On the heterogeneity of human population as reflected by the mortality dynamics

Séverine Arnold (-Gaille)
Faculty of Business and Economics,
University of Lausanne (HEC Lausanne)

Joint work with
Demetris Avraam (University of Bristol),
Olga Vasieva and Bakhtier Vasiev (University of Liverpool)

Longevity 12
September 29, 2016

Table of contents

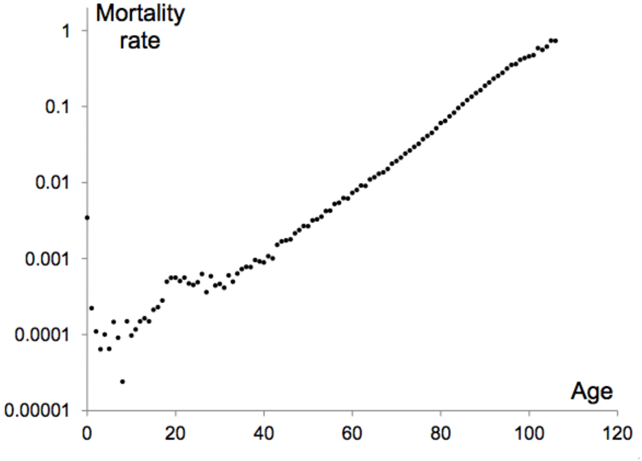

Figure: Mortality Rates, Sweden, 2000

Gompertz law of mortality

[Gompertz, 1825]:

$$m_x = m_0 e^{\beta x}$$

Gompertz law of mortality

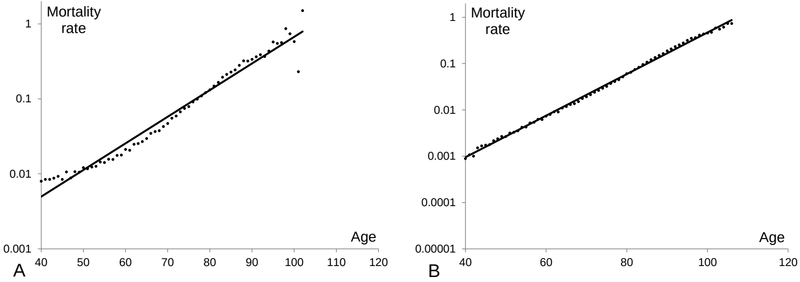

Figure: Mortality Rates, Sweden, 1900 (Panel A) and 2000 (Panel B)

Aim of this work

Populations are heterogeneous.

→ Each subpopulation obey the exponential law.

→ [Avraam et al., 2014] showed that the mortality of the entire population can be modeled as a mixture of weighted exponential terms.

→ Can we explain old-age mortality within that framework?

→ Can we explain the homogenisation of the population through natural selection?

Gompertz and an extension

Gompertz law of mortality [Gompertz, 1825]:

$$m_x = m_0 e^{\beta x}$$

An extension of [Avraam et al., 2013]

$$m_x = \sum_{j=1}^{n} \rho_{jx} m_{jx} = \sum_{j=1}^{n} \rho_{jx} m_{j0} e^{\beta_j x}$$

Fit

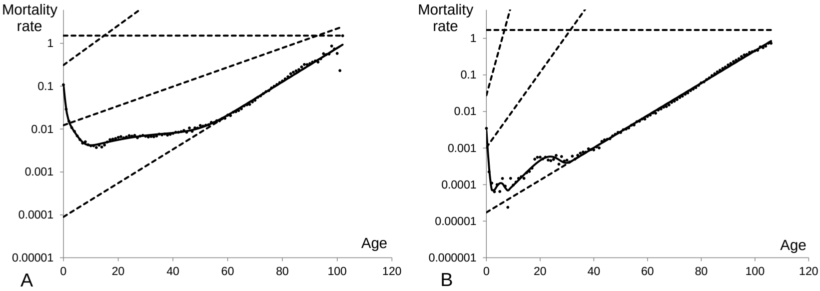

Figure: Heterogeneous model, Sweden, 1900 (Panel A) and 2000 (Panel B)

Fit

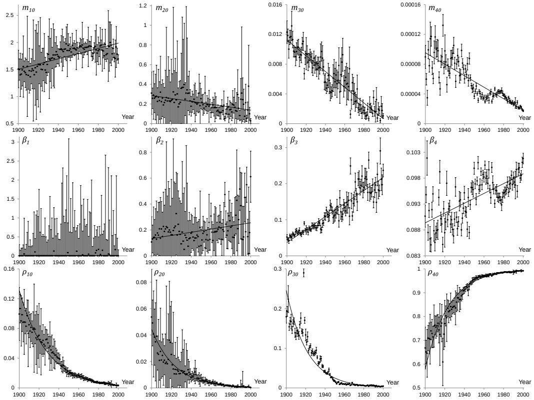

Figure: Evolution of the parameters of a four-subpopulation model, Sweden

→ homogenisation of the population

Mortality at extreme old ages - Different theories, no common agreement

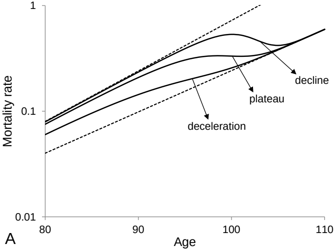

Figure: Theoretical trajectories (solid curves) of old-age (80-110) mortality dynamics of an heterogeneous population composed by two subpopulations

Mortality at extreme old ages - Different models

Model	Equation	Number of parameters	*BIC*
Gompertz	$m_x = \alpha e^{\beta x}$	2	-151.731
Makeham	$m_x = \gamma + \alpha e^{\beta x}$	3	-148.297
Weibull	$m_x = \alpha x^{\beta}$	2	-161.819
Heterogeneous 2-subpopulations	$m_x = \sum_{j=1}^{2} \rho_{j,x} m_{j,0} e^{\beta_j x}$	5	-167.380
Heterogeneous 3-subpopulations	$m_x = \sum_{j=1}^{3} \rho_{j,x} m_{j,0} e^{\beta_j x}$	8	-154.080

Figure: Models fitted to the Swedish average 1970-2010 death rates for ages 80+

Mortality at extreme old ages - Different models *cont'd*

Perks	$m_x = \gamma + \frac{\alpha e^{\beta x}}{1+\delta e^{\beta x}}$	4	-150.755
3-parameter Logistic	$m_x = \gamma + \frac{\alpha e^{\beta x}}{1+\alpha e^{\beta x}}$	3	-127.547
Beard	$m_x = \frac{\alpha e^{\beta x}}{1+\delta e^{\beta x}}$	3	-154.189
Kannisto	$m_x = \frac{\alpha e^{\beta x}}{1+\alpha e^{\beta x}}$	2	-122.069
Michaelis-Menten	$m_x = \alpha e^{\beta x/(1+\gamma x)}$	3	-158.714
Exponential-Quadratic	$m_x = e^{\alpha+\beta x+\gamma x^2}$	3	-149.078

Figure: Models fitted to the Swedish average 1970-2010 death rates for ages 80+

Mortality at extreme old ages - Fitted heterogeneous model

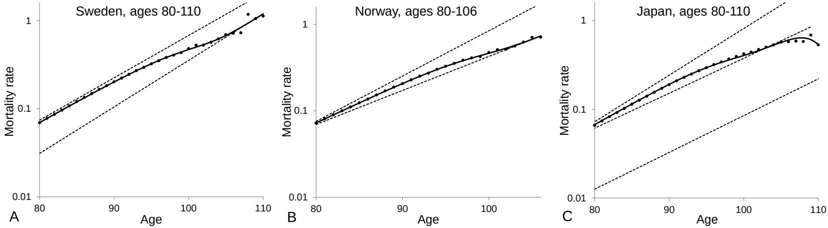

Figure: Model of heterogeneous population fitted to average 1970-2010 death rates for ages 80+ in Sweden (A), Norway (B) and Japan (C)

Mortality at extreme old ages - Different theories, no common agreement

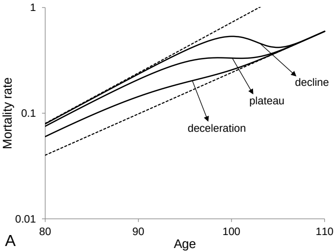

Figure: Theoretical trajectories (solid curves) of old-age (80-110) mortality dynamics of an heterogeneous population composed by two subpopulations

Natural selection - General idea

Individuals with certain heritable traits have the ability to survive and reproduce offspring more often than individuals deficient of those traits.

- $\rightarrow$ The proportion of individuals carrying genotypes that express these traits is gradually increasing over time;
- $\rightarrow$ The more likely is an individual to survive and live long enough to mate and reproduce, the higher his ability to pass his genes to the next generation $\rightarrow$ Average number of children with a specific genotype used as indicator.

$\rightarrow$ Base of our model framework

Fit

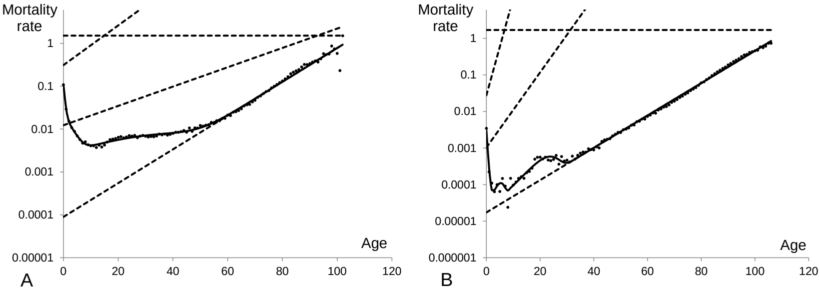

Figure: Heterogeneous model, Sweden, 1900 (Panel A) and 2000 (Panel B)

Natural selection - Assumptions

- $\rightarrow$ Alleles A and B: 2 distinct traits related to mortality dynamics;
- $\rightarrow$ Allele A is dominant $\rightarrow$ AB and AA follow the same mortality dynamics;
- $\rightarrow$ Third subpopulation: individuals carrying genotypes AA and AB;
- $\rightarrow$ Forth subpopulation: individuals carrying genotype BB;
- $\rightarrow$ Reproductive behaviour does not depend on genotype;
- $\rightarrow$ Reproductive ages: 20-40;
- $\rightarrow$ Fertility does not depend on age.

Natural selection - Results

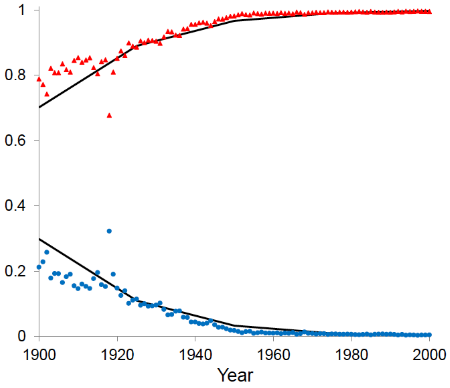

Figure: Population homogenisation and natural selection

Concluding remarks

We consider a model of heterogeneous population composed of several subpopulations having different mortality dynamics.

→ Each subpopulation follows the Gompertz law of mortality.

Two main findings:

→ The model can explain controversial observations in late-life mortality;

→ By assuming that the population heterogeneity reflects genetic variation between subpopulations, we showed that natural selection can explain the homogenisation of the Swedish population within one century.

Bibliography

Avraam, D., Arnold, S., Jones, D., and Vasiev, B. (2014).
Time-evolution of age-dependent mortality patterns in mathematical model of heterogeneous human population.
Experimental Gerontology, 60:18–30.

Avraam, D., de Magalhaes, J., and Vasiev, B. (2013).
A mathematical model of mortality dynamics across the lifespan combining heterogeneity and stochastic effects.
Experimental Gerontology, 48:801–811.

Gompertz, B. (1825).
On the nature of the function expressive of the law of human mortality and on a new mode of determining life contingencies.
Philosophical Transactions of the Royal Society of London, 115:513–585.

Thank you for your attention!

Severine.Arnold@unil.ch