

Research Article

More on the Mortality Conjecture: The Components of Demographic Mortality

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Abstract

In a previous preprint article, the author presented a conjecture on the trend of demographic mortality as the life span progresses. That article also provided a mathematical formulation of the statistical distribution to which mortality would tend in this case. In the present work, we show the possibility that the demographic mortality at high ages would be given by the sum of four main components. The four components were derived by iteratively solving the Fredholm equation that can be associated with the model. These solutions are presented for three demographic cases based on statistical data available in the public databases and literature. These are: mortality data in the US from 1970 to 2017, in Italy from 1974 to 2019 and in Japan from 1974 to 2019. In all cases, similarities and invariant components are noted and presented in graphs and numerical data. The four aforementioned components appear on average equally spaced in the age peaks (in the case of females ~50, ~63, ~77, ~90 ages) and are always present for all sample years and in all three countries. These same components can be used to reconstruct the q_x datum, at advanced ages, of the considered Life Tables. A correlation with a more recent study using a multi-omics approach is pointed out.

Keywords

Demographic Mortality, S-System Distribution, Demographic Life Tables, Fredholm Equation

1. Introduction

In the study of demography in various countries around the world, an important role is played by Life Tables in which, among other aspects of people's life data, mortality data (i.e. the deaths of people according to various age and population groups) are also presented. An example of these mortality data is given in the Appendix I where deaths by age group of five years and survey year are given for three countries in the case of the females. Analysis of the data reveals some common and recurring features. Firstly, the sum of all data in the columns is centered on 100000. This is due to the convention with which the data are normally presented in Life Tables. Furthermore, if we look at the vertical sequences of the data, we see that at the

beginning of the columns the infant mortality figure appears to be present in the initial 0-4 age group. Thereafter, with increasing ages, the number of deaths appears almost independent of age up to the average of 40 years. After the age of 40-50, mortality starts to increase more sharply and reaches a statistical peak after which it decreases to zero at the age of the life limit. For brevity and in the following, we call area 'A' the area of infant mortality, 'B' the area of nearly flat mortality and 'C' the area of 'peak' mortality. In the paper in Ref. [1], the author presented a conjecture on mortality at high ages in which the mortality of zone C is predicted to tend toward a theoretical curve as lifespan increases. This theoretical func-

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tion, called $mTC(a, TC)$, is defined by an age variable 'a' and a single parameter TC (which coincides with the area under the curve plotted when $0 < a < \infty$) and has been analytically described and characterized in the works of Ref. [1] and [2]. The theoretical basis for the derivation of this function had been laid in Ref. [2] paper in which the Fermi statistic method was used to generate the function. In Appendix II the aforementioned function is recalled in various analytical versions and useful formulas. To clarify how these relationships can be used in the case of real mortality data, consider the examples in Figure 1 and Figure 2 below:

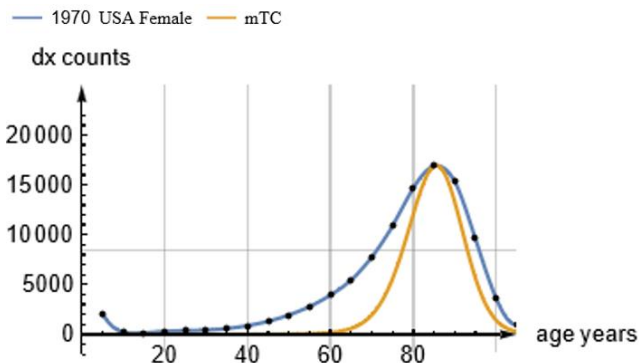


Figure 1. USA 1970 curve superimposed on the theoretical mTC curve.

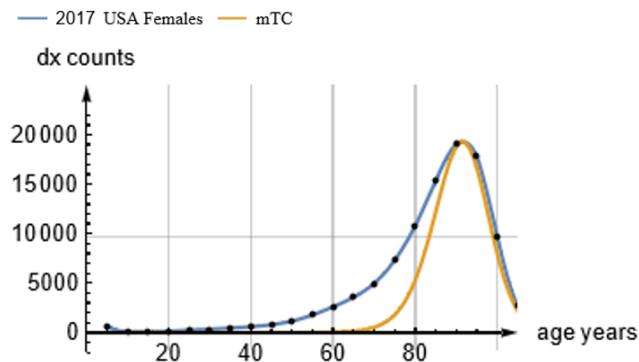


Figure 2. USA 2017 curve superimposed on the theoretical mTC curve.

Figure 1 shows the mortality data (dots as per Figure A1 in Appendix I) for the USA 1970 interpolated with a continuous curve. Below this curve a second curve mTC is presented whose peak coincides with the interpolated mortality peak. This last curve is a mTC function curve with $ap = 85.5761$ years (where 'ap' is the age corresponding at the peak), $TC = 70986$ and a peak height equal to 16932. The overlap of the curves in the peak is obtained, using the formulas in Appendix I, by: 1) finding the age of the maximum of the interpolated curve and choosing this as 'ap' value, 2) calculating the TC parameter corresponding to the mTC with the same 'ap' and appropriately scaling the mTC curve by multiplying the

$mTC(a, 70986)$ function by a computed constant factor. Looking at Figure 1, you can see two distinct areas to the left and right of the peak not covered by the mTC curve. The area under the mTC curve indeed turns out to be 57881 dx cases, which means that the theoretical curve only partially covers the total cases of 100000 deaths and this is evident in the graphics of Figure 1. For Figure 2 (2017 data with the same graphics meaning of Figure 1), it can be seen that the peak of maximum mortality has shifted to a higher age (about 91.5 years) and that the area of difference between the two curves to the left of the mTC still persists, even if the interpolated curve shape shrinks, while the area of difference to the right minimizes. Areas A and B have also shrunk. Mortality coverage by the 2017 mTC curve is increased to 65940 dx over 100000 dx and the peak height becomes 19290 and the full width at half maximum (FWHM) is reduced, as can be seen by the interception of the FWHM horizontal line on the curve. This trend is consistent with the conjecture mentioned above. This conjecture predicts indeed that as the 'ap' increases, the two difference areas shrink until they disappear for very high 'ap' values. The calculations indicated above are carried out using the formulas in the Appendix II while the continuous interpolating function is generated through a well-known and widely used mathematical computer application. The present study aims to analyze in detail the possible components that give rise to the difference area to the left of the theoretical mTC curve. The study also wants to assess whether there are differences between these possible components when dealing with surveys in different countries. For these purposes, mortality data from the USA, Italy and Japan in the years 1970-2017 (USA) and 1974-2019 (Italy and Japan) will be considered. In order to search for 'hidden' components of the left-hand skewness of the mortality curve, the next section presents a Fredholm integral equation that in general can answer the problem posed. In the third section, an iterative solution based on graphical methods for this equation is proposed. In the following sections, the results obtained are presented and discussed with preliminary conclusions.

2. The Fredholm Equation

In the work of Ref. [1], it was seen how the area to the left of the mTC curve takes on the appearance of a second similar peak when graphed in isolation. This fact, together with the presence of the main peak, may lead us to hypothesize that the demographic experimental curve -in the high ages C zone sector- may be obtained from the multiple composition of theoretical mTC curves with different parameters and sizes. This can be expressed in general by the Fredholm integral equation of the first kind as follows:

$$mdx(a, t_0) = \int_0^{TC_{max}} f(t_0, TC) mTC(a, TC) dTC \quad (1)$$

In eq. (1), the term mdx represents the interpolated demographic data that is a function of the age and year t_0 in which

the demographic estimate is made (e.g. $t_0=1970$ or 2017 in the cases depicted above in [Figures 1 and 2](#)). The mTC function is the one discussed above and detailed in Appendix II while the function $f(t_0, TC)$ identifies the 'weight' of the specific mTC function at the polling time t_0 and with parameter TC. The integral in eq. (1) then gives us for each age 'a' and demographic sampling t_0 the sum of the various mTC components that contribute to construct the $mdx(a, t_0)$ when weighted by the function $f(t_0, TC)$. Our problem is therefore to find the solution of the integral in eq. (1) in terms of the unknown function f , the mTC functions being known analytically and the mdx function numerically. In the case where the mTC components are present in discrete numbers of TC parameters and not continuous, eq. (1) becomes:

$$dx_{a,t_0} = \sum_{i=1}^n f(t_0)_i mTC(a, TC_i) \quad (2)$$

where n represents the number of possible discrete TC components and similarly the i -th $f(t_0)$ refers to the weight of the i -th mTC. Recalling the formulas in the Appendix II, it will also be possible to express eq. (2) using the normalized function $mTCnp$ which depends on the usual variable 'a' and a parameter 'ap' equal to the age of the curve peak. Consequently, a weight i -th $w(t_0)$ will appear in the equation to represent exactly the number of dx cases relevant to the single component $mTCnp(a, ap)$ with i -th parameter ap . Under these conditions, eq. (3) can be defined:

$$dx_{a,t_0} = \sum_{i=1}^n w(t_0)_i mTCnp(a, ap_i) \quad (3)$$

To the author's knowledge, no general solution of the Fredholm integral equation of the first type is known. Numerical solution methods do exist in the literature, but these can lead to oscillating terms and non-unique solutions (see e.g. Ref. [3] and [4]). A possible practical approach is therefore to be guided by the specific physical problem and to bind the method of solution to it.

3. The Solutions of the Fredholm Integral Equation

To find a possible solution to eq. (3) in real cases, we used mortality data from three different countries: USA, Italy and Japan. It should be noted that these three countries are not only characterized by different lifestyles and social realities, but also have different population sizes (USA about 333 million people, Japan about 125 million and Italy about 60 million). Among these data we have chosen -for all three countries- the subset of the female case, which presents a lower dispersion (FWHM) of the mortality peak than the totals. The data used are available in Appendix I. In Ref. [1] a graphical-analytical method was used to identify a second peak component to the left of the main peak. This method is extended here recursively. In practice, a third peak is identified from the second peak and so on by iteration. This procedure is based on the assumption that the peak of the

actual curve can be approximated to a large extent by a single mTC function, which leaves a small portion of the curve not covered by the mTC to the left. The numerical and graphical calculations are done with the aid of a mathematical application and ad-hoc written software that runs with the mathematical application itself. The Appendix II equations are used for the computations. To clarify this method, the following [Figures 3 and 4](#) (relevant e.g. to the Italy case) are useful. The dotted curve represents actual demographic data appropriately interpolated with a continuous curve ¹(*). The mTC curve is our mTC function scaled to match the current peak. The [Figure 4](#) show a "difference curve" obtained by subtracting the scaled mTC from the current curve. Note that in this figure two vertical lines show the location of the current peak and also the location of the previous figure peak. Similar operations are then applied in sequence to this 'difference' curve generating [Figures 5, 6, 7, 8, 9, 10](#). It must be noted that in the [Figure 4](#), we only consider the difference to the left of the subtraction of the curves, as the right-hand lobe tends - in general - to shrink faster than the left-hand one. This right-hand lobe is therefore omitted in the figures and in the calculations.

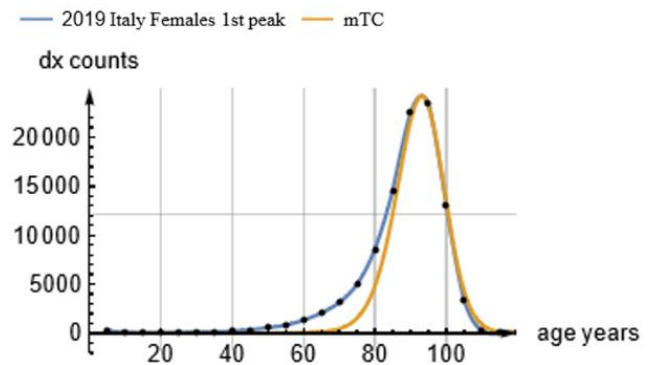


Figure 3. Plots of interpol. demogr. data and a compliant mTC.

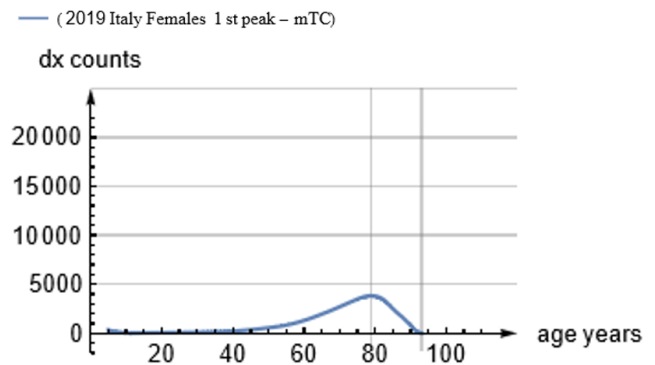


Figure 4. Plot of difference between curves giving a 2nd peak.

¹ (*) The constraint assumed for the continuous curve implies a possible shift (about 2.5 years) to the right of the simulated curve with respect to the real curve. This is not critical for our analysis, as we are looking for structural effects (not influenced by an offset component) and not for an absolute age effect.

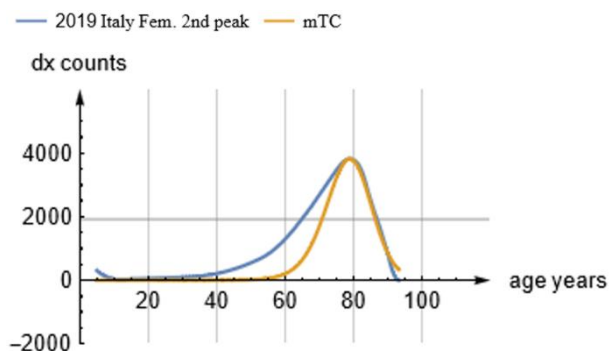


Figure 5. Plots of 2nd peak curve and a compliant mTC.

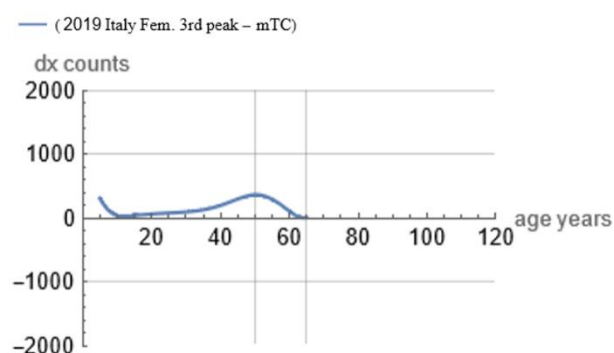


Figure 8. Plot of difference between curves giving a 4th peak

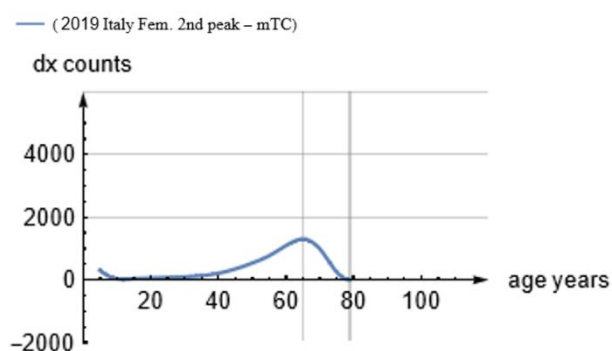


Figure 6. Plot of difference between curves giving a 3rd peak.

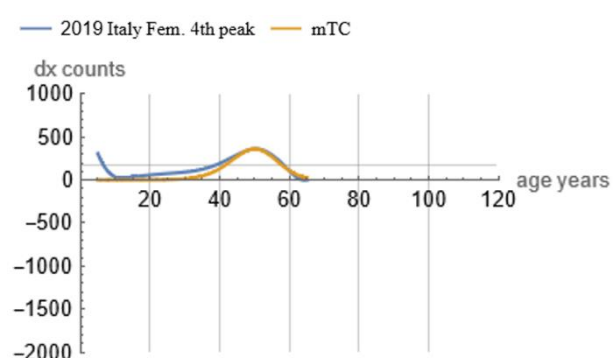


Figure 9. Plots of 4th peak curve and a compliant mTC.

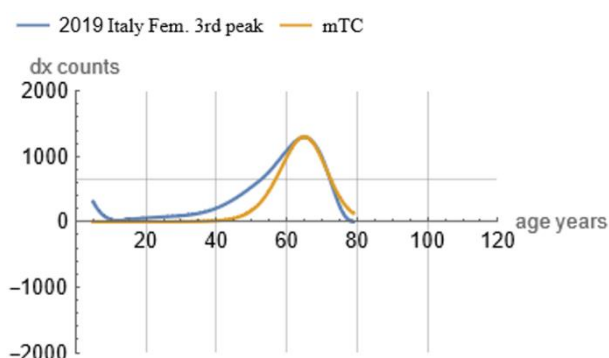


Figure 7. Plots of 3rd peak curve and a compliant mTC.

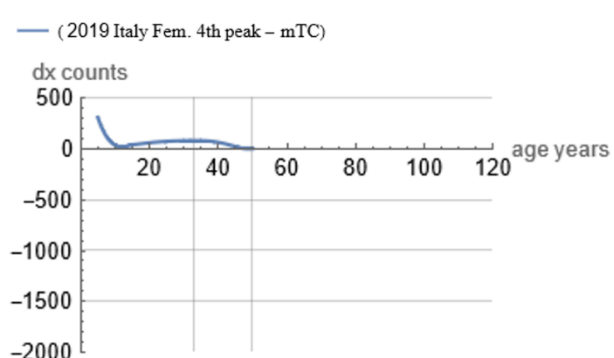


Figure 10. Plot of difference between curves giving a flat zone.

Year	Sex	B max height	B age of max height	No.cases	4th Peak age	No.cases	3rd Peak age	No. cases	2nd Peak age	No. cases	Main Peak age	Deviation % to 100k
1970	US Female	321	24.1	2523	43.6	7722	57.3	20 057	71.4	57 881	85.6	-12.0%
1980	US Female	286	26.2	2448	47.7	7651	60.6	21 357	74.	59 708	88.3	-8.8%
1990	US Female	287	34.1	2183	48.6	7841	61.9	23 106	75.2	59 685	89.6	-7.2%
2003	US Female	236	26.4	2727	49.1	7271	63.1	21 683	76.	60 857	90.	-7.5%
2017	US Female	312	33.6	2208	47.7	7651	62.6	19 625	77.6	65 940	91.5	-4.6%

Figure 11. USA female mortality components summary data.

Year	Sex	B max height	B age of max height	No.cases	4th Peak age	No.cases	3rd Peak age	No. cases	2nd Peak age	No. cases	Main Peak age	Deviation % to 100k
1974	ISTAT Female	210	33.5	1764	46.6	5445	59.1	15551	71.5	68939	85.5	-8.3%
1979	ISTAT Female	222	38.6	2323	51.	5518	62.4	17337	73.7	69145	86.7	-5.7%
1984	ISTAT Female	121	30.	1352	45.	4476	58.5	17711	73.	72941	87.8	-3.5%
1989	ISTAT Female	155	31.8	1500	48.9	4642	60.1	18968	75.	71453	88.6	-3.4%
1994	ISTAT Female	227	35.1	2022	52.4	6179	65.	20043	78.6	74038	90.	2.3%
1999	ISTAT Female	139	33.7	1163	47.6	3994	60.	13735	74.9	73741	89.4	-7.4%
2004	ISTAT Female	106	31.1	1199	49.8	4054	62.2	11605	75.6	80445	90.5	-2.7%
2009	ISTAT Female	131	41.1	1918	54.6	5999	67.3	15207	80.8	80887	92.4	4.0%
2014	ISTAT Female	88	37.6	1188	50.3	3924	63.5	12434	77.	79976	92.5	-2.5%
2019	ISTAT Female	78	32.9	1240	50.	4454	65.	13057	78.9	82788	93.1	1.5%

Figure 12. Italy female mortality components summary data.

Year	Sex	B max height	B age of max height	No.cases	4th Peak age	No.cases	3rd Peak age	No. cases	2nd Peak age	No. cases	Main Peak age	Deviation % to 100k
1974	Japan Female	218	30.	1525	42.8	4961	56.7	15854	71.5	71782	85.	-5.9%
1979	Japan Female	200	30.2	1614	47.1	4957	59.7	15376	73.9	72294	86.8	-5.8%
1984	Japan Female	185	31.6	1832	49.	5102	62.2	14630	75.9	74486	88.3	-4.0%
1989	Japan Female	144	30.	1342	46.8	4689	61.1	14200	76.3	76879	89.8	-2.9%
1994	Japan Female	156	35.	1577	50.3	4302	62.8	12746	76.2	76943	90.3	-4.4%
1999	Japan Female	170	35.	1779	51.5	4871	64.4	14594	78.7	75868	91.9	-2.9%
2004	Japan Female	206	40.	2183	54.7	5304	67.3	15162	81.5	76388	93.8	-1.0%
2009	Japan Female	175	39.6	1868	53.4	4808	66.9	14608	81.8	79866	94.6	1.1%
2014	Japan Female	160	38.8	1829	54.3	4975	67.6	13368	82.1	83130	95.	3.3%
2019	Japan Female	133	38.4	1627	53.8	4106	66.8	10793	80.4	85209	95.	1.7%

Figure 13. Japan female mortality components summary data.

A recurrence of the shape (self similarity-like) of the new peaks found can be seen in the above Figures, which show a persistent asymmetry to the left. Also noticeable is the reduction in heights and consequently in the areas subtended by the curves (note the change in scale of the y-axis for the various Figures). Finally, recursion stops when the new curve obtained by difference from the previous one no longer shows evidence of peaks to be mapped with mTC or reaches an age range near to the B zone. This is the case in Figure 10 where after the last graphical subtraction, only an almost flat area appears. This flat zone can be assimilated to the aforementioned zone B of the demographic tables. This recurring exercise was applied to all of the population cases considered in Appendix I (Figures A1, A2 and A3). The outcomes led to the significant result that in all of the situations considered, no more than four mTC curves can cover the zone C of the population curves. For all the cases indeed, after the fourth iteration the resulting graphical curve appears semi-flat and/or distributed over an age range corresponding to the age range of zone B. Accordingly, we can consider the above Fredholm's equations solved with four mTC functions each characterized by a specific i -th TC (and consequently an ap) and an i -th weight f (or w). These results are summarized in Figures 11, 12 and 13 for the case of females in the USA, Italy and Japan.

These data show in the third column the maximum height level of the last iteration in zone B, while the fourth column indicates the age of maximum height in zone B itself. The subsequent columns indicate the area (No. cases) of the single-component mTC curve and the relevant peak age in years (' ap ' parameter). The ' ap ' parameter is used in the data to

allow an immediate view of the position of the mTC peak. These data can also be used to reconstruct the dx function using eq. (3) as follows in the next section. Finally, the last column defines an accuracy value in the calculations measured as the percentage fraction between the sum of the areas of the four mTC functions compared to the total number of cases of 100000. This sum should theoretically always be less than 100000 since it does not include data areas A and B and the right lobe of the difference curves but only considers the reconstruction of area C with the four identified mTC functions. To these theoretical errors, it must be added the possible inaccuracies related to interpolations and peak searches. The data also show the growth in longevity over the years and from country to country.

4. Reconstructing the dx Curve with the Solutions Found

From the graphs and data shown above for the three cases study, we can verify the correctness of the solutions found. To this task we use eq. (3) where $w(t_0)$ corresponds to the individual areas (No. cases) in Figures 11, 12, 13 and $mTC_{np}(a, ap)$ will be given by a relevant formula in the Appendix II with the parameter ' ap ' taken from the above data Figures. Then we can numerically calculate the second member of eq. (3) and compare the result with the actual demographic data dx . The plots of the results are given hereunder for e.g. US 2017 with log scale and linear scales. In the first two figures we give the individual plots of the four components that build up the mortality data. In the next two figures the sum of the com-

ponents is given compared with dots corresponding to the demographic table sampling. The A, B and C zones are also addressed.

A similar exercise was carried out for the Italy 2019 and Japan 2019 data as shown in the following figures. The fourth (small) peak curve is almost invisible in the linear plot due to the low cases count. From the above examples, it can be seen that the reconstruction of the actual mortality data by means of the four mTC functions identified as solutions of the Fredholm equation is quite accurate in the age range from 40 years to 105 years, i.e. in most of zone C of interest. Zones A (infant mortality) and B (flat mortality probability) are highlighted and are as expected outside our study data interval. Similar figures are obtained for all the other cases from different years of mortality sampling and in the different considered countries.

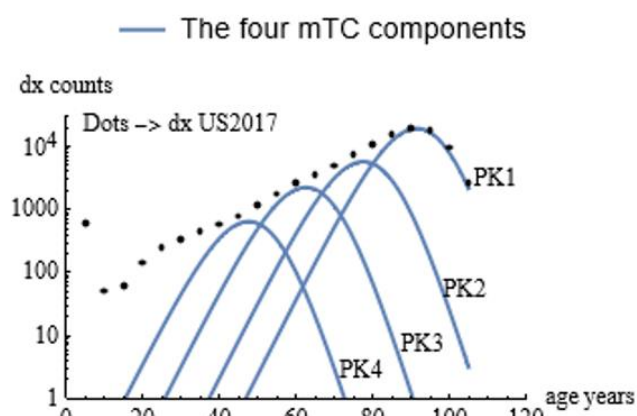


Figure 14. Peaks subsets for fem. US2017 table (Log scale).

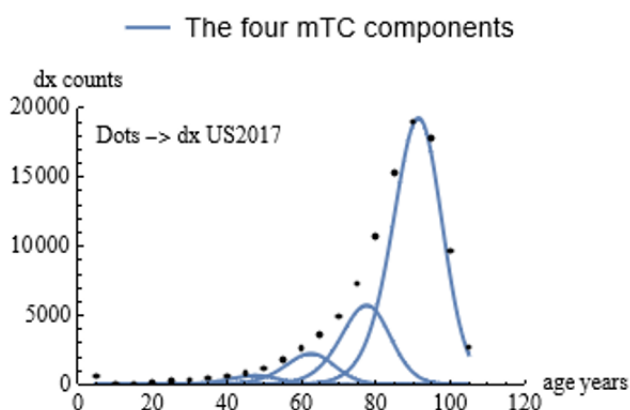


Figure 15. Peaks subsets for US2017 table year (linear).

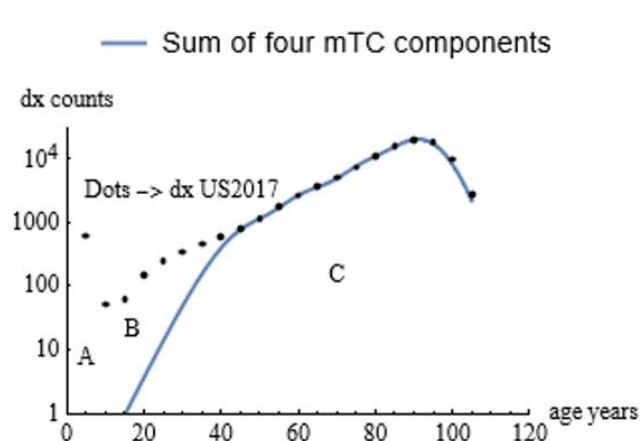


Figure 16. Plot of subsets sum for fem. US2017 (Log scale).

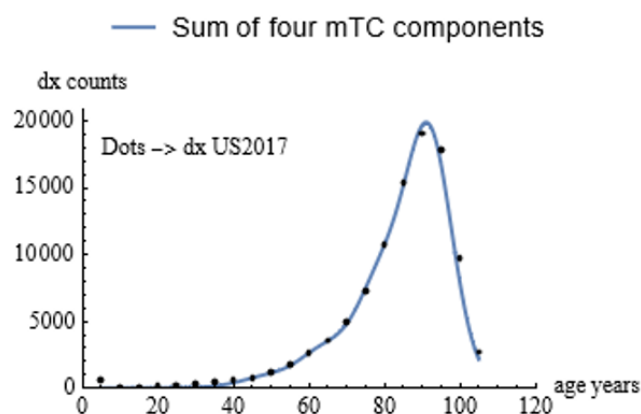


Figure 17. Plot of subsets sum for fem. US2017 (linear scale).

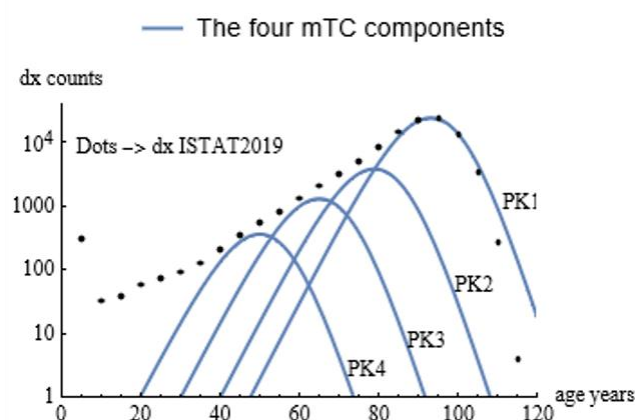


Figure 18. Peaks subsets for fem. Italy 2019 dx table (Log scale)

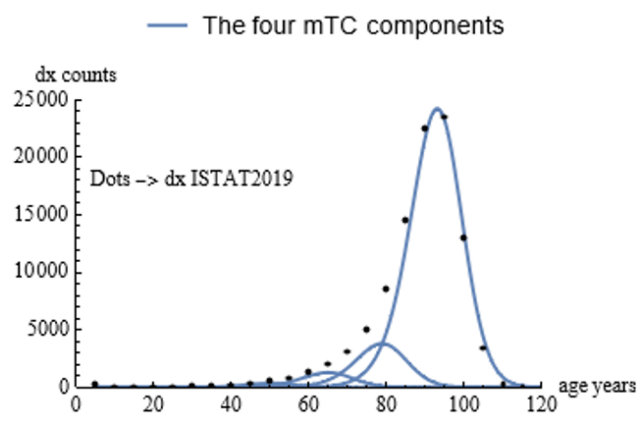


Figure 19. Peaks subsets for fem. Italy 2019 dx table (linear scale).

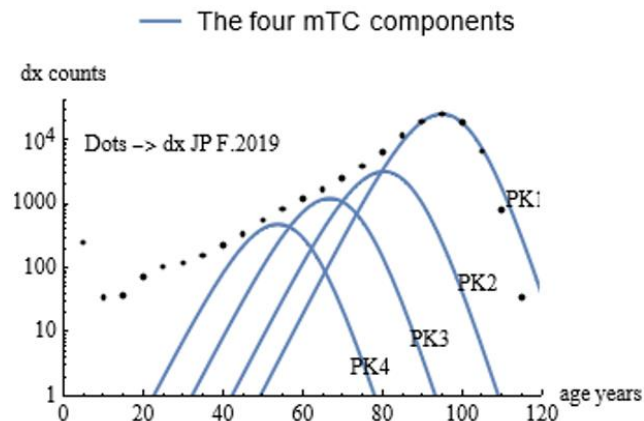


Figure 22. Peaks subsets for fem. Japan 2019 dx table (Log scale).

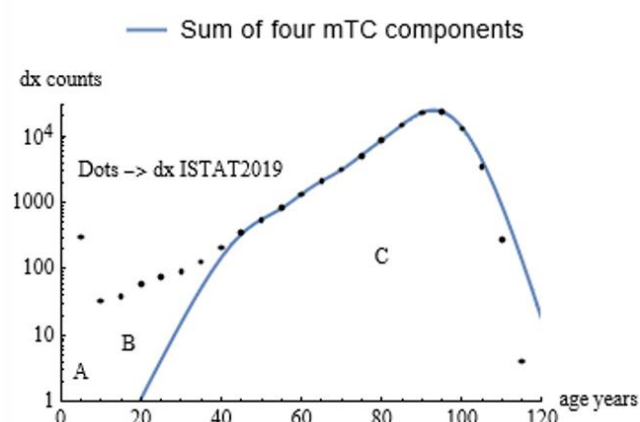


Figure 20. Plot of subsets sum for fem. Italy 2019 (Log scale).

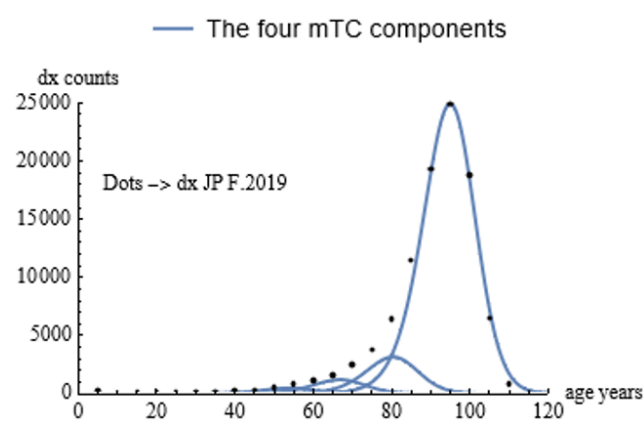


Figure 23. Peaks subsets for fem. Japan 2019 dx table (linear scale).

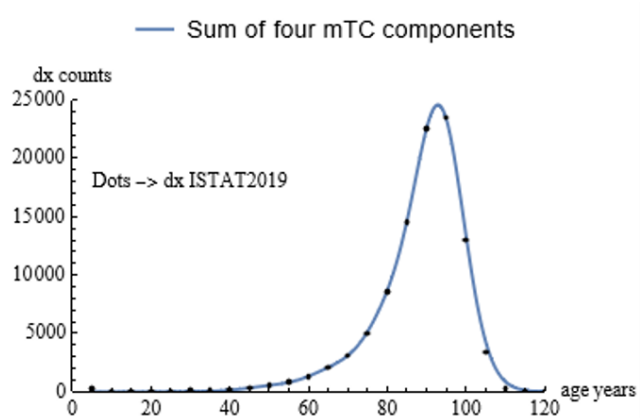


Figure 21. Plot of subsets sum for fem. Italy 2019 (linear scale).

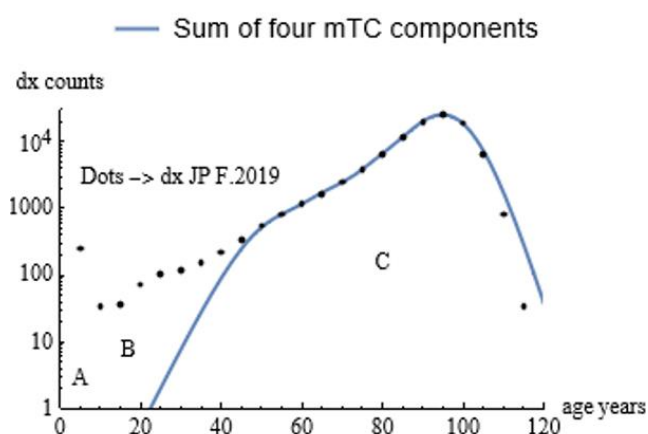


Figure 24. Plot of subsets sum for fem. Japan 2019 (Log scale).

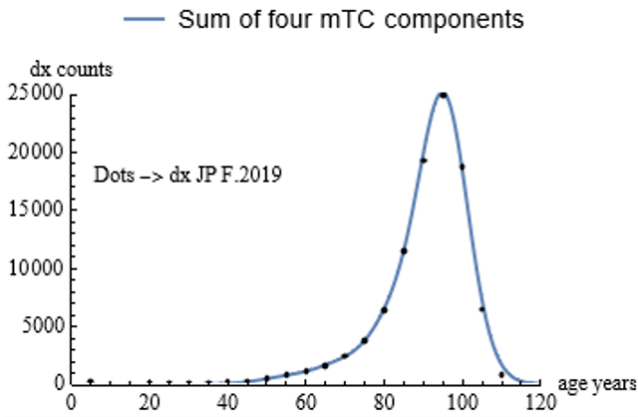


Figure 25. Plot of subsets sum for fem. Japan 2019 (linear scale).

From the above examples, it can be seen that the reconstruction of the actual mortality data by means of the four mTC functions identified as solutions of the Fredholm equation is quite accurate in the age range from 40 years to 105 years, i.e. in most of zone C of interest. Zones A (infant mortality) and B (flat mortality probability) are highlighted and are, as expected, outside our study data interval. Similar figures are obtained for all the other cases from different years of mortality sampling and in the different countries considered.

5. Reconstructing the qx Curve with the Solutions Found

In the Life Tables, in addition to the dx data, also the qx data are present. These data represent the ratio between the deaths -in a given age period- and the number of survived subjects entering at the beginning of this period. These qx's data depict therefore the probability to die in the age period considered. In Ref. [2] the author derived an explicit continuous time (age) function form for the qx data based on the mTC continuous function model. We recall here this form as defined:

$$qx(t) = \frac{mTC(t, TC)}{N(t, TC)}$$

where $N(t, TC)$ is given by:

$$N(t, TC) = TC - \int_0^t mTC(\tau, TC) d\tau + gg \ mTC(t, TC);$$

$gg=0.5;$

We see from above that, given the mTC function, also the

$qx(t)$ function can be derived by integration of the mTC.

This integration is indeed possible and therefore an analytic expression of the $N(t, TC)$ is made available in Appendix II. Now, coming back to the four mTC components that build-up the most part of the dx profile of the various demographic data presented in Section 4., one can wonder if these components -when mixed in the same proportions and TC's parameters considered for the dx study- can lead also to a reconstruction of the correlated mixed qx datum. We consider then the equation:

$$qx_{mix}(a) = \frac{\rho_1 m(a, TC1) + \rho_2 m(a, TC2) + \rho_3 m(a, TC3) + \rho_4 m(a, TC4)}{\rho_1 N(a, TC1) + \rho_2 N(a, TC2) + \rho_3 N(a, TC3) + \rho_4 N(a, TC4)}$$

where a is the age of the population and $\rho_i = w_i / TC_i$. The w_i and the TC_i parameters are the same used in eq. (3) and Section 4 for the reconstruction of the dx data. The Figure 26 shows the result of this exercise for the case of Italian females in year 2019 when compared with qx's Life Table data. A good fitting is obtained for ages over about 40 years.

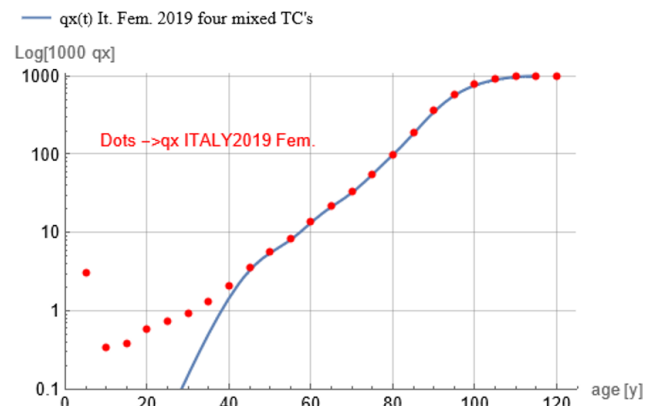


Figure 26. Plot of 1000 qxmix for Italy females 2019.

6. Discussion of the Results

Two main aspects emerge from the data collected:

- *Similarity*

Data in Figures 11, 12 and 13 show that the four peaks are almost equally spaced (between 11-15 years interval) for almost all cases/countries considered. This is also shown in Figure 27. These graphs plot the areas (weight) of the component's vs the ap parameter. It is seen that four clusters of points identify the four components of mortality. This feature - common for the US, Italy and Japan - leads to a similarity in peaks shape for the three countries.

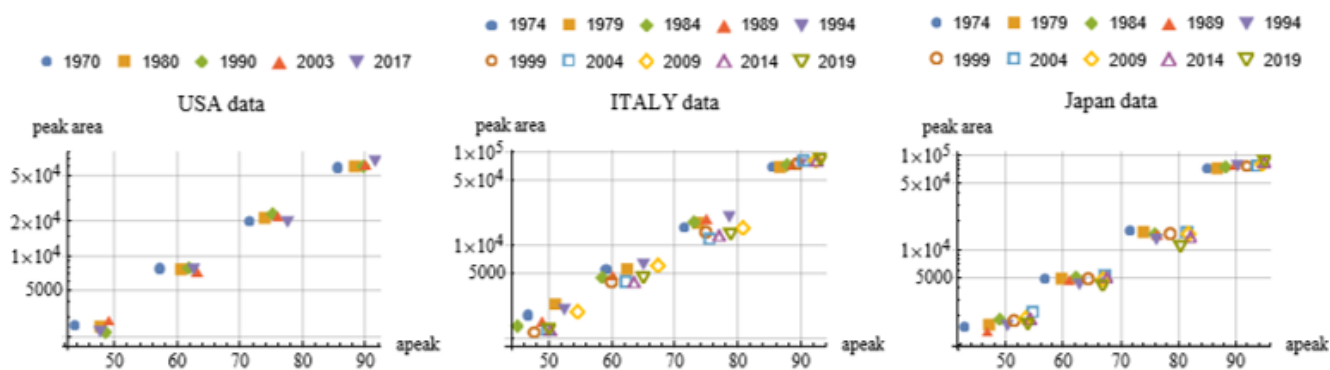


Figure 27. Plot of peaks areas vs peak ages & fem. Demographic Table year for the three countries.

In the Log-scale graphs of Figure 27, we see a steady shift of the positions of the component peaks age to the right from old to more recent years of demographic sampling, a fact consistent with an improvement in lifespan.

- Invariant structure

The following pie charts show the relative share of mortality cases (areas of the mTC peak's curves) between the com-

ponents for initial years of sampling and final years of sampling. We see that the four components pattern is permanent in the two extreme dates of the demographic sample years. The four components structure is always present also for the other sample years (omitted for brevity). The shrinking trend of the other components vs the main peak is also evident from old sample year to recent sample year.

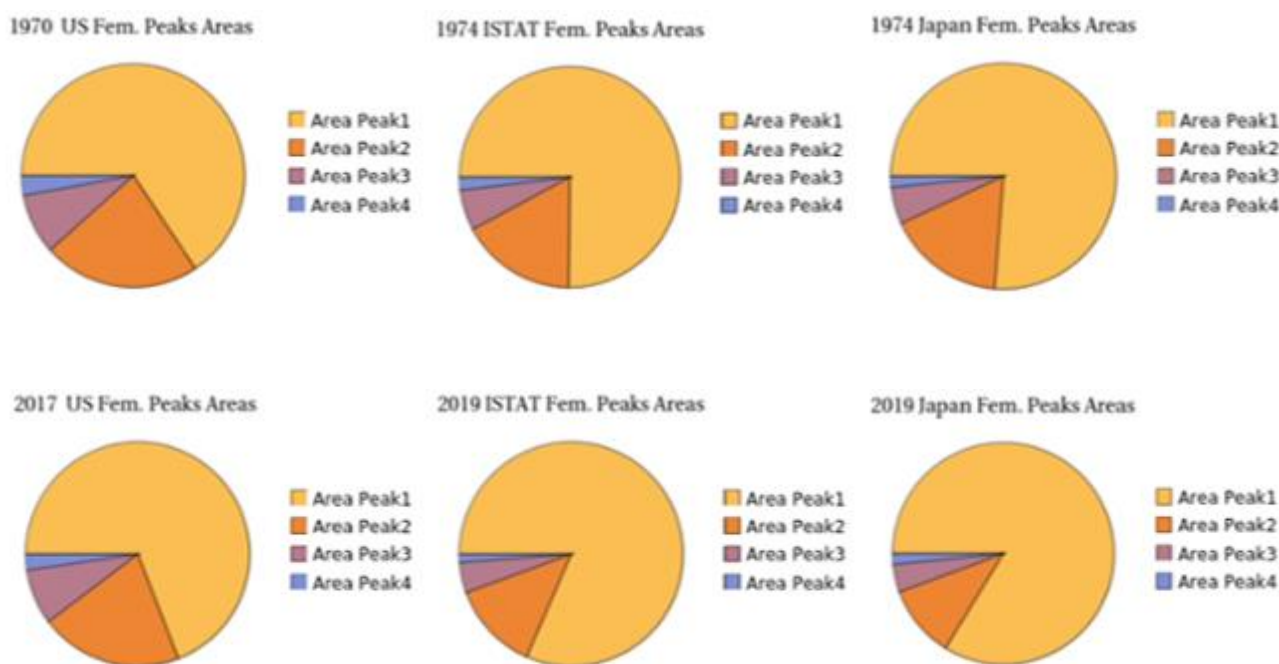


Figure 28. Share of mortality components for initial/final years of sampling and countries.

7. The Male Data

Up to this point, all the data considered concern the case of the female sex. A similar exercise was carried out for the male case (Figure 29). In this case, the data show a certain greater statistical dispersion (e.g. peak's FWHM), which leads to a relatively greater inaccuracy in the reconstruction of the

Fredholm equation. Despite this, however, the results for males also confirm the invariances found for females, i.e. the presence of four main components similarly spaced by age and with a similar structure of relative weights. This is true for the three countries considered and for all sampling years. In order not to burden the reader, the graphs and data for the male case are omitted here with exception of the following Figure 29. These graphs also reveal the well-known difference in longevity between males and females, the various

male data clusters being all on average backward in age compared to the female clusters seen in Figure 27.

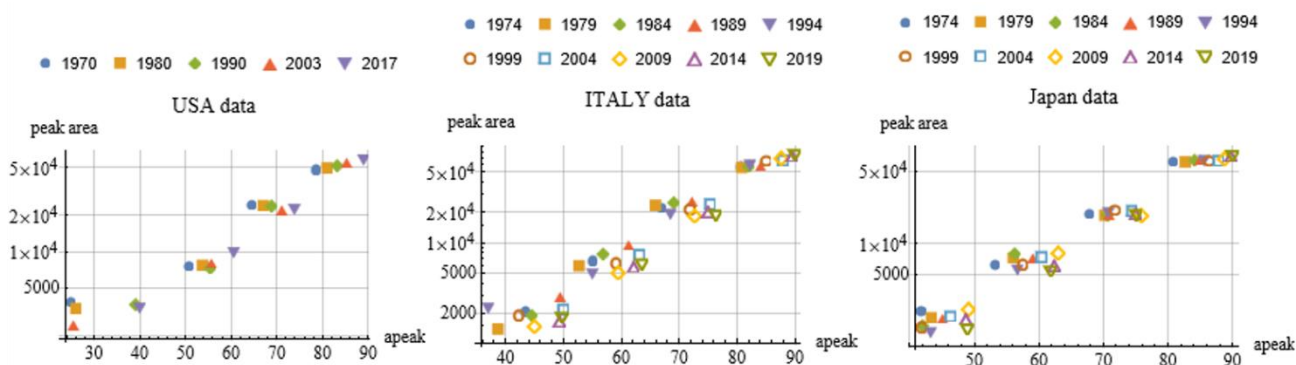


Figure 29. Plot of peaks areas vs peak ages & male dem. Table year for the three countries.

8. Summary and Conclusions

A number of facts emerge from the results outlined above:

- the large part of zone C (that of maximum mortality vs. age) can be represented by the linear combination of four main components that can be described analytically by mTC functions. This holds for both dx and qx Life Tables data.

- this feature is true for all countries and for all sampling years taken into account, so it appears to be an invariant characteristic of demographic mortality for these instances

- the four aforementioned components appear on average equally spaced in the age peaks (for females ~50, ~63, ~77, ~90 ages) and are always present for all sample years and in all three countries

- the three minor components decrease as a share of the total with increasing sample years and lifespan, which is consistent with Ref. [1] conjecture that demographic mortality at older ages will converge to a single mTC function (the big Peak 1) as lifespan increases.

At this point, our findings on the components of demographic mortality should be compared with the discussion in the literature on whether there are subcomponents of mortality in the aging process. Some studies highlight a non-linear growth in aging and the possible presence of population subgroups (Ref. [9-13]). Other studies consider mortality differences on a microscopic basis, i.e., at the cellular level or in subsystems capable of self-repair (Ref. [14-16]), or explain mortality data with a mixture of models (Ref. [17, 18]).

In particular, a correlation with a recent study using a multi-omics approach must be highlighted: in a paper published in August 2024 in the journal Nature Aging (Ref. [19]), researchers highlighted a non-linear disease risk that accumulates with the biological ageing process. "The analysis revealed consistent nonlinear patterns in molecular markers of aging, with substantial dysregulation occurring at two major periods occurring at approximately 44 years and 60 years of chronological age" (cit. from Ref. [19]). This study involved a

sample of US persons aged 75 years and under. In our present study, we showed the possible existence of discrete components of demographic mortality with age clusters. These two approaches - conducted in completely different ways - show a correlation of results.

In conclusion, the issue of mortality in old age, i.e., the issue of aging, is subject to multiple hypotheses about its possible causes. Our study proposes the following conclusions: there are six overall components of demographic mortality, namely: infant mortality, the flat area in middle age and four components in higher ages, the latter being almost equidistant in age intervals and distributed with exponential relative weights and described by mTC functions. These six components change in their relative weights as lifespan changes. In particular, as lifespan increases, all components except the main one decrease but do not disappear altogether. In the long run, it can be foreseen that the main mortality peak will converge towards a single prevailing mTC function.

Abbreviations

FWHM Full Width at Half Maximum
TC Total Cases

Author Contributions

Giuseppe Alberti it is the sole author. The author read and approved the final manuscript.

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Data Availability Statement

The data supporting the outcome of this research work has

been referred in this manuscript.

Conflicts of Interest

The author declares no conflicts of interest.

Appendix

Appendix I: Mortality Data

The following numerical data are derived from Ref. [5-8]

Age interv. [y]	1970	1980	1990	2003	2017
0-4	2045	1334	994	718	607
5-9	171	122	95	65	52
10-14	148	112	97	74	61
15-19	305	248	217	194	146
20-24	365	301	272	246	251
25-29	422	332	312	273	340
30-34	578	411	417	358	460
35-39	869	609	563	562	590
40-44	1304	961	811	869	796
45-49	1941	1510	1290	1267	1154
50-54	2786	2300	2051	1808	1775
55-59	3927	3346	3139	2694	2606
60-64	5441	4894	4667	4159	3566
65-69	7743	6800	6553	6001	4959
70-74	10 848	9534	9235	8633	7293
75-79	14 662	12 814	12 301	12 018	10 753
80-84	16 907	16 600	15 871	15 870	15 327
85-89	15 378	17 194	17 449	17 803	19 042
90-94	9595	12 716	14 320	15 027	17 839
95-99	3611	5935	7095	8408	9686
>100	954	1927	2251	2952	2697
Total	100 000	100 000	100 000	99 999	100 000

Figure A1. USA female mortality from 1970 to 2017 years.

Age interv. [y]	1974	1979	1984	1989	1994	1999	2004	2009	2014	2019
0-4	2412	1742	1206	951	791	590	408	350	323	305
5-9	144	113	98	77	81	59	43	42	34	33
10-14	125	114	90	81	84	67	48	44	40	38
15-19	183	154	139	125	136	123	96	86	65	58
20-24	224	176	153	158	150	147	104	98	80	75
25-29	251	215	179	182	220	161	122	106	97	92
30-34	369	284	258	242	277	226	160	144	133	128
35-39	499	462	380	379	361	316	256	222	224	208
40-44	798	684	662	570	530	488	402	376	352	349
45-49	1271	1131	1011	981	829	795	668	620	581	550
50-54	1865	1778	1576	1429	1316	1178	1065	1018	906	828
55-59	3033	2583	2437	2172	1928	1783	1600	1513	1395	1322
60-64	4331	4345	3770	3408	3085	2697	2453	2327	2160	2063
65-69	6860	6461	6351	5375	4913	4439	3745	3580	3299	3124
70-74	10 825	10 375	9546	9249	7885	7280	6167	5722	5270	5000
75-79	16 790	15 818	14 897	13 451	13 604	11 735	10 410	9881	8690	8573
80-84	20 142	19 922	20 321	19 358	18 257	19 401	16 351	16 591	15 252	14 569
85-89	17 798	18 907	20 624	20 657	21 659	21 525	23 489	22 727	22 398	22 507
90-94	9557	11 251	12 428	14 844	16 353	17 830	19 820	22 284	22 334	23 485
95-99	2332	3168	3522	5492	6470	7696	9924	9947	13 000	13 014
100-104	187	310	345	785	1021	1380	2480	2182	3150	3404
105-109	4	8	9	33	49	79	187	139	215	271
110-114	0	0	0	0	1	1	3	2	3	4
115-119	0	0	0	0	0	0	0	0	0	0
Total	100 000	100 001	100 002	99 999	100 000	99 996	100 001	100 001	100 001	100 000

Figure A2. Italy female mortality from 1974 to 2019 years.

Age interv. [y]	1974	1979	1984	1989	1994	1999	2004	2009	2014	2019
0-4	1240	909	715	571	528	425	349	292	272	248
5-9	139	102	82	75	68	56	39	44	35	34
10-14	99	74	61	60	49	51	38	35	33	36
15-19	181	136	121	118	98	105	95	80	62	72
20-24	281	201	172	150	142	143	135	141	113	104
25-29	324	243	214	181	158	165	156	165	141	117
30-34	413	317	276	230	220	224	202	195	181	155
35-39	565	454	398	353	309	296	305	286	250	221
40-44	847	681	616	535	483	469	427	421	378	337
45-49	1260	1067	932	808	761	746	674	635	588	544
50-54	1916	1570	1381	1238	1147	1115	1042	927	883	815
55-59	2845	2338	2016	1836	1638	1593	1465	1298	1264	1168
60-64	4443	3588	3117	2696	2526	2317	2021	1830	1795	1633
65-69	7305	5816	5099	4350	3902	3611	3043	2720	2620	2466
70-74	11 709	9956	8434	7180	6438	5740	4937	4340	4070	3802
75-79	17 533	15 654	14 101	12 093	10 916	9819	8180	7485	6946	6424
80-84	20 999	20 751	20 419	19 258	17 588	15 892	13 850	12 877	12 402	11 477
85-89	17 154	19 784	21 349	22 484	22 493	21 669	20 371	20 031	19 936	19 303
90-94	8494	11 849	14 433	17 016	19 152	20 740	22 100	23 336	24 319	24 927
95-99	2033	3900	5165	7260	9188	11 473	14 842	16 393	17 195	18 767
100-104	213	575	842	1395	2016	3020	5000	5663	5764	6505
105-109	9	36	56	107	174	316	691	767	720	809
110-114	0	1	2	3	6	13	37	38	32	34
115-119	0	0	0	0	0	0	0	0	0	0
Total	100 002	100 002	100 001	99 997	100 000	99 998	99 999	99 999	99 999	99 998

Figure A3. Japan female mortality from 1974 to 2019 years.

Appendix II: Mathematical Formulas

Below we provide a summary of the main relationships that characterize the theoretical mTC function identified in the work of Ref. [1] and Ref. [2]. Log[n] means the natural logarithm of the number n. The mTC is presented in the specific conventional case where the species 'u' constant (see Ref. [2]) is equal to five and the demographic Life Tables dx and qx data are given at 5 years intervals. Then we have:

-The general mTC function of the variable a (age) and a parameter TC (referring to Total Cases) proportional to the area underlying the function curve:

$$mTC(a, TC) = -4^{a/5}(-1 + TC - \text{Log}[2])^{1 + \frac{1}{1 - \text{Log}[2]}}(-2 + \text{Log}[2])\text{Log}[2](-2 + 2^{a/5} + TC - 2^{a/5}\text{Log}[2])^{\frac{3 - \text{Log}[4]}{-1 + \text{Log}[2]}}$$

- The normalized function $mTCn(a, TC)$ where the area under the curve is constant and independent from TC:

$$\llbracket mTCn(a, TC) = (mTC(a, TC))/TC$$

- The normalized $mTCnp(a, ap)$ function with parameter ap equal to the year at which peak of the function is reached:

$$mTCnp(a, ap) = -\frac{1}{4 + 2^{ap/5}} 2^{a/5} \left(1 + 2^{-1 + \frac{ap}{5}} - \text{Log}[2] \right)^{\frac{1}{1 - \text{Log}[2]}} (-2 + \text{Log}[2])\text{Log}[2] \left(2^{a/5} + 2^{-1 + \frac{ap}{5}} - 2^{a/5}\text{Log}[2] \right)^{\frac{3 - \text{Log}[4]}{-1 + \text{Log}[2]}} (2 + 2^{ap/5} - \text{Log}[4])$$

- Some mTC additional features are:

$$\int_0^\infty m(a, TC) da = 5 TC; \int_0^\infty m(a, TC) 2^{-a/5} da = 5;$$

- The relations between a_{peak} and TC:

$$a_{peak} = 5 \frac{\text{Log}[2(-2+TC)]}{\text{Log}[2]};$$

$$TC = 2 + 2^{-1+\frac{a_{peak}}{5}};$$

-The curve max height value (peak value) with vs TC parameter:

$$\begin{aligned} mmax(TC) = & -4 \frac{\text{Log}\left[\frac{(-2+TC)\text{Log}[4]}{\text{Log}[2]}\right]}{\text{Log}[2]} (-1 + TC - \text{Log}[2])^{1+\frac{1}{1-\text{Log}[2]}} (-2 + \\ & \text{Log}[2])\text{Log}[2] \left(-(((-2 + TC)(-3 + \text{Log}[4]))^{\frac{3-\text{Log}[4]}{-1+\text{Log}[2]}}) \right); \end{aligned}$$

-The $N(a, TC)$ explicit function to be used for the continuous calculation of qxmix:

$$\begin{aligned} N(a, TC) = & TC - 4^r gg(-2+k)k(-1-k+TC)^{1+\frac{1}{1-k}}(-2+2^r-2^rk+ \\ & TC)^{\frac{3-\text{Log}[4]}{-1+k}} + (-1-k+TC)^{1+\frac{1}{1-k}} \left((k-TC)(-1-k+TC)^{-1+\frac{1}{-1+k}} + \right. \\ & \left. (-2+2^r-2^rk+TC)^{-1+\frac{1}{-1+k}}(-2+2^{1+r}-2^rk+TC) \right); r = a/5; k = \\ & \text{Log}[2]; gg = 0.5 \end{aligned}$$

References

- [1] G. Alberti "A conjecture on demographic mortality at high ages." <https://doi.org/10.48550/arXiv.2307.10279>
- [2] G. Alberti "Fermi statistics method applied to model macroscopic demographic data" <https://doi.org/10.48550/arXiv.2205.12989>
- [3] S. Twomey "On the numerical solution of Fredholm integral equations of the first kind by the inversion of the linear system produced by quadrature." J. ACM 10 (1963), 79-101.
- [4] Fredholm Integral Equations, web site: Available from: <https://inteq.readthedocs.io/en/latest/fredholm/index.html> [Accessed 13 November 2025]
- [5] L. A. Gavrilov and N. S. Gavrilova, "Mortality Measurement at Advanced Ages: a Study of the Social Security Administration Death Master File", North American Actuarial Journal. 15(3): 432-447. <https://doi.org/10.1080/10920277.2011.10597629>
- [6] Elizabeth Arias and Jiaquan Xu, "United States Life Tables, 2017", NVSS, Volume 68, Number 7, June 24, 2019.
- [7] Istituto Italiano di Statistica, "ISTAT Data", Available from: <https://esploradati.istat.it/databrowser/#/en> [Accessed 13 November 2025]
- [8] National Institute of Population and Social Security, "The Japanese Mortality Database", Available from: <https://www.ipss.go.jp/p-toukei/JMD/index-en.asp> [Accessed 13 November 2025]
- [9] Jacques Demongeot, Pierre Magal, 'Population dynamics model for aging', <http://dx.doi.org/10.3934/mbe.2023870>
- [10] F. Zane, C. MacMurray, C. Guillermain, C. Cansell, N. Todd and M. Rera, 'Ageing as two-phases process: a theoretical framework' <https://doi.org/10.3389/fragi.2024.1378351>
- [11] J. D. Zazueta-Borboa, J. M. Aburto, I. Permanyer, V. Zarulli & F. Janssen, 'Contributions of age groups and causes of death to the sex gap in lifespan variation in Europe', <https://doi.org/10.1080/00324728.2023.2222723>
- [12] A. Golubev, 'A previously unrecognized peculiarity of late-life human mortality kinetics?', <https://doi.org/10.21203/rs.3.rs-3316407/v1>
- [13] M. Tuğrul and U. K. Steiner, 'Demographic consequences of damage dynamics in single-cell aging', <https://doi.org/10.1103/PhysRevResearch.7.013327>
- [14] N. Shimoyama, M. Hosonuma, 'Application of the first exit time stochastic model with self-repair mechanism to human mortality rates', <https://doi.org/10.1007/s00285-024-02150-4>
- [15] P. Y. Nielsen, M. K. Jensen, N. Mitarai, S. Bhatt, 'A Systems Level Explanation for Gompertzian Mortality Patterns is provided by the "Multiple and Inter-dependent Component Cause Model"', <https://doi.org/10.1101/2023.06.20.545709>
- [16] J. Shi, Y. Shi, P. Wang and D. Zhu, 'Multi-population mortality modelling: a Bayesian hierarchical approach', <https://doi.org/10.1017/asb.2023.29>
- [17] S. C. Patricio, F. Castellares, B. Queiroz, 'Mortality modeling at old-age: an mixture model approach', <https://doi.org/10.48550/arXiv.2301.01693>
- [18] S. C. Patricio, T. I. Missov, 'Makeham Mortality Models as Mixtures', <https://doi.org/10.48550/arXiv.2304.08920>
- [19] X. Shen, C. Wang, X. Zhou, W. Zhou, D. Hornburg, S. Wu & M. P. Snyder "Nonlinear dynamics of multi-omics profiles during human aging", Nature Aging, <http://dx.doi.org/10.1038/s43587-024-00692-2>