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2020 Living to 100 Discussant Comments
5A: Multi-Population Mortality Modeling

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Discussant Comments Session 5A: Multi-Population Mortality Modeling

Leonid Gavrilov, Ph.D.

Calibrating Mortality Processes with Trend Changes to Multi-Population Data – Matthias Börger Ph.D., Justin Schoenfeld, Johannes Schupp, Ulm University

This is an invited discussion of two papers presented at the Living to 100 Symposium. The first paper entitled "Calibrating Mortality Processes with Trend Changes to Multi-Population Data" is provided by Matthias Börger, Justin Schoenfeld and Johannes Schupp from the Ulm University. This paper described rather sophisticated approach to mortality projections using a large volume of historical mortality data. Despite the complexity of the suggested approach the accuracy of projections looks rather low. We see very high uncertainty of life expectancy projections when the projected range of possible life expectancy estimates is about 50 years. There may be two possible solutions for improving the accuracy of projections. First, it is important to take into account that rates of mortality change over time are different for different ages. For example, recent scientific publications suggest that human longevity records stopped increasing [1]. Our finding that the mortality of U.S. centenarians has not decreased noticeably in recent decades is consistent with this suggestion [2]. It is noteworthy that mortality of centenarians in the United States does not demonstrate an obvious tendency to decline over time, in contrast to mortality at younger ages. This stability of mortality of centenarians over time was first observed for Swedish centenarians [3] and also was reported for centenarians in the United Kingdom [4]. Thus, it is important to take into account different rate of mortality decline over time for different ages.

Second, it is important to keep in mind that the way of mortality decline may be different for different historical periods. For example, it was found that the age-dependent component of mortality (Gompertz term) in the well-known Gompertz-Makeham formula demonstrates surprising historical stability before the 1960s, despite rapid decline in age-independent mortality, that is, the Makeham term [5]. Further more careful investigation confirmed the validity of this phenomenon [6] and demonstrated that the background component of mortality was the only mortality component, which has significantly changed over the studied period (1900–1970). Later Bongaarts developed further the method based on studying historical trends of the Gompertz-Makeham parameters, suggesting the use of a logistic formula for mortality forecasting [7].

The Lee-Carter method, currently used for mortality forecasting, assumes that the historical evolution of mortality at all age groups is driven by one factor only. This approach cannot capture an additive pattern of mortality decline observed before the 1960s and shown using the Gompertz-Makeham formula. Thus, the limitation of this method is related to the assumption that historical evolution of mortality at all age groups is driven by one factor only [8]. However, a factor analysis of mortality dynamics over the period of 1900–2014 in developed countries found that at least two time-dependent factors are responsible for the observed decline of mortality (younger age groups have a different factor of mortality decline compared to the older groups) [9]. A one-factor model could be applicable to earlier historical periods (before the 1960s), when a decline in mortality rates was driven mainly by a decrease in the background mortality, that is, the Makeham parameter of the Gompertz-Makeham law [5, 6]. It is obvious that the Lee-Carter model is not well applicable to mortality modeling during the period 1900–1960 because of the additive rather than multiplicative pattern of mortality decline during this time.

Observations made before 1960 enrich the historical data but are liable to distort the results of mortality projections. For mortality projections, it is better to use more recent data that take account of the change in the patterns of mortality decline. This factor analysis approach has several advantages. First, it can determine the total

number of independent factors affecting mortality changes over time. Second, this approach allows researchers to determine the time interval, in which underlying factors remain stable or undergo rapid changes. Most methods of mortality projections are not able to identify the best base period for mortality projections, attempting to use the longest-possible time period instead. Thus, for mortality projections based on multiplicative model of mortality changes it would be better to use mortality for more recent historical periods rather than long-term series of mortality data.

The Mathematical Mechanism of Biological Aging – Boquan Cheng; Bruce Leonard Jones, FSA, FCIA, PhD.; Xiaoming Liu, Ph.D.; Jiandong Ren, Ph.D., University of Western Ontario

The second paper entitled "The Mathematical Mechanism of Biological Aging" is provided by Boquan Cheng, Bruce Jones, Xiaoming Liu and Jiandong Ren (University of Western Ontario) and presented by Xiaoming Liu. This is an interesting model that has two major assumptions. The first assumption is that the transition rates (λ) between stages are equal for all states of organism's aging. What is the rationale for this assumption? It is more natural to suggest that rates of transition are increasing with each stage of aging. This suggestion about increasing rates of transition is made in the alternative avalanche-like model of aging [In the Cheng's paper this model is named the Le Bras model although both notation and interpretation of this model were first published in [6]]. According to avalanche-like model, in the initial state (S0) organism has no defects. Then, as a result of random damage, it enters states S1, S2, …Sn, where n corresponds to the number of defects. Rate of new defects has avalanche-like growth with the number of already accumulated defects and hazard rate also has avalanche-like growth with number of defects.

Second assumption of the model is that there are approximately 100 or 200-250 stages of organism's aging. What is the rationale to use this relatively small number of stages in order to describe aging? Alternative avalanche-like model uses unlimited number of stages that allows us to obtain analytical solution for mortality in a closed form [6]. 100-250 stages of aging appear to be very small number taking into account huge number of cells in a multicellular human organism. This may be the point of further model improvement and its further development.

Overall, these are two good and interesting papers!

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Society of Actuaries
475 N. Martingale Road, Suite 600
Schaumburg, Illinois 60173
www.SOA.org