Title: Senescence: Still an Unsolved Problem of Biology

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Contributions

M.R. and R.S.G. conceived the project. M.R. and P.C conducted the analyses with input from R.S.-G. and produced all visualisations. M.R drafted the first version and, together with P.C. and R.S.-G., revised and edited the manuscript.

Competing interests

The authors declare no competing interests.

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Abstract (150 words), Main text (3957 words), 44 references, 4 figures. Supplementary Info (separate file) contains R code, 3 figures, and 3 tables.

Data accessibility statement

Data are available from the COMPADRE Plant Matrix Database and COMADRE Animal Matrix Database (www.compadre-db.com). Code used for analysis is available in the supplementary information. Should the manuscript be accepted, the data supporting the results will be archived in an appropriate public repository (Dryad, Figshare or Hal) and the data DOI will be included at the end of the article.

Abstract

Despite *ca.* seven decades of theoretical elaboration since Peter Medawar's foundational 'An Unsolved Problem of Biology', we argue that the fundamental problem of the evolution of senescence, *i.e.* the increasing risk of mortality and decline in reproduction with age after maturity, remains unsolved. Theories of senescence predict the inescapability of senescence, or its universality at least among species with a clear germ-soma barrier. Here, using demographic information for 475 multicellular species, we exemplify the discrepancy between these theoretical predictions and currently available data. We derive age-based trajectories of mortality and reproduction whose form cannot be satisfactorily explained by the theories of senescence, and show that species' may often display senescence for one fitness component but not the other. We propose that theories of senescence must be extended beyond merely individual chronological age; size, the species' ecological context, and kin selection may all play hidden, yet integral roles in shaping patterns of senescence.

Main text

Introduction

The evolution of senescence has long been explained by a collation of theories defining the 'classical evolutionary framework of ageing'. The central logic common to these theories argues that the force of natural selection weakens with age (1-4); selection becomes too weak to oppose the accumulation of genes that negatively affect older age classes (1), or favours these genes if they also have beneficial effects at earlier ages in life (3), when the contribution individuals make to future populations is assumed to be greater. Selection, therefore, should favour resource investment into earlier reproduction rather than late-life maintenance (4). Ultimately, these theories predict, directly (2) or indirectly (1,4), that senescence is inescapable (2), or at least inevitable in organisms with a clear germline-soma separation (3,4).

A recent comparative depiction of demographic ageing patterns across 46 species of animals, plants, and algae (5) has contradicted the expectations of the classical evolutionary framework. Many of the examined species display negligible (6) or even negative (7) senescence, where the risk of mortality remains constant or decreases with age, and reproduction remains constant or increases with age. This mismatch between expectations and observations renders the classical evolutionary framework insufficient to explain the diversity of senescence across the tree of life. Why do some species succumb to senescence, and what allows others to escape its forces? We now need to examine the mechanisms behind such variation of ageing patterns (8, 9), and how prevalent such "exceptions" are to the assumed rule of universal senescence.

Here, we utilise high-resolution demographic information for 80 animal (10) and 395 plant (11) species worldwide (See Materials and Methods) to (i) provide a quantitative evaluation of the rates of actuarial senescence – the increase in mortality risk with age after maturation – across multicellular organisms, (ii) test whether the classical

evolutionary framework explains the examined diversity of senescence rates, with special attention to predictions from germ-soma separation, and (iii) propose how to widen the classical evolutionary framework of ageing to better encompass the study of senescence across the tree of life.

Briefly, we first derived life tables (12) from a selection of species' matrix population models (13), each of which summarise the population dynamics of the studied species under natural conditions (See Materials and Methods). We then quantified the rate of actuarial senescence on the survivorship trajectory of each species' life table using a 'shape' metric of senescence (14). Our analysis uses a 'pace-shape' framework of ageing (15,16), where the pace of ageing quantifies the speed of life via mean life expectancy (16). The shape of ageing quantifies the spread and timing of mortality events, normalised by mean life expectancy, which facilitates cross-species comparison. The shape metric, S, is bound between -0.5 and 0.5 (See Materials and Methods), where $S>0$ indicates that most mortality events occur at advanced ages (*i.e.* actuarial senescence), while $S<0$ indicates low mortality late in life, *i.e.* escape from actuarial senescence**.** We determined a bound around zero using a root mean square distance measure (See Materials and Methods), with values of S that fall within the bound deemed to be indifferent from zero. We therefore describe species with such values as displaying *negligible* actuarial senescence.

Previous studies have suggested that phylogenetic relatedness play a role in determining whether a given species displays positive, negligible or negative actuarial senescence (8). Here, we quantify the role of evolutionary history on actuarial senescence across our 475 species by estimating its phylogenetic signal (17) using phylogenies for animals (18) and plants (19) respectively. Finally, the central assumption of the classical evolutionary framework of ageing, that the force of natural selection weakens with age, rests on the assumption that older individuals contribute less to future populations (1,4-6). This is both

because the theories assume fewer individuals survive to later age classes (1), and that individuals are expected to favour reproduction at young rather than old ages (1,5,6). To observe how different age classes contribute to future populations in our study species, we use the derived life tables (12) to quantify age-specific reproduction rates (*m(x)*) to see if they match the pattern of actuarial senescence already quantified (See Material and Methods).

Results

Actuarial senescence is not the rule

The majority of animal species in our study (59/80) display no change in their risk of mortality with age. In particular, *increases* in the risk of mortality with age are especially scarce across invertebrates in our data, with the water flea (*Daphnia pulex* – Fig.1) as the sole example of positive actuarial senescence. The remaining 14 invertebrate species display negligible actuartial senescence, as in the case of the long-wristed hermit crab (*Pagurus longicarpus* – Fig. 1), or even negative actuarial senescence, for example the sea whip (*Leptogorgia virgulata* – Fig 1), actuarial senescence. Across vertebrates, 72% of species, including the guppy (*Poecilia reticulata* – Fig 1), display no change in risk of mortality with age (Fig. 1; Table S1). Positively senescent species, however, are more common in vertbrates (18%;12/65) than invertebrates (6%;1/15); these species are primarily mammals (75%; Table S1) such as the moose (*Alces alces* – Fig.1). Further species such as the eastern mud turtle (*Kinosternum subrubrum)* and two birds: the white-tailed eagle (*Haliaeetus albicilla)* and Heermann's gull (*Larus heermanni)* also display positive actuarial senescence. The six negatively senescent vertebrate species span across mammals *(3),* ray-finned fish *(1),* and reptiles *(2)* (e.g. the South American river turtle *Podocnemis expansa* – Fig.1; Table S1).

The majority of examined plant species also display negligible senescence. Indeed, only 2% of 375 plant species exhibit positive senescence, including the scots pine (*Pinus sylvestris*)

and the great laurel (*Rhododendron maximum*; Fig. 1). Approximately 23% of angiosperms show a decreasing risk of mortality with age (e.g. *Opuntia rastrera* – Fig. 1), compared to 40% of gymnosperm species (e.g. *Pinus lambertiana* – Fig 1). Overall, 98% of our studied plant species do not undergo actuarial senescence.

Patterns of senescence are driven by phylogenetic relatedness in plants, but not animals.

Estimates of phylogenetic signal on actuarial senescence were insignificant across the pool of examined animals (Fig S1; Table S3). Specifically, Pagel's λ (17) was not significantly different from zero for the both the full phylogenetic analysis across animals (λ = 0.22, p = 0.18), and also when considering vertebrates and invertebrates separately (Table S3). These results indicate that the patterns of senescence across animals cannot be explained by phylogenetic relatedness, under a brownian model of evolution. On the other hand, phylogenetic relatedness plays some role in senescence patterns across plants (Fig. S2; Table S3). A full analysis including both angiosperms and gymnopserms raised a Pagel's λ of 0.31 ($p < 0.001$), most likely due to the significant phylogenetic signal in angiosperms (λ = 0.27, p = 0.001). Independent phylogenetic analysis of actuarial senescence across gymnosperms raised a non-significant signal (λ = 0.27, p = 0.08), likely due to the small sample size of gymnosperms (n = 25 species).

Patterns of reproduction and actuarial senescence are somewhat independent across animals and plants.

Patterns of *m(x)* are diverse and not always determined by whether the examined species display or escape actuarial senescence (Fig.2; Fig.S3). In plants, for example, both the scots pine and the great laurel display actuarial senescence (Fig. 1), but their reproductive outputs do not decline with age (Fig. 2). This pattern is contrasting to both examples of animals displaying

positive senescence, where the moose and water flea also display reproductive decline with age (Fig. 2).

The patterns of actuarial senescence and reproductive output do not always align in species that display negligible or negative senescence. The flatweed provides an example of where both components of senescence align with both species exhibiting negligible senescence and a relatively constant *m(x)* trajectory. The long-wristed hermit crab and the sugar pine, however, also display negligible senescence but have increasing *m(x)* trajectories. It appears from our study species that both components of senescence can sometimes follow variable, independent, trajectories.

Discussion

The senescence landscape that emerges from our study of 475 species indicates that (i) senescence is not inescapable across the tree of life, (ii) senescence is not inevitable in species with a germ-soma barrier, and (iii) senescence is prevalent in some species without a clear germ-soma barrier. These findings are in direct contradiction with the predictions of the classical evolutionary framework of ageing (1,4-6). Our comparative ageing analyses, the largest to date, provides a clear view of the discrepancy between senescence theory and data.

Considering first the analysis of actuarial senescence, most of our study species fall into the bound of neglgible actuarial senescence *i.e.* no significant change in the risk of mortality with age (Fig. 1; Table S1; Table S2). Generally, this finding supports the orginal conundrum that the presence of senescence is inherently paradoxical. If natural selection is a fitness-maximising agent (20), then one would *a priori* not expect the evolution of a phenomenon so seemingly detrimental. Perhaps a determination to label senescence as universal force is born out of its obvious effects in humans when, in reality, it is mostly absent from nature (Fig. 1). In addition, while our analyses include species that display both positive and negative actuarial

166 senescence (Fig.1; Table S1; Table S2), not all of these can be explained under the classical
167 evolutionary framework (1,4-6). For example, although a small proportion, seven angiosperms
168 – species with no clear germ-soma separation – display positive actuarial senescence (Table
169 S2). On the other hand, three mammals, species with a clear germ-soma barrier, display
170 negative actuarial senescence (Table S1).

171 Our results also show that age-trajectories of mortality and reproduction are often
172 independent (Fig. 2; Fig. S3). For each species in our study, we only consider a single studied
173 population, and so this decoupling is not be an artefact of intra-specific variation across
174 different populations. It follows that species may display actuarial senescence, but not
175 reproductive senescence, and *vice versa*. Thus, we urge future work to consider that senescence
176 is a two-component phenomenon of which, as displayed here, both are not destined to the same
177 fate, unlike commonly assumed in ageing research (21). To fully divulge the senescence profile
178 of a species, one must consider both mortality and reproduction.

179 Studies on reproductive senescence are sparser than their actuarial senescence
180 counterparts. Some important longitudinal investigations into reproductive senescence have
181 been conducted (21-23), and current data suggest that rates of reproduction, like mortality
182 hazards, can also both increase or decrease with age. Our results support observations that
183 reproductive patterns are variable across species (Fig. 2; Fig. S3). Recently, Baudisch & Stott
184 (14) have developed a methodology to quantify reproductive senescence patterns using a metric
185 parallel to the one we use here, *S*, for actuarial senescence.

186 In general, our results display the discrepancy between the predictions of the classical
187 evolutionary framework of ageing and empirical data. We suggest that researchers must widen
188 the framework to better encompass the biology of a more diverse range of taxa. For example,
189 the models of the classical evolutionary framework are purely age-structured, yet, in some

species, demographic patterns of survival and reproduction may be influenced equally or even more by factors besides age (13). Indeed, the force of selection does not always decline with age for some species (24), which contrasts with widely accepted predictions (4,5). The organisms that display demographic trajectories of survival and reproduction that defy such predictions are better predicted by size rather than age, such as sessile, modular species (25,26), or species with indeterminate growth forms (11). Perhaps not by coincidence, in our analyses, 98% of studied plants and all of our studied corals show no increase in risk of mortality with age (e.g. *Paramuricea clavata;* Fig. 1; Table S1; Table S2).

Many of the predictions made explicit from the classical framework of ageing have, until recently, long stood the test of time. Higher rates of extrinsic mortality, *i.e.* deaths due to the background environment, are expected to accelerate rates of senescence, whereas juvenile mortality is predicted not to play a role in the evolution of senescence (5). Theoretical advancements, however, have shown that, for extrinsic mortality to have a significant effect on the evolution of senescence, it must be age-dependent (27). Also, by biasing the stable age distribution of a population towards younger ages, high birth rates can also reduce the strength of selection with age (28). The strength of selection at a given age is dependent on both the abundance of individuals in a given age class *and* the respective reproductive value of that age class (4,28). Following this logic, some species that display senescence yet retain high reproduction at old ages (e.g. *Pinus sylvestris*; Fig. 2) may have a stable age distribution biased towards younger individuals. This outcome would render selection too weak to promote an escape from senescence. Ultimately, how the environment shapes patterns of birth and deaths will dictate both the reproductive value of age classes and the stable age-distribution of the classes. In turn, the resulting dynamics of these pressures will affect the relative strengths of age-specific selection gradients (29) for mortality and reproduction, and therefore patterns of senescence.

Finally, we have only considered patterns of survival and reproduction with respect to effects on the focal individual. If, however, an individual's survival and/or reproduction affects the fitness of others and the interacting individuals are relatives, selection on the demographic age trajectories will also be weighted by these effects (30). In our study, the killer whale (*Orcinus orca*) experiences negligible actuarial senescence (S= 0.037) (Table S1; Fig. S3). Killer whales are an exemplar where post-reproductive survival is hypothesised to have evolved due to the positive effects individuals can have on the survival and reproduction of grand-offspring, *i.e.* the 'grandmother hypothesis' (4,5,31,32,33). Although, on the other hand, post-reproductive survival is also suggested to have evolved because of similar benefits in Elephants, yet the Asian elephant population in our study (*Elaphus maximus*) displays positive actuarial senescence (S = 0.247) (Table S1; Fig. S3). Our study is not suited to provide a detailed account of the effects of sociality on the evolution of senescence. Further evidence, however, is beginning to accrue elsewhere that it may play an important role beyond the remits of 'grandmothering' (33,34,35).

In summary, the emerging picture of senescence across multicellular organisms is at odds with the widely cited predictions of the classical evolutionary framework (1,4-6). We propose that the field would benefit significantly from shiften attention towards the underlying mechanisms allowing species to *escape* from senescence. We expect the greatest progress to be made by researchers honing their focus to widening the classic evolutionary theories to a framework not solely focused on age, but instead inclusive of the aforementioned factors and with a special focus on actuarial and reproductive senescence as potentially differing trajectories. Most ageing research likely stems from human desire to increase human health and life span (36). This desire requires understanding the variation in patterns of senescence across the tree of life. For now, senescence remains an unsolved problem of biology.

Material and Methods

Data

We used the COMADRE Animal Matrix Database (v. 3.0.0) (2) and COMPADRE Plant Matrix Database (v. 5.0.0) (3) to obtain age trajectories of survival and reproduction. These open-access data repositories consist of a collection matrix population models[13] (MPMs) incorporating high-resolution demographic information on the survival and reproduction patterns of over 1,000 animal and plant species worldwide and associated metadata (2,3). Both databases include information on species for which the data have been digitised and thoroughly error-checked. In addition, we contacted authors for clarifications when any doubt about the interpretation of the life cycle of the species emerged. We imposed a series of selection criteria to restrict our analyses to data of the highest quality possible.

(i) MPMs were parameterised with field data from non-disturbed, unmanipulated populations (*i.e.* natural populations) to best describe the species' age trajectories.

(ii) MPMs had dimension ≥3 × 3 (i.e. rows × columns). Generally, low dimensions MPMs lack quality for the estimation of life history traits (37). This selection criterion also helps avoid problems with quick convergence to stationary equilibrium, at which point the estimates of life history trait values and rates of senescence become unreliable (8,38).

(iii) MPMs were only used when the entire life cycle was explicitly modelled including recordings of survival, development, and reproduction for all life cycle stages.

(iv) When multiple studies existed for the same species, we considered only the study of greater duration to ensure the highest temporal variation in the population dynamics was captured.

(v) Studies of annual plant species modelled using seasonal projection matrices were not included; we chose only species using an annual time step. This is due to the difficulties of converting their population dynamics to an annual basis to compare with all other species' models.

(vi) Included MPMs have stage-specific survival values ≤ 1. In a small number of published models, the stage-specific survival values can exceed 1 due to clonality being hidden in the matrix, rounding errors, or other mistakes in the original model (2,3).

(vii) MPMs were from species of which phylogenetic data was available, to ensure we were able to account for phylogenetic relatedness on our models.

The result of these criteria was a subset of 475 species of animals and plants from the initial databases, which we used for our analysis. Of these, 80 were animals, with 15 invertebrates and 65 vertebrates. The remaining 395 species were plants, with 25 gymnosperms and 370 angiosperms. We provide a list of all the species used, their categorisation of senescence including a value of *S*, and their relevant source study in the supplementary information.

Quantifying actuarial senescence

MPMs are a summary of the population dynamics of a given species, from which we can calculate several life history traits. To do so, we first must decompose an MPM (***A)*** into its sub-components (13):

U **–** containing the stage-specific survival rates

F – containing the stage-specific per-capita reproduction rates

C – containing stage-specific per-capita clonality rates

$$\boldsymbol{A = U + F + C} \qquad \text{equation 1}$$

This decomposition facilitates the estimation of key life history traits, including a rate of senescence (*S*) (14). Calculating *S* requires first obtaining the age-specific survivorship curve $l(x)$ from $\boldsymbol{U}$. To obtain $l(x)$ we first have to define age, and the definition of age requires a choice of a stage that corresponds to "birth". Following Jones *et al.* (8), 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, nor larvae or propagules in animals) due to the estimate uncertainty of parameters involved in those stages. The calculation of $l(x)$ was then implemented according to Caswell (p. 118-21) (13).

$$l(x) = e^t U^x e^j \qquad x = 0, 1,\ldots. \qquad \text{equation 2}$$

Where *e* is a vector of ones, and we start with a single individual in the stage *j* defined to correspond to birth.

We considered survivorship trajectories beginning at the age of maturity (α - calculated following 5.47–5.54 in Caswell (13)) and ending at the age at which 5% survivorship from maturity occurs (ω). This is because a cohort modelled by iteration of the $\boldsymbol{U}$ matrix eventually decays exponentially at a rate given by the dominant eigenvalue of $\boldsymbol{U}$, and converges to a quasi-stationary distribution given by the corresponding right eigenvector **w**. Once this convergence has happened, mortality remains constant with age, and so to prevent our conclusions 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 (8,38).

Following Baudisch & Stott (14), the function *H(x)* defines the cumulative hazard of mortality up to age x as

$$H(x) = \int_{\alpha}^{x} \mu(t)dt \qquad \text{equation 3}$$

Where $\mu(x)$ denotes the age-specific mortality function capturing the average hazard of death of an individual at age *x*, and *H(x)* corresponds to the logrartihmic transformation of the survivorship trajectory (*H(x) = -lnl(x)*).

S is quantified as the difference in areas under the age-specific survivorship curves of a standardised survivorshop curve that assumes constant mortality, and therefore has a value of 0.5, and the survivorship curve in question:

$$S = 0.5 - \int_{\alpha}^{\omega} H(x) \qquad \text{equation 4}$$

Theoretically, the maximum and minimum values of the second term in equation 4 are 1 and 0 respectively. The value of S is therefore bound between -0.5 and 0.5. If most mortality occurs later in life, $S > 0$, and individuals in the population display actuarial senescence. On the contrary, if $S < 0$, the risk of mortality declines with age and the individuals in the population escape actuarial senescence. Values of $S \sim 0$ indicate negligible senescence, where risk of mortality remains relatively constant with age. We decided to determine a bound around zero to infer which values of *S* should be considered as negative, negligible, or positive senescence respectively for the species in our dataset. For both animals and plants separately, we assumed that the root mean squared difference between a species' value of *S* and zero is less than or equal to some value, ε, such that:

$$\sqrt{\frac{\sum(S(i)-0)^2}{n}} \leq \varepsilon$$

Where *S(i)* is the value of s for species i, and n is the total number of species in our dataset which are animals (80) or plants (395), respectively.

We quantified bounds of $\mathbf{-0.109 \leq S \leq 0.109}$ for animals and $\mathbf{-0.129 \leq S \leq 0.129}$

for plants. For each taxonomic kingdom, values of *S* that fall within the bound are considered not different from zero and therefore categorised as negligible senescence. The inequality assumes no statistical distribution of the values of *S* across species.

Phylogenetic analyses for actuarial senescence

After quantifying each species' rate of actuarial senescence, we accounted for the phylogenetic relatedness of the species studied to determine the influence of a species' evolutionary history on its value of *S*. To explore the effects of phylogenetic relationships between the species included in this study, we obtained animal and plant phylogenies from different sources. The plant phylogeny was obtained using the *V.PhyloMaker* R package (19). *V.PhyloMaker* allows to build a rooted and time-calibrated phylogeny using a species list, based on already built plant phylogenies (39,40). The animal phylogeny was produced using the *datelife* R package (18), a service that uses publically accessible phylogenetic source data to build a chronogram – rooted and time-calibrated tree - given an input phylogeny that we sourced from the Open Tree of Life (41). In some cases, for both plant and animal phyologenies, we detected polytomies (*i.e.* >2 species with the same ancestor), which can interfere in our phylogenetic signal analyses (see 42). Polytomies were resolved using the function "multi2di" from *ape* package (43), which transforms polytomies into a series of random dichotomies with one or several branches of length zero. Trees were visualised using the *ggtree* R package (44).

To evaluate the role of phylogenetic relatedness in determining the patterns of variation of actuarial senescence we estimated Pagel's λ (17). This metric is an index bounded between zero and one, where values ~0 indicate that the evolutionary history of the species explains little about the variation of the trait measured, and values ~1 suggest that that evolutionary history mostly explains the observed variation of the trait across the studied species. To

estimate Pagel's λ we used the R package *phytools* (42). A full summary of the phylogenetic signals obtained for each of the four monophyletic groups can be found in the Supplementary Information (Table S3).

Reproduction analysis

We calculated reproductive age-trajectories for the species in our analysis to investigate whether reproductive senescence followed the same pattern as actuarial senescence in species that display *vs.* escape actuarial senescence. Age-specific reproduction (*m(x)*) was calculated following Caswell (p. 118-21) (13). Briefly, the proportional structure of the cohort at age *x* is given by

$$\mathbf{p}(x) = \frac{U^x e_j}{e^T U^x e_j} \quad x = 0,1,\ldots. \qquad \text{equation 4}$$

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

$$m(x) = \mathbf{e^T F p}(x) \qquad \text{equation 5}$$

For the remaining 463 species that aren't displayed in Figure 2, the *l(x)* and *m(x)* trajectories are found in the Supplementary information (Fig.S3).

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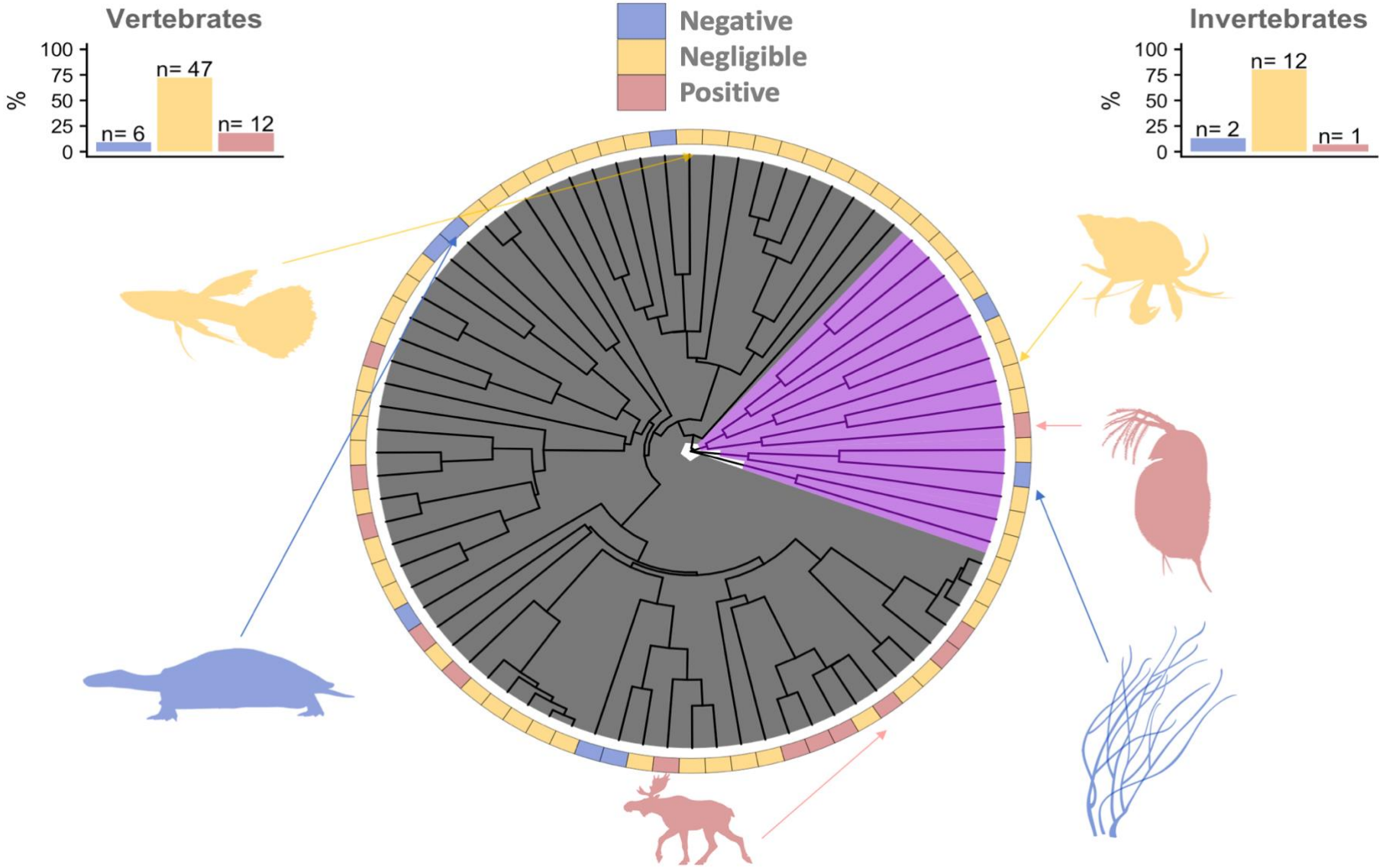
474

Figure Legends

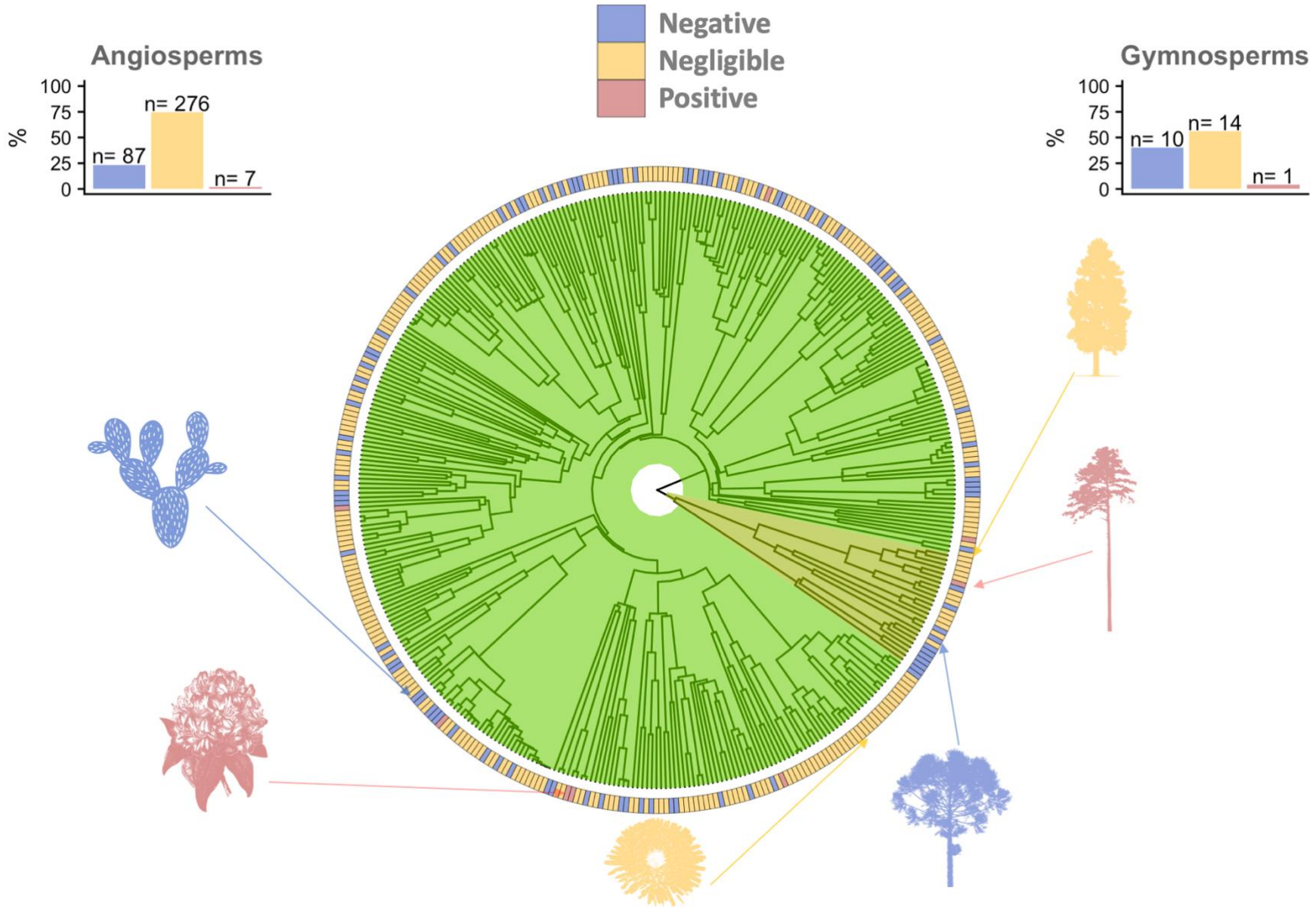
Figure 1 The evolution of and escape from senescence across multicellular life. The classical evolutionary framework of ageing does not explain the evolution of actuarial senescence across our study species. Positive, negligible and negative patterns of senescence are dispersed throughout the four examined clades, with the percentages of each pattern within each clade shown in the bar charts of each of the figures. **a)** Acturial senescence across animals. Depicted around the phylogeny are six representative species, displaying positive (red), negligible (yellow), and negative (blue) senescence from each clade. Clockwise, representing invertebrates, these species are *Pagurus longicarpus*, *Daphnia pulex* and *Leptogorgia virgulata.* For vertebrates, again clockwise, these species are *Alces alces*, *Poecilia reticulata,* and *Podocnemis expansa.* **b)** Acturial senescence across plants. Depicted around the phylogeny are six representative species, displaying positive (red), negligible (yellow), and negative (blue) senescence from each clade. For gymnosperms, these species are *Pinus lambertiana*, *Pinus sylvestris,* and *Taxus floridana.* For angiosperms, these species are *Hypochaeris radicata, Rhododendron maximum,* and *Opuntia rastrera.*

Figure 2 Age-based patterns of survivorship (*l(x)* - red) and reproduction (*m(x)* - black) are often decoupled, as shown for a selected subset of the examined species in Figure 1. **a)** *l(x)* and *m(x)* trajectories for the six selected animal species from Figure 1 and **b)** *l(x)* and *m(x)* trajectories for the six selected plant species from Figure 1. Species are representative of vertebrates, invertebrates, gymnosperms, and angiosperms. Trajectories are conditional upon reaching the age of maturity, at which the mature cohort is defined to have entered adulthood with a survivorship of 1. The trajectories of *l(x)* and *m(x)* run from age at maturity to the age at which 5% of the mature cohort is still alive.

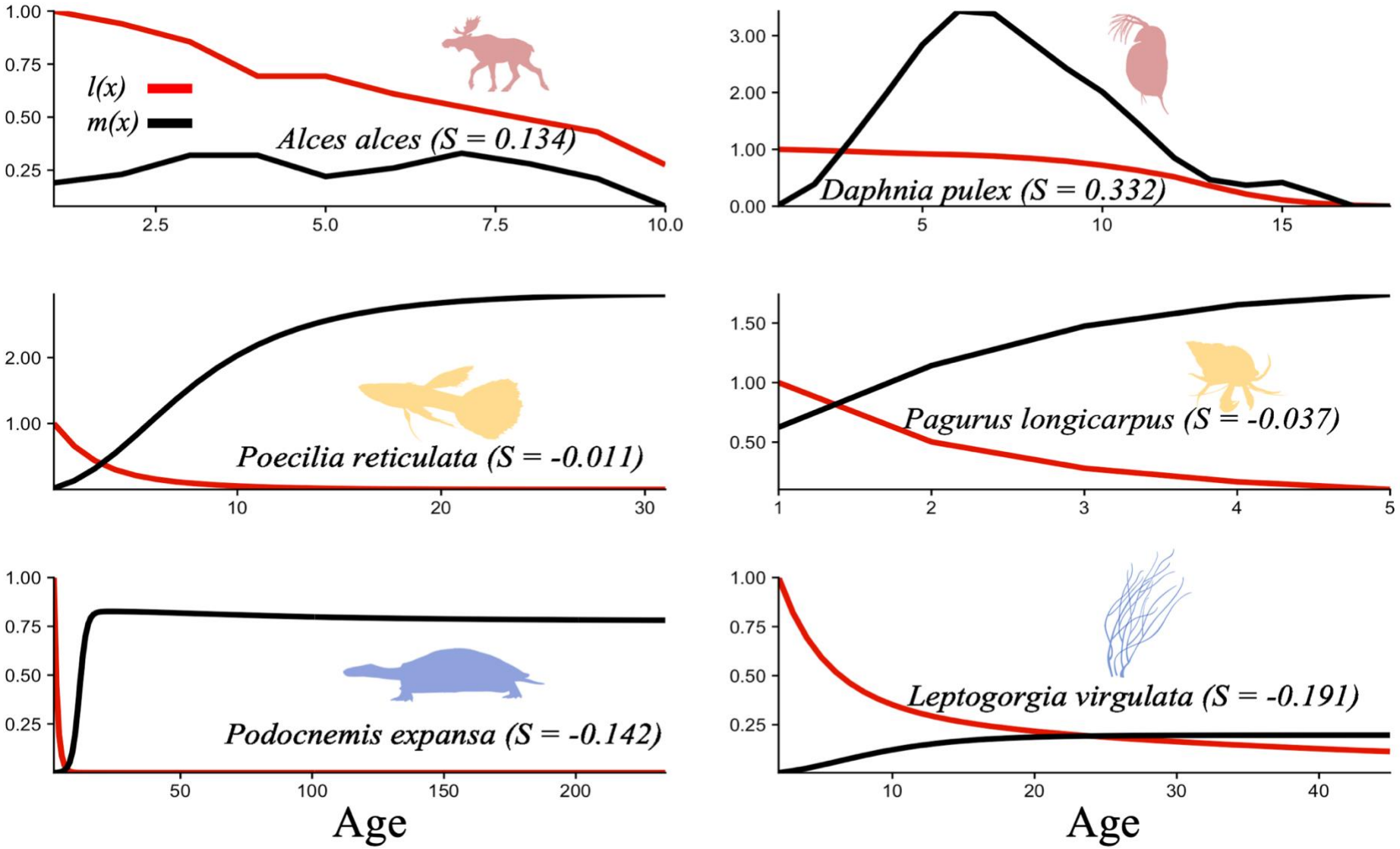
Digital Figures – Figure 1a



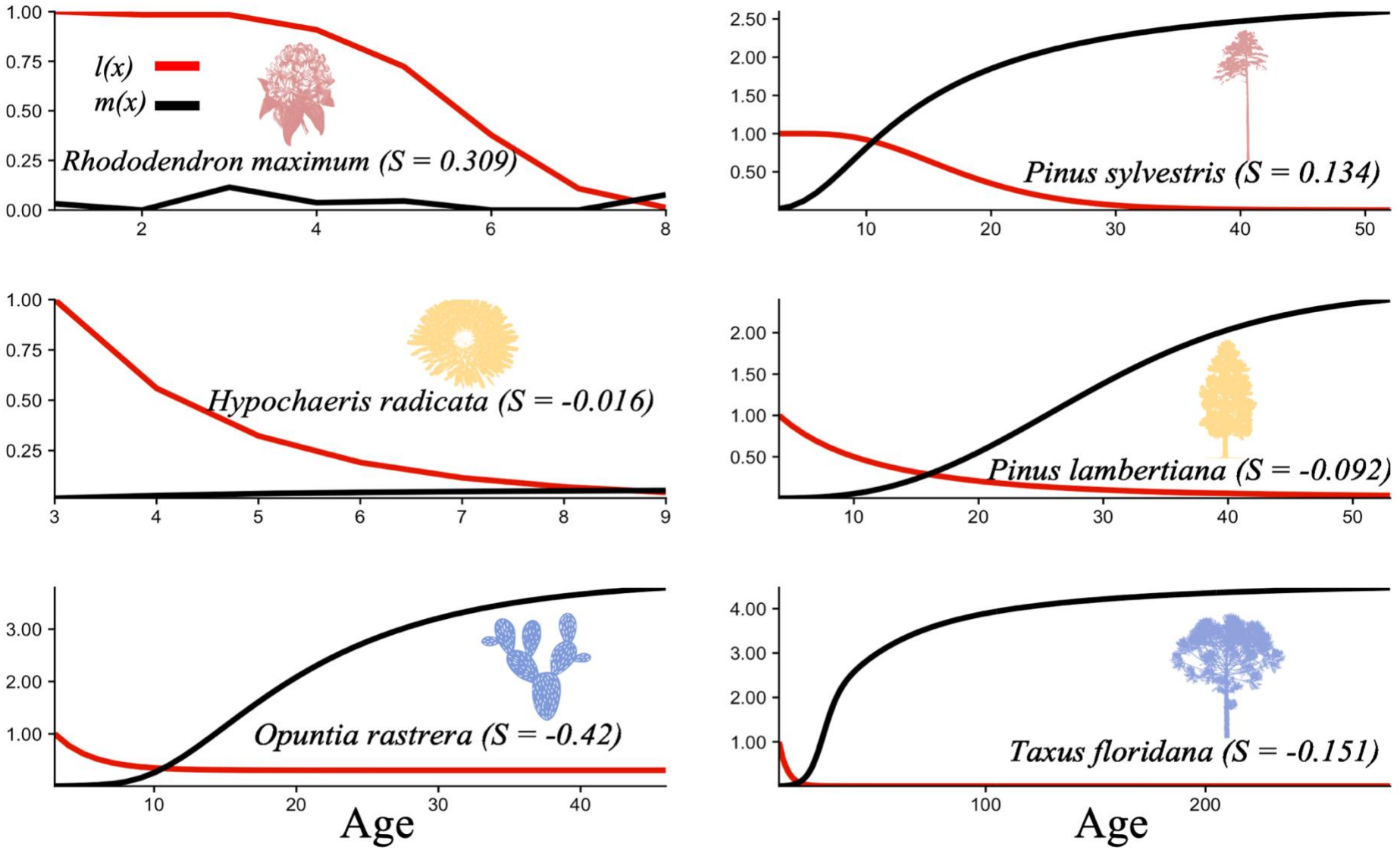
1b)


Angiosperms
100
75
50
25
0
%
n= 87
n= 276
n= 7
Negative
Negligible
Positive
Gymnosperms
100
75
50
25
0
%
n= 10
n= 14
n= 1

501 **2a)**


l(x)
m(x)
Alces alces (S = 0.134)
Daphnia pulex (S = 0.332)
Poecilia reticulata (S = -0.011)
Pagurus longicarpus (S = -0.037)
Podocnemis expansa (S = -0.142)
Leptogorgia virgulata (S = -0.191)
Age
Age

2b)


l(x)
m(x)
Rhododendron maximum (S = 0.309)
Pinus sylvestris (S = 0.134)
Hypochaeris radicata (S = -0.016)
Pinus lambertiana (S = -0.092)
Opuntia rastrera (S = -0.42)
Taxus floridana (S = -0.151)
Age
Age