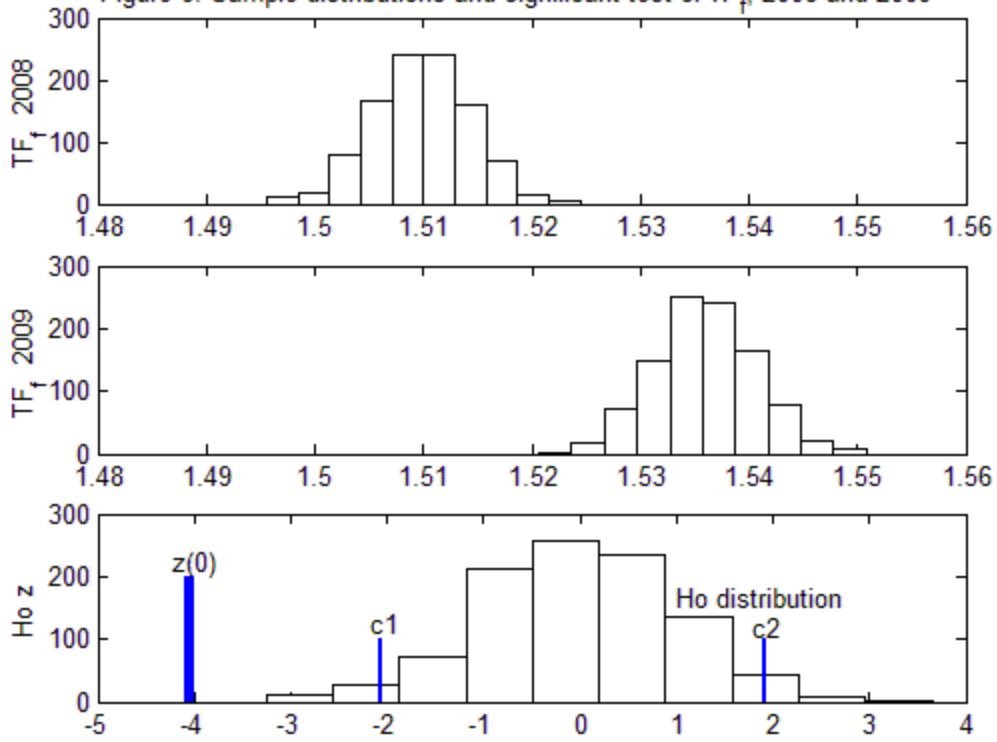Figure 6. Sample distributions and significant test of $TF_f$, 2008 and 2009



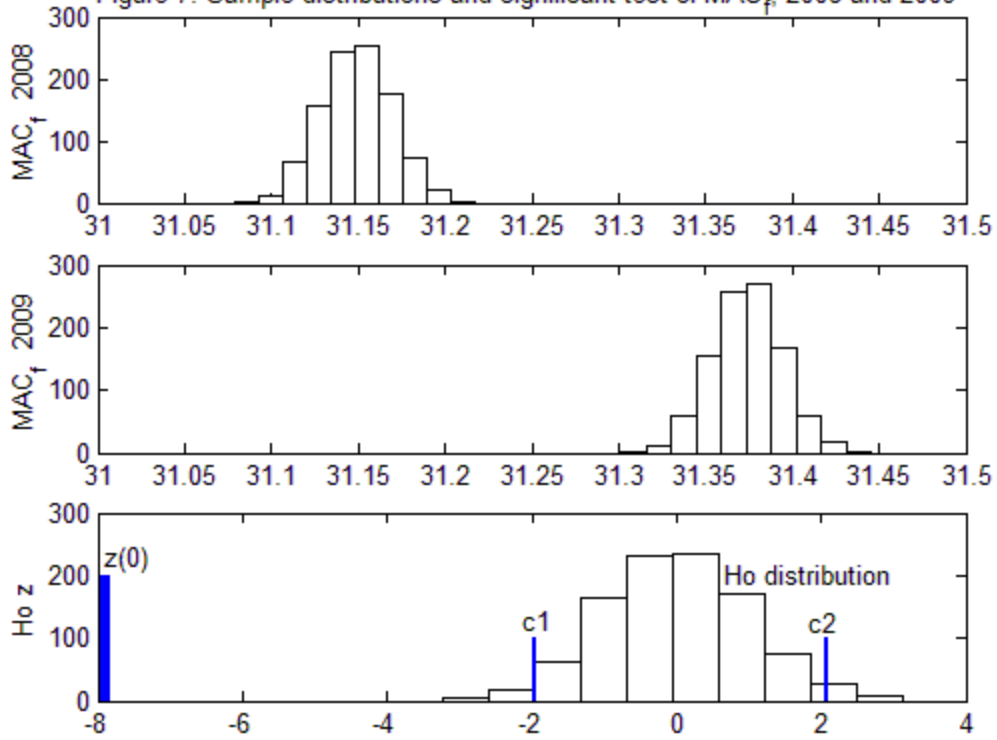Figure 7. Sample distributions and significant test of $MAC_f$, 2008 and 2009

Between 2008 and 2009, $TF_f$ and $MAC_f$ both increased significantly. It is interesting to note that this is different from the argument that, postponing childbearing (an increase of $MAC_f$) would cause the level of fertility to decline (a decrease of $TF_f$). Furthermore, the test can be extended to specific birth parities, and to family structures, when they are required.

The above examples indicate that the concise and probabilistic fertility tables could provide relevant insights into family structures and fertility change. These insights are especially informative for low-fertility countries, where the changes of fertility are subtle and important, for example, to population and other projections. Nonetheless, the conclusions obtained from these examples are based on one country in three recent successive years, and may not apply to other countries and times.

## Summary

This paper proposed a concise fertility table, which requires a demographic definition of the probability of childbearing by age and parity, and two assumptions, namely that a woman can bear at most one birth in a year and this birth occurs by even chance during the year. Using a concise fertility table, family structures such as the proportion of families by the number of children, or the proportion of children by the number of siblings, can be explored. The concise fertility table is deterministic, because it is based on the demographic definition of probability.

A concise fertility table only describes a sample scenario of the uncertain childbearing process of the hypothetic cohort. To model the uncertain childbearing process itself, this paper extended the concise fertility table from deterministic to probabilistic, using the statistical definition of probability and the approach used for probabilistic life tables (Li and Tuljapurkar, 2013). This extension does not require additional data, but needs two additional assumptions, which are independent birth deliveries between individual women and unbiased data. In a deterministic fertility table, a variable has a sample value for a given parity and age. In a probabilistic fertility table, a variable has a probability distribution for a given parity and age.

Using probabilistic fertility tables, the statistical significance of a difference, between the values of a fertility-table variable observed in two countries or at two times, can be tested. This test could help avoid two mistakes: explaining a difference that might be a random event, or ignoring a difference that may turn out important.

 In this paper, the data used to compute probabilistic fertility tables are collected from the Human Fertility Database (2013). Such data can be assumed unbiased, and could also be available for most developed countries and some developing nations. When the observed data cannot be assumed unbiased, however, computing probabilistic fertility

tables may not make much sense, because the resulting probability distributions may not refer to the estimate true values, and what they refer to are unknown.

## Appendix

This appendix discusses how to compute $q_i(a)$. Using population data from census and estimates and vital registration for births, the values of the age-parity-specific fertility rate for a certain period can be computed as:

$$M_i(a) = \frac{Number\ of\ births\ delivered\ by\ below\ women}{Person-years\ of\ women\ having\ (i-1)\ children\ at\ ages\ [a, a+1)}. \qquad (a.1)$$

In (a.1), both the numerator and the denominator refer to a certain period, which may or may not be a calendar year. It should be mentioned that, although the age interval must be one year for the concise fertility table, the period to which a fertility table refers can be flexible such as 5 years. This is important for small populations, of which a longer period should contain more births and hence make the age-parity-specific fertility rates more robust.

Because fertility may change only slightly in one year interval of age and a moderate period of time, there is approximately (see Preston, Heuveline, and Guillot, 2001)

$$M_i(a) = m_i(a), \qquad (a.2)$$

where $m_i(a)$ represents the age-parity-specific fertility rate of the hypothetic cohort, and is defined as

$$m_i(a) = \frac{b_i(a)}{L_{i-1}(a)}. \qquad (a.3)$$

The target of this appendix is to compute $q_i(a)$ using $m_i(a)$.

In (a.3), $L_{i-1}(a)$ represents the person-years of the (i-1)th parity in [a,a+1):

$$L_{i-1}(a) = \int_{y=a}^{a+1} l_{i-1}(y)dy, \qquad (a.4)$$

where $l_{i-1}(y)$ represents the number of woman of parity i-1 at age y. For i=1, $L_0(a)$ is the population exposed to the chance of having the first child at ages [a,a+1). For i>1, however, $L_{i-1}(a)$ is not the population exposed to the chance of having the (i)th child at

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ages *[a,a+1)*, because some women entered parity *(i-1)* by bearing the $(i-1)th$ child at ages *[a,a+1)* and thence are not exposed to the chance of having the *ith* child within the rest of the calendar year, according first assumption that a woman can bear at most one birth in one year.

Under the second assumption that the births occur evenly in each age interval, both the decline (due to delivering the *(i)th* births) and the increase (due to delivering the *(i-1)th* birth) of $l_{i-1}(a)$ are linear functions of age. Thus, $l_{i-1}(a)$ changes with *a* linearly and therefore

$$L_{i-1}(a) = 0.5 \cdot [l_{i-1}(a) + l_{i-1}(a+1)]. \qquad (a.5)$$

For the case of *i=1*, (a.5) leads to

$$m_1(a) = \frac{b_1(a)}{L_0(a)} = \frac{q_1(a)l_0(a)}{0.5 \cdot [l_0(a) + l_0(a+1)]} . \qquad (a.6)$$

Using the first line of (5), (a.6) is rewritten as

$$m_1(a) = \frac{q_1(a)}{0.5 \cdot [1 + l_0(a+1)/l_0(a)]} = \frac{q_1(a)}{0.5 \cdot [1 + (1 - q_1(a))]}, \qquad (a.7)$$

which yields

$$q_1(a) = \frac{m_1(a)}{1 + 0.5 \cdot m_1(a)} . \qquad (a.8)$$

Equation (a.8) is identical to the corresponding formula in life tables, because $L_0(a)$ is the population exposed to the chance of having the first child at ages *[a,a+1)*.

For the cases of $m > i > 1$, (a.5) still yields

$$m_i(a) = \frac{b_i(a)}{L_{i-1}(a)} = \frac{q_i(a)l_{i-1}(a)}{0.5 \cdot [l_{i-1}(a) + l_{i-1}(a+1)]} . \qquad (a.9)$$

But now the second line of (5) applies and leads to

$$m_i(a) = \frac{b_i(a)}{L_{i-1}(a)} = \frac{q_i(a)l_{i-1}(a)}{0.5 \cdot [l_{i-1}(a) + l_{i-2}(a)q_{i-1}(a) + l_{i-1}(a)(1 - q_i(a))]} . \qquad (a.10)$$

Rewriting (a.10), there is

$$q_i(a) = \frac{m_i(a)}{1+0.5 \cdot m_i(a)}[1 + \frac{0.5 \cdot l_{i-2}(a)q_{i-1}(a)}{l_{i-1}(a)}], \quad i > 1. \tag{a.11}$$

The difference between (a.8) and (a.11) is caused by that, although $L_{i-1}(a)$ is still the person years, it is no longer the population exposed to the chance of having the $(i)th$ child at ages $[a,a+1)$ for $i>1$. This provides an explanation as below. For $i>1$, the $(i-1)th$ births make $L_{i-1}(a)$ larger than the population exposed to the chance of bearing the $(i)th$ birth, and the $m_i(a)$ smaller, comparing to that of $i=1$. Thus, as a compensation, (a.11) includes an additional term, compared to (a.8). This additional term makes the calculation slightly complicated.

In (a.11), $q_i(a)$ and $l_{i-1}(a)$ are unknown, and can be solved iteratively together with the second line of (5):

$$l_{i-1}(a) = l_{i-2}(a-1)q_{i-1}(a-1) + l_{i-1}(a-1)[1-q_i(a-1)],$$
$$q_i(a) = \frac{m_i(a)}{1+0.5 \cdot m_i(a)}[1 + \frac{0.5 \cdot l_{i-2}(a)q_{i-1}(a)}{l_{i-1}(a)}]. \tag{a.12}$$

The iteration starts from $i = 2$, of which $q_1(a)$ and $l_0(a)$ for all $a$ are already computed as the result of $i = 1$. Using the first line of (a.12), $l_1(a_{\min} + 1)$ is obtained, because it is known that $q_2(a_{\min}) = 0$ according to the assumption that a woman could deliver only one child in a year. Subsequently, $q_2(a_{\min} + 1)$ is obtained from the second line of (a.12). When $q_2(a_{\min} + 1)$ is known, $l_1(a_{\min} + 2)$ is obtained from the first line of (a. 12), and so is the $q_2(a_{\min} + 2)$ from the second line of (a.12). Repeating this process, $q_2(a)$ and $l_1(a)$ for all $a$ are obtained. Now the iteration reaches $i = 3$, of which of which $q_2(a)$, $q_1(a)$, $l_1(a)$ and $l_0(a)$ are already computed. Here $q_3(a)$ and $l_2(a)$ for all $a$ can be computed in the way similar to that of $i = 2$, starting from $q_3(a) = 0$ for $a \leq (a_{\min} + 1)$ according to the assumption that a woman could deliver only one child in a year. Repeating the process, $q_i(a)$ and $l_{i-1}(a)$ for all $i \leq (m-1)$ are obtained.

For the open parity $q_{m+}(a)$, the assumption that the births occur evenly in each age interval still leads to

$$m_{m+}(a) = \frac{b_{m+}(a)}{L_{(m-1)+}(a)} = \frac{q_{m+}(a)l_{(m-1)+}(a)}{0.5 \cdot [l_{(m-1)+}(a) + l_{(m-1)+}(a+1)]}. \tag{a.13}$$

Using (6), there is

$$m_{m+}(a) = \frac{b_{m+}(a)}{L_{(m-1)+}(a)} = \frac{q_{m+}(a)l_{(m-1)+}(a)}{0.5 \cdot [l_{(m-1)+}(a) + l_{(m-1)+}(a) + l_{(m-2)}(a)q_{(m-1)}(a)]}, \qquad (a.14)$$

which is

$$q_{m+}(a) = m_{m+}(a)[1 + \frac{0.5 \cdot l_{m-2}(a)q_{m-1}(a)}{l_{(m-1)+}(a)}] . \qquad (a.15)$$

Different from the case of $i<m$ in which $q_i(a)$ are computed iteratively, all $q_{m+}(a)$ can be computed by (a.15), this is because $l_{(m-1)+}(a)$ can be calculated according to that the hypothetical cohort subjects neither mortality nor migration:

$$l_{(m-1)+}(a) = l_0(a_{\min}) - \sum_{i=0}^{m-2} l_i(a) . \qquad (a.16)$$

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