

Consiglio Ordine Nazionale degli Attuari





L'ATTUARIO GLOBALE PER UN MONDO SOSTENIBILE **TRA TRADIZIONE** NOVAZIONE **RISCHI EMERGENTI**

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Special session in memory of Ermanno Pitacco: Science in the knowledge.

A biologically inspired perspective in longevity risk management: which implications for actuaries?

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- Over the last century, populations worldwide have experienced continuous longevity growth;
- Globally, life expectancy has increased by more than 6 years between 2000 and 2019 from 66.8 years in 2000 to 73.4 years in 2019. While healthy life expectancy has also increased by 8% from 58.3 in 2000 to 63.7, in 2019.



On the left: life expectancy at birth, both genders, in 2000. On the right: life expectancy at birth, both genders, in 2019. Source: WHO.







- However, country-specific mortality trends and disparities in the age-at-death distribution are observed;
- Indeed, mortality reductions arose from several heterogeneous factors affecting the human lifespan:
 - <u>Social and environmental risk factors</u>, that is exogenous factors such as socio-economic status, diffusion of healthy lifestyles, the use of preventative medicine, climate warming, and so on;
 - <u>Biological risk factors</u>, that is endogenous factors represented by clinical or molecular biomarkers of aging, such as epigenetic clocks, DNA methylation, telomere length, etc.
- By means of biomarkers, the biological science literature tells us that each individual may have an age different from the chronological age: the so-called **biological age** (see, e.g., Jackson et al. (2003))
- <u>Key fact</u>: A person's age does not move necessarily in lockstep with calendar time, meaning there exists a nonchronological age descending from a (random) shift of the corresponding chronological age. Then, a direct impact on the human lifetime emerges, as well as a new perspective on managing longevity risk.







Biological Science in the Actuarial Knowledge

How define and measure a non-chronological age?

- Biological science perspective: biological age vs. chronological age (see, e.g., Ferrucci et al. (2019)). 1. In this case, biological age measurement requires gathering data from a large group of people and collecting samples of their physical, physiological, and molecular variables. Then, by regression, the set of significant variables is inferred, i.e. the biomarkers, and the sign of their coefficients identifies if there is an increment or a reduction of the corresponding chronological age;
- **Demographic perspective**: longevity-risk-adjusted global age vs. chronological age (Milevsky (2020)). 2. In this case, collecting data on mortality rates as a function of chronological age, a multi-step procedure is proposed to derive (on average) the non-chronological age for a national population;
- **Demographic perspective**: <u>survivorship age vs. chronological age</u> (Alvarez, Vaupel (2023)) 3. In this case, it is possible to derive the corresponding non-chronological age by inverting the survival function describing the survival of a population.

We will consider the latter perspective by exploiting the Gompertz mortality law.







The Gompertz model

• Let be T_0 the lifetime for a newborn. Then, if $Y \sim Exp(1)$ we have:

 $T_0 = a + b \ln Y \sim Gompertz(a, b), \quad a, b > 0$

So that the survival function and the force of mortality are, respectively,

$$S_0(x) = \mathbb{P}(T_0 > x) = \exp\left(\exp\left(-\frac{x-a}{b}\right)\right)$$
$$\mu(x) = -\frac{d}{dx}\ln S_0(x) = \frac{1}{b}\exp\left(\frac{x-a}{b}\right)$$

• **Re-parametrize** $\mu(x)$: h, g > 0 such that $b = \frac{1}{g}, a = \frac{1}{g} \ln\left(\frac{g}{h}\right)$. Then, it holds that:

$$\mu(x) = h e^{gx}$$

with h the initial mortality level and g the rate of ageing.







Mortality as function of survival (Alvarez, Vaupel (2023))

• The so-called **survivorship age** (s-age) is introduced:

$$x(s) = S_0^{-1}(x)$$

Then, the age is a function of the survival level s and it indicates the age at which proportion s of a person's birth cohort is still alive. The s-age x(1) is the s-age at which everyone is alive and the s-age x(0) denotes the age at which there are no survivors left in the population.

• In addition, the force of mortality is expressed in terms of the survival level *s*:

$$\mu(x) = -\frac{d}{dx} \ln S_0(x) = \frac{1}{s} \left(-\frac{d}{ds} x(s) \right)^{-1} = \mu(s)$$

The $\mu(s)$ measures the risk of dying for the proportion s of the population that is still alive. Moreover, $\mu(s)$ links mortality and survival without the influence of chronological ages.







Mortality as function of survival (Alvarez, Vaupel (2023))

Assuming the (*h*, *g*)-Gompertz framework, the s-age is given by the following expression: •

$$x(s) = \frac{1}{g} \ln\left(1 - \frac{g}{h} \ln(s)\right)$$

While the s-age based force of mortality is:

 $\mu(s) = h - g \ln(s)$







Survivorship-Age: the case of Italian Males









Mortality as function of frail-survival

- As highlighted in Olivieri (2006) and Pitacco(2019), the mortality phenomenon is affected by heterogeneity.
- The heterogeneity in mortality among different individuals can be attributed to several risk factors, some of which are not directly observable and generate heterogeneity in mortality expressed through the concept of individual frailty.
- Formally, let us to the so-called multiplicative frailty model

$$\mu_z(x) = Z_0 \mu(x), \qquad Z_0 \sim Gamma(\alpha, \beta), \qquad \alpha, \beta > 0$$

where $\mu(x)$ is the standard force of mortality, that is with Z = 1.

• If $\mu(x) = he^{gx}$, the following Gamma-Gompertz's survival function for the whole population holds

$$\bar{S}_0(x) = \left(\frac{\beta}{\beta + \frac{h}{g}(e^{gx} - 1)}\right)^{\alpha}$$







Mortality as function of frail-survival

- **Question**: Is the frailty linked to the shift between the chronological age and the non-chronological age?
- **Ongoing answer(s)**: Research project "A biologically inspired perspective in longevity risk management: which implications for actuaries?", financed by Society of Actuaries, Research Institute.
- For instance, exploiting the s-age based approach, we can derive the **frailty-adjusted s-age** as:

$$\bar{x}(s) = \frac{1}{g} \ln\left(1 - \frac{g\beta}{h}(1 - (\bar{s})^{-\alpha})\right), \qquad \alpha > \frac{\ln\left(\frac{g\beta - h}{g\beta}\right)}{\ln(s)}$$

Such that the following s-age-based force of mortality holds:

$$\mu(\bar{s}) = \frac{h}{\alpha\beta}(\bar{s})^{-\alpha} + \frac{g}{\alpha}(1 - (\bar{s})^{-\alpha})$$







Frail-Survivorship-Age: the case of Italian Males



Data from Human Mortality Database. Condition: $\alpha > 0.0935$, then $\alpha = 0.1$ (heterogeneous population); setting $\theta = 20$, the expected frailty is 0.005, then lower mortality w.r.t. the baseline one (on average).







Frailty impact on s-age

| Year | x(s) | | $x(\overline{s})$ | | $\mu(s)$ | | $\mu(ar{s})$ | |
|------|----------|----------|-------------------|-----------------|----------|----------|------------------|------------------|
| | s = 0, 1 | s = 0, 9 | $\bar{s} = 0, 1$ | $\bar{s} = 0,9$ | s = 0, 1 | s = 0, 9 | $\bar{s} = 0, 1$ | $\bar{s} = 0, 9$ |
| 1960 | 84.18 | 45.47 | 94.43 | 54.14 | 0.1821 | 0.0086 | 0.1623 | 0.0084 |
| 1990 | 88.3 | 51.4 | 98.04 | 59.71 | 0.1918 | 0.0089 | 0.1712 | 0.0088 |
| 2017 | 92.76 | 63.63 | 100.42 | 70.23 | 0.2437 | 0.0111 | 0.2177 | 0.0111 |

- Mortality over chronological ages differs over time, but the relationship between survival and the risk of dying is more regular (conditioned to survival level);
- As the frailty is considered, a **shift among s-ages emerges**;





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Frailty, survival and lifetime shifting

Willemse, Kaas (2007) show that if the following assumptions hold:

- $T_0|(Z_0 = 1) = a + b \ln Y \sim Gompertz(a, b, 1), Y \sim Exp(1)$
- $Z_0 = b \ln Y \sim GenGompertz(0, b, \alpha), Y \sim Gamma(\alpha, 1)$

Then

$$T_0|(Z_0 = z) \sim T_0|(Z_0 = 1) - Z_0$$

And

$$\left(P(T_0 > x | Z_0 = 1)\right)^z = P(T_0 - Z_0 > x) = \left(\frac{1}{1 + \exp\left(\frac{x - a}{b}\right)}\right)^{\alpha}$$







Frailty, survival and lifetime shifting: Work in progress

- The above approaches are static: only the age structure of mortality is considered;
- The next goal consists of generalizing the results in Willemse, Kaas (2004) considering Gompertz processes for the frailty-conditioned lifetime:

$$dT_x(t) = T_x(t)(1 - \alpha \ln T_x(t)) + T_x(t)dW(t)$$

- Then, impacts on actuarial assessments will be considered. For instance:
 - Construction of a dynamic (and rational) age-shifting procedure for mortality differentiation;
 - Solvency: underestimation of longevity risk?
 - Impacts on natural hedging strategies and their optimality





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THANKS FOR YOUR ATTENTION

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