LIVING to 100
SOCIETY OF ACTUARIES
INTERNATIONAL SYMPOSIUM

Compiling a Very Large Sample of Centenarian Pedigrees to Ascertain Patterns of Inheritance and a "Familial Propensity for Longevity Score"

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Presented at the Living to 100 Symposium
Orlando, Fla.
January 4–6, 2017

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Abstract

It is apparent that a large portion of the baby boomer population will live beyond the age of 90 years. Entitlement programs and various insurance products have thusly become interested in longevity risk. Beyond period life table predictions, actuaries have little to go on in determining which individuals or portions of populations are at increased risk of living to 90 or 100 or even older. We and others have noted strong familial risk for living beyond the oldest one percentile of survival for a birth cohort. However, just because one is at increased risk, the odds of achieving such a milestone are still small if the event is very rare. We hypothesized that determining common patterns of longevity (e.g., paternal, maternal, skipping generations) and level of risk according to which of one's relatives were long-lived can help inform actuaries about longevity risk. To explore this hypothesis, we proposed to perform network analyses of thousands of pedigrees that provide vital information for each family member. An important step of this work is to compile the largest possible samples of pedigrees with and without long-lived family members. Here, we describe our process of hand-curation of centenarian pedigrees and the software we have developed for the automated construction of such pedigrees.

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