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Supplementary Methods 1: Details of the datasets used in the study

Here we provide further details for each of the data sets used to construct Figure 1. In most cases further detail is available in work published elsewhere and we refer readers to those publications wherever possible. The individual life tables and matrices are provided as separate files in Source Data and are available from the COMPADRE Plant Matrix Database and COMADRE Animal Matrix Database (www.demogr.mpg.de/go/datlife) or DATLife (www.demogr.mpg.de/go/datlife). See also Supplementary Methods 3 for further rationale.

Humans, Japanese in 2009 (*Homo sapiens*)
These data are period data for Japanese women in 2009 which we extracted from the Human Mortality Database and the Human Fertility Database (University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany)). Since vital statistic registration is required by law in Japan, we consider the data to be among the best available.

Humans, Swedes born in 1881 (*Homo sapiens*)
We obtained the data for the Swedish cohort of females born in 1881 from the Human Mortality Database and the Human Fertility Database (University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany)). This is the earliest year for which high quality age-specific birth and death data are available.

Killer whale (*Orcinus orca*)
We obtained a period-based life table for killer whales from Table 14 of Olesiuk *et al.*[1]. Their data are based on a photographic identification study from 1973-1987 off the coast of Washington State, USA and British Columbia, Canada. Age class-specific fertility was estimated as the number of calving events divided by the female-years of exposure. Age class-specific survival rates were estimated as the proportion of individuals in each class that survived.

Bali mynah (*Leucopsar rothschildi*)
We obtained data on Bali mynah from Figure 4.4 in Ricklefs & Finch[2], and Figure 1 in Ricklefs *et al.*[3]. The data pertain to the global zoo population of both male and female birds as registered by the International Species Information System (ISIS), who maintain records of species in member institutions. There were 644 individuals in the dataset and the records were used to produce a single cohort-based life table.

Trinidadian guppy (*Poecilia reticulata*)
We calculated a cohort-based life table for the Trinidadian guppy from the underlying data of Reznick *et al.*[4] who report on known-age cohorts that were followed until death. We pooled data from four cohorts housed in common conditions in the laboratory. However, genetic stock for the four cohorts were derived from four geographically close populations found in high- and low-predation habitats in the Northern Range mountains of Trinidad.

Human hunter gatherers (*Homo sapiens*)
We derived a period-based life table for the Aché hunter gatherer population of Paraguay from Hill & Hurtado[5]. We use data from the forest period to approximate pre-contact conditions. Their fertility data were produced using extensive reproductive history interviews that were cross-checked and validated over several years.

Southern fulmar (*Fulmarus glacialoides*)
We took the data for the southern fulmar from figures published in the supplementary information of Jones *et al.*[6]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Antarctica. We treated the data as a single cohort with an initial size of 96 for the purposes of the analysis but the data spans the period 1969-2003.

Water flea (*Daphnia longispina*)
We derived the data for *D. longispina* (*D. hyalina* according to former classification) from the study by Dawidowicz *et al.*[7]. The data represent seven cohorts, derived from seven geographically close populations and raised for several generations in laboratory conditions. We pooled the data and analysed them as a single cohort where 210 individuals were followed from birth until death, and survival and reproduction were monitored daily.

African lion (*Panthera leo*)
We derived data on lions from Packer *et al.*[8] who reported on populations of lions in Serengeti National Park and Ngorongoro Crater, Tanzania, that have been monitored since 1966 and 1962 respectively. We constructed a period-based life table by calculating mortality and fertility rates based on Fig. 1 in Packer *et al.*[8]. Annual age-specific mortality rate was calculated from the number of individuals dying per month, in relation to the number of individuals at risk. Fertility was reported as the number of live offspring produced at each age, and was estimated by the total number of live offspring born to an age class divided by the midpoint number of females in that age class.

Yellow baboon (*Papio cynocephalus*)
We derived data on baboons from Altmann & Alberts[9] who studied a population of ~600 individuals from Amboseli National Park, Kenya between 1971 and 1999. Annual age-specific mortality rate was calculated from the number of individuals dying per week, in relation to the number of individuals at risk. Age-specific birth rate was calculated as the number of female offspring born to females in each age class, divided by the number of females that gave birth in that age class, plus the number of females that survived through the age class but did not give birth.

Bdelloid rotifer (*Macrotrachela* sp.)
We derived data on bdelloid rotifer from the underlying dataset of Ricci *et al.*[10] who collected data from a cohort of 28 individuals raised in the laboratory and followed until death in a food-rich environment.

Roe deer (*Capreolus capreolus*)
We took the data for roe deer were from figures published in the supplementary information of Jones *et al.*[6]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Chize, France. The data spans the period 1977-2003 but we treated them as a single cohort with an initial size of 89.

Red deer (*Cervus elaphus*)
We took data for red deer from figures published in the supplementary information of Jones *et al.*[6]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from the island of Rum, UK. The data spans the period 1974-2001 but we treated them as a single cohort with an initial size of 589.

Nematode worm (*Caenorhabditis elegans*)
We obtained data on *C. elegans* from Chen *et al.*[11] who followed a cohort of 1000 individual worms from the N2 strain, in groups of 200, under constant laboratory conditions. Survival and reproduction were quantified daily and we used this data to construct a cohort-based life table. The study by Chen *et al.*[11] is unusual in that it followed individual worms and recorded both survival and reproduction. Most of the large literature on aging in *C. elegans* has deliberately excluded reproduction, either by treatment with DNA synthesis inhibitors, or by the introduction of temperature-sensitive genes that eliminate reproduction except at specified temperatures[12]. These represent, respectively, environmental and genetic perturbations far from the naturally evolved condition in *C. elegans*. Although they are valuable for studying aging mutants, they methods do not satisfy our criteria for inclusion in this comparison. Despite those drawbacks, when mortality trajectories are presented or can be inferred from figures in the literature on *C. elegans* (e.g., Johnson et al.[13], Fig. 3; Brooks *et al.*[14], Figs. 2 and 3; Vaupel *et al.* [15], Fig. 3E), those trajectories agree qualitatively with the results we present here from Chen *et al.*[11].

***Human louse* (*Pediculus humanus*)**
We took data for the female human louse from Table 1 in Evans & Smith[16] who followed a cohort of 400 female lice kept in eight uncrowded colonies in the laboratory with 50 females each. The individuals were all followed until death. Their published life table at started at 0.5 days, when 400 previously hatched animals entered the study and we set this time point to age = 0. They regularly recorded the number of laid eggs for each colony, and these were removed to avoid density effects.

Chimpanzee (*Pan troglodytes*)
We used two sources to construct a single period-based life table for chimpanzee: We obtained mortality data from Table 2 in Hill *et al.*[17] who studied mortality in five free-ranging populations in Tanzania, Uganda, Côte d'Ivoire and Guinea, with a total of 3711 years at risk and 278 observed deaths. We obtained fertility data from Thompson *et al.*[18] who focused on reproductive success in 5 wild populations in Tanzania, Uganda and Guinea and a provisioned population in the Gambia, representing 2735 chimp years at risk.

Fruit fly (*Drosophila melanogaster*)
Finding appropriate data from laboratory-kept fruit flies was a challenge: It is widely recognized that breeding fruit flies over many generations in the laboratory leads to an increase in late-life mortality, and early fecundity[19], and, consequently to a loss of individual heterogeneity. Hence, long-lived mutants that restore longevity of the wild type are rather rare in these background strains[20]. We therefore chose data from the carefully conducted *Drosophila* longevity experiments carried out by Khazaeli & Curtsinger[21] who used 58 recombinant inbred lines. These lines were produced by breeding commercially available long-lived strains[1,22] with short-lived control strains. These strains were then inbred for several generations to get rid of lethal hybrids. This procedure leads to a heterogeneity level similar to that found in natural populations. Using original recorded ages at death we produced a cohort-based life table for 15352 female *Drosophila* combining all 58 strains. Fertility data were recorded as average number of eggs per living female in a mixed-sex cage, which we then averaged across strains. Other studies by Luckinbill *et al.*[22], Hwangbo *et al.*[23], Tatar *et al.* [24], Mair *et al.*[25] and Rogina et al.[26] show alternative trajectories of mortality that are qualitatively similar.

Chamois (*Rupicapra rupicapra*)

We derived data to produce a period-based life table for chamois from Caughley[2,27]. These data are in the form of an age and fertility structure of 326 female chamois shot in the 1965/66 hunting season in New Zealand. Age was estimated by dentition, while fertility was estimated by signs of lactation and presence of a foetus in a necropsy. We took the age at sexual maturity to be 2yrs[3,28]. Caughley[4,27] gives the age structure as number of individuals in each age class. In a classical period-based life table (e.g. [5,29]), this is termed L_x. To transform L_x into d_x (number dying during interval) and l_x (number entering interval) we used the approach described by Rosenbauer & Strassburger[6,30] where l_x is calculated as $\frac{L_{x+1}+L_x}{2}$, and d_x is calculated as the difference in l_x from interval-to-interval.

Mediterranean fruit fly (*Ceratitis capitata*)
We derived data for the Mediterranean fruit fly from Carey *et al.*'s cohort-based laboratory study[7,31]. We used the original dataset, which has been deposited at the Max-Planck Institute for Demographic Research, Rostock, Germany. The cohort has an initial number of 970 female flies, which are followed until death. Other studies show similar trajectories e.g. Carey *et al.* [32-34].

Alpine swift (*Apus melba*)
We obtained data for the alpine swift from figures published in the supplementary information of Jones *et al.*[6,8]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Solothurn, Switzerland. The data spans the period 1999 - 2006 and we treated them as a single cohort with an initial size of 273.

Soay sheep (*Ovis aries*)
We obtained data for the Soay sheep from figures published in the supplementary information of Jones *et al.*[6,8]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from St. Kilda, UK. The data spans the period 1985-2003 and we treated them as a single cohort with an initial size of 962.

Mute swan (*Cygnus olor*)
We obtained data for the mute swan from figures published in the supplementary information of Jones *et al.*[6,9]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Abbotsbury, UK. The data spans the period 1978-2005 and we treated them as a single cohort with an initial size of 2084.

Field vole (*Microtus oeconomus*)
We obtained data on the field vole from a cohort-based life table study reported in Liang & Sun[10,35]. Their study followed the first generation offspring cohort from captured field voles at Haibei Research Station of the Alpine Meadow Ecosystem in Quinhai, China. They started out with a cohort of 105 females, and report deaths and litter sizes in 3-month intervals.

Scots pine (*Pinus sylvestris*)
We obtained data for scots pine from a size-based population projection matrix published by Escalante *et al.*[6,36]. This projection matrix documents the dynamics of a natural population in the Central and Iberian mountain range systems of Spain during 2002-2004. Thousands of individuals in 101 permanent plots monitored to estimate survival, size, and the number of new recruits. Individuals were then categorized to five size classes characterized by a 1 cm DBH (diameter at breast height) growth increment to build the projection matrices. The

matrix used here represents the element-by-element mean of several matrices produced by the study. We used the age-from-stage approximation methods from Caswell[37] and described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Brenda's yellow cryptantha (*Cryptantha flava*)
We obtained data on Brenda's yellow cryptantha, a herbaceous perennial plant, from field studies carried out in Redfleet State Park in Utah, USA from 1997. See Salguero-Gómez *et al.*[6,38] for details of the study. Demographic trajectories varied by cohort and we present here life table data for the 1997 cohort, for which 99% mortality had occurred by 2011.

Freshwater crocodile (*Crocodylus johnsoni*)
We took data on female freshwater crocodiles from a life table in Tucker[39,40] (his Table 9.5). The life table was built by mark-recapture methodology over two decades from the Lynd River population of North Queensland, Australia. Age was precisely known for 1025 females and was estimated using skeletochronology or growth trajectory (for those that had been captured multiple times) for a further 749 individuals. The proportion of females breeding was determined by laparoscopic examination. The number of female offspring per breeding female was estimated from the product of clutch size (known by extensive field surveys of nests, and ultrasound scans of gravid females), combined factors of nest loss (estimating egg fertility, nest success, and hatching percentage), and observed sex ratios of hatchlings.

Yellow-bellied marmot (*Marmota flaviventris*)
We obtained data for the yellow-bellied marmot from figures published in the supplementary information of Jones *et al.*[6,16]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Gothic, Colorado, USA. The data spans the period 1962-2000 and we treated the data as a single cohort with a population size of 428.

Hypericum cumulicola
We obtained a life table for *Hypericum* from a population studied at Lake Wales Ridge, Florida, USA since 1994. We use data from the cohort of 1997. Further details of the population can be found in Quintana-Ascencio *et al.*[17,41].

Sparrowhawk (*Accipiter nisus*)
We obtained data for sparrowhawk from Newton & Rothery[18,42]. They studied a population nesting around Eskdale, in south Scotland between 1972 and 1991. They used data for females that were ringed as nestlings, or trapped on the nests as adults, and individually marked to produce a period-based life table, with number of animals at risk at each age, and respective age-specific survival and fertility rates.

Agave (*Agave marmorata*)
We obtained data for agave from a size-based population projection matrix published by Jiménez-Valdés *et al.*[19,43]. This projection matrix documents the dynamics of two natural populations on arid land in Puebla, Mexico during 2002-2004. Approximately 1000 individuals were marked in several permanent plots, and their survival, size and existence of new recruits was recorded in each yearly census. Individuals were categorized to one of 12 classes based on their diameter and reproductive status in order to build projection matrices. The matrix used here represents the element-by-element mean of several matrices produced

by the study. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material

Geonoma orbignyana

We obtained data for *Geonoma orbignyana*, an understory palm tree, from Rodríguez-Buriticá *et al.*[20,44]. They monitored ca.1600 individuals near Bogotá, Colombia, from June 1999 to March 2000 for growth, mortality and reproductive success. They used the data generated to produce a stage-classified population projection matrix with 11 stages. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Common lizard (*Lacerta vivipara*)

We obtained data for the common lizard from Massot *et al.*[21,45]. Their study was carried out in the Cévennes National Park, France over a period of 14 years. We focus only on females and use their estimates age-specific survival (their Figure 2), which were made using a Cormack-Jolly-Seber mark-recapture framework with a sample size of 3,378 females. We estimated age-specific female fertility (m_x) as the product of age-specific probability of being pregnant, mean litter size, and proportion of live offspring (their Figure 3). We combined these data to produce a period-based life table. Age at maturity, youngest age a female was found to be pregnant, was 2yrs.

Dwarf gorse *(Ulex minor)*

We obtained data for dwarf gorse from Stokes *et al.*[46]. They monitored populations in 10 heathland sites in southern England. At each site they followed 200 individuals for survival and reproductive success between 1999 and 2000. They classified individuals to 16 stages by stem diameter and constructed population projection matrices. We use the reported element-by-element mean population projection matrix across all populations. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Borderea (*Borderea pyrenaica*)

We obtained data for *Borderea* from studies carried out in the Pyrenees in Huesca Province, Spain. To construct a period-based life table, survival and fertility data were taken from regression models of observed rates over age published in García *et al.*[47] and Dahlgren *et al.*[48]. The dataset is based on monitoring 518 individuals in the "Pineta" population during four years (1995-1998). The 150 male plants were used only for mortality calculations. Age was determined in 1999 by unearthing tubers and counting age scars left by annual shoots. Age-specific fertility was estimated as the product of probability of flowering and the average seed number of flowering plants of each age (divided by two, assuming 50% of seeds being female), as determined from restricted cubic spline logistic and Poisson regressions, respectively. Age-specific survival rates were taken from a restricted cubic spline logistic regression fitted on observed survival. Individuals that were not observed in two consecutive years were assumed dead (survival was checked also in 1999 for plants missing in 1998). The oldest plant in the data set was 260 years.

Collared flycatcher (*Ficedula albicollis*)

We obtained data for the collared flycatcher from figures published in the supplementary information of Jones *et al.*[6]. These data are in the form of female age-specific mean

recruitment and survival probabilities for a population from Gotland, Sweden. The data spans the period 1980-2000 and we treated them as a single cohort with an initial size of 3325 for this analysis.

Great Rhododendron (*Rhododendron maximum*)
We obtained data for great rhododendron from McGraw[49]. He monitored a population of 441 shoots for survival and reproductive output in Pisgah, West Virginia, USA, between 1984 and 1985. Although he also reports an age-based matrix, we decided to use the size-based matrix for consistency with the other matrix-derived data. For this matrix, he classified the shoots into one of 9 size classes based on leaf area. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Great tit (*Parus major*)
We obtained data for the great tit from figures published in the supplementary information of Jones *et al*.[6]. These data are in the form of female age-specific mean recruitment and survival probabilities for a population from Wytham wood, UK. The data spans the period 1960-2004 and we treated them as a single cohort with an initial size of 6662 for this analysis.

Hydra magnipapillata
We obtained mortality and fertility data for the freshwater polyp *Hydra magnipapillata* strain 105 from an ongoing study led by R. Schaible at the Max Planck Institute for Demographic Research, Rostock, Germany. A cohort of polyps were cultured under the identical and constant laboratory conditions documented in Schaible *et al*.[50]. The initial cohort was of 1019 individuals and there have been a total of 1,610,818 hydra-days of observation during which time only 42 deaths were recorded. All budding events were recorded and the buds were discarded as soon as they detached from the mother. No sexual reproduction was recorded.

***Hermit crab* (*Pagurus longicarpus*)**
We derived data for the hermit crab from Damiani[51]. This paper reports on matrix projection models for a captive crab population of 145 females held in various conditions at Duke University Marine Laboratory. The study produced a number of matrices, each with three stages, but we use an element-by-element mean matrix from the annual-based control treatments. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Armed saltbush (*Atriplex acanthocarpa*)
We obtained the data the armed saltbush from Verhulst *et al*.[52], which reports on a study focusing on a population in the Chihuahuan Desert, Mexico between 1995-1998. They constructed size-based matrices with five stages and we use the reported average matrix (an element-by-element mean). We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Red abalone (*Haliotis rufescens*)
We obtained data for the red abalone from a size-based population projection matrix published by Rogers-Bennett et al.[53]. This projection matrix details the dynamics of five natural populations of individually tagged animals in northern California, USA, during 1971-

1978. The populations were censused annually and individuals were assigned to one of nine size classes based on shell length. Data from the five populations were pooled to provide a single matrix. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Red-legged frog (*Rana aurora*)
We obtained the data for the red-legged frog from Biek *et al.*[54]. This paper presents parameterized matrices with three stages, based on field data collected from British Columbia, Canada and Oregon and Wyoming, USA. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Viburnum (*Viburnum furcatum*)
We obtained data from viburnum from Hara *et al.*[55]. This paper presents a stage-classified matrix for a population from the southern slope of Mt. Kurikoma, Japan. Seven stages were used, based on ontogeny and plant height. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Red gorgonian (*Paramuricea clavata*)
We extracted data for the red gorgonian from a population projection matrix published by Linares *et al.*[56] which included seven size-based stages. They obtained their data from two marine protected areas off the NW Mediterranean coast of Spain (Cap de Creus and Medes Islands) at depths of 15-25m. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Oarweed (*Laminaria digitata*)
We obtained data for oarweed, a green alga, from Chapman[57] who used a matrix projection approach to document the demography of a stand in south west Nova Scotia, Canada, over a nine year period. Individuals were sampled annually to estimate their survival, persistence, and emergence of new recruits. Individuals were then categorized into five classes according to vertical length. Spore production and fecundity were calculated using allometric equations. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Netleaf oak (*Quercus rugosa*)
We obtained data for netleaf oak via personal communication from C. Bofil and T. Valverde (UNAM, Mexico). Their study details the dynamics of a population in oak-pine woodland in the Parque Ecológico of Mexico City, Mexico, from 1991 to 1994, using population projection matrix methods. They sampled individuals annually for survival, persistence, and emergence of new recruits, and they categorized individuals into seven classes based on ontogeny and size. We consider age 0 to be the time when seeds emerge from seedbank dormancy. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Desert tortoise (*Gopherus agassizii*)

We derived data for the desert tortoise from Turner *et al*.[58]. They studied five populations from San Bernardino County, California, USA, between 1983 and 1986. They used mark-recapture methods to construct a period-based life table from 1257 capture events and to estimate fertility they radiographed females to quantify the number of eggs present. We use their table 30, which is a single life table integrating data from all five populations.

White mangrove (*Avicennia marina*)

We obtained data for white mangrove from Burns & Ogden[59]. This paper reports on a study of a population of mangrove trees monitored in Ohiwa Harbour, New Zealand between 1980-1981. We used the age-from-stage approximation methods described in Supplementary Methods 2 to produce a life table from these matrix data. An R script is also provided in the Supplementary Material.

Supplementary Methods 2: Further rationale on data set selection given as response to reviewer.

After addressing the reviewers' comments on earlier drafts, we provided further explanation of our decisions to include/not include species in our analysis. At the request of the editor, we include this response verbatim below:

We thank the reviewers for their additional comments on our manuscript "*Varieties of ageing across the tree of life*". Only one reviewer had comments that need to be addressed and we answer him/her below.

Reviewer: *The data shown for model laboratory organisms such as D. melanogaster and C. elegans are each derived from one study. The mouse is not included at all. The fly data are carefully chosen but are they representative? There are dozens of studies and the arguments put forward for using a set of inbred strains in the face of known and dramatic inbreeding depression are unclear. Both here and in the nematode data, some further discussion in the text and some further elaboration in appendices is warranted. There is abundant data from several additional studies that should be mentioned and cited.*

The major purpose of our paper is to highlight the vast variety of shapes of mortality and fertility trajectories that have evolved across the tree of life. It is precisely in the context of evolution that it becomes so important to include both fertility and mortality from the *same* study, since these quantities are likely to trade off. In the present work we have carefully considered study species for which both demographic trajectories were quantified for the same individuals of the population. Unfortunately for our purposes, in a significant number of demographic studies researchers focus exclusively on mortality and ignore fertility. This is often done for good practical reasons; in the wild, quantifying reproduction may be impracticable due to the difficulties of estimating reproductive output and assigning parenthood to new recruits. In laboratory studies, a natural breeding environment would be difficult to attain for many species. Such lab species include mice and rats. This is the primary reason we do not include them in Figure 1 of our manuscript.

Many laboratory studies focus on mutations that strongly influence mortality or fertility. These often offer valuable insight into the mechanisms of ageing. However, we also know that strains with these mutations are not the "wild type" (term used in its off-hand sense) of the naturally occurring species. Therefore we excluded such studies from our compilation.

Our results for *Caenorhabditis elegans* are extremely rare, probably unique, in that they are based on a study (Chen et al.[11]), that followed individual worms and recorded both survival and reproduction. To our knowledge, all the rest of the large literature on aging in *C. elegans* has deliberately excluded reproduction, either by treatment with DNA synthesis inhibitors, or by the introduction of temperature-sensitive genes that eliminate reproduction except at specified temperatures (Fabian and Johnson[12]). These represent, respectively, environmental and genetic perturbations far from the naturally evolved condition in *C. elegans*. Although they are valuable for studying aging mutants, they do not satisfy our criteria for inclusion in this comparison.

In spite of those drawbacks, when mortality trajectories are presented or can be inferred, for wild-type strains, from figures in the literature on *C. elegans* (e.g., Johnson et al.[13], Fig. 3;

Brooks et al.[14], Figs. 2 and 3; Vaupel et al.[15], Fig. 3E), those trajectories agree qualitatively with the results we present here from Chen et al.[11].

For *Drosophila* we highlight in the supplementary material several additional studies that show qualitatively similar mortality to the ones derived from the study we chose to use : Luckinbill et al.[22], Hwangbo et al.[23] , Tatar et al.[24], Mair et al.[25] and Rogina et al.[26]. For medflies (*Ceratitis capitata*) we point the reader to further work by Carey et al. [32-34], also showing qualitatively similar trajectories at the ages used in our Figure 1 in our manuscript. At more extreme ages, when far fewer than 5% of adult medflies are still alive, Carey et al.[32] report declining mortality. In Carey et al. [33,34] life expectancy and the steepness of the rise of mortality with age vary depending on diet regimes but in all cases death rates increase with age.

Reviewer: *A number of papers have appeared that address mortality and fertility and several of these publications show data that may be at variance with the data cited… The authors should provide additional analyses of these various populations in a series on supplemental figures and analyses. The mouse, rat and naked mole rat are not included and this seems odd and should be remedied for completeness sake.*

We acknowledge the existence of variation among different populations and strains within a species, but this is not our focus in this study. Such variation is exemplified by the inclusion of 3 human populations and is acknowledged in explicit statements on Page2 Line 21, and Page 10 Lines 10-12 of our manuscript. To highlight this variation further, we now include a Supplementary Analysis of the mortality trajectories of laboratory mice and rats of different strains, sexes and from different studies[60-65] (we refer to it in the manuscript on Page 10 Lines 12-14). We note, however, that fertility data were unavailable. The analyses ([Extended Data Figure 1]) do show variation in the standardized mortality trajectories, and this is most pronounced in the mouse. The curves have to be treated with caution because of small sample sizes. Furthermore, without detailed further analysis, the roles of demographic, environmental, and genetic heterogeneity remain a mystery. We are currently working on a separate research project to explore the sources of variation in trajectories of mortality and fertility within species.

The inclusion of the mice and rat trajectories addresses the referee's request for inclusion of mice and rats "for completeness sake". Unfortunately, we were unable to find suitable data on the other requested species, the naked mole rat (*Heterocephalus glaber*). The mortality rates published by Buffenstein[66] are not explained: it is not clear how "mortality rates" were calculated and what age-specific death and population counts were used to do. The value given for the "mortality rate (qx)" at age 0 is 3, which cannot be the probability of death qx and must have some other, unspecified, interpretation.

Supplementary Methods 3: Computation of age-specific mortality and fertility from stage-classified models

Matrices

The calculation begins with a stage-classified population projection matrix $\mathbf{A}$. To separate the processes of survival and reproduction, the matrix is decomposed into

$$\mathbf{A} = \mathbf{U} + \mathbf{F} \tag{1}$$

where $\mathbf{U}$ contains transition probabilities for extant individuals and $\mathbf{F}$ contains production of new individuals by reproduction.

The definition of age requires a choice of a stage that corresponds to "birth." In age-classified models, and in many stage-classified models, there is only one such stage. But in some stage-classified models new individuals may start their lives in different stages (e.g., small or large seedlings). In such cases, more than one row of the matrix $\mathbf{F}$ will contain non-zero entries. In our analyses, we defined the stage corresponding to birth as the first established non-propagule stage (e.g., not seeds or seed bank in the case of plants).

Demographic calculations

Calculation of age-specific demographic outcomes from the stage-specific matrices proceeds as described in Section 5.3 of Caswell[37]. For our analyses, we require life expectancy, age-specific survivorship, age-specific fertility, the mean age at first reproduction, and the age at which the cohort has converged to within 5% of its quasi-stationary structure.

1. Life expectancy. Let stage j be the stage defined to correspond to birth. Life expectancy at birth is given by

$$\eta = \mathbf{e}^{\mathsf{T}} \left(\mathbf{I} - \mathbf{U}\right)^{-1} \mathbf{e}_j \tag{2}$$

where $\mathbf{e}$ is a vector of ones, $\mathbf{e}_j$ is the jth unit vector, and $\mathbf{I}$ is the identity matrix.

2. Age-specific survivorship $\ell(x)$. As in Section 5.3.1of Caswell[37], start with a single individual in the stage j defined to correspond to birth. Survivorship is given by

$$\ell(x) = \mathbf{e}^{\mathsf{T}}\mathbf{U}^{x}\mathbf{e}_{j} \qquad x = 0, 1, \ldots. \tag{3}$$

3. Age-specific fertility $m(x)$. The proportional structure of the cohort at age x is given by

$$\mathbf{p}(x) = \frac{\mathbf{U}^{x}\mathbf{e}_{j}}{\mathbf{e}^{\mathsf{T}}\mathbf{U}^{x}\mathbf{e}_{j}} \qquad x = 0, 1, \ldots. \tag{4}$$

The total sexual reproductive output per individual at age x is given by

$$m(x) = \mathbf{e}^{\mathsf{T}}\mathbf{F}\mathbf{p}(x). \tag{5}$$

4. Age at first reproduction. Calculation of the mean age at first reproduction is described in detail in Section 5.3.3 of Caswell[37]. Briefly, we defined the set of reproductive stages $\mathcal{R}$ as those columns of $\mathbf{F}$ that contain at least one non-zero element. We created an new absorbing state corresponding to the event of reproducing at least once before death, and used the resulting absorbing Markov chain to compute the probability of reproducing. That probability was then used to create a conditional Markov chain, and we computed the mean age at first reproduction as the mean time to absorbtion in this conditional chain. The exact calculations are given in eqs. 5.47–5.54 of Caswell[37].

5. Convergence to the quasi-stationary distribution. A cohort modelled by iteration of the transient matrix $\mathbf{U}$, as in (3) above, eventually decays exponentially at a rate given by the dominant eigenvalue of $\mathbf{U}$, and converges to a quasi-stationary distribution given by the corresponding right eigenvector $\mathbf{w}$. Once this convergence has happened, mortality remains constant with age, because the stage-classified model explicitly assumes that age is, ultimately, irrelevant. To prevent our conclusions about age trajectories being overly influenced by this assumption, we calculated the age at which the cohort had converged to within a specified percentage (5%) of the quasi-stationary distribution.

Without loss of generality, we scaled the eigenvector so that the 1-norm, $|\mathbf{w}| = 1$. We used Keyfitz's Δ; for example, see eq. (4.100) of Caswell[37], to measure the convergence of the proportional cohort structure $\mathbf{p}(x)$, given by (4), to the quasistationary distribution, where

$$\Delta(x) = 0.5 \left\| \mathbf{p}(x) - \mathbf{w} \right\| . \tag{6}$$

We defined the age of convergence, as shown in Figure 1, as the minimum age x_c at which

$$\Delta(x_c) \leq 0.05. \tag{7}$$

Computer code

We provide an R script below to implement the above routine on the matrices provided as Source Data files in the Supplementary Information.

Supplementary Methods: 'R' computer code to extract age trajectories of fertility and mortality from stage-based population projection matrices.

```
#Code to extract lx, mx and L_alpha from stage-based population projection
#matrices.

#Presented as part of the Supplementary Methods for the manuscript:
#Owen R. Jones, Alexander Scheuerlein, Roberto Salguero-Gómez, Carlo Giovanni
#Camarda, Ralf Schaible, Brenda B. Casper, Johan P. Dahlgren, Johan Ehrlén, María
#B. García, Eric Menges, Pedro F. Quintana-Ascencio, Hal Caswell, Annette Baudisch,
#James W. Vaupel
#Varieties of Ageing Across the Tree of Life. Submitted to Nature.

#Code developed by R. Salguero-Gomez (University of Queensland & Max Planck
#Institute for Demographic Research), O. R. Jones (University of Southern Denmark &
#Max-Planck Odense Center on the Biodemography of Aging) and Hal Caswell (Woods
#Hole Oceanographic Institute & Max-Planck Institute for Demographic Research)
#Email: Roberto Salguero-Gomez <r.salguero@uq.edu.au>
#Using equations from H. Caswell (2001) Matrix Population Models. 2nd Edition.
#Sinauer, Sunderland, MA. Specific equations and pages within the references are
#cited in each of the functions below.

#Last modified: August 11th, 2013

# For this script, the matrix data must be arranged in a CSV as follows:
# The first column, "classOrganize" indicates the stage-type for each row/column of
#the matrix.
# This is a re-classification of the stages indicated by the authors (see variable
#"classAuthor" below) according to five possible general classes:
#                 - prop: propagule that has not yet been established (seeds in the
#seedbank of a plant, spores in some sessile animals)
#                 - pre_rep: pre-reproductive stages.
#                 - rep: sexually reproductive stages.
#                 - post_rep: post-reproductive stages, where the individual is not
#dormant/hybernating.
#                 - dorm: dormant/hybernating individuals. By default individuals
#in this class are non-reproductive.
# The second column, "classAuthor" gives the description of the stages in the
#population matrix model as defined by the author in the pertinent publication.
# The second column, "classNumber" gives the numerical ordination of the classes,
#from 1 to n, where n is the last class.
# There then follow n rows each for the U, F and C matrices. U gives the survival
#probabilities while F and C give the sexual reproduction and clonal reproduction
#respectively
#   - U1-Un: matrix of survival probabilities (u[i,j]), where n is the largest
#class number in the matrix model.
#   - F1-Fn: matrix of per-capita sexual contributions (f[i,j]), where n is the
#largest class number in the matrix model.
#   - C1-Cn: matrix of per-capita clonal contributions (c[i,j]), where n is the
#largest class number in the matrix model.
#
# Note: there are several examples in the Supplementary Information (Source Data).

#Packages necessary:
require(MASS, popbio)

#Read in the csv file containing the matrix for the species of interest
Dataset = read.csv("PATH TO MATRIX CSV FILE")

#Define possiblie class categories
Classes = c("prop", "pre_rep", "rep", "post_rep", "dorm")

#Simple re-statement of each of the variables as "character" or as "numeric" for
#later calculations.
for(i in 1:dim(Dataset)[2]){
  if(i   <   which(colnames(Dataset)   ==   "classNumber")){Dataset[   ,   i]   =
as.character(Dataset[ , i])
    }else{
      Dataset[,i]=as.numeric(Dataset[,i])
```

```
    }
}

#Matrix dimension:
matDim = dim(Dataset)[1]

#Read the different sub-matrices:
  #U matrix (transition probabilities):
        Umat     =     as.matrix(Dataset[     ,     which(colnames(Dataset)     ==
"U1"):(which(colnames(Dataset) == "U1") + matDim - 1)])
  #F matrix (per-capita sexual contributions):
    Fmat      =      as.matrix(Dataset[      ,      which(colnames(Dataset)      ==
"F1"):(which(colnames(Dataset) == "F1") + matDim - 1)])
  #C matrix (per-capita asexual contributions):
    Cmat      =      as.matrix(Dataset[      ,      which(colnames(Dataset)      ==
"C1"):(which(colnames(Dataset) == "C1") + matDim - 1)])
  #The full projection matrix is thus calculated as:
    Amat = Umat + Fmat + Cmat

#The life stages of this model are:
lifeStages = Dataset[ , "classOrganized"]

#The calculations here employed define the beginning of life when an individual
#become established. Thus, we do not consider transitions from the "prop" stages
notProp = min(which(lifeStages != "prop"))

#Mean life expectancy based on the fundamental matrix (See bottom equation of page
118 in Caswell 2001):
N = solve(diag(matDim) - Umat)

#The life expectancy conditional on entering the life-cycle of the species in the
#first non-propagule stage as per the fundamental matrix of A, N, is:
lifespanFundamental = colSums(N)[notProp]

#Age-specific survivorship (lx) (See top function on page 120 in Caswell 2001):
       Umat2 = Umat
       survivorship <- array(NA, dim = c(1000, matDim))
      for (o in 1:1000){
        survivorship[o, ] = colSums(Umat2 %*% Umat)
        Umat2 = Umat2 %*% Umat
      }

      lx = survivorship[, notProp]

      #The following line makes sure that survivorship at age 0 is 1:
      lx = c(1, lx[1:(length(lx) - 1)])

  #Probability of survival to first sexual reproductive event (See Eq 5.19 onwards
  #on page 114 of Caswell 2001)
      u = colSums(Umat)
       Uprime = Umat
       Uprime[, (lifeStages == "rep")] = 0
       Mprime = matrix(0, 2, matDim)
       for (p in 1:matDim){
        if (lifeStages[p]=="flow") Mprime[2,p]=1
        }else{
        Mprime[1, p] = 1 - u[p]
       }

       Bprime = Mprime %*% (ginv(diag(matDim) - Uprime))
       prob1stReprod = Bprime[1, notProp]

  #Mean age at sexual maturity  (See pages 124-125 in Caswell 2001)
       D = diag(c(Bprime[2, ]))
       Uprimecond = D%*% Uprime %*% ginv(D)
       expTimeReprod = colSums(ginv(diag(matDim) - Uprimecond))
       La=expTimeReprod[notProp]

       #Age-specific fertility (mx, Caswell 2001, p. 120)
       ageFertility = array(0, dim = c(1000, matDim))
```

```
      fertMatrix = array(0, dim = c(1000, matDim))
       Umat3 = Umat
       e = matrix(rep(1, matDim))
       for (q in 1:1000) {
         fertMatrix = Fmat %*% Umat3 * (as.numeric((ginv(diag(t(e) %*% Umat3)))))
         ageFertility[q, ] = colSums(fertMatrix)
         Umat3 = Umat3 %*% Umat
       }
      mx = ageFertility[, notProp]

  #The following line ensures that mx at age 0 is 0:
    mx = c(0, mx[1:(length(mx) - 1)])

#Function to determine the cutoff age at quasi-convergence for lx and mx (Code
#adapted from H. Caswell's matlab code):
    qsdConvergence <- function(survMatrix, beginLife){
      uDim = dim(survMatrix)
      eig = eigen.analysis(survMatrix)
      qsd = eig$stable.stage
      qsd = as.numeric(t(matrix(qsd / sum(qsd))))

      #Set up a cohort
      nzero = rep(0, uDim[1]) #Set a population vector of zeros
      nzero[beginLife] = 1 #Set the first stage to =1
      n = nzero #Rename for convenience

      #Iterate the cohort (n= cohort population vector, p = proportional structure)
      dist = p = NULL
      survMatrix1 <- survMatrix
      for (j in 1:1500){ #j represent years of iteration
        p = n / sum(n) #Get the proportional distribution
        dist[j] = 0.5 * (sum(abs(p - qsd)))
        n = survMatrix1 %*% n #Multiply the u and n matrices to iterate
      }
      #Find the ages for convergence to 0.1, 0.05, and 0.01
          pick1 = min(which(dist < 0.1))
          pick2 = min(which(dist < 0.05))
          pick3 = min(which(dist < 0.01))
          convage = c(pick1, pick2, pick3)
        return(convage)
    }

  Convergence=qsdConvergence(Umat, notProp)

#Save the age-specific trajectories as a lifetable, and write out as a CSV file.
  lifetable = matrix(NA, nrow = 1000, ncol = 5)
  colnames(lifetable) = c("x", "lx", "mx", "La", "QSD")
  lifetable[ , "x"] = c(0:999)
  lifetable[ , "lx"] = lx
  lifetable[ , "mx"] = mx
  lifetable[1, "La"] = La
  lifetable[1:3, "QSD"] = Convergence

       write.csv(lifetable, "Lifetable.csv", row.names = FALSE)
```

Supplementary Note: Intraspecific variation in standardised mortality trajectories of laboratory rat and mouse

We acknowledge the existence of intraspecific variation among populations and strains. To highlight this variation, we include the following supplementary analysis of the standardised mortality trajectories (see main methods) of laboratory mice (*Mus musculus*) and rats (*Rattus norvegicus*) of different strains, sexes and from different studies. Fertility data were unavailable. The analyses (Extended Data Figure 1) show variation in the standardized mortality trajectories and this is most pronounced in the mouse. The curves should be treated with caution because they are derived from relatively small cohort sizes. Furthermore, without detailed further analysis, the roles of demographic, environmental, and genetic heterogeneity remain a mystery.

Rat (*Rattus norvegicus*)

Data on rat mortality were taken from three classic studies that investigated the effects of food restriction on mortality schedules. Mortality data for five different cohorts of Sprague-Daley rats were taken from table 4 in Ross[64], with cohort sizes ranging from 120 to 200 animals. Yu *et al*.[65] in their figure 6 show survival data for specific pathogen free (SPF) Fischer 344 male rats in a food restricted (115 individuals) and a control cohort (115 individuals). Four additional mortality curves were taken from figure 2 in Holloszy's[63] study of the effects of exercise and restricted feeding on survival. Cohort sizes for these ranged from 31 to 65 individuals.

Mouse (*Mus musculus*)

We took mortality data for 33 cohorts from figures 2, 3, 4 and 5 from the classical study by Smith and Wolford[60] on mouse strains of both sexes that differed in their histocompatibility systems. For these data, the cohort size ranged from 38 to 61 animals. Additional data from 3 cohorts of wild-derived mice and one lab-bred cohort were taken from figure 1 in Miller *et al.*[61]. These cohorts each contained 50 animals and were of mixed sex. Further data were taken from survival curves for two mixed-sex cohorts of wild-derived mice shown in figure 3A of Harper *et al*.[62]. One of these cohorts was food-restricted (124 individuals) while the other served as control (127 individuals).

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