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Byung Mook Weon

bmweon@skku.edu

Sungkyunkwan University

Article

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Centenarian population growth does not require extension of the fitted lifespan tail across five countries

Byung Mook Weon[1*]

[1]Soft Matter Physics Laboratory, School of Advanced Materials Science and Engineering, Sungkyunkwan University, Suwon, 16419, Republic of Korea.

Corresponding author(s). E-mail(s): bmweon@skku.edu;

Abstract

Centenarian populations are growing rapidly, but an increasing number of people aged 100 years or older need not indicate extension of the extreme lifespan tail. We analyzed harmonized population counts and sex-specific period life tables from the Human Mortality Database for Japan, Sweden, France, Italy, and South Korea. We linked old-age population stocks to a modified stretched-exponential survival representation and evaluated 317 one-year-ahead centenarian-population predictions. The pooled mean absolute percentage error was 3.02%, compared with 3.02% for a direct mortality-data benchmark and 8.34% for naive persistence. Thus, forecasting accuracy primarily reflects explicit accounting for entry at age 100 and survival of existing centenarians rather than superiority of the fitted survival function. The representation also supplies a characteristic age ($\boldsymbol{\alpha}$) and a model-derived upper-tail descriptor ($\boldsymbol{\omega}$). Across all five countries, $\boldsymbol{\alpha}$ increased, whereas $\boldsymbol{\omega}$ showed no comparable long-term rise; recent estimates were approximately 117–122 years. Exploratory scenarios suggest further centenarian growth to 2050 but are sensitive to calibration assumptions. These findings distinguish growth in centenarian abundance from changes in the fitted lifespan tail without implying a fixed biological maximum lifespan.

Keywords: centenarians, human longevity, biodemography, survival analysis, Human Mortality Database, modified stretched-exponential model

1 Introduction

Centenarians are an increasingly visible component of aging populations and an important model of exceptional human longevity. Across low-mortality countries, the number of people surviving beyond age 100 has increased by orders of magnitude during the past several decades (Robine and Cubaynes 2017; Teixeira et al. 2017). Clinical and biological studies additionally show that exceptional longevity is often accompanied by delayed disease, preserved autonomy, and distinctive immune and inflammatory phenotypes (Andersen-Ranberg et al. 2001; Zhang et al. 2025; Plaza-Florido et al. 2026). These observations raise two related but distinct demographic questions: *how many* people will reach extreme old age, and *how far* the survival distribution itself continues to extend.

Japan provides one of the clearest examples of rapid centenarian growth. Previous studies documented an approximately 100-fold increase from the early 1960s to 2000 and showed that both cohort size and improved survival contributed to the expansion (Robine and Saito 2003; Robine et al. 2003). Subsequent work extended the demography of Japanese centenarians and supercentenarians and clarified the strengths and limitations of extreme-age data (Saito et al. 2012, 2020; Matsukura 2015; Aoki 2023). Comparable growth has occurred in European populations, although the timing, scale, sex composition, and old-age mortality schedules differ across countries (Robine and Cubaynes 2017; Teixeira et al. 2017). A cross-national test can therefore assess whether the relationship between population growth and survival-tail geometry is specific to Japan or recurs in other mortality regimes.

Several complementary forecasting traditions are relevant. Kestenbaum and Ferguson projected U.S. centenarian numbers from the population aged 90+ and age-specific mortality trends (Kestenbaum and Ferguson 2006); Leeson showed that different mortality trajectories generate widely different future centenarian populations in England and Wales (Leeson 2017); and Lee–Carter-type models provide a general framework for forecasting age-specific mortality (Lee and Carter 1992). At still older ages, extreme-value approaches focus on survival beyond age 110 and on maximum reported age at death (MRAD) (Rootzén and Zholud 2017; Pearce and Raftery 2021). Importantly, a record age can increase simply because more people are exposed to the extreme tail even if old-age death probabilities do not change substantially (de Beer et al. 2017). Population abundance and tail geometry must therefore be separated explicitly.

In parallel, our recent analysis of 46 Human Mortality Database populations described survivorship using the same modified stretched-exponential formulation and characterized each annual survival curve by a characteristic age α and a model-derived upper-tail parameter ω (Gonçalves and Weon 2026). The characteristic age generally increased, whereas ω declined or stabilized, narrowing the interval $\delta = \omega - \alpha$. A value of ω near 120 years was interpreted as a model-dependent descriptor of the fitted upper tail, not as a fixed biological maximum.

The central question here is whether changes in centenarian population abundance track changes in the fitted survival tail. To test this question independently of visual agreement between historical time series, we evaluate genuine one-year-ahead population predictions and compare the fitted survival model with direct mortality accounting

and naive persistence. Relative to our previous 46-population lifespan-geometry analysis, the present study adds a distinct population-dynamic test: annual survival curves are combined with observed old-age population stocks and evaluated against realized centenarian counts one year later. The analysis therefore moves from describing survival geometry to prospectively testing population dynamics, while separating the predictive value of demographic accounting from the interpretive value of α and ω. We analyze Japan, Sweden, France, Italy, and South Korea using the same HMD population and mortality definitions. The first four provide long historical series, whereas South Korea contributes a shorter 2003-onward series during a period of rapid mortality improvement; together they differ substantially in population size and demographic trajectory. We then test whether the long-run expansion of N_{100+} occurs in parallel with α and ω, and finally construct harmonized conditional scenarios to 2050.

2 Methods

2.1 Harmonized annual population and mortality data

All primary cross-national analyses use the Human Mortality Database (HMD) (Human Mortality Database 2026; Wilmoth et al. 2017). For each country and sex, we use the annual population-size series at single-year ages and the annual period life tables containing m_x, q_x, l_x, d_x, L_x, T_x, and e_x. To make the five-country comparison strictly comparable, the principal analysis uses HMD population estimates for all countries, including Japan. Japanese administrative MHLW counts and JMD estimates remain useful independent sources (National Institute of Population and Social Security Research n.d.; Robine and Saito 2003; Saito et al. 2020), but they are not mixed with HMD population stocks in the harmonized validation.

For Japan, Sweden, France, and Italy, the comparative historical analysis is restricted to 1950 onward even where much longer series are available. South Korean HMD population and life-table series begin in 2003 and are analyzed from that point. Population observations extend through 2025 for Japan, Sweden, France, and South Korea and through 2024 for Italy; the uploaded life tables extend through 2024 for Japan, Sweden, and South Korea, 2023 for France, and 2022 for Italy. Consequently, the latest mortality-supported one-year-ahead validation targets are 2025, 2025, 2024, 2023, and 2025, respectively. Missing annual population years are omitted rather than interpolated, leaving 74 Japanese, 76 Swedish, 75 French, 70 Italian, and 22 South Korean target years.

The population and mortality-data coverage and the validation-year counts are summarized in Supplementary Table S1. Missing annual population observations were excluded rather than interpolated.

For every base year t, we use the observed sex-specific population at exact age 99 and aggregate the single-age HMD stocks into ages 100–104, 105–109, and the open 110+ interval. This reproduces the same demographic accounting structure in all five countries while retaining an exact age-99 inflow.

2.2 Modified stretched-exponential survival model

For sex s, country c, and calendar year t, the normalized survival curve is represented as

$$S_{c,s,t}(x) = \exp\left[-\left(\frac{x}{\alpha_{c,s,t}}\right)^{\beta_{c,s,t}(x)}\right], \tag{1}$$

where the characteristic age α satisfies

$$S_{c,s,t}(\alpha_{c,s,t}) = e^{-1}. \tag{2}$$

The age-dependent shape parameter is written

$$\beta_{c,s,t}(x) = \frac{\ln[-\ln S_{c,s,t}(x)]}{\ln(x/\alpha_{c,s,t})}, \tag{3}$$

and is fitted at old ages by a quadratic function of age, following the procedure used in our previous study (Gonçalves and Weon 2026). Because the stretching exponent $\beta(x)$ varies with age rather than remaining constant, we refer to Eq. (1) as a modified stretched-exponential survival function. The model-derived upper-tail parameter ω is determined by the fitted-tail condition

$$\beta(\omega) + \omega \ln(\omega/\alpha) \left.\frac{d\beta}{dx}\right|_{x=\omega} = 0. \tag{4}$$

We fit the tail over ages 80–109 and exclude the open-ended 110+ life-table point from the polynomial fit. This fixed specification is applied identically to every country, sex, and year and is retained to preserve comparability with the previous international analysis. The 80–109 interval includes the late-life curvature used to estimate the tail while avoiding the open-ended 110+ category. As before, ω is a model-dependent descriptor of the fitted survival geometry, not the observed maximum age and not a deterministic biological lifespan limit (Gonçalves and Weon 2026). Because ω is obtained from an extrapolated quadratic tail fit and is more variable in periods with sparse oldest-age exposure, individual annual estimates should not be overinterpreted; the substantive inference rests on the cross-national long-run pattern and recent clustering. Old-age mortality deceleration and heterogeneity provide additional reasons not to interpret any extrapolated tail parameter as a literal hard boundary (Kannisto 1988; Vaupel et al. 1979; Horiuchi and Wilmoth 1998).

2.3 One-year-ahead centenarian population model

Let $N_{99,c,s,t}$ denote the observed population exactly age 99, and let $N_{100-104,c,s,t}$, $N_{105-109,c,s,t}$, and $N_{110+,c,s,t}$ denote the corresponding old-age stocks. The probability of surviving from 99 to 100 is

$$p_{99,c,s,t} = \frac{S_{c,s,t}(100)}{S_{c,s,t}(99)}. \tag{5}$$

For an age group $[a, b]$, the fitted survival curve gives a one-year retention ratio

$$R_{c,s,t}^{[a,b]} = \frac{\sum_{x=a}^{b} S_{c,s,t}(x+1)}{\sum_{x=a}^{b} S_{c,s,t}(x)}. \tag{6}$$

For the open 110+ interval we use

$$r_{110,c,s,t} = \frac{S_{c,s,t}(111)}{S_{c,s,t}(110)}. \tag{7}$$

The next-year centenarian population is then

$$\begin{aligned} \widehat{N}_{100+,c,s,t+1} = {} & N_{99,c,s,t} p_{99,c,s,t} + N_{100-104,c,s,t} R_{c,s,t}^{[100,104]} \\ & + N_{105-109,c,s,t} R_{c,s,t}^{[105,109]} + N_{110+,c,s,t} r_{110,c,s,t}. \end{aligned} \tag{8}$$

Male and female predictions are summed. No population observation from the target year enters Eq. (8), so each retained point is a genuine one-year-ahead prediction conditional on the previous year's population structure and mortality schedule.

Prediction accuracy is summarized with R^2, RMSE, bias, and

$$\text{MAPE} = \frac{100}{n} \sum_{i=1}^{n} \left| \frac{\widehat{N}_i - N_i}{N_i} \right|. \tag{9}$$

Because HMD supplies single-age population stocks through age 109, we also repeat the analysis by propagating every age 100–109 separately. That sensitivity analysis is reported in Supplementary Information.

2.4 Benchmark models

We compare the modified stretched-exponential model with two benchmarks using identical observed population stocks. A naive persistence model assumes

$$\widehat{N}_{100+,c,s,t+1}^{\text{naive}} = N_{100+,c,s,t}. \tag{10}$$

A direct-HMD cohort model replaces the fitted modified stretched-exponential probabilities with the original HMD death probabilities. At age 99,

$$p_{99,c,s,t}^{\text{HMD}} = 1 - q_{99,c,s,t}. \tag{11}$$

For an interval $[a, b]$, relative weights are generated recursively by

$$w_a = 1, \qquad w_{x+1} = w_x (1 - q_{x,c,s,t}), \tag{12}$$

and

$$R_{c,s,t}^{\text{HMD},[a,b]} = \frac{\sum_{x=a}^{b} w_x (1 - q_{x,c,s,t})}{\sum_{x=a}^{b} w_x}. \tag{13}$$

For the HMD 110+ open interval, where $q_{110+} = 1$ by life-table construction, one-year survival is approximated by $\exp(-m_{110+})$. This benchmark isolates the incremental value of the smooth modified stretched-exponential representation from the more general predictive value of mortality-informed cohort accounting.

2.5 Centenarian growth and lifespan geometry

Population levels, α, and calendar time all contain strong secular trends. We therefore avoid interpreting simple level correlations as evidence that changes in α or ω cause changes in centenarian abundance. For each country and sex we examine annual first differences,

$$g_{c,s,t} = \Delta \ln N_{100+,c,s,t}, \tag{14}$$

together with $\Delta\alpha_{c,s,t}$ and $\Delta\omega_{c,s,t}$. The purpose is descriptive: to determine whether short-term centenarian growth is consistently accompanied by short-term movement of the fitted upper tail.

2.6 Harmonized recent-trend scenarios to 2050

For each country and sex, annual centenarian growth is modeled from 2001, or from the first available annual transition in 2004 for South Korea, through the latest year supported by the life-table series, as

$$\begin{aligned}\widehat{g}_{c,s}(t) = {} & a_{0,c,s} + a_{1,c,s}(t - 2000) + a_{2,c,s}\Delta\alpha_{c,s}(t) \\ & + a_{3,c,s}\Delta\omega_{c,s}(t) + a_{4,c,s} \ln N_{100+,c,s}(t-1).\end{aligned} \tag{15}$$

Recent trajectories of α and ω are extrapolated linearly from 2000 through each country's calibration endpoint (from 2003 onward for South Korea),

$$\begin{aligned}\alpha_{c,s}(t) &= u_{0,c,s} + u_{1,c,s}(t - 2000), \\ \omega_{c,s}(t) &= v_{0,c,s} + v_{1,c,s}(t - 2000).\end{aligned} \tag{16}$$

Equation (15) is then iterated to 2050. Male and female growth residuals are resampled as paired year-level vectors for 3,000 residual-bootstrap paths; the 2.5th and 97.5th percentiles define a conditional 95% interval.

These are harmonized *recent-trend scenarios*, not official cohort-component projections. They hold the fitted model structure and extrapolated parameter trends fixed and therefore do not capture alternative future mortality regimes, migration, or structural demographic change. Calibration-window sensitivity is evaluated separately in Supplementary Information.

3 Results

3.1 Centenarian populations increased across all five countries

Figure 1 shows the HMD population aged 100+ over each country's available period. The absolute scales differ greatly, but all five countries show sustained growth. The

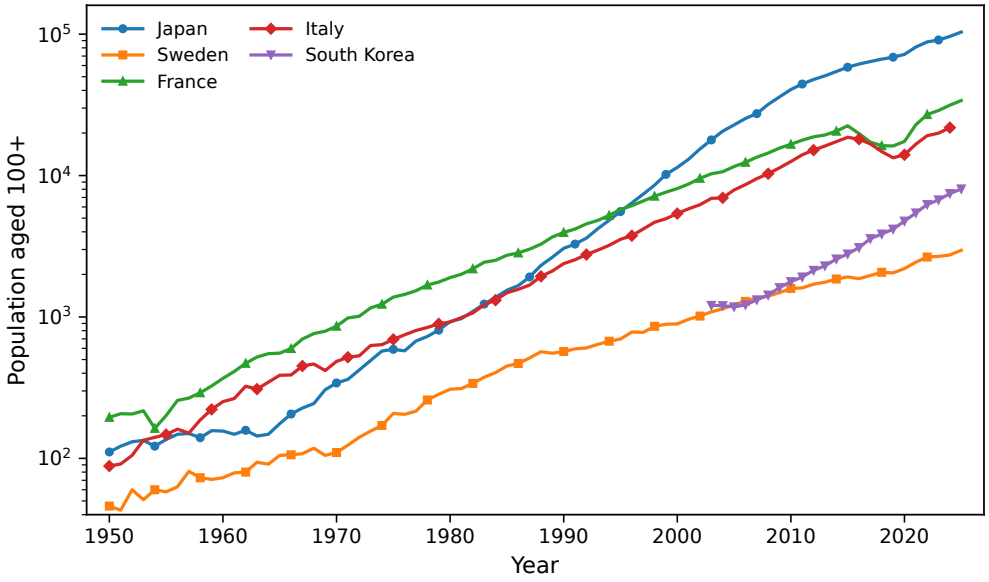


Fig. 1 Annual HMD population aged 100 years and older in Japan, Sweden, France, Italy, and South Korea over their available HMD periods. The logarithmic scale allows direct comparison across countries that differ greatly in absolute population size.

Japanese population increases from approximately 111 in 1950 to 103,411 in 2025, Sweden from 46 to 2,961, France from 195 to 33,931, and Italy from approximately 88 in 1950 to 21,833 in 2024. South Korea, whose harmonized series begins later, increases from approximately 1,208 in 2003 to 8,042 in 2025. The Korean series therefore provides a shorter but independent test during a period of rapid centenarian expansion.

3.2 The characteristic age rises while the upper-tail parameter does not

Figure 2 shows the sex-specific annual trajectories of α and ω. In every country, α rises strongly over the long run. The fitted ω is much more variable in earlier periods but does not show a comparable sustained rise; since 2000 it generally declines or stabilizes.

The latest values cluster much more tightly for ω than for the centenarian population itself. Across the ten country–sex series, latest ω lies between 116.78 and 122.18 years. Women have higher α than men in every country, whereas sex differences in ω are much smaller. This pattern indicates that the female longevity advantage is expressed mainly through a larger fraction of women surviving closer to a similar upper-tail region.

Table 1 Latest HMD-derived characteristic age α, upper-tail parameter ω, and interval $\delta = \omega - \alpha$ (years).

Country	Sex	Year	α	ω	δ
Japan	Male	2024	87.30	122.18	34.88
Japan	Female	2024	92.71	120.89	28.19
Sweden	Male	2024	88.25	118.40	30.15
Sweden	Female	2024	90.67	118.41	27.74
France	Male	2023	87.48	120.13	32.65
France	Female	2023	91.75	118.34	26.59
Italy	Male	2022	86.71	117.77	31.06
Italy	Female	2022	90.01	116.78	26.77
South Korea	Male	2024	87.10	122.11	35.00
South Korea	Female	2024	91.51	119.39	27.88

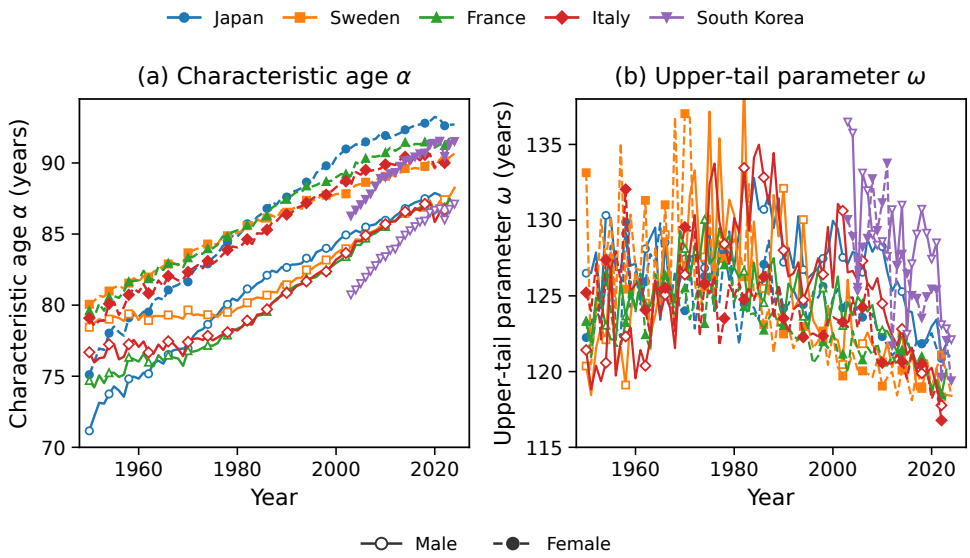


Fig. 2 Annual lifespan-geometry parameters for males and females in Japan, Sweden, France, Italy, and South Korea. (a) Characteristic age α. (b) Model-derived upper-tail parameter ω. Colors and marker shapes distinguish countries, while solid and dashed lines denote males and females, respectively. A common legend is placed below the two panels to improve readability. The cross-national pattern is clear: α rises over the observed interval, whereas ω shows no comparable secular increase.

3.3 One-year-ahead prediction generalizes across countries

Figure 3 compares observed and modified stretched-exponential predictions of centenarian populations. Prediction accuracy is high in each population despite large differences in scale and demographic history. Country-specific R^2 ranges from 0.99564 to 0.99989 and MAPE from 1.97% to 3.49% (Table 2).

Across all 317 country-year forecasts, pooled MAPE is 3.02%. The high R^2 values should not be interpreted in isolation, because N_{100+} spans several orders of magnitude

Table 2 Modified stretched-exponential one-year-ahead prediction performance for total population aged 100+.

Country	n	Target years	R^2	MAPE (%)	RMSE	Bias (%)
Japan	74	1950–2025	0.99983	2.811	372.2	-1.48
Sweden	76	1950–2025	0.99951	3.489	17.8	+1.31
France	75	1950–2024	0.99961	3.424	158.9	+2.58
Italy	70	1950–2023	0.99989	2.630	63.8	+1.05
South Korea	22	2004–2025	0.99564	1.967	139.9	-1.59

and is strongly persistent. The percentage-error metrics and benchmark comparison below are therefore more informative about incremental predictive performance.

3.4 The historical trajectories are reproduced over several orders of magnitude

Figure 4 plots the annual observed and predicted series directly. The model reproduces the transition from small postwar centenarian populations to the much larger modern stocks in all five countries. Errors are larger in relative terms when populations are very small, but the predictions continue to track the observed trajectories during periods of rapid expansion.

3.5 Modified stretched-exponential and direct HMD mortality perform similarly

The cross-national benchmark clarifies the source of predictive skill. Pooled over 317 forecasts, MAPE is 3.02% for the modified stretched-exponential model, 3.02% for direct HMD mortality, and 8.34% for naive persistence. At the country level, the modified stretched-exponential model is slightly better than direct HMD in Japan, Sweden, and South Korea, whereas direct HMD is slightly better in France and Italy. The differences between the two mortality-informed models are small relative to their common advantage over persistence.

This result limits claims that the modified stretched-exponential functional form itself is responsible for short-horizon accuracy. The dominant predictive information is the demographic accounting in Eq. (8): the age-99 inflow plus mortality among people already aged 100+. The modified stretched-exponential model's distinctive contribution is instead to represent the same mortality schedule smoothly while simultaneously supplying interpretable descriptors α and ω. Full benchmark results are given in Supplementary Information.

3.6 Annual growth is not consistently tied to annual movement of ω

First-difference analysis shows no uniform positive relationship between annual centenarian growth and $\Delta\omega$. Correlations differ in sign and magnitude by country and sex. Some individual series show statistically detectable associations, but the direction is not consistent across populations. The same is true for $\Delta\alpha$. Thus, short-term

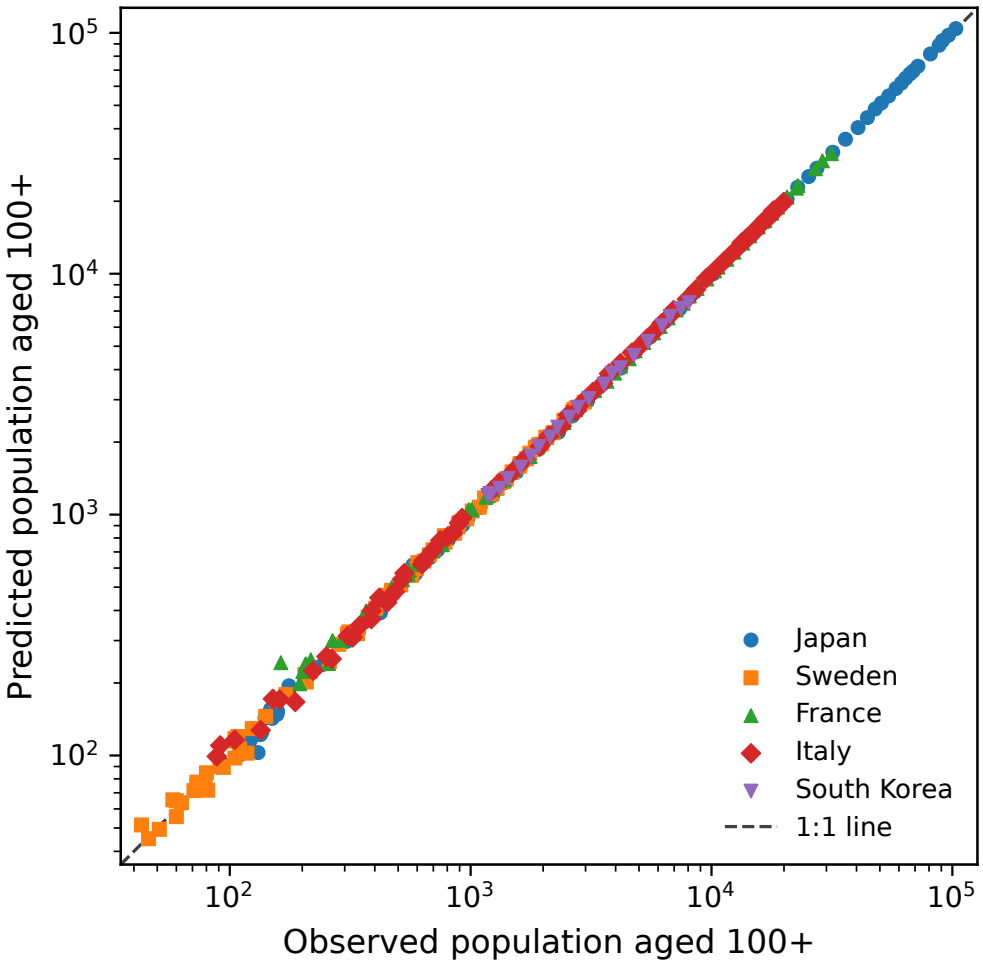


Fig. 3 Observed versus one-year-ahead modified stretched-exponential prediction of the population aged 100+ for the five countries. Each point uses the previous year's observed population stocks and mortality schedule. The dashed line is the line of identity.

fluctuations in the fitted survival geometry do not provide a universal explanation of year-to-year centenarian growth. The long-run contrast is more robust: N_{100+} rises by orders of magnitude while ω does not.

3.7 Conditional 2050 scenarios differ substantially across countries

Figure 5 shows harmonized recent-trend scenarios using the same model specification in all five countries. Under the primary calibration, the 2050 central scenario is approximately 273,585 for Japan, 115,429 for South Korea, 77,731 for France, and

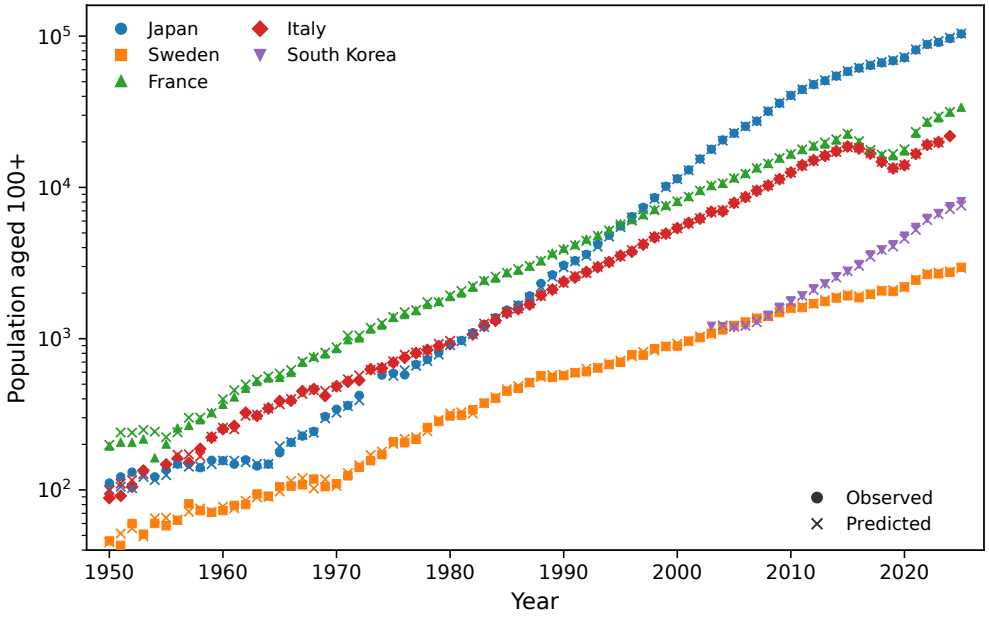


Fig. 4 Observed HMD population aged 100+ and one-year-ahead modified stretched-exponential predictions. Filled country-specific symbols denote observed values, whereas × symbols denote predictions. The logarithmic scale permits comparison across five countries and multiple orders of magnitude.

Table 3 Harmonized recent-trend centenarian scenarios to 2050. Intervals are conditional 95% paired-residual-bootstrap intervals.

Country	Calibration endpoint	2050 central scenario	Lower 95%	Upper 95%
Japan	2024	273,585	249,878	302,241
Sweden	2024	7,966	7,473	8,429
France	2023	77,731	58,878	98,744
Italy	2022	32,471	23,544	43,060
South Korea	2024	115,429	109,962	120,834

32,471 for Italy. The corresponding value for Sweden is 7,966 (Table 3). The residual-bootstrap intervals quantify only year-to-year variation conditional on the model and extrapolated parameter trends.

As a short-horizon check on the scenario equation itself, the first post-calibration observation is predicted within −2.36% in Japan (2025), −3.80% in Sweden (2025), −5.85% in France (2024), and −1.60% in Italy (2023), while South Korea is within +2.81% in 2025. Long-horizon values are much less stable: changing the calibration start from 2000 to 2005 or 2010 materially changes the 2050 scenario in several countries, especially France and Italy. South Korea is comparatively stable across the tested starts (approximately 110,000–122,000 by 2050), although its calibration series is much shorter. Those sensitivity results are reported in Supplementary Information.

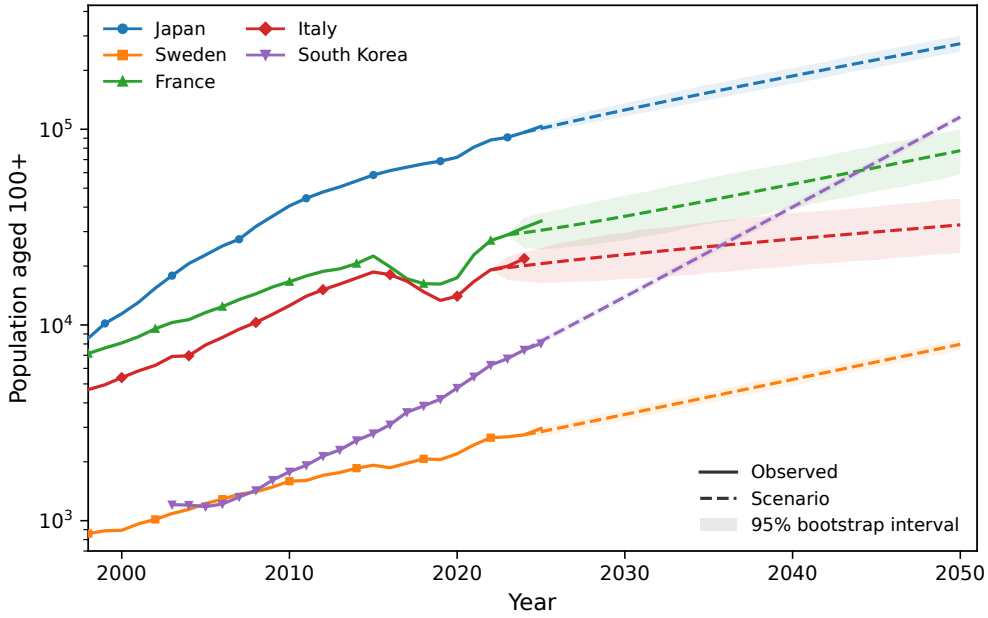


Fig. 5 Observed HMD populations aged 100+ and harmonized recent-trend scenarios to 2050 for Japan, Sweden, France, Italy, and South Korea. Solid lines show observations, dashed lines show model-based scenarios, and shaded bands show conditional 95% paired-residual-bootstrap intervals. A logarithmic scale is used so that all five countries remain visible on the same graph.

4 Discussion

4.1 Cross-national validation changes the interpretation of the model

The main advance of the present analysis is the transition from survival-curve description to population-dynamic validation, together with external replication. The earlier α–ω study characterized how annual survival geometry changes across populations; the present analysis asks whether that geometry, combined with observed old-age stocks, reproduces realized centenarian population dynamics. A survival–population model first developed around the unusually rich Japanese record also reproduces annual centenarian dynamics in Sweden, France, Italy, and South Korea. The countries differ greatly in population size, historical mortality, timing of centenarian expansion, and latest data year, yet one-year-ahead MAPE remains between 2.0% and 3.5%. South Korea is notable because the validation begins only in 2004, but accuracy remains high during a period of rapid mortality improvement and centenarian growth. The result therefore cannot be attributed solely to a peculiarity of the Japanese demographic series.

At the same time, the benchmark comparison makes clear what has and has not generalized. What generalizes most strongly is the demographic identity underlying the model: next year's centenarian stock is largely determined by the previous year's

age-99 population and survival among existing centenarians. The precise modified stretched-exponential representation is not uniquely necessary for accurate one-year forecasting, because direct HMD mortality performs almost identically. This distinction strengthens rather than weakens the interpretation: the population forecast and the survival-tail geometry can be evaluated as related but separate components.

4.2 What the modified stretched-exponential representation adds

The modified stretched-exponential framework is useful because a single fitted survival representation serves two functions. First, it supplies smooth retention probabilities for propagating old-age population stocks. Second, it maps the same annual survival curve to compact geometric descriptors, especially α and ω. Raw HMD probabilities provide an excellent forecasting benchmark but do not by themselves yield an equivalent two-parameter description of how the survival curve shifts and compresses over time.

Accordingly, the present results do not support a claim of strong predictive superiority for the modified stretched-exponential model over direct HMD mortality. In pooled cross-national prediction, their MAPEs differ by less than 0.01 percentage points. The added value of the modified stretched-exponential representation is interpretive: it permits the population trajectory to be compared directly with the long-term movement of the characteristic age and upper tail.

4.3 More centenarians do not require a rising lifespan boundary

The most consistent cross-national result is the divergence between population abundance and upper-tail geometry. At calendar time t, the centenarian stock is the sum of the age-specific populations above 100,

$$N_{100+}(t) = \sum_{x \geq 100} N_x(t). \tag{17}$$

This stock reflects the sizes of cohorts reaching old age together with survival to age 100 and survival thereafter. Growth in N_{100+} can therefore arise from cohort size, improved survival to age 100, or improved post-100 survival; none of these requires ω to increase proportionally.

This distinction is visible in every country studied. Between 1950 and the latest available population observation, N_{100+} rises by roughly 64-fold in Sweden, 174-fold in France, 247-fold in Italy, and more than 900-fold in Japan. South Korea increases by approximately 6.7-fold from 2003 to 2025. Over the corresponding observation periods, α moves substantially to older ages, whereas recent ω values cluster around 117–122 years. The results are consistent with a changing shape of the modeled survival distribution, but the numerical tail location remains conditional on the chosen quadratic fit.

This interpretation also helps reconcile population-based and record-based measures of extreme longevity. As the number of people exposed to ages above 100 or 110

increases, the expected maximum observed age can rise even without a parallel shift in a population-level tail parameter (de Beer et al. 2017; Pearce and Raftery 2021). Thus, a growing number of extreme-age observations does not by itself identify an expanding underlying lifespan boundary.

4.4 Cross-country and sex differences

The common qualitative pattern does not imply identical demographic trajectories. Japan exhibits the largest modern centenarian population and the greatest proportional increase from 1950. Sweden has a much smaller population but provides the longest continuous national mortality record. France and Italy occupy intermediate positions and show different recent growth rates. South Korea contributes a shorter 2003–2025 series but one characterized by rapid mortality improvement and a steep rise in centenarian abundance, broadening the validation beyond the four long historical European/Japanese series.

Sex differences are also systematic. In the latest life tables, female α exceeds male α by approximately 2.4–5.4 years across the five countries, whereas male–female differences in ω are much smaller. Within this fitted representation, the female advantage is more pronounced in the characteristic age than in the tail descriptor; this pattern should not be interpreted as a direct estimate of sex-specific biological longevity limits.

4.5 Short-horizon validation and long-horizon uncertainty are different problems

The accuracy of one-year-ahead prediction should not be extrapolated mechanically to 2050. The one-year model conditions on observed age-99 and 100+ population stocks and an observed mortality schedule; the long-range scenario must instead extrapolate growth and survival trends recursively. Small changes in those assumptions accumulate.

This distinction is evident in the calibration-window sensitivity. Japan and Sweden are comparatively stable across some alternative starts, whereas France and Italy show much larger changes; South Korea is relatively stable across the tested windows but is based on fewer calibration years. The recent-trend regression also has limited explanatory power for some country–sex series. The 2050 values should therefore be read as conditional scenarios illustrating the consequences of recent trajectories, not as replacements for national cohort-component projections.

5 Limitations

First, HMD data are harmonized and high quality, but very old-age population counts and mortality rates remain vulnerable to small exposures, age misstatement, registration differences, and historical reconstruction. Data quality is not identical across countries or periods.

Second, to preserve a common formulation we aggregate ages 100–104 and 105–109 in the primary one-year model even though HMD provides single-age population stocks. A full single-age sensitivity analysis changes predictions only minimally: the

mean absolute grouped-versus-single prediction difference is approximately 0.19–0.23% across the five countries, and country-level MAPE changes by less than 0.06 percentage points.

Third, the 110+ interval is open-ended. Its contribution to the total centenarian stock is small, but dedicated analysis of supercentenarians requires validated individual-level ages and specialized extreme-age mortality models (Rootzén and Zholud 2017; Pearce and Raftery 2021).

Fourth, the one-year prediction holds the base-year period mortality schedule fixed over the forecast interval. This design is deliberately prospective and transparent, but unexpected within-year mortality shocks or rapid improvement can generate error.

Fifth, the modified stretched-exponential model does not materially outperform direct HMD mortality in short-horizon prediction. Claims about this model should therefore concern its combined forecasting and geometric interpretation, not unique predictive superiority.

Sixth, the 2050 scenarios are structurally uncertain. The residual-bootstrap intervals capture historical residual variation conditional on the fitted regression and extrapolated α and ω trends; they do not include alternative mortality-improvement paths, future cohort-size uncertainty, migration, registration changes, or model misspecification. Calibration-window sensitivity is large in some countries.

Seventh, the absolute value of ω is conditional on the specified quadratic tail fit over ages 80–109. The same fitting rule is applied throughout, which supports internal cross-country and temporal comparison, but the present analysis does not quantify sensitivity to alternative fitting windows or polynomial orders. The recent 117–122-year range should therefore be interpreted as a feature of this fixed modified stretched-exponential specification rather than as an invariant biological boundary. Dedicated fitting-specification sensitivity using the raw annual life tables would be a useful extension.

Finally, the five countries are high-longevity populations with unusually strong demographic data systems. South Korea also has a substantially shorter HMD series (2003 onward) than the other four countries, so its long-horizon trend estimates are based on fewer observations. The five-country set provides useful external validation but is not globally representative. Extension to a broader range of HMD populations is needed to determine how far the findings generalize.

6 Conclusions

Using a single harmonized HMD framework, we analyzed centenarian population dynamics in Japan, Sweden, France, Italy, and South Korea. Across 317 available one-year-ahead forecasts, the modified stretched-exponential survival–population model reproduces the observed population aged 100+ with country-level MAPE between 1.97% and 3.49%. Direct HMD mortality performs almost identically, while naive persistence is substantially less accurate. The robust demographic result is therefore the value of explicit age-99 inflow and survival accounting; the distinctive contribution of the modified stretched-exponential representation is to connect that accounting to interpretable lifespan geometry.

Across all five populations, the characteristic age α has increased strongly, whereas the model-derived upper-tail parameter ω has not risen in parallel and recently lies in a relatively narrow range near 117–122 years. The number of centenarians can therefore increase dramatically without a commensurate rightward movement of the fitted survival tail.

This cross-national separation between *how many* people reach extreme old age and *how far* the survival distribution extends provides a more general interpretation of modern centenarian growth than the Japanese case alone. It also clarifies why short-horizon population prediction can be highly accurate while long-horizon scenarios remain structurally uncertain. Harmonized recent-trend scenarios imply continued centenarian growth through 2050, but their country-specific levels depend materially on calibration choices and should therefore be interpreted as conditional demographic scenarios rather than deterministic forecasts.

Supplementary information

The accompanying Supplementary Information contains supplemental methods, complete validation and benchmark results, single-age sensitivity analysis, first-difference associations, recent-trend model coefficients, and uncertainty analyses for the conditional 2050 scenarios.

Author contributions

B.M.W. conceived the study, developed the methodology, performed the analysis, interpreted the results, prepared the figures and tables, and wrote and revised the manuscript.

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Competing interests

The author declares no competing interests.

Ethics approval and consent to participate

Not applicable. The study analyzes publicly available aggregate population and life-table data and does not use identifiable individual-level human-subject data.

Consent for publication

Not applicable.

Data availability

The primary data used in the cross-national analysis are publicly available from the Human Mortality Database (HMD) (Human Mortality Database 2026). The analysis uses annual population size by single year of age and sex and sex-specific annual period life tables for Japan, Sweden, France, Italy, and South Korea. The Japanese Mortality Database and other Japanese administrative sources discussed in the manuscript provide complementary demographic context but are not mixed into the harmonized five-country one-year validation. Derived annual α, ω, validation predictions, and scenario outputs can be reproduced from the HMD files and the equations reported here and in Supplementary Information. No restricted individual-level data were used.

Code availability

The equations and analytical procedures required to reproduce the modeling framework are described in the Methods and Supplementary Information. Custom analysis code was used to produce the reported results; the author will provide the analysis scripts and processing details upon reasonable request.

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