



# DEMOGRAPHIC RESEARCH

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## ***DEMOGRAPHIC RESEARCH***

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*Replication*

**The question of the human mortality plateau:  
Contrasting insights by longevity pioneers**

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# Contents

1	Introduction	322
2	Data	323
3	Methods	325
4	Results	328
4.1	Constant vs. Gompertz mortality after age 105	328
4.2	Cohort and gender effects on mortality after age 105	331
5	Discussion	332
6	Conclusion	333
	References	335

## **The question of the human mortality plateau: Contrasting insights by longevity pioneers**

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### **Abstract**

#### **BACKGROUND**

The debate about limits to the human life span is often based on outcomes from mortality at the oldest ages among longevity pioneers. To this day, scholars disagree on the existence of a late-life plateau in human mortality. Amid various statistical analysis frameworks, the parametric proportional hazards model is a simple and valuable approach to test the presence of a plateau by assuming different baseline hazard functions on individual-level data.

#### **OBJECTIVE**

We replicate and propose some improvements to the methods of Barbi et al. (2018) to explore whether death rates reach a plateau at later ages in the French population as it does for Italians in the original study.

#### **METHODS**

We use a large set of exceptionally reliable data covering the most recently extinct birth cohorts, 1883–1901, where all 3,789 members who were born and died in France, were followed from age 105 onward. Individual life trajectories are modeled by a proportional

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hazards model with fixed covariates (gender, birth cohort) and a Gompertz baseline hazard function.

## **RESULTS**

In contrast with Barbi et al. (2018)'s results, our Gompertz slope parameter estimate is statistically different from zero across all model specifications, suggesting death rates continue to increase beyond 105 years old in the French population. In addition, we find no significant birth cohort effect but a significant male disadvantage in mortality after age 105.

## **CONCLUSIONS**

Using the best data currently available, we did not find any evidence of a mortality plateau in French individuals aged 105 and older.

## **CONTRIBUTION**

The evidence for the existence of an extreme-age mortality plateau in recent Italian cohorts does not extend to recent French cohorts. Caution in generalizations is advised, and we encourage further studies on long-lived populations with high-quality data.

## **1. Introduction**

The shape of the mortality curve at very old ages has long been a subject of heated debate, with opinions divided mainly on whether death rates at the most advanced ages continue to increase exponentially or at a slower pace (i.e., decelerate). The latter, if true, leads to another possible scenario, where death rates not only decelerate but eventually become constant after a certain age, reaching the so-called 'plateau of human mortality'. Acknowledging the mortality plateau means validating the existence of mortality deceleration in humans, but the opposite is not necessarily true.

Our ability to study mortality deceleration and the existence of a mortality plateau depends chiefly on having high-quality data on death counts and population size at very high ages, where we can expect to observe these two phenomena. The methods used to analyze the trustworthy data also matter and should be adapted to the type of data at hand (censored, truncated, period- or cohort-based, individual- or aggregated-level, etc.). Different combinations of data and methods continue to fuel the long-standing debate, provoke controversies, and make it difficult to reach a single conclusion. For instance, several works published during the late 1990s based on aggregated period mortality data from the 1950s onward documented the deceleration in the age pattern of mortality at advanced ages in a large set of low-mortality countries (Horiuchi and Wilmoth 1998; Thatcher, Kannisto, and Vaupel 1998; Thatcher 1999). More recently, mortality deceleration was also observed in a thoroughly validated set of data on French-Canadian cen-

tenarians born to (extinct) cohorts 1870–1896 (Ouellette 2016), as well as thanks to an extensive testing of mortality models after age 80 on 360 high-quality cohort data sets (Feehan 2018). Evidence of such a late-life mortality deceleration seems consistent with various theoretical explanations (Beard 1959; Vaupel et al. 1979; Wachter and Finch 1997; Wilmoth and Horiuchi 1999; Steinsaltz and Wachter 2006; Mueller et al. 2011). Still, no consensus has yet been reached because other scholars have found that in some period and cohort settings, the death rate increases exponentially up to at least ages 105 to 106 (Gavrilov and Gavrilova 2011; Gavrilova and Gavrilov 2015; Gavrilov and Gavrilova 2019b; Gavrilova, Gavrilov, and Krut’ko 2017).

In this article, we focus on a possible mortality plateau in humans. The last 15 years have yielded more and more reliable individual-level data on deaths at the latest ages, thereby creating new research opportunities. Gampe (2010) for instance implements a nonparametric approach and estimated a mortality plateau at a (constant) hazard level of about 0.7 for females after age 110, using individual-level data from the 2008 edition of the International Database of Longevity (IDL) on 11 countries. A decade later, the updated version of the IDL, which included roughly twice as many individuals as previously, permits a re-analysis of the late-age trajectory of human mortality and confirms the constant hazards of death above age 110 (Gampe 2021). The study also renews warning against drawing any conclusion beyond the age of 114 due to data scarcity. Meanwhile, in 2018, the journal *Science* had released a paper by Barbi and colleagues in which the authors use newly available Italian individual-level data on survivors and deaths above age 105 to claim evidence for the “existence of extreme-age mortality plateaus in humans” (p. 1459). The latter study generates a great debate, with opinions ranging from agreement (Mueller and Rose 2018), to reservations (Camarda et al. 2018), to opposition (Beltrán-Sánchez, Austad, and Finch 2018; Olshansky and Carnes 2018; Newman 2018; Gavrilov and Gavrilova 2019a), fueling long-standing discussions on the possible limits to human life span, where various means of statistical analysis have been applied to different sources of data (Aarssen and de Haan 1994; Barbi, Caselli, and Vallin 2003; Dong, Milholland, and Vijg 2016; Gbari et al. 2017; Vijg and Le Bourg 2017; Rootzén and Zholud 2017; Einmahl, Einmahl, and de Haan 2019). We find Barbi and colleague’s (2018) approach interesting and worthy of replication on our large set of exceptionally high-quality data, consisting of 3,789 French longevity pioneers born in France between 1883 and 1901, each followed from age 105 until death.

## 2. Data

Our data come from the Répertoire national d’identification des personnes physiques (RNIPP), a database maintained by the French National Institute for Statistics and Economic Studies (Institut national de la statistique et des études économiques, or INSEE).

RNIPP data include a list of individual records linking each person to an identification number, thus identifying specific individuals without error. In 2014, INSEE signed an agreement with the French Institute for Demographic Studies (Institut national d'études démographiques, or INED), whereby INSEE provides INED with an RNIPP extract of all records of individuals born in France whose differences between alleged years of death and birth are at least 105. INSEE updates this extract for INED on a yearly basis, which allows for continuous empirical studies on mortality at extreme ages in France.

**Table 1: Number of validated deaths by birth cohort and sex, French population, ages 105 and above**

Birth cohort	Number of deaths	
	Females	Males
1883	71	10
1884	73	5
1885	79	11
1886	95	10
1887	124	8
1888	123	11
1889	148	13
1890	142	15
1891	164	13
1892	150	14
1893	204	22
1894	207	21
1895	223	12
1896	240	21
1897	264	19
1898	279	20
1899	236	20
1900	308	27
1901	355	30
<b>Total</b>	<b>3,485</b>	<b>304</b>

Source: Répertoire national d'identification des personnes physiques (RNIPP).

Due to its long history of well-developed civil registrations, France is one of the few countries that have gathered comparably vast amounts of data on deaths at ages 105 and above. For the sake of population homogeneity and accuracy, we included in our dataset only individuals who were born and died in metropolitan France, excluding all cases of deaths that occurred outside the country, as well as births and/or deaths pertaining to French overseas departments and territories (so-called *DOM-TOM*). Moreover, we kept data on extinct birth cohorts exclusively to follow all members of the various cohorts

from age 105 until extinction (i.e., up to age 115 in the present study). Therefore, we have neither left-truncated nor right-censored data in our analyses, but right truncation exists, and our models will take it into account. These data are available in the IDL (2022), where data are provided free of charge after registration.

The distribution of deaths by birth cohort and sex is presented in Table 1. Altogether, there are 19 extinct cohorts born between 1883 and 1901, covering 3,789 deaths above age 105 that occurred during the 1988–2016 period. Females outnumber males considerably at the oldest ages (3,485 vs. 304), and the number of female survivors also increases steadily across birth cohorts.

Since data quality at the oldest ages depends heavily on the accuracy of reported ages at death, the data we use here were validated following a strict protocol for thoroughly verifying the coherence between the information recorded on the person's official birth and death certificates. The details and results of the age-validation procedure on the French dataset can be found in Ouellette et al. (2021). In summary, for deaths that occurred at ages 110 onward (so-called supercentenarians), exhaustive validation was performed. All birth and death certificates were recovered and confirmed the accuracy of age at death (to the nearest day) for the vast majority of cases: 92% of the 213 cases were correct (i.e., 18 erroneous cases were found). For deaths registered at ages 105 to 109 (so-called semi-supercentenarians), which are quite numerous, the validation process was applied to a set of extracted RNIPP data that covers 1,050 deaths from years 1988 to 2002. This set was checked exhaustively for the oldest individuals (alleged ages of 107, 108, and 109). For the remainder of the set, a random sample made of half the cases at alleged age 106 and one third of those at alleged age 105 was drawn and checked. All birth and death certificates for these French alleged semi-supercentenarians were recovered (except for 4 individuals), and the registered ages had a very high degree of accuracy: 99.7% of the 2,031 cases were correct (i.e., only 3 erroneous cases). We therefore concluded that these most recent data from the RNIPP extracts require no further validation for ages 105 to 109. Globally, according to the IDL – which collates data on deaths at ages 105 and above from countries with reliable civil registration (or equivalent) systems – the French data validation procedure meets the highest criteria.

### **3. Methods**

Individual life trajectories leading to death provide continuous information over time without requiring data to be aggregated by age and birth cohort. We model these trajectories from age 105 until death using a parametric proportional hazards model with fixed covariates (gender and birth cohort), in which the baseline hazard function follows

the Gompertz model (Gompertz 1825). The formula for the individual hazard is given by

$$h(t_i) = h_0(t_i) \exp(\beta_1 C_i + \beta_2 M_i) = a \exp(bt_i) \exp(\beta_1 C_i + \beta_2 M_i),$$

where  $C_i$  is the individual's birth year minus 1891,  $M_i = 1$  for males and 0 for females, and  $t_i$  is the survival duration (in years) of each individual after age 105.

Consequently,  $\beta_1$  and  $\beta_2$  capture the cohort and gender effects, respectively;  $a$  is the initial hazard at starting age 105; and  $b$  is the Gompertz slope. The baseline hazard function  $h_0(t_i)$  can thus be interpreted as the hazard for female subjects born in 1891. With this type of model, a straightforward test can establish the significance of each parameter and evaluate the effect of explanatory variables. For instance,  $\beta_2$  measures the difference in hazards between males and females, given equal birth cohorts and controlling for age.

The vector of parameters  $\theta = (a, b, \beta_1, \beta_2)'$  is estimated using the method of maximum likelihood. For individuals who have survived to the age of 115 or beyond our last date of observation, the right-truncated duration,  $R$ , is the difference between that last date of observation and the date on which these individuals attained age 105 ( $0 < t < R$ ). Given  $\theta$ , the contribution to the likelihood function is

$$L(t, R; \theta) = \frac{f(t; \theta)}{F(R; \theta)},$$

where  $f(\cdot)$  and  $F(\cdot)$  are the density and distribution functions, respectively.

Taking logarithms on both sides of the previous equation and applying survival analysis relationships, we obtain the contribution to the log-likelihood function

$$\ln L(t, R; \theta) = \ln(h(t; \theta) - H(t; \theta) - \ln(1 - S(R; \theta)),$$

where  $h(\cdot)$  and  $H(\cdot)$  are the hazard and cumulative hazard functions evaluated at the duration lived, respectively. The last term,  $S(R; \theta)$ , is the survival function at the time of right truncation. For further details on these survival analysis derivations, see for example Hosmer and Lemeshow (1998) and Klein and Moeschberger (2003).

In this article, maximum likelihood estimation is performed using the R package `flexsurv` (Jackson 2016: v2.0), which has an option to take into account the right truncation present in our data scheme. Reproducible R code is provided with this paper, and readers are invited to refer to these materials for more details.

A major objective in our study is to test the hypothesis of constant mortality above age 105 against the hypothesis that mortality continues to increase after this age. In order to reproduce the analysis presented in Barbi et al. (2018), we first focused on the

hypothesis testing performed in the original article where

$$H_0 : b = 0 \quad \text{vs.} \quad H_1 : b \neq 0.$$

This type of test is, however, unsuitable when dealing with survival data because  $H_1 : b \neq 0$  allows for eventual negative values of  $b$ , which in the Gompertz model leads to a defective distribution where a fraction of the individuals could live forever.

Consequently, we decided to go beyond the mere purpose of replicating the Barbi et al. (2018) analysis on our high-quality data of the French population aged 105 and above. Hence, we also perform a more suitable hypothesis testing where  $b > 0$  is opposed to the null hypothesis of a mortality plateau, which is

$$H_0 : b = 0 \quad \text{vs.} \quad H_1 : b > 0.$$

In this case, parameter  $b$  is on the boundary of the parameter space, which makes the standard assumptions on asymptotic properties of likelihood-based inference inappropriate. Therefore, the likelihood ratio test should be done using another asymptotic distribution of the likelihood ratio test statistic. In a demographic setting, Bohnstedt and Gampe (2019: p. 71) show that we should use a mixture of a chi-squared distribution with one degree of freedom and a point mass at 0, given by  $\frac{1}{2}\chi_1^2 + \frac{1}{2}\chi_0^2$ .

We ran statistical hypothesis tests on all model specifications to assess the relevance of gender and cohort effects. Associated coefficients are tested by opposing  $\beta = 0$  to  $\beta \neq 0$  (i.e., by performing a conventional likelihood ratio test as models are nested).

The performance of all possible models can be compared using the Akaike information criteria (AIC) (Akaike 1973). This criterion, which balances a model's fidelity to data and complexity, is computed as

$$\text{AIC} = -2L + 2k,$$

where  $L$  is the maximized likelihood value and  $k$  is the number of parameters estimated for each model. The absolute values of AIC are not interpretable per se, but the difference between AIC scores allows us to assess the associated models' fit while accounting for the number of estimated parameters. The smaller the AIC score, the better the model performs.

## 4. Results

### 4.1 Constant vs. Gompertz mortality after age 105

To assess the significance of the additional Gompertz slope,  $b$ , with respect to a constant mortality scenario, we performed two statistical hypothesis tests in which parameter  $b = 0$  is opposed to either  $b \neq 0$  or to a strictly positive  $b$ . The former approach allows us to replicate the test conducted by Barbi et al. (2018) using our French dataset, while the latter is more appropriate for our setting by avoiding immortal individuals (see Section 3 for details).

Table 2 presents the outcomes of the two hypothesis tests on all model specifications. Interaction effects are not considered, as in the original study by Barbi et al. (2018). In any case, these interactions were not statistically significant in our data. For every model specification, a likelihood ratio test rejects the null hypothesis of a constant hazard after age 105. This outcome holds regardless of the hypothesis test performed. In fact, by imposing a nonnegative constraint on parameter  $b$ , the test becomes one- rather than two-tailed and  $p$ -values are consequently halved, giving an even higher level of significance for the Gompertz slope parameter in all our model specifications.

**Table 2:**  $p$ -values for two hypothesis tests on Gompertz slope parameter,  $b$ , across all model specifications, French birth cohorts 1883–1901, ages 105 and above

Models	$p$ -values: $H_0 : b = 0$ vs.	
	$H_1 : b > 0$	$H_1 : b \neq 0$
No covariate	7.011e-08	1.402e-07
With gender effect	4.389e-08	8.778e-08
With cohort effect	7.063e-08	1.413e-07
With gender and cohort effects	4.380e-08	8.761e-08

Source: Authors' calculations based on data from the Répertoire national d'identification des personnes physiques (RNIPP).

A comparison based on AIC is presented in Table 3, and it also shows that the model with the Gompertz slope,  $b$ , describes the data better (e.g., 10,878.00 vs. 10,904.63 for the model with gender effect only). In sum, based on the reported parameter estimates, on the hypothesis tests (one- and two-sided) and on the AIC, the Gompertz slope,  $b$ , is highly significant in the French data. To put it another way, the observed data is sufficiently inconsistent with the null hypothesis of a constant mortality pattern.

**Table 3: Parameter estimates in model specifications with different combinations of variables, French birth cohorts 1883–1901, ages 105 and above**

Baseline	Covariates	Parameter estimates	95% CI	Log-likelihood	AIC	Rank	
Constant hazard, $a$	No covariates	$a$ 0.645	[ 0.625 , 0.666 ]	-5,452.094	10,906.19	7	
	Cohort	$a$ 0.645	[ 0.621 , 0.670 ]	-5,452.087	10,908.17	8	
		$\beta_1$ -0.00035	[-0.0065, 0.0058]				
	Sex	$a$ 0.638	[ 0.617 , 0.659 ]	-5,449.319	10,902.64	5	
		$\beta_2$ 0.144	[ 0.027 , 0.261 ]				
	Cohort+Sex	$a$ 0.645	[ 0.614 , 0.664 ]	-5,449.317	10,904.63	6	
$\beta_1$ 0.000		[-0.006 , 0.006 ]					
Gompertz ( $a, b$ )	No covariates	$a$ 0.589	[ 0.562 , 0.617 ]	-5,438.235	10,880.47	3	
		$b$ 0.061	[ 0.039 , 0.083 ]				
	Cohort	$a$ 0.588	[ 0.559 , 0.619 ]	-5,438.234	10,882.47	4	
		$\beta_1$ 0.000	[-0.006 , 0.006 ]				
	Sex	$a$ 0.581	[ 0.554 , 0.609 ]	-5,435.006	10,876.01	1	
		$b$ 0.062	[ 0.040 , 0.084 ]				
	Cohort+Sex	$\beta_2$ 0.155	[ 0.038 , 0.273 ]	-5,435.002	10,878.00	2	
		$a$ 0.580	[ 0.550 , 0.612 ]				
		$b$ 0.062	[ 0.040 , 0.084 ]				
		$\beta_1$ 0.00028	[-0.006 , 0.007 ]				
			$\beta_2$ 0.156	[ 0.038 , 0.273 ]			

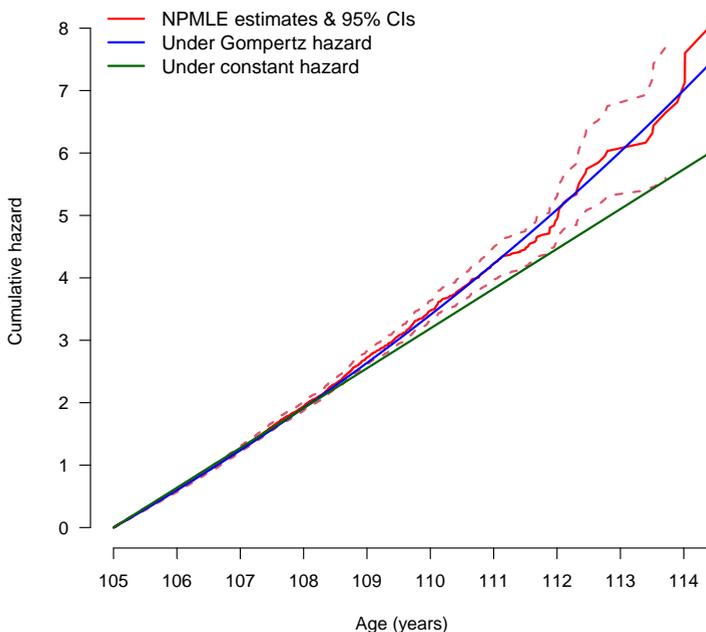
Notes: CI is for confidence interval, AIC is for Akaike information criterion. Letters  $a$  and  $b$  refer to Gompertz parameters from the model  $h(t) = a \exp(bt)$ ;  $\beta_1$  and  $\beta_2$  capture cohort and sex effect, respectively.

Source: Authors' calculations based on data from the Répertoire national d'identification des personnes physiques (RNIPP).

To assess departure from the data due to the parametric assumption of the baseline, we also computed the cumulative hazard using both nonparametric and parametric approaches, following the idea of Barbi and colleagues (2018). For the former, since right truncation is present in our study framework, instead of using the conventional Kaplan-Meier estimator, we relied on the estimator proposed by Shen (2010) and implemented in the function `cdfDT` provided by the R package `SurvTrunc` (Rennert 2018). A small modification was made to the code of the `cdfDT` function to extract the cumulative hazard estimates needed for this visual inspection. As done for the parametric approach, we computed the cumulative hazard from both the constant and Gompertz hazards according to the relationship  $H(t) = -\ln[S(t)]$  and using the parameter estimates in Table 3

for models including a statistically significant gender effect. Figure 1 presents estimates for the French female cohort, and it shows that the Gompertz hazard model (blue line) is closer to the nonparametric estimates (in red) than the fitted constant hazard (green line). The gap between the two lines (blue and green) becomes more noticeable as age increases, and at the highest ages, the cumulative hazard curve under constant hazard (green line) is often found to lie below the lower bound of the nonparametric confidence interval estimates. These observations strengthen our finding that the Gompertz baseline performs best in modeling hazard rates above age 105.

**Figure 1: Estimated cumulative hazard using nonparametric and parametric approaches, French females born 1883–1901, ages 105 and above**

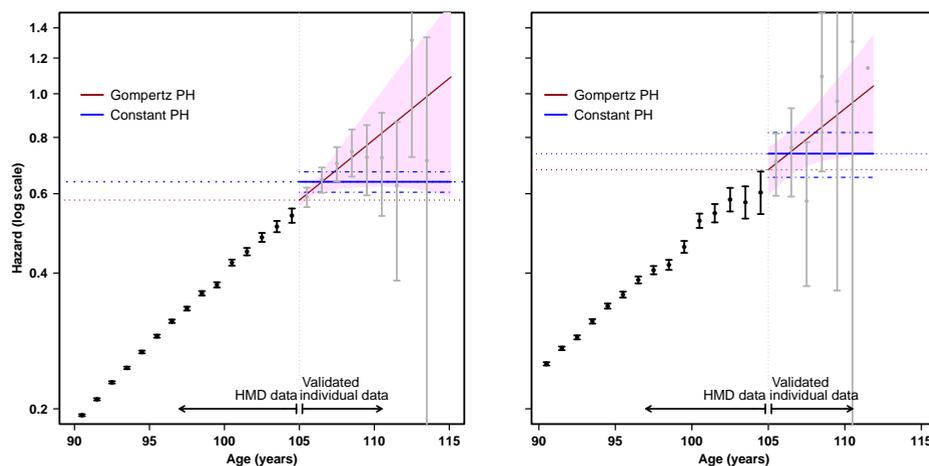


Notes: NPMLE is for nonparametric maximum likelihood estimate. This figure is equivalent to Figure 2 in Barbi et al. (2018: p. 1461).  
Source: Authors' calculations based on data from the Répertoire national d'identification des personnes physiques (RNIPP).

Going one step further, we consider that a useful model should not only fit the data

well over a specific age range (i.e., from age 105 onward here), but it should also be able to summarize the transition from younger old ages as smoothly as possible. As *natura non facit saltus*, the force of nature upon human mortality shall change gradually in absence of specific reasons for irregularities. To check for conformity, we plotted in Figure 2 observed death rates at ages 90 to 104 taken from the Human Mortality Database (2020) for the cohort of French females and males born in 1891. We then superposed the associated sex-specific fitted curves from age 105 given by our models with a Gompertz and a constant hazard baseline. Despite the relatively large confidence intervals (shaded purple area) due to small population sizes, especially beyond age 110, a Gompertz baseline aligns better with the mortality trend at younger old ages. This confirms once more that a Gompertz baseline function is more reasonable for our data when modeling hazard rates above age 105.

**Figure 2: Observed and fitted hazards, French females (left) and males (right), born in 1891**



Notes: PH is for proportional hazards. Associated confidence intervals do not account for right truncation scheme and are included for illustrative purposes only. This figure is equivalent to Figure 1 in Barbi et al. (2018: p. 1461).

Source: Authors' calculations based on data from the Répertoire national d'identification des personnes physiques (RNIPP) and Human Mortality Database (HMD).

## 4.2 Cohort and gender effects on mortality after age 105

We investigated other model specifications, first to test the sensitivity of our parameter estimates and second to choose the best-performing model for reliable conclusions on

birth cohort and gender effects. The results across all model specifications are reported in Table 3. Precisely, we performed likelihood ratio tests between models having different baseline functions without cohort or gender effects ( $p = 1.402e-07$ , see Table 2), between models with gender effect only ( $p = 8.778e-08$ ), and between models with cohort effect only ( $p = 1.413e-07$ ). We find that the Gompertz slope parameter,  $b$ , is positive and statistically different from zero regardless of the model specification (Table 3). According to the AIC, models including the Gompertz slope consistently perform better than those assuming constant hazard. Among them, the model with a Gompertz baseline hazard and a gender covariate has the lowest AIC, thereby showing that gender still has a significant effect on mortality after age 105. Assuming all else being equal, male subjects have a hazard rate that is 1.168 times higher than their female counterparts (hazard ratio of  $\exp(0.155) = 1.168$ ). Hence, according to our data for France, a male disadvantage persists even at the highest ages. No significant cohort effect is detected in any of the model specifications.

## 5. Discussion

Our replication study is based on Barbi et al. (2018)'s paper, in which the authors rely on an Italian dataset that appears to support the existence of a mortality plateau in humans beyond 105 years old. We investigated the generalizability of the original study by using data for France and found no evidence of a plateau after the age of 105. Because the methods in both studies are the same, explanations for the contradictory results likely come from the data. The Italian and French datasets are similar in terms of sample size (3,836 vs. 3,789) and hence of comparable statistical power. The latter set includes individuals who were born and died in metropolitan France only, while the former has a small share of individuals born outside Italy (under 4% according to the authors). The age-validation procedure for both sets of data consists in coupling birth and death certificates for all native alleged supercentenarians (110 and above). For younger old ages, the French data go a little further as this coupling procedure was extended to a large number of alleged semi-supercentenarians (105 to 109 years). With 99.7% of the 2,031 cases checked having exact dates of birth and death, the very high quality of France's RNIPP data is confirmed.

Another key advantage of the French dataset is that all individuals belong to extinct birth cohorts. Unlike in the original study, these data are thus free from any left truncation and right censoring, minimizing sources of uncertainty in mortality models' parameter estimates. After careful examination, the right truncation, though theoretically present in our data, does not have much of an effect on the parameter estimates in the extinct-birth-cohorts data scheme. Our estimated value of the Gompertz slope parameter,  $b$ , is much higher than that reported by Barbi et al. (2018) (0.062 vs. 0.013). With a rela-

tively comparable sample size, a higher level of  $b$  grants higher chances of detecting the true trajectory instead of the simpler constant baseline hazard model that supports the existence of a mortality plateau. The low estimate of  $b$  in the study using Italian data might be one of the reasons why constant baseline hazard model is selected even if the true underlying mortality pattern could have been more likely Gompertzian (Camarda 2022).

We considered the same covariates as those of the original study, namely gender and birth cohort. Despite the small number of male survivors at extreme ages ( $N = 304$ ), we found a significant gender effect on mortality after age 105 at the 5% level, indicating a persistent male disadvantage even at the highest observed ages. Being male increases the risk of death by a factor of 1.168 compared to females, all else being equal. Males having a higher hazard than females of equal age agrees with the observation made by Barbi and colleagues (2018). However, the increased risk of death for males, as indicated by the gender parameter estimated from the Italian dataset, is of smaller magnitude compared to ours (1.034 vs. 1.167) and did not lead to a significant gender effect at the 5% level ( $p = 0.058$ ) (Barbi et al. 2018: Table 2). Regarding the birth cohort covariate, it showed no significant effect based on our French data, as opposed to what was found in the Italian dataset. In addition to the fact that French birth cohorts are generally older than that of Italy (1883–1901 vs. 1896–1910), the lack of a cohort effect in our analysis might also come from the absence of clear mortality reductions after ages 90 to 92 in the French population (Meslé and Vallin 2020). It is therefore probably still too early to observe any mortality improvement among semi- and supercentenarians in our birth cohorts, hence the lack of a cohort effect. At this point, these are solely possible explanations, and since no underlying mechanism has yet been confirmed, it is therefore worthy of further research.

The choice of the age range over which modeling is performed in our study (105 and above) was made to fully replicate the study by Barbi and colleagues (2018). It is, however, an arbitrary choice, and it may have a direct effect on our modeling of age patterns in mortality at the oldest ages. Although we found no sign of a mortality plateau beyond age 105 in the French dataset, we cannot rule out the possibility of such a plateau at later ages that our dataset does not allow us to study. Nor do we dismiss the possibility of mortality deceleration above age 105; models are those of the original study and they consider either constant or linear (Gompertz) mortality trends, not decelerating mortality patterns.

## 6. Conclusion

Using a standard survival analysis procedure on French data that comprise all individual deceased above age 105 in extinct birth cohorts ranging from 1883 to 1901, we found no evidence of a plateau in human mortality after 105. Our estimate of the (baseline) Gompertz slope parameter,  $b$ , is statistically different from zero across all model specifications

studied. Such a finding suggests the Gompertz baseline is valid within a proportional hazards framework and that death rates continue to increase beyond 105 years. This disagrees with what Barbi and colleagues (2018) find in their study, which our paper aimed to replicate by using French instead of Italian mortality data.

While many controversies have arisen as a result of different combinations of data and methods, every new study should be seen as providing additional insight into the continuing debate about the shape of the mortality curve at very old ages, rather than granting a final universal answer valid for all human populations. With each improvement in data quality, increase in population size, and advance in statistical methodology, it is highly probable that new outcomes will emerge. At present, however, it would be more prudent to admit that no definitive conclusion about the existence of a plateau in human mortality at very high ages can be reached. Nevertheless, the advancing frontier of survival will likely come to a point where the population surviving to current highest ages will no longer be considered ‘pioneers’, and consequently there will be more solid knowledge about mortality at these extreme ages. Until then, comprehensive and comparative studies based on longevity data from different countries ought to be most welcome.

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