

VIENNA INSTITUTE OF DEMOGRAPHY

Working Papers

09 / 2005

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Long-Term Effects of Childbearing Postponement



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Abstract

Long-term consequences of childbearing postponement for the population size are considered. General relations are obtained, which imply that the cohort NRR, the final generation length, and dynamics of the number of genealogical lines determine the final population trend. The period fertility rates are not relevant to ultimate population size in the case of stationary population and have only moderate effect when cohort NRR differs from unity. Relations obtained are also of value for formal demography and can be applied to the fertility transition modeling, population forecasting, and population genetics.

Keywords

Childbearing postponement, genealogical lines, cohort rates, long-term population dynamics

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Acknowledgements

The work was supported in part by the Russian Foundation for Fundamental Research under Grant #05-06-80432 “Development of mathematical models and methods for estimating the reproduction characteristics of a small-size population”.

Long-term effects of childbearing postponement

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1. Introduction

The work of Bongaarts and Feeney (1998) stimulated a broad research on fertility postponement consequences for fertility measures and population reproduction perspectives (e.g. Lesthaeghe and Willems 1999; Kohler and Philipppov 2001; Zeng and Land 2002; Kohler and Ortega 2002a, 2002b; Lutz, O'Neill, and Scherbov 2003; Goldstein, Lutz, and Scherbov 2003; Schoen 2004). The subject is rather complicated due to interplay of period and cohort factors as reflected in controversial comments to the aforementioned work and to earlier works concerned with cohort-related fertility measures (Hajnal 1947; Ryder 1964, 1965; Ni Bhrolchain 1992; Van Imhoff and Keilman 2000; Kim and Schoen 2000; Bongaarts and Feeney 2000). Schoen and Jonsson (2003), who put the problem into a stimulating form of a demographic paradox, illustrated the complicated nature of the problem. They demonstrated that populations may shrink even if every cohort has completed fertility rate above the replacement level. They show that such a paradoxical situation can last for a very long period due to declining cohort size.

The works mentioned attract attention to the effect of childbearing postponement on fertility rates while not directly discussing long-term consequences for the population size. We look at the problem from another angle, by studying what happens to the population size during and after shifts in the fertility schedule. Here I turn to this aspect of the fertility postponement phenomenon and argue that cohort fertility measures as well as 'corrected' period fertility measures do matter in the long run. As we will see, when fertility schedule alters, population passes from one global trend to another, and period fertility pattern can differ substantially from cohort patterns only during the transition. Our results are especially clear in the case of population whose cohorts simply replace themselves. In this case, the ultimate population size depends neither on period manifestations of the fertility transition, nor on the duration of the transition. Rather, the ultimate population size in this case depends on population characteristics before and after the fertility transition only. Even more, if population – after an arbitrary period – will return to its original fertility patterns, the population size will also return to its original trend. Interestingly, an analogous to the population momentum can be introduced, which relates the ultimate change in population size during the fertility transition to pre-transition population structure and ultimate reproduction regimen.

First, we will discuss the concept in the case of population with cohorts simply replacing themselves. The concept of genealogical lines crossing the time line will facilitate our derivations. We will see that this quantity is constant if every cohort simply replaces itself. The population stationary size depends on this quantity and fertility timing. Hence, ultimate fertility pattern determines the population size in the long run irrespective to the transient fertility patterns. Then, we will turn to the case of arbitrary population and

derive general relations. In the conclusion, we undertake a discussion of some implications to population reproduction measurement, population modeling, and genetics.

2. Population dynamics under simple reproduction of cohorts

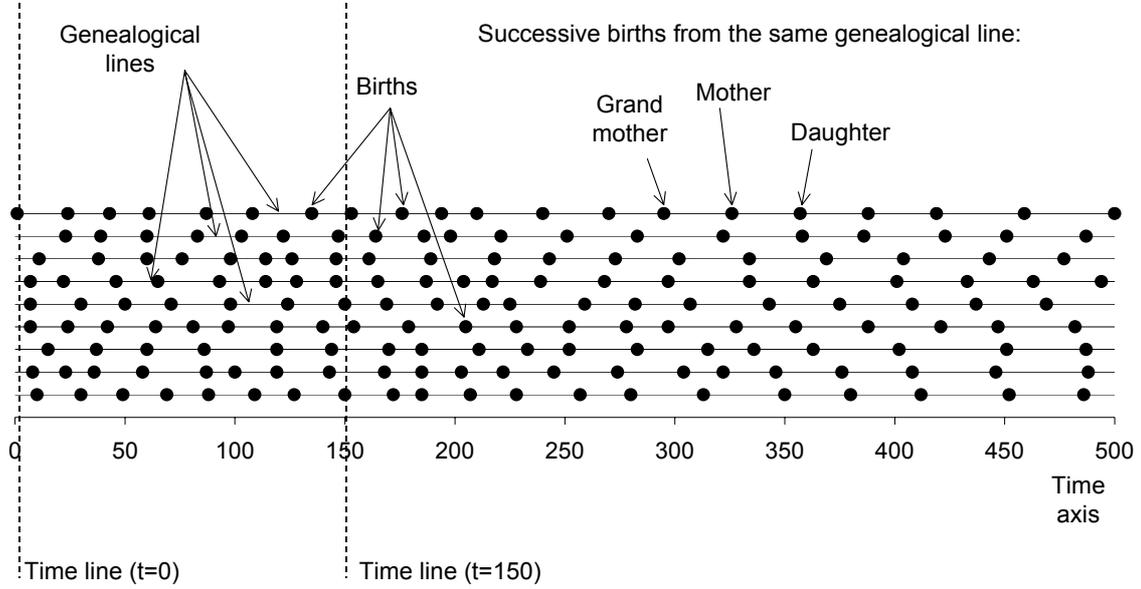
Let us consider the population whose cohorts simply replace themselves, i.e. every cohorts' net reproduction rate (NRR) equals to unity. What could happen to the population size when intergeneration intervals became longer? Intuitively it is clear, that in such circumstances births will be distributed within longer time intervals. Therefore, the intensity of births, i.e. the number of births per time unit, should become lower. This, in turn, implies that the population size should also decrease, as the stationary population size is a product of the births intensity and of the expectation of life at birth. At the same time, it is clear that the births intensity as well as the population size will not diminish constantly. As soon as the fertility timing will stop changing, the births intensity and the population size will also stabilize. Hence, it is natural that during the transition, when fertility timing shifts from one pattern to another, the period fertility rates will be below the replacement level, as the initially stationary population should decrease in size. However, the period fertility rates should again return to the replacement level and synchronize with the cohort rates after completion of the transition. In view of this population dynamics, the following crucial questions arise, which need an in-depth study: Which factors determine the final births intensity and the population size? How does the final population size depend on duration of the transition? How is it related to what happens during the transition (e.g. to period fertility measures observed during the transition)? What would happen to the population size if fertility pattern returned to its original pre-transition shape?

Let us turn to quantitative concepts in order to carry a formal study of the questions presented. When every cohort simply replaces itself, every newborn on average will give birth to one successor. For further derivations it will be helpful to put the cohort reproduction model into the following shape. We will consider that every newborn gives birth to *exactly one* successor. In reality some newborns have no successors at all, and others have more than one successor. Yet, we can formally distribute all births in a given cohort among all newborns of this cohort in a way presented above. This is possible as the cohort net reproduction rate equals to unity. Obviously, the fertility rates, inter-generation intervals, period and cohort fertility rates and population dynamics will not be affected by the new interpretation of the reproduction model.

The following visualization of the reproduction process will facilitate our study. We will depict births as dots and connect together dots of successive births. As anyone in our interpretation has exactly one successor, the reproduction process will be depicted as a chart of genealogical lines, which never intersect, never split, and never end. Illustrative example is presented on figure 1. Horizontal lines correspond to the genealogical lines, vertical lines correspond to a given time moment. Number of dots between two time lines is a number of births in the corresponding time interval. When childbearing postpones, interval between dots on the chart became wider, and their intensity, i.e. intensity of births, decreases. In the example presented on the figure, fertility timing alters during the period

from year 200 until year 400. Mean age at childbearing rises from the initial level of 20 years to the level of 35 years.

Figure 1. Illustrative example of the chart depicting the population reproduction process in the case of simple reproduction



The key observation from the presented reproduction model is that the number of genealogical lines crossing any time line is invariant of shifts in fertility timing as long as cohorts' net reproduction rates remain equal to unity. Given the number of genealogical lines crossing any given time line and the fertility timing, one can estimate the births intensity. It is the product of the number of genealogical lines by the births intensity per one line. For any genealogical line, there is one birth per interval between two successive births. Expected duration of this interval equals to the mean age at childbearing. Hence, average births intensity for one genealogical line is a reciprocal of the mean age at childbearing. This average intensity will approximate the expected value of real births intensity if, under the ergodic property, the population structure is randomized enough. Finally, the births expected intensity $B(t)$ at time t can be obtained by the following relation:

$$B(t) = \frac{G(t)}{\mu(t)}, \quad (1)$$

here $G(t)$ is a number of genealogical lines crossing the time line t , and $\mu(t)$ is an expected age of childbearing for those who have been born before the time t and will give birth after that moment. We reserve the prefix 'expected' for a small population, whose births intensity can fluctuate substantially. For large populations equation (1) corresponds to the observed level of births intensity.

One can compute the population size $N(t)$ at time t , given the births dynamics and mortality schedule:

$$N(t) = \int_0^X l(x, t-x) B(t-x) dx, \quad (2)$$

here $l(x, t)$ is a survivorship function, i.e. the accumulated probability of surviving from age 0 to age x for those born at time t ; X is the upper age, to which people can survive.

If the number of genealogical lines, fertility patterns, and survivorship function remain constant for at least X years, and the population structure has been randomized, we can obtain from (1), (2) for the expected population size:

$$EN(t) = \frac{G(t)}{\mu(t)} \int_0^X l(x, t) dx = \frac{e_0(t) \cdot G(t)}{\mu(t)}, \quad (3)$$

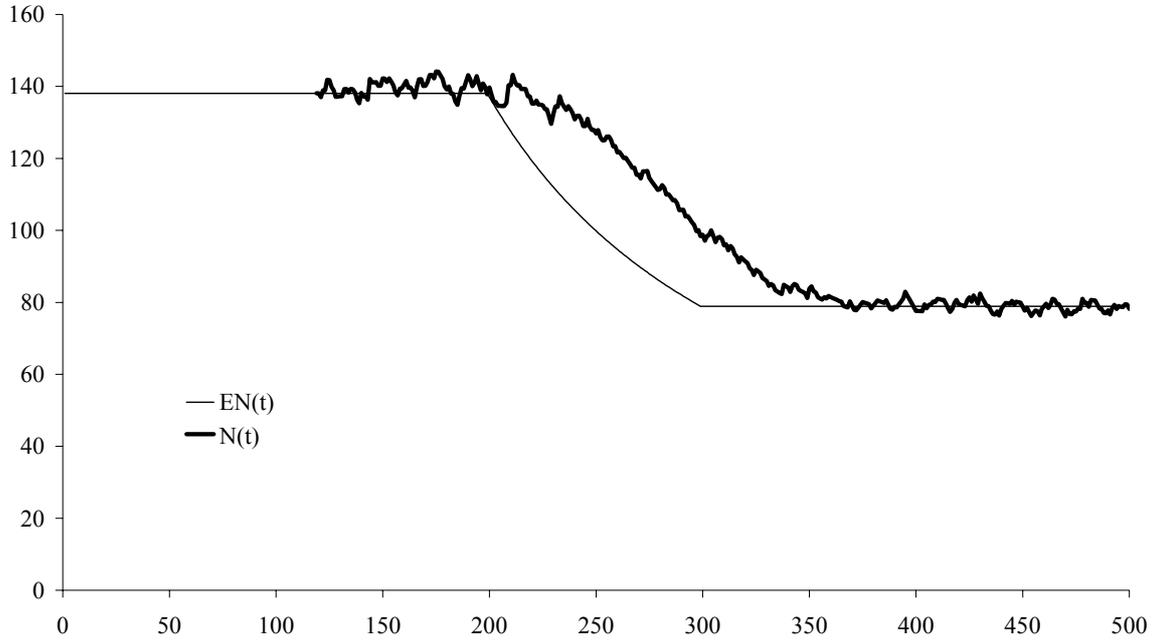
where $e_0(t)$ is the life expectancy at birth for those born at time t . Relations (1), (3) can also be applied to the births intensity and the population size of the stationary population equivalent to the population under study.

Figure 2 illustrates relation (3). It depicts the simulated population dynamics for a small population consisting of 40 genealogical lines. Mean age at childbearing changes in the period between year 200 and year 300 from 20 to 35 years. The thin and smooth line presents the population size expected under relation (3). It is clearly seen that, although the population size fluctuates randomly and changes dramatically during the fertility transition, its average level is well explained by the relation obtained.

Now we can answer the key questions stated above:

1. The final births intensity and the population size are fully determined by the number of genealogical lines, the life expectancy at birth, and the mean age at childbearing. Neither the shape of the fertility and survivorship functions, nor the reproduction history affect the final population size as long as the cohort NRR equals to unity. In particular, changes in variance of the fertility function and changes of fertility rates by birth order have no effect on the ultimate population size as long as the NRR and the mean age at childbearing are controlled.
2. The final births intensity and the population size depend neither on duration of the transition, nor on what ever happens during the transition. In particular, period fertility measures observed during the transition are not relevant to the population asymptote.
3. The population size will return exactly to the same level as before the transition, if fertility pattern will return to its original shape.
4. Transitional process could affect the population size and the age structure during and right after the transition only.

Figure 2. Illustrative dynamics of the population size. Population consists of 40 genealogical lines with mean age at childbearing that equals to 20 in the period before year 200 and equals to 35 after year 300



As the ultimate population size does not depend on how exactly passes the transition, one can use the concept close to the population momentum. Let the initial population structure be stationary, i.e. its expected size can be estimated using relation (3). Then the following *momentum of population change* can approximate the ratio of the ultimate population size to its pre-transition level:

$$\Omega_T = \frac{e_0 \cdot \mu^0}{e_0 \cdot \mu}, \quad (4)$$

here upper-case index '0' denotes pre-transition population measures. If the structure of the initial population is not stationary, then the total population momentum can be obtained by multiplying the timing factor given by relation (4) to the common momentum of the age structure. If, for example, the life expectancy at birth rises from 65 years to 70 years, and the mean age at childbearing rises from 22 years to 25 years, then the momentum of population growth implied by these changes will be equal to $\Omega_T = \frac{70 \cdot 22}{65 \cdot 25} = 0.95$. Hence, the changes in mortality and fertility will result in a 5% decrease of the population.

Another example of application of formula (4) concerns to 'neutral' demographic transition, which results in changes in mortality and fertility levels having no effect on cohorts' NRRs. In other words, fertility level decreases during such a transition simultaneously with the mortality level. As the fertility decreases, the proportion of lower birth orders rises, and the mean age at childbearing decreases. Hence, the neutral demographic transition could result in population changes described by the momentum formulae (4) despite having no effect on cohorts' reproduction. If, for example, the life

expectancy rises from 35 years to 65 years, and mean age at childbearing drops from 30 years to 23 years, then the population should increase by the product of $\Omega_T = \frac{65 \cdot 30}{35 \cdot 23} = 2.42$.

Amazingly, population can remarkably gain in size even when gains in survivorship are instantly leveled off by fertility decline.

In reality, it is useful to work with genealogical lines in common sense, i.e. those lines, which connect births of persons descending from one predecessor. For a large population the number of real genealogical lines will be equal to that presented above. In a small population, however, this number can fluctuate substantially. Yet, expected number of genealogical lines should also be constant in a small population as long as the cohort NRR remains equal to one. Formal proof of this proposition can be derived from the results in a general case of arbitrary NRRs, which is the subject of the next section. Hence, the results obtained are fully applicable if we consider the $G(t)$ being an expected number of genealogical lines in common sense.

3. Effects of childbearing postponement in a general case

In general, when one cannot point to such a simple invariant as the number of genealogical lines, study of the problem becomes cumbersome and needs a new approach. As the number of genealogical lines in this case could not be constant, the graphical illustration of the population reproduction presented above becomes useless. Hence, hereinafter we will consider the $G(t)$ being a number of common genealogical lines crossing the time line t . This number will grow on average when cohort NRR is above unity. It will decline with NRR below unity. In a small population this general trend will be accompanied by random fluctuations, see figure 3.

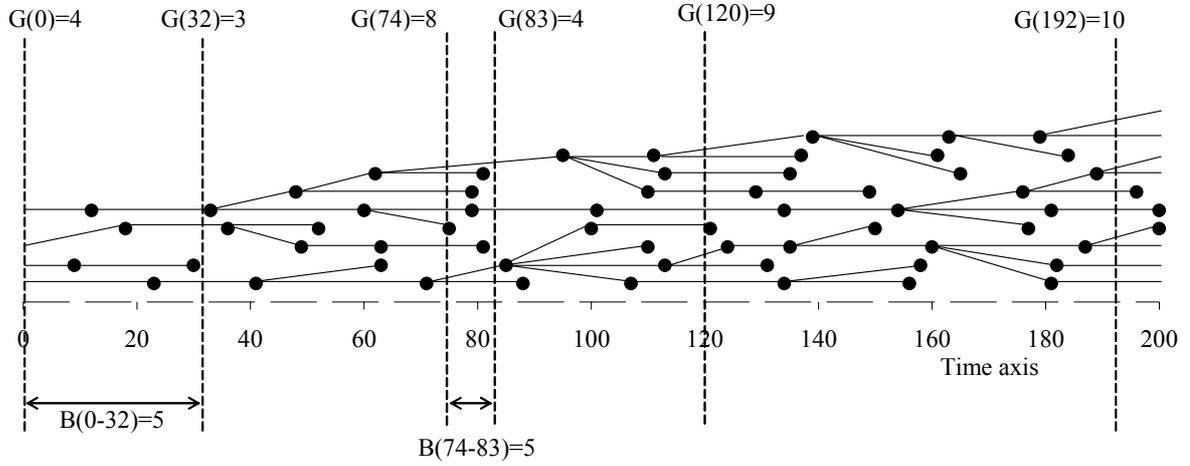
Basic equation (1) should be replaced in this section, as we cannot assume that births will be distributed uniformly even when fertility timing stabilizes. In order to derive the general relation, we can note that each birth dot presented on the genealogical chart marks the end of one genealogical line to the left. At the same time, number of genealogical lines can start from each birth dot. Expected number of these lines is the NRR of the cohort, which the birth belongs to. The expected number of genealogical lines crossing the right border of some short time interval $(t, t + \Delta)$ will exceed the number of lines crossing the left border to approximately $NRR(t) - 1$ times the number of births during the interval:

$$G(t + \Delta) - G(t) = (NRR(t) - 1)B(t)\Delta + o(\Delta), \quad (5)$$

where $o(\Delta)$ is a remaining part of order less than Δ . Dividing equation (5) by Δ and approaching the Δ to null, we obtain the following general relation between genealogical lines number and births intensity:

$$B(t) = \frac{1}{NRR(t) - 1} \cdot \frac{dG(t)}{dt}. \quad (6)$$

Figure 3. Genealogical chart depicting the population reproduction process with NRR above one



Now let us assume the population reproduction parameters and age structure to be stable. Under such circumstances all population indexes, including the number of genealogical lines, will grow at rate given by Lotka's r :

$$\frac{dG(t)}{dt} = rG(t), \quad (7)$$

where Lotka's r is related to the NRR by the common relation:

$$r = \frac{\ln NRR(t)}{T(t)}. \quad (8)$$

Here $T(t)$ is the generation length for the cohort born at time t .

Combining relations (6)-(8), we obtain finally for the stable population:

$$B(t) = \frac{\ln NRR(t)}{NRR(t) - 1} \cdot \frac{G(t)}{T(t)}. \quad (9)$$

When NRR is close to the level of simple replacement (one) then generation length turns into mean age at childbearing, $\ln NRR(t)$ approaches $NRR(t) - 1$, and formula (9) turns into formula (1) obtained earlier for stationary populations. Using general relation (2), we obtain for the expected stable population size:

$$EN(t) = \frac{r}{e^{rT} - 1} \cdot G(t) \int_0^X l(x, t) e^{-rx} dx = \frac{\ln NRR(t)}{NRR(t) - 1} \cdot \frac{G(t)}{T(t)} \int_0^X l(x, t) e^{-rx} dx. \quad (10)$$

Now we are ready to discuss consequences of different transition scenarios for the population size. If nothing alters except for the fertility timing, then NRR and survivorship function in (10) remain constant through time. Generation length widens or shortens reflecting the shifts in fertility tempo, and Lotka's r alters following relation (8). Both the generation length and Lotka's r depend neither on duration nor on timing of the transition, however. Instead, they depend on final fertility patterns and will return to their original

values, if the fertility patterns will return to their pre-transition shapes. The only component in relation (10), which does depend on how passes the transition is the number of genealogical lines $G(t)$. Nonetheless, nothing could reverse the dynamics of this component as long as the cohort NRR remains unchanged. It grows with NRR above unity and declines with NRR below unity. Peculiarities of the transition can affect only the rate at which $G(t)$ grows or declines. When demographic rates alter monotonically during the transition, then the rate at which $G(t)$ changes during the transition can attain any value between the initial and final levels of Lotka's r .

Numerical simulations show that the most important factor, which affects the population size after shifts in fertility timing, is the generation length. Figure 4 presents results of simulating the population dynamics with generation length linearly changing from initial level of 25 years to the level of 35 years in period from year 150 till year 200. Two values of cohort NRR are concerned: 1.05 and 0.95. For both values, two scenarios are presented on the figure. In the first scenario (upper graphs on the figure) generation length remains at the level attained after the transition and never changes afterwards. In the second scenario generation length returns to its original level after second transition. This second transition occurs from year 250 until year 300. Period NRRs during the transition depend on the intensity of fertility timing changes and are presented on the charts. Figure 5 illustrates simulation results for the same scenarios with generation length changing from the initial level of 35 years to the level of 25 years and then back to its original value. Lotka's r alters following relation to the generation length (8), and the number of genealogical lines assumed to follow relation (7) all the period concerned. Births intensity and population size are calculated using general relations (2) and (6), and size of the stable equivalent population $EN(t)$ is estimated from equation (8). Such simulations correspond to special type of transitions, when the number of genealogical lines follows the model presented above. Yet, results of such simulations still represent the qualitative properties of population dynamics with constant cohort NRR and changing fertility timing.

All scenarios presented illustrate that population changes during the transitions can be described as movement from one global trend to another. The generation length change is the most important single factor of population dynamics. Duration and intensity of the transition affect only the point where the population converges to the new global trend. Lags or overtakes in time schedule occurred during the transition affect the dynamics of the number of genealogical lines and prevent the population size from returning to its original trend.

Period NRRs, which are presented on the charts, correspond to the population changes during the transition and show how quickly population moves from one trend to another. This is clearly seen from figure 6, where population dynamics is presented for similar transitions, which occur at different speed (0.2, 0.1, 0.05, and 0.04 years of generation length change per one calendar year), i.e. during transitions of different length. If fertility timing changes very fast, then the situation of paradox proposed by Schoen and Jonsson (2003) can arise. In such case, ultimate global trend and dynamics during the transition from one trend to another have different directions as reflected in controversial values of the cohort and period NRRs.

Figure 4. Population dynamics in simulation experiments with generation length changing from the initial value of 25 years to 35 years (upper charts) and then back to its original value (last two charts). Initially all populations consist of 100 000 genealogical lines.

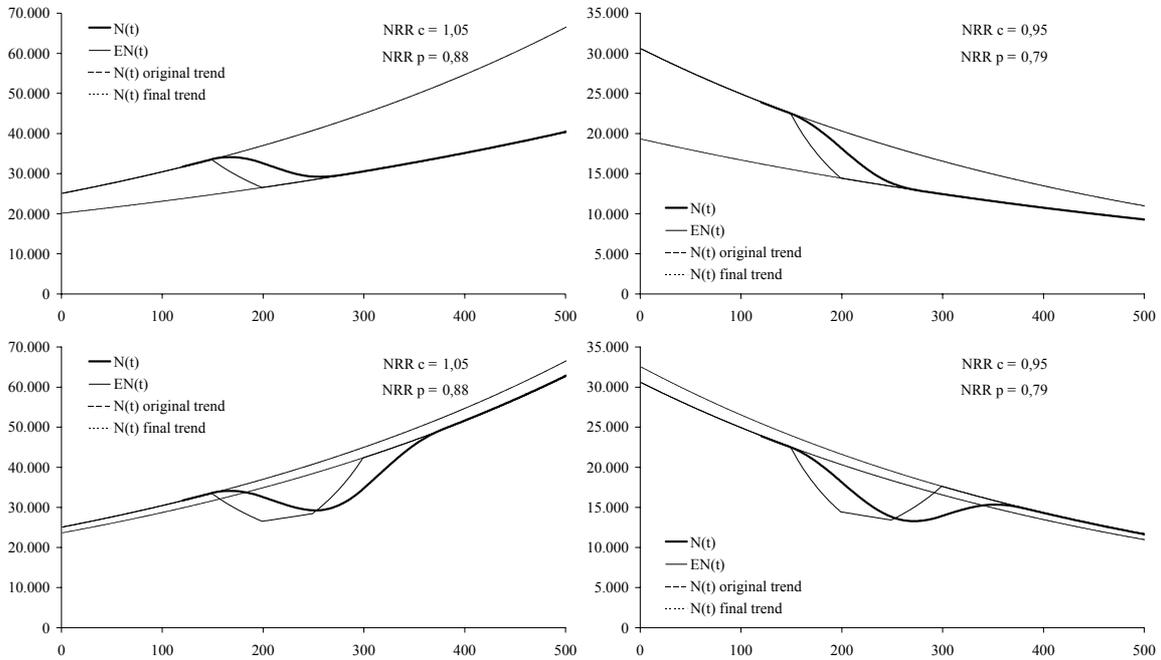


Figure 5. Population dynamics in simulation experiments with generation length changing from the initial value of 35 years to 25 years (upper charts) and then back to its original value (last two charts). Initially all populations consist of 100 000 genealogical lines.

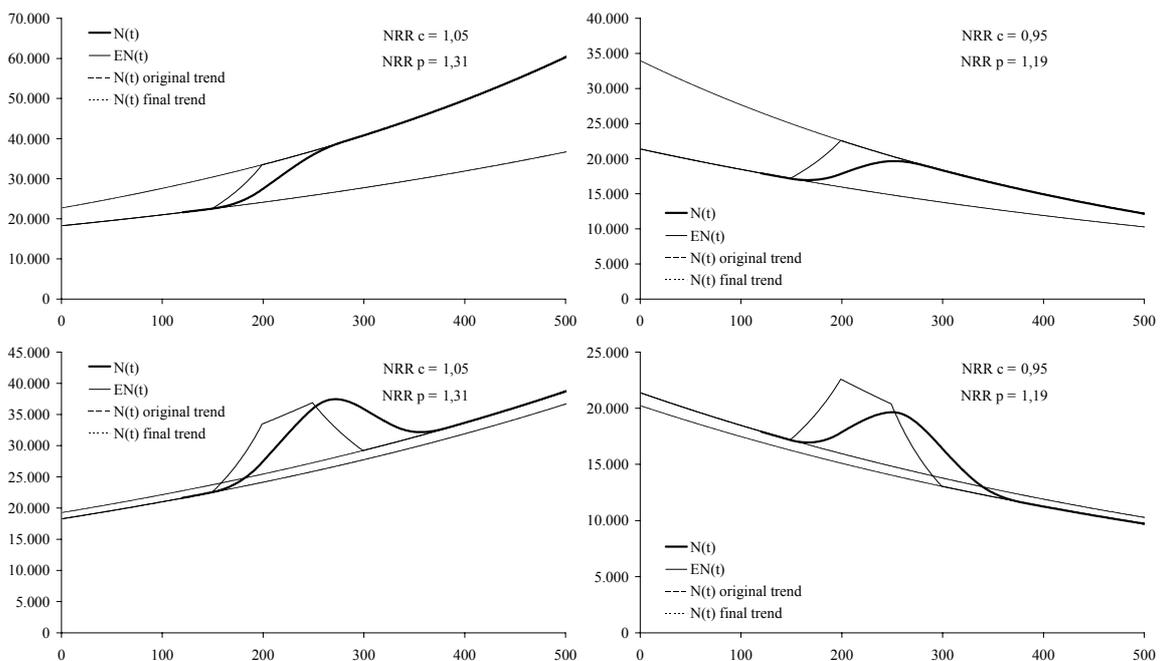
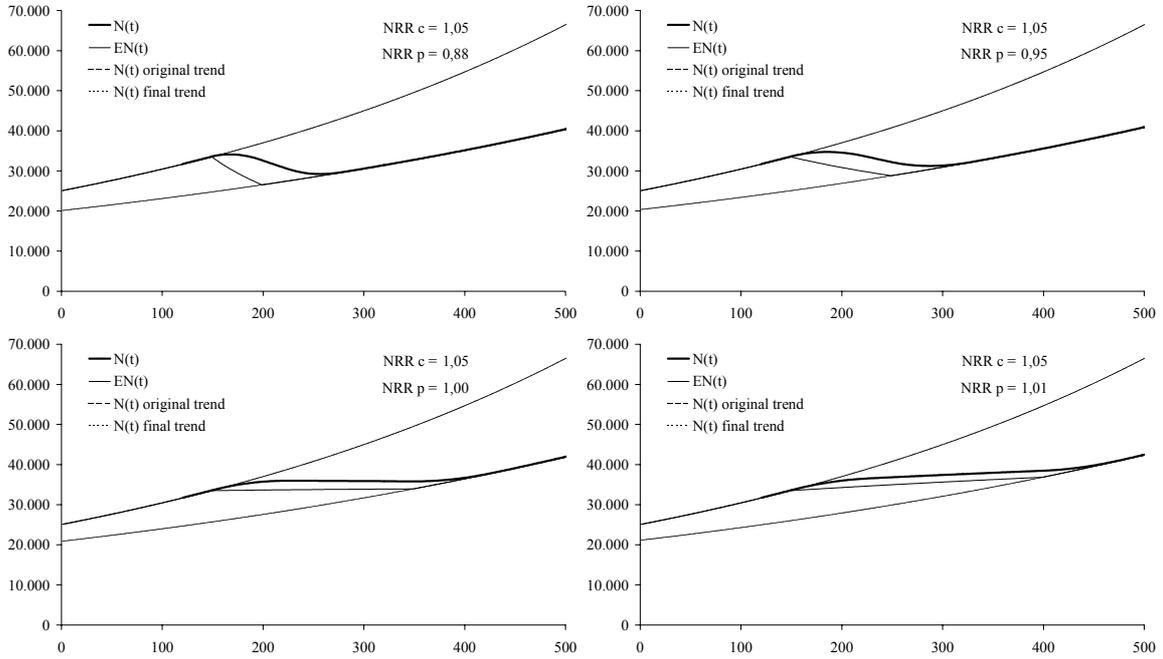


Figure 6. Population dynamics in simulation experiments with generation length changing from the initial value of 35 years to 25 years with different speeds (0.2, 0.1, 0.05, and 0.04 years of generation length change per one calendar year).



4. Implications

Our findings show that cohort reproduction measures (the NRR in particular) could be a very important source of information about future population trend. With the cohort NRR above unity the population will eventually rise. It will eventually decline with the cohort NRR below unity. This information cannot be derived directly from period measures. Instead, the period measures should be corrected in order to estimate the cohort rates if fertility timing alters substantially (see the aforementioned works on fertility postponement consequences). Cohort NRRs, however, do not provide full quantitative information about long-term population perspectives. They should be supplemented by information about fertility timing. The generation length affects both Lotka's r and, more important, the ultimate population size itself through relations (3) and (10). Cohort reproduction rates determine the topology of births, i.e. the structure of the genealogical chart, while the fertility timing determines time distribution of births and metrics of the genealogical tree.

The number of genealogical lines crossing a time line is also of value for analyzing and modeling the population reproduction. This quantity has convenient properties. In particular, direction of its dynamics does not depend on current population structure. It is fully determined by the value of the cohort NRR as it is clearly seen from relation (6), which can be rewritten as follows:

$$\frac{dG(t)}{dt} = B(t)(NRR(t) - 1) \quad (11)$$

If cohort NRR is above/below unity, then the number of genealogical lines should

grow/decline. Hence, dynamics of the number of genealogical lines could be an indicator of the population reproduction regimen. In this context the number of genealogical lines is close to the demographic potentials (Ediev 2001, 2003a) as the dynamics of latter indexes is also not affected by current population structure. Indeed, both concepts coincide in the case of the population with cohort NRR equal to unity. The number of genealogical lines crossing any given time line equals to expected number of births from the population alive at that time. In particular, we have for a person aged x , who was born at time t :

$$g(x,t) = \int_x^X \frac{l(y,t)}{l(x,t)} f(y,t) dy, \quad (12)$$

where $g(x,t)$ is an expected number of genealogical lines emanating from the birth point of the person, which continue till the time when the person ages to the age of x , and $f(x,t)$ is a fertility function for the cohort born at time t . Total number of genealogical lines for arbitrary population can be derived by integrating age-specific coefficients (12) with the population age composition. Dynamics of the demographic potential coefficients is given by the similar equation:

$$c(x,t) = \int_x^X \frac{l(y,t)}{l(x,t)} f(y,t) c(0,t+y) dy, \quad (13)$$

where potential of the newborn is a solution of the following integral equation:

$$c(0,t) = \int_0^X l(y,t) f(y,t) c(0,t+y) dy. \quad (14)$$

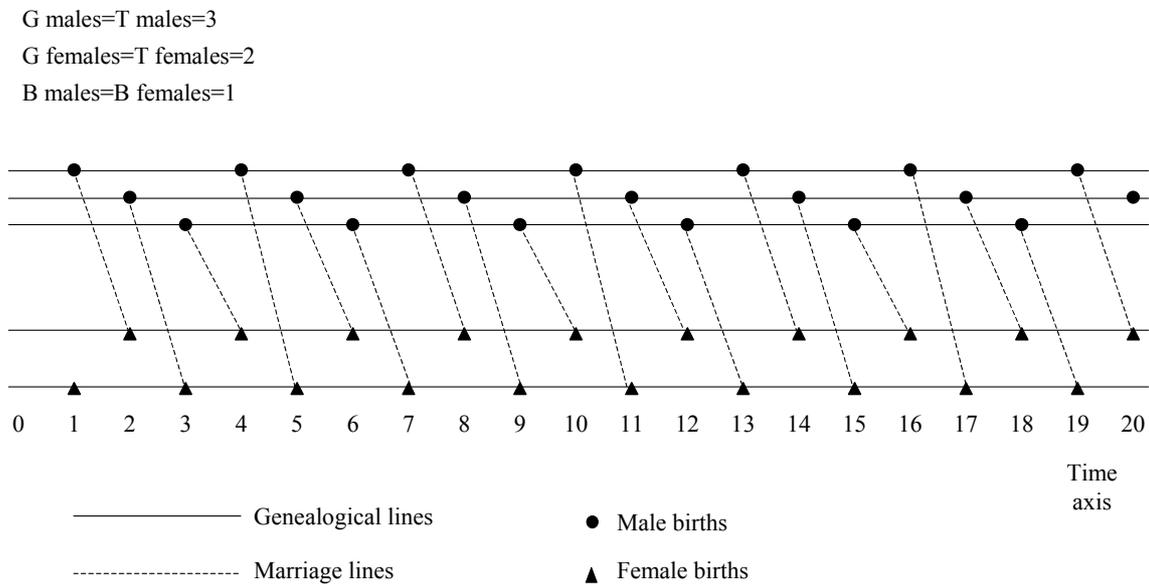
When the cohort $NRR(t) = \int_0^X l(y,t) f(y,t) dy$ equals to unity, then all solutions of (14) are time invariant. Choosing the solution with the newborn's potential equal to unity, $c(0,t) \equiv 1$, we can turn relation (13) into relation (12) and demonstrate equality of the genealogical lines and the demographic potential concepts.

When the cohort NRR is not constant through time or it is not equal to unity, then the concepts of genealogical lines and demographic potential differ substantially. Although both concepts seem to be helpful in monitoring and modeling the population reproduction, the concept of demographic potential provides more precise and more flexible tools of population reproduction measurement (Ediev 2001, 2003a, 2003b, 2004, 2005a, 2005b, 2005c). Main advantage of the demographic potential concept is that both the direction and rate of its change do not depend on population structure. On the other hand, the number of genealogical lines does not depend on model assumptions about long-term population reproduction perspectives. It seems to be a robust indicator of qualitative characteristics of the reproduction process.

The number of genealogical lines can not be measured directly as cohort NRR can not be obtained until completion of the reproduction history of the cohort. It can be approximated, however, using the estimations for cohort NRRs, age-specific demographic potentials, and results of the longitudinal surveys revealing the expected number of children to be born.

Aside from helping to understand the population dynamics, results obtained here are helpful in other areas of demographic research as well. Resemblance between the number of genealogical lines and the demographic potential brings us to the possibility of developing innovative methods of population modeling and forecasting. Population models consisted of relations for the demographic potential dynamics and for the dynamics of the average demographic potential have proven their efficiency (Ediev 2000, 2001a, 2001b, 2003a, 2005c). Similar models consisting of sub-models for the number of genealogical lines and for the ratio of this quantity to the population size could also be of value in demographic studies.

Figure 7. Illustrative genealogical chart of a two-sex population with a genealogical paradox: number of genealogical lines (G) for males is higher than the number of genealogical lines for females due to the longer generation length (T). Sex ratio at birth is set to be unity implying equal births intensity (B) for males and females



An interesting application could be made for two-sex models. Indeed, our results bring us to a new two-sex paradox: they imply that the number of male and female genealogical lines in the population should substantially differ even when the stationary population is concerned. Given the sex ratio at birth γ , one can derive from relation (1) for the stationary population:

$$\frac{G^{males}}{G^{females}} = \gamma \frac{\mu^{males}}{\mu^{females}}, \quad (15)$$

hereinafter we omit the time variable for stationary populations. As the mean age at childbearing is usually higher for males, and the sex ratio at birth is above unity, we obtain from (15) that the number of male genealogical lines should substantially exceed the number of female genealogical lines in a stationary population. If, for example, the mean age at childbearing is 28 for females and 30 for males, and the sex ratio at birth equals to

1.055, then the number of male genealogical lines will exceed the number of female genealogical lines by the product of $1.055 \cdot \frac{30}{28} = 1.13$, i.e. by 13% (!). Figure 7 illustrates

how such a paradoxical situation can exist. Similar results can be obtained for a stable population from relation (9). These results have further implications for population genetics. They could explain the source of higher genetic diversity among males. As the size of the genetic pool seems to be proportional to the number of genealogical lines, male population can support higher genetic diversity than the female population. This question deserves further study, however, as the genetic diversity is also affected by the topology of the real genealogical tree.

Another implication for population genetics concerns the evolutionary theory of ageing. From relation (3) we have for the number of genealogical lines of a stationary population:

$$G = \frac{\mu \cdot N}{e_0}. \quad (16)$$

Hence, genetic diversity in a stationary population is proportional to its size and to the mean age at childbearing and reciprocal to the life expectancy at birth. The population size is given by the ecological capacity. Therefore, the genetic diversity is determined by the ratio of the mean age at childbearing to the life expectancy at birth. This could explain wide variety of life expectancies in the nature: the life expectancy alone does not matter for the genetic diversity. Genetic diversity is a competitive advantage for a species. Hence, ratio of the mean age at childbearing to the life expectancy at birth should be maximized during the evolutionary process. This ratio cannot exceed the unity, however, if parents do not die before giving the last birth. Under such circumstances, the maximum genetic diversity will be attained if the fertile ages are close to the life expectancy at birth. Hence, zero fertility at young ages and genetic mechanisms of ageing after attaining the upper fertile ages could be interpreted as evolutionary advantages.

5. Conclusion

Along with cohort rates, period measures are also of importance for forecasting and modeling the population dynamics. We agree with Schoen and Jonsson, who showed that population dynamics could deviate from the dynamics determined by the cohort NRR during considerably long periods. However, our results show that duration and intensity of the transition have no effect on final population trend, except for moderate effect on the genealogical lines dynamics in the case of NRR different from unity. Intensity of the transition determines only how fast the population will pass from one global trend to another. Hence, analysis of the period data is valuable for modeling and forecasting the short-term population perspectives while keeping in mind the long-term population asymptote determined by the cohort indicators. This brings us to the point that it is the combination of period and cohort perspectives, which provides adequate tools of demographic analysis.

Relations obtained in the paper are of importance *per se* as they allow better understanding the population dynamics and could have important implications in many

fields of population research including population forecasting, population policy, reproduction analysis, population genetics, and evolutionary genetics.

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