

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

Lisa Nussbaum

Department of Biostatistics, Boston University School of Public Health

Giacomo Nebbia

Department of Medicine, Boston Medical Center and Boston University School of Medicine

Annie Helmkamp

Department of Medicine, Boston Medical Center and Boston University School of Medicine

Stacy Andersen

Department of Medicine, Boston Medical Center and Boston University School of Medicine

Thomas Perls

Department of Medicine, Boston Medical Center and Boston University School of Medicine

Paola Sebastiani

Department of Biostatistics, Boston University School of Public Health

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

Copyright © 2017 by the Society of Actuaries.

All rights reserved by the Society of Actuaries. Permission is granted to make brief excerpts for a published review. Permission is also granted to make limited numbers of copies of items in this monograph for personal, internal, classroom or other instructional use, on condition that the foregoing copyright notice is used so as to give reasonable notice of the Society’s copyright. This consent for free limited copying without prior consent of the Society does not extend to making copies for general distribution, for advertising or promotional purposes, for inclusion in new collective works or for resale.

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

Lisa Nussbaum,¹ Giacomo Nebbia,² Annie Helmkamp,³ Stacy Andersen,⁴ Thomas Perls,⁵ Paola Sebastiani⁶

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.

¹ Department of Biostatistics, Boston University School of Public Health, Boston, MA, USA.

² New England Centenarian Study, Geriatrics Section, Department of Medicine, Boston Medical Center and Boston University School of Medicine, Boston, MA, USA.

³ New England Centenarian Study, Geriatrics Section, Department of Medicine, Boston Medical Center and Boston University School of Medicine, Boston, MA, USA.

⁴ New England Centenarian Study, Geriatrics Section, Department of Medicine, Boston Medical Center and Boston University School of Medicine, Boston, MA, USA.

⁵ New England Centenarian Study, Geriatrics Section, Department of Medicine, Boston Medical Center and Boston University School of Medicine, Boston, MA, USA. Correspondence: thperls@bu.edu.

⁶ Department of Biostatistics, Boston University School of Public Health, Boston, MA, USA.