

A Physics Model for Analysis on Demographic Structures

Wenjie Zhou¹

¹ Jupi-Kern Technology Limited, Hongkong, China

Correspondence: Wenjie Zhou, Jupi-Kern Technology Limited, Hongkong, China. E-mail: wjzhou_2000@163.com

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Abstract

Differing from statistics models for analysis on demographic structures, a physics model based on a set of assumptions is presented. The mortality probability function for a single person is derived to approach an approximation of analytic solutions for population evolution equations. This physics model has offered a kinetic method to forecast demographic structures and population evolution. Furthermore, the cause-and-effect relationship between demographic structures and nature or social forces can be discovered through higher-order solutions in this theory. Indeed, the life expectancy of an individual person can be possibly predicted as well. As an example, the calculated results on major parameters, such as, population structures, population size evolution, survival ratios and life expectancy at birth, show out well matching between zero-order approximations by this model and the real data from China census in the year of 2010.

Keywords: demographic structures, mortality probability function, population evolution equation, power-law forces

1. Introduction

The evolution of demographic structures in one region is of importance to macroeconomics and government policies. The demographic database can be maintained through regular population census and routine population records. However, kinds of demographic models are continuously developed to seek for *nature* rules governing in demographic structures so as to forecast the population evolution in the future.

The law of mortality is the foundation rules for mathematically studying on demographic structures. Several statistical models, such as well-known Heligman-Pollard model (Heligman et.al, 1980) and Lee-Carter model (Ronald et.al, 1992), were used to describe the law of mortality. The Heligman-Pollard model once succeeded in fitting for historical mortality rates by an empirical formula with 3 terms and 8 parameters, unfortunately, it could not be utilized to forecast population evolution due to lack of time factor in its complex formula. The Lee-Carter model was widely cited for historical data fitting and population forecasting, however, it was a statistics model based on relevance analysis, and did not find out the *cause-and-effect* rules in demographic structures.

Just like that Newton's law of gravity contributed to predict the discovery of Neptune, physics laws rather than statistical analysis can possibly reveal the fundamental mechanics in the evolution of demographic structures and thus provide reasonable forecasts by such *nature* rules.

If the plenty of cellules in human body are taken an analogy to the elemental particles in subatomic structures where weak interaction among particles giving rise to the law of radioactive decay in sub-atoms, the death probability ratio of a single person is supposed to obey the similar power-law, albeit the biological forces among different types of cellules to impact on the death of human body are still unknown at all. Based on such assumptions, the mortality probability function (MPF) by ages of a single person is his or her death probability at specific age, which corresponding to the age-specific mortality rates (ASMR) in the specific cohort.

2. Physics Model

2.1 Power-Law Assumptions

A set of power-law assumptions as follows are promoted to build a physics model to discover the kinetics of demographic structures.

i) Each of the biological forces in a single person contributes to the death probability ratio as a power law of time

t , or

$$\frac{\Delta\mu(t)}{\mu(t)} \propto \Delta(t^k) \quad (1)$$

where, $\mu(t)$ is the death probability at the time t , with the characteristic index k by this specific force.

ii) All the biological forces are catalogued into two opposite types as, the *growth forces* with negative indices k to decrease the death probability over time, and, the *decay forces* with positive indices k to increase the death probability over time.

iii) The death probability ratio of a single person is the sum of both contributions from these two different types of biological forces.

2.2 Mortality Probability Function

From abovementioned assumptions, the death probability or mortality probability function of a single person can be written as

$$\ln[\mu(\tau)] = A(\tau + \tau_0)^{-\alpha} + B(\tau + \tau_0)^\beta + C \quad (2)$$

Here, $\mu(\tau)$ is the mortality probability function over the age τ , and

τ_0 is taken as value of 0.8 for the normal gestation period of 0.8 years before his/her birth, and

$\alpha(>0)$ is growth index determined by nature effects from average growth forces, and

$\beta(>0)$ is decay index determined by nature effects from average decay forces, and

A, B, C are parameters determined by long-term social effects from such as medical level and nutritional structures.

2.3 Population Evolution Equation

For sake of a continuous and deterministic model for the evolution of demographic structures, we start from the population evolution equation (PEE).

The parameters in the PEE are catalogued into two types, i) N-parameters which impacting on the nature physiology in human bodies, such as, physiologic evolution, ethnicities, chronic hereditary diseases, medical level and nutritional structures; and ii) S-parameters which being caused by social behaviors with minor effects on human physiology, such as, population migration, large-areas acute diseases, accident, catastrophe and war.

The difference between N-parameters and S-parameters is an important clue to understand the mathematical principles in the PEE. In the nature N-parameters, the two variables, age τ and time t , are interdependent by an implicit relationship of $\Delta\tau = \Delta t$, which denoting the physiology rules in human bodies. Thus, N-parameters are multiplicative terms to the population density in the PEE. By contrast, the social S-parameters have two independent variables, τ and t , and thus are additive terms simply appending to the population density in the PEE.

The multiplicative terms by N-parameters in the PEE are taken into priority considerations. The governing equation for population evolution (Olsder et.al, 1975) by N-parameters is re-written as follows

$$p(\tau + \Delta\tau, t + \Delta t)\Delta\tau = p(\tau, t)\Delta\tau - \mu(\tau, t)p(\tau, t)\Delta\tau\Delta t \quad (3)$$

where, $\mu(\tau, t)$ is the mortality probability function at the age τ and the time t , and $p(\tau, t)$ is the population density function (PDF) with corresponding to the time-variant population size $N(t)$ as

$$\int_0^\infty p(\tau, t)d\tau = N(t) \quad (4)$$

General efforts (Olsder et.al, 1975) in mathematical derivation on the governing equation (3) gave rise to a partial differential equation with two independent variables (τ and t), in need of numerical calculations rather than explicit expresses for analysis on demographic structures.

In this physics model, due to the implicit relationship of $\Delta\tau = \Delta t$ in N-parameters, a single ordinary differential

equation can be derived from the governing equation. And in the zero-order approximation, an explicit solution for the PEE with N-parameters is finally obtained as

$$\ln\left[\frac{p(\tau, t)}{p(0, t - \tau)}\right] = M(0) - M(\tau) \quad (5)$$

with the time-independent function $M(\tau)$ in zero-order approximation as

$$M(\tau) = \frac{\exp(a_0\tau + b_0)}{a_0} \quad (6)$$

where, the coefficients, a_0, b_0 can be derived from those five parameters in eq. (2).

Thus, the total PEE is obtained by simply adding the S-parameters term into the population density function as

$$p(\tau, t) = p(0, t - \tau) \exp[M(0) - M(\tau)] + S(\tau, t) \quad (7)$$

where, $M(\tau)$ is given by eq. (6), and the S-parameters term $S(\tau, t)$ is the absolute deviation in the population density function $p(\tau, t)$ which can be calculated from historical demography records.

3. Result

3.1 Parameters Fitting

Those five characteristic parameter, α, β and A, B, C in the mortality probability function in eq. (2) can be determined by fitting into the real age-specific mortality rates (ASMR) in the population censuses. As an example, the data in China census in the year of 2010 (Cui et.al, 2013) are taken as the reference to the calculated results by this model (Figure 1). It shows that the model is well matching to the actual census data except for the age range from 15 to 25, where the ASMR deviation was caused by so-called accident mortality in Heligman-Pollard model (Heligman et.al, 1980). However, the accident mortality, in this model, is regarded as an additive term by social S-parameters in eq. (7) rather than nature N-parameters in human bodies, and thus excluded in the mortality probability function in eq. (2).

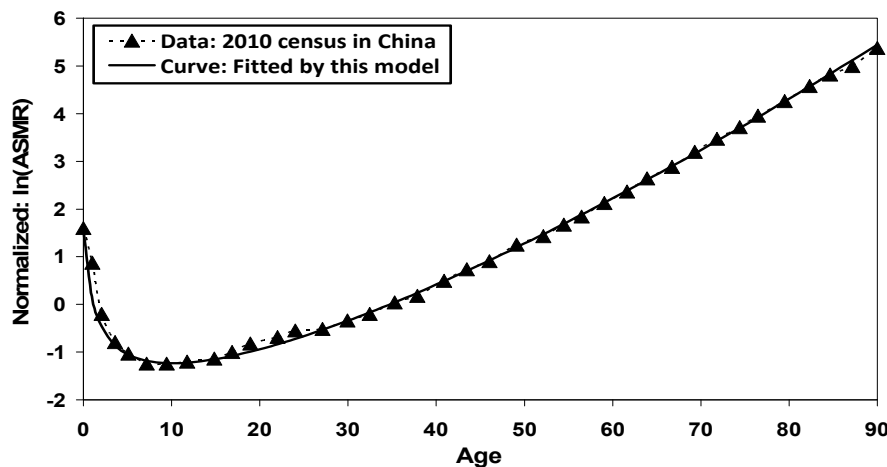


Figure 1. Log(ASMR): 2010 Census in China and Fitting Results by This Model

3.2 Number of Live-Birth and Population Structures

As a qualitative analysis on the cause-and-effect relationship between the number of live-birth and demographic structures as in eq. (5), a linear variation in live-birth number in first-order approximation is supposed as

$$p(0, t - \tau) = B_0[1 + k(t - \tau)] \quad (8)$$

where, B_0 is the initial number of live-birth (NLB). And k is the variation rate of NLB with three different types:

grow type when $k > 0$; flat type when $k = 0$; and descend type when $k < 0$.

The normalized population structures under different type of birth rates are calculated as shown in Figure 2. Compared to the grow-type, the descend-type NLM appears of an inverted pyramid-like shape in population structures sequentially, implying a higher proportion of aging population.

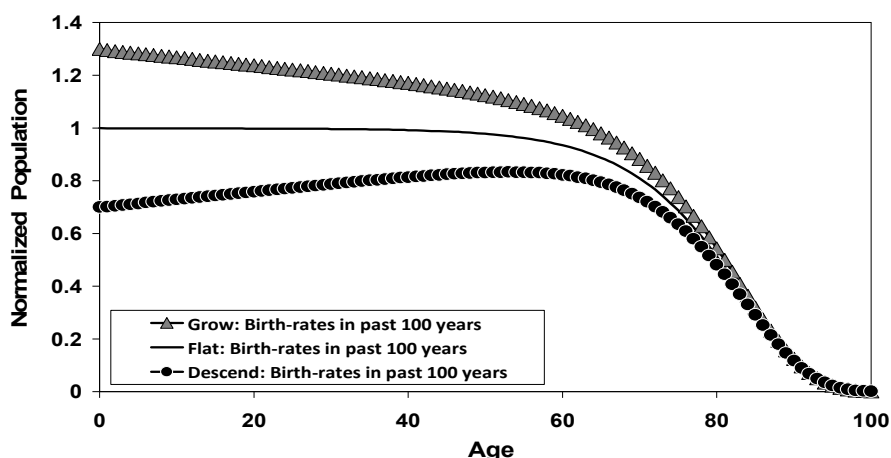


Figure 2. Population Structures under Different Type of Birth Rates

The evolution of population structures in China as shown in Figure 3 could be well explained by this qualitative theory. Before 1953, the NLB in China kept high growth rates without any population controls, thus the demographic structures in 1953 was in a grow-type pyramid albeit a sharp drop in youth population due to long-time wars. The single-child policy starting from 1970s' changed the birth rate from grow-type to descend-type, an inverted pyramid appeared sequentially in the demographic structures after 1982. One more stringent wave of single-child policy in 1990s' then caused the double peaks in the inverted pyramid between 2000 and 2010. By estimations, China is expected to fall into a seriously aging society from 2030 if still keeping the single-child policy.

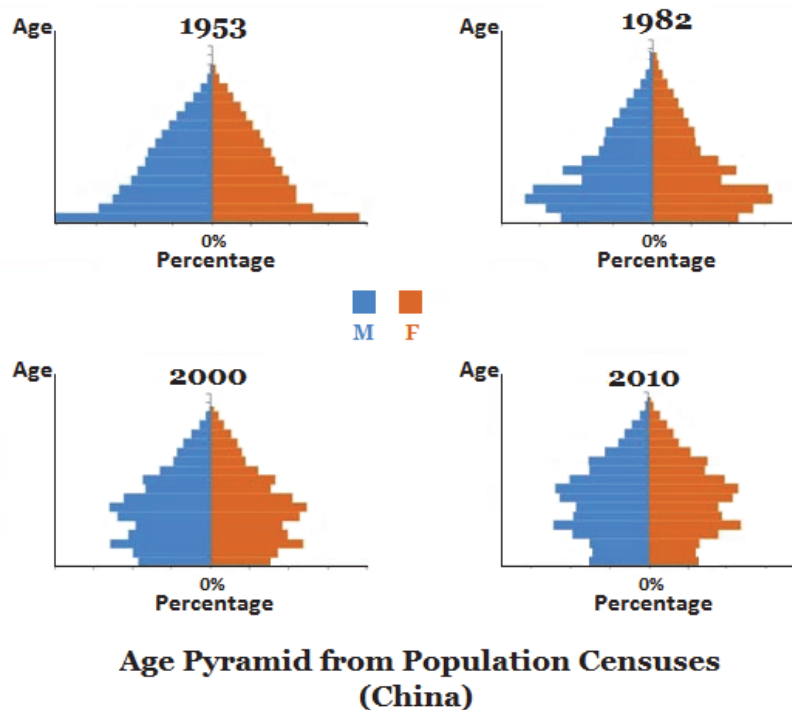


Figure 3. Evolution of Population Structures in China

3.3 Evolution of Population Size

The population size $N(t)$ is given by

$$N(t) = N(0) \exp\left[\int_0^t (B(t) - \delta) dt\right] \quad (9)$$

where, $B(t)$ is time-variant birth rates, and differential death-rate δ is given by

$$\delta = \frac{\int_0^\infty \mu(\tau) \exp[M(0) - M(\tau)]}{\int_0^\infty \exp[M(0) - M(\tau)]} \quad (10)$$

Usually the value of δ can be approximated as a constant in a short period, and in the example of 2010 China census (Cui et.al, 2013), this value is 0.0127.

As qualitative calculations on a first-order approximation of birth rates $B(t)$,

$$B(t) = B_0 (1 + kt) \quad (11)$$

where, B_0 is the initial birth rates in present time ($t=0$), and k is the time-variant slope of birth rates.

The population evolution trends in different type of birth rates are shown in Figure 4. It shows that the slope of birth rates is governing the convex-concave properties of the population evolution curve.

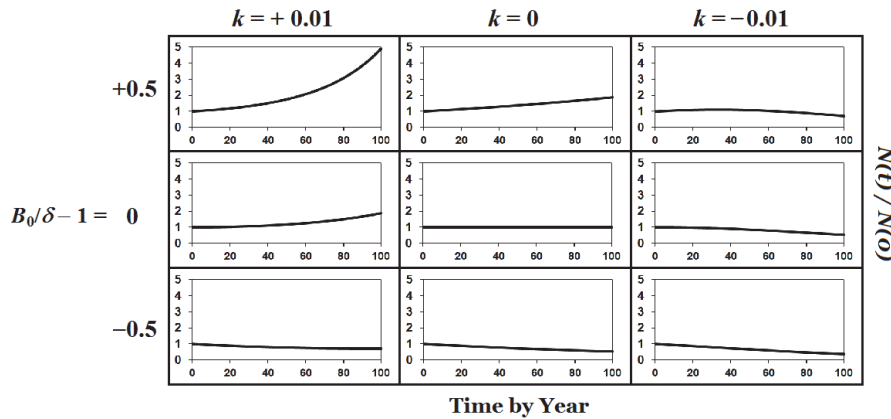


Figure 4. Population Evolution in Matrix of Birth Rates

3.4 Survival Ratios

The survival ratios $R(\tau, \Delta T)$ can be described as ratios of the population after an interval ΔT to the population in age of τ in present time, or

$$R(\tau, \Delta T) = \frac{p(\tau + \Delta T, \Delta T)}{p(\tau, 0)} = \exp[M(\tau) - M(\tau + \Delta T)] \quad (12)$$

The fitting results by this equation on the survival ratios comparing to the data from China census in 2010 (Cui et.al, 2013) is shown in Figure 5, with a RMS error of 0.0075.

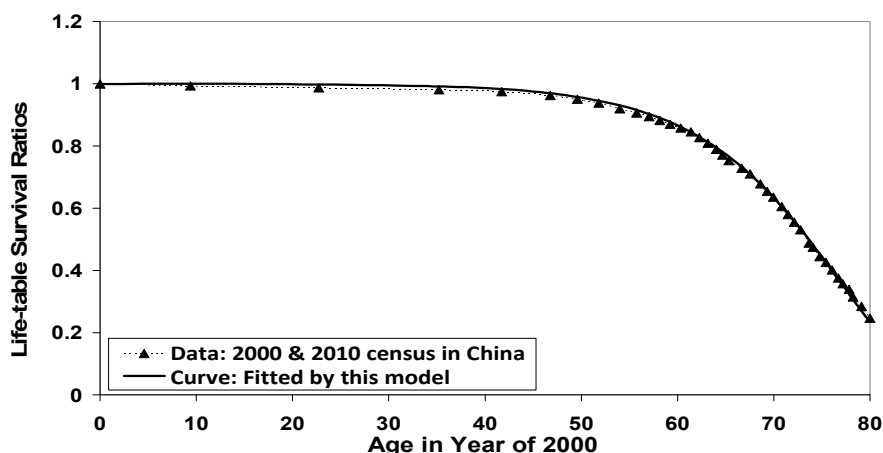


Figure 5. Survival Ratios: 2010 Census in China and Fitting Results by Model

3.5 Life Expectancy at Birth

The life expectancy at birth, $LEB(T)$, is defined as the average life-time in years that a newborn could expect to live with subject to the age-specific mortality rates of a given period, say T . It is simply described in this model as the average lift-time of the population in age of $t_0 = 0$ and in present time of $t_0 = T$, with the present MPF $\mu(\tau, T)$, or

$$LEB(T) = \frac{\int_0^{\infty} \mu(\tau, T) p(\tau, T + \tau) d\tau}{p(0, T)} = \int_0^{\infty} \mu(\tau) \exp[M(0) - M(\tau)] d\tau \quad (13)$$

As an example, the calculated result on LEB by this equation is 78.38, by compared to 74.83 from China census in 2010 (Cui et.al, 2013).

4. Discussion

In this article, the zero-order approximation in the physics model is presented to illustrate the kinetics of demographic structures and population evolution, with being exemplified by the data from China census in the year of 2010. Furthermore, through the higher-order parameters α , β and A , B , C in this model, the relationship between demographic structures and the long-term nature factors, such as physiologic evolution and ethnicities, or long-term social factors, such as medical level and nutritional structures can be further investigated. Indeed, the life expectancy forecast of an individual person can be even predicted by this physics model with enough accuracy in future,

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