

# Life Table and Accelerated Failure Time Model in Individual based Biodemography and Theory of Ageing.

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## Abstract

With very detailed individual information being available, we are able to study individual based biodemography and theory of aging, and look beyond life table based classic demography. The backbone of such individual based population dynamics is a class of (heteroscedastic) accelerated failure time model (AFTM) with time-dependent covariates, which is shown as an ideal model for the trade-off relationship between the two major life history trajectories: age-specific fecundity and mortality, and, at the same time, accommodating effects of gene  $\times$  environment interaction. The statistical inference approach, the overidentified estimating equation (OEE) as well as a theoretical construct of the biodemography and related issues in theory of ageing would be discussed.

Some keywords: Euler-Lotka equation; Local confounding; Log-rank test; Martingale central limit theorem; Reaction normal.

## 1 Introduction

Despite a vast literature in biology on animal's life history theory, surprisingly little detailed empirical information exists on relationships between trajectories of age-specific mortality and fecundity over the lifetime of even a single animal species. One of the broad consequences of the lack of such understanding is that life table and the Euler-Lotka equation are still applied under the independent assumption of the two trajectories ever since the works of Euler and Lotka. Especially, the equation is the key construct underpinning classic demography for determining the growth rate of a population as well as evolutionary theories on animal population dynamics for defining the fitness value of a genotype.

However violations of this simplistic assumption is called upon in Vaupel, et al (1998), where the term biodemography is coined for a mating between biology and demography. Since even genetically identical population by display phenotypic (observable) differences by altering physiological modes for coping with fluctuating conditions, especially in the process of growing into mature adults. From this aspect, the Euler-Lotka equation might as well valid on a local scale, but not on the global one where a fitness landscape is created. The forces driving the creation of such landscape could be ranging from social

economics to family planing in human, and from heterogeneity of environmental conditions to pheynotypic adaptivness. For this reason, the individual based model might be a reasonable starting points for the new era of biodemography.

On individual level, the relationship between trajectories of age-specific mortality and fecundity along the lifetime of an animal species has recently studied in Hsieh (2001b) via the accelerated failure time model (AFTM). The relationship was used to derive Weibull as well as Gompertz mortality functions from constant Exponential mortality function via suitably chosen time-dependent covariates. Also it is applied to calculate the evolutionary force on molding senescence by natural selection.

In section 2, the distinguish feature of our setting is that, the time-dependent covariates is not age-specific fecundity itself, but is its time-dependent impacts speculated as synthesized from the short term, parental care and lasting damages caused by each individual reproduction. Statistical inferences pertaining to AFTM is based on the overidentified estimating equation (OEE) approach developed in Hsieh (1997,2001a) to provide a relatively simple, but nearly (asymptotically) efficient estimations for statistical inferences.

In section 3, based on AFTM, issues of population dynamics as an algorithmic compositions and theory of aging are discussed with emphasis on differences between individual and life-table based biodemographies, such as proportion of elder population.

## 2 Linking age-specific mortality and fecundity via AFTM and its heterogeneous version.

Let  $\tilde{m} = \{m(i), i = 1, 2, \dots, M\}$  denote the age-specific fecundity with  $m(i)$  the number off-springs are reproduced at the age  $i$ , and  $M$  is taken as a large default number. Here  $m(0)$  is taken to be 0 and the age 1 is taken as the age at sexual maturity. For expositional convenience, let  $\tilde{m}_0 = \{0, i = 1, 2, \dots, M\}$ , and it renders a random survival time is denoted by  $U$  and its corresponding mortality function is then denoted by  $\lambda_0(t)$  for  $t \in [0, M]$ . Further the survival time and its corresponding age-specific mortality pertaining to the individual, who indeed experienced the reproductive scheduling specified by  $\tilde{m}$ , is denoted as  $T$  and  $\lambda(t; \theta, \tilde{m})$ , respectively, where  $\theta$  a vector of unknown parameters would be defined below.

Further, with a particular age-specific fecundity, let  $Z(s)$  stand for the impacts function induced by  $\tilde{m}$  and specifically defined as

$$Z(s) = \sum_{i=1}^M m_i K(s - i);$$

$$K(s) = \sum_{j=0}^k \beta_j I_{[j, j+1]}(v) + \beta_\infty I_{[0, \infty]}(v)$$

where  $I_{[a, b]}$  is the indicator function on interval  $[a, b]$ , the kernal function  $K(s)$  is thought of as the impact caused by a single reproduction. The idea behind the defintion of  $Z(s)$  is to recognize it as a synthesized wave of impact functions, or flows of information created

by the  $\tilde{m}$ . This idea has its fundamental significance in our development of individual biodemography.

The structure of AFTM is described as follows. The observable random survival time  $T$  associated with the covariate history:  $\bar{Z}(T) = \{Z(t)|0 < t < T\}$  satisfies the following equation

$$U = \int_0^T e^{\beta' Z(s)} ds, . \quad (1)$$

here, most importantly, the baseline survival time,  $U$ , would be observed if  $Z(t) \equiv 0$ .

To account for heterogeneous environmental conditions, denoted by covariate  $X$ , the model (??) is further generalized to the following heterogeneous accelerated failure time model (HAFTM) as

$$U^{1/\alpha(X)} = \int_0^T e^{\beta' Z(s)} ds, . \quad (2)$$

That is, with  $X$ , the corresponding baseline survival is changed into  $U^{1/\alpha(X)}$ , and it is related to the observable survival time  $T$  associated with  $X$  and covariate history:  $\bar{Z}(T) = \{Z(t)|0 < t < T\}$ , in the same way as in the model (??). Here, for expositional simplicity, we take  $\alpha(X) = \exp\{\gamma X\}$ .

### 3 Individual based Biodemography via algorithmic composition and theory of ageing.

With the relation between age-specific mortality and fecundity established via AFTM or HAFTM together with estimated impact and baseline mortality functions, we are able to make more precise prediction of the mortality function pertaining to a group of individuals having a specific reproduction schedule than using classic life-table approach. The essential implication of such understanding is that it becomes the construct of the individual based biodemography, and paves the way for studying evolutionary theories of population dynamics and of ageing. Below we briefly outline the ideas of population dynamics pertaining to such biodemography as an algorithmic composition, and issued could resolved theory of aging.

Dynamics of a population is now known as a complex information processing system. And it is also recognized that such dynamics is shaped by natural selection, learning or other optimizing processes. However each of such molding forces is involving with different time scale. Hence any demographic prediction should be made according to a proper time scale. For example, the prediction of an age class fraction within a generation time should be considered very differently from that of many generations away. In fact, if human population is concerned, most demographic predictions in social economics and politics are of rather short in generation terms. That is, the local trajectory of dynamical behavior of the population of interest within a short time period must be carefully studied and taken into consideration in making such predictions.

For this reason, we propose to view the population dynamics of interest as an algorithmic compositions, or a computer program consisting of a hierarchy of algorithms. Heuristically, the structure of hierarchy is as follows.

1. The main program, an algorithm on the top level of the hierarchy, is constructed based on a rugged multipeak fitness landscape with a geometry structured by a defined neighborhood system. Such fitness landscape is referring to social economic status for human or quality of habitat for animal. And the algorithm is referring to a movement scheme on the neighborhood system to capture the correlations of each life history pattern between parent and offspring generations.
2. A subroutine, an algorithm in the lower level of the hierarchy, is specified on each peak to capture individual life history patterns.

In the main program, peaks of different height would be equipped with different environmental condition for the development of offspring of the occupant of the peak. Based on this setting, the HAFTM would be used as the backbone of the individual based biodemography. Furthermore evolutionary molding forces pertaining to this biodemography can be derived by tuning parameter values in both top and lower levels in the hierarchy of algorithms via computer simulations, or theoretical treatments.

Further, in theory of aging, three issues are related to our discussion here.

1. whether a single reproduction could cause lasting damage on a female;
2. the level-off phenomenon on mortality function of oldest-old population;
3. whether there is a limit of maximum attained age.

In summary, we would demonstrate that the biased demographic predictions would certainly be resulted by using life table ignoring the possible subpopulation heterogeneity. And, in AFTM, or HAFTM, our estimated impact function would provide a way to resolve the above issues of theory of aging.

## References

- [1] Hsieh, F. (1997), Estimations in homoscedastic linear regression models with censored data: An empirical process approach. *Ann.Statist.* **25**, pp. 2665-2681.
- [2] Hsieh, F. (2000), A note on an asymptotically efficient statistical procedure for an accelerated failure time model with time-dependent covariates. (Revised for JMVA)
- [3] Hsieh, F. (2001a), On heteroscedastic hazards regression model: theory and application. *J. R. statist. Soc. B* **63** pp. 63-79.
- [4] Hsieh, F. (2001b), An accelerated failure time model, the Gompertz law and molding of senescence by natural selection.(Submitted to Theoretical Population Biology).
- [5] Stearns, S.C. (1992). The evolution of life histories. Oxford University Press, Oxford, UK.
- [6] Vaupel, W. et. al. (1998). Biodemographic trajectories of longevity. *Science* Vol. 280, May, pp.855-860.