Inevitable Senescence?
Contributions to
Evolutionary-Demographic Theory

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ABSTRACT

The main thrust of my dissertation is to understand whether and when senescence is an inherent characteristic of life. Hamilton (1966) claimed to have proven that "senescence is an inevitable outcome of evolution". One major result of my work is that no dogmatic statement can be made about the universality of senescence. By carefully studying Hamilton's paper on the moulding of senescence, I show that Hamilton did *not* prove that senescence "cannot be avoided by any conceivable organism".

I have developed simple models that contribute general insights to evolutionary demographic theory. The models are designed to shed light on whether and when non-senescent life-history strategies could be optimal. All models show that senescence is not inevitable. Sustenance can be an optimal life-history strategy. The results of my size-based models suggest that species with the capability of continued growth after the onset of reproduction are candidates for non-senescence. The results of my vitality-based model suggest that the costs of growth and maintenance and, to an almost equal extent, the costs of reproduction are major determinants of the choice between senescence and sustenance.

My dissertation can be viewed as a theoretical exploration of the inter-species diversity of aging, i.e., of how varied aging can be for different species and of what factors determine whether a species' strategy involves sustenance or senescence. My models suggest that a remarkable variety of patterns may be optimal under different circumstances. The limited empirical data available suggests that species may show a rich diversity of age-schedules of mortality, fertility and growth.

This dissertation shows that senescence and sustenance are two complementary sides of the process of aging. One cannot be deeply understood without the other. The new, burning question that arises from my work is: In what kind of species does senescence evolve and in what kind of species is it sustenance that evolves?

CONTENTS

LIST OF TABLES

LIST OF FIGURES

ACKNOWLEDGEMENTS

I thank my supervisor Linda Partridge for her advice and support and her continuous monitoring of my work.

I am grateful to my colleagues at the Max Planck Institute for Demographic Research in Rostock and especially thank my supervisor James W. Vaupel for detailed, intensive discussions and my mentor Jutta Gampe for her support.

This dissertation has greatly benefited from the excellent working conditions and from the warm and friendly atmosphere at the Max Planck Institute for Demographic Research in Rostock.

The International Max Planck Research School of Demography provided my doctoral training in demography. I further benefited from being part of the Research Training Network created by Europe's leading demographic research centres with financial support from the European Commission. The network enabled me to spend 4 month at the Vienna University of Technology carrying out my research and receiving training in dynamic optimization and demography under the supervision of Gustav Feichtinger and Alexia Fuernkranz-Prskawetz.

I gratefully acknowledge guidance from Kenneth Wachter and Brian Charlesworth. I have also benefitted from helpful discussions with Peter Abrams, James Carey, Hal Caswell, Kaare Christensen, James Curtsinger, Martin Dölling, Patrick Doncaster, David Gems, Ronald Lee, Daniel Martinez, Anatoli Michalski, Steven Orzack, Daniel Promislow, Roland Rau, Debbie Roach, Arthur Robson, Maria Shkolnikova, David Steinsaltz, Francois Taddei, Marc Tatar and Vladimir Veliov.

I thank my family and my friends.

1. INTRODUCTION

1.1 Synopsis

Death is part of life, and it can strike any time. The question is whether death necessarily becomes more likely as life proceeds. William D. Hamilton (1966), one of the leading biologists of the last century claimed that senescence is inevitable because the force of selection declines with age, making later ages unimportant to evolution. Survival and reproduction are the key players in this game and they are the traits negatively affected when selection loosens its grip.

Since 1966 it has been dogma among gerontologists that a decline in physiological functioning with age, i.e. senescence, is an inherent, inescapable part of life. Humans inevitably grow old, which is probably why it seems so unlikely to us that other forms of life could escape senescence. Biologists, however, often observe that functioning improves as individuals develop. Therefore the idea of living beings that perform equally well or better over their life course until they eventually meet the Grim Reaper might not be so strange after all.

One major result (Baudisch, 2005) of my dissertation is that no dogmatic statement can be made about the universality of senescence. By carefully studying Hamilton's work on the molding of senescence I show that Hamilton did not prove that senescence is unavoidable. He claimed that the force of selection must decrease with age for any conceivable organism. The weaker the force of selection, the more unfavorable mutations might sneak in, constituting a mutational burden. Contrary to his results, I point out that the force of selection can increase with age and, in this case, will counteract mutational burden at higher ages more strongly than at younger ages. The specific nature of a mutational effect, i.e. whether a mutation affects mortality in an additive or in a proportional way, determines the dynamics of the force of selection with age.

Combining Hamilton's analysis with the concept of mutation-selection balance and providing a critical analysis of theoretical issues and empirical evidence, I strengthen the view that the age-patterns of mortality and fertility are largely shaped by optimization rather than by the accumulation of deleterious mutations. However, the question on mutational burden vs. optimization is not yet closed.

Building on the insight that senescence is likely to be a byproduct of an adaptive process, I developed simple state-dependent models, three based on size and one on vitality.

The size-based models show that negative senescence can be an optimal life-

history strategy (Vaupel, Baudisch et al., 2004). The trajectory of growth is a crucial determinant in tipping the scale between senescence and sustenance. Indeterminate growers, i.e. species that exhibit a period of parallel growth and reproduction as part of their life history, are likely candidates for sustenant strategies, whereas senescence is expected for species that stop growing at about the age of reproductive maturity.

A fundamental insight gained from the vitality-based optimization approach, vitality being the size of an individual weighted by functioning, is the major importance of the costs of maintenance and growth for the determination of senescence versus sustenance. The model shows that a rich diversity of age-patterns of mortality can be optimal. Sustenance (or virtual sustenance) outplays senescence whenever maintenance costs are low. I show that changes in intrinsic and extrinsic mortality can switch the life history between senescence and sustenance strategies if the level of costs of reproduction and growth is not too high. The model is a first step in identifying the characteristics in a species that predict whether the species follows a senescent or a non-senescent life history.

A further insight from the vitality model concerns a mortality paradox. Contrary to "Williams' Hypothesis" that species living under more hazardous extrinsic conditions should exhibit faster senescence, I show that an increasing extrinsic hazard could switch an optimal life history from a senescent to a non-senescent one if maintenance costs are low.

In all my models, optimal equilibrium is assumed, something that might never be reached in nature. The variability of the environment is neglected. Competition between individuals in a population and among populations as well as the resulting interdependent population dynamics are not taken into account. One might perhaps claim that I study evolution without evolution. I defend my approach with the argument that I wish to study whether and when senescence can be avoided by any conceivable organism. The idea is that if senescence is not inevitable and is only one of many options for the age-patterns of life in optimal equilibrium, then this is a hint that the real world may provide these options as well.

1.2 Background

1.2.1 Senescence - Paradox? - Inevitable?

Life is shaped by evolution as described by Darwin (1964, pg. 5):

> "As many more individuals of each species are born than can possibly survive; and as, consequently, there is a frequently recurring struggle for existence, it follows that any being, if it vary however slightly in any manner profitable to itself, under the complex and sometimes varying conditions of life, will have a better chance of surviving, and thus be *naturally selected*. From the strong principle of inheritance, any selected variety will tend to propagate its new and modified form".

The key players in evolution are survival and reproduction. To reproduce you have to be alive, to be selected you need to reproduce more successfully than your competitors, and finally you have to transmit this ability to your offspring. Senescence is a process of decline in physiological functioning that results in a decrease in survival and/or reproduction with age. Therefore, senescence is an unfavorable process in the struggle for existence. The question arises: Why, then, could it evolve at all? Clearly, senescence did evolve – but did it in all forms of life? This is the burning question I wish to answer from a theoretical perspective. Is senescence an inherent part of life or could it be that some species have escaped senescence?

William D. Hamilton wrote a very influential article in 1966 on "The moulding of senescence by natural selection," in which he claimed that senescence is inevitable. Hamilton states that "no life schedule, even under the most benign ecology imaginable, could escape my spectrum of forces of senescence ... in the farthest reaches of almost any bizarre universe" (Hamilton, 1996, pg. 90). "[F]or organisms that reproduce repeatedly, senescence is to be expected as an inevitable consequence of the working of natural selection" (Hamilton, 1996, pg. 109). Did Hamilton really prove that senescence is inevitable? I will treat this question in Chapters 2 and 3, and the answer is: No, he did not.

1.2.2 Evolutionary theories of senescence

Two main approaches have been developed to explain the evolution of senescence: The first approach assumes that senescence is due to a burden of deleterious

mutations at later ages, whereas the second approach assumes that senescence is a negative byproduct of an adaptive process constrained by trade-offs. Both approaches hinge on the assumption that the force of selection declines with age.[1] The force of selection is determined by differences in reproductive success. The larger the difference in reproductive success between two alternative variants of a trait, the stronger the force of selection on that trait. Reproductive success is determined by survival and reproduction. Consequently, the force of selection is determined by survival and reproduction.

Since death is certain, the number of survivors of a birth cohort declines with age. Medawar (1952) conjectured that, because fewer and fewer individuals survive up to higher and higher ages, those ages matter less and less to lifetime reproductive success, leading to a decline in the force of selection with age. Hamilton (1966) thought he had proved that the force of selection must decline with age, but I will show later that, under some circumstances, the force of selection can increase with age.

Medawar (1952) proposes the theory of mutation accumulation. Mutations occur recurrently. To the extent that reproduction or survival are in any way negatively affected, an individual carrying such a mutation will be at an evolutionary disadvantage relative to non-carriers of that mutation. Clearly, the force of selection would tend to wipe out deleterious mutations. However, as the force of selection peters out, bad mutations manage to creep in, being less and less strongly opposed by evolutionary forces. Medawar argues that the smaller the force of selection, the more mutations would accumulate.

Williams (1957) proposes the theory of antagonistic pleiotropy after the basic idea was initially formulated by Medawar (1952, pg. 64). Like the theory of mutation accumulation, Williams's approach is based on the precondition that the force of selection decreases with age. Genes are considered that have fitness enhancing effects earlier in life and fitness depressing effects later in life. Because the force of selection decreases with age, the advantage early in life receives a much stronger weighting than the disadvantage late in life. Unlike the passive process underlying mutation accumulation, mutations are actively selected that imply a deleterious effect at older ages, since the balance between costs and

[1] I give a limited proof in Appendix A that, if selection pressure increases, then the optimal life history has to be non-senescent. It is not clear for the general case whether an optimal life history could be senescent at an age when selection pressure increases.

benefits favors younger ages.

Note that the general idea underlying antagonistic pleiotropy is to actively balance linked traits that affect survival and reproduction in opposite ways. Genes with antagonistic and pleiotropic effects are a specific case of a trade-off affecting fitness. The general idea of trade-offs underlies the disposable soma theory proposed by Thomas Kirkwood (Kirkwood (1977), Kirkwood (1981)). Kirkwood's approach is based on the observation that the critical part of an individual that must survive is the genetic code. The genetic code contains all information needed to ensure the persistence of a lineage. It is therefore economic to separate the germ cells from the rest of the body cells, the soma, and to protect only the germ line from the ubiquitous occurrence of damage. The soma merely serves as a vehicle for the genetic code to be transported over generations. Kirkwood conjectures that the costs required for the persistent repair of the soma is too high and evolution therefore trades off the protection of the germ line against senescence of the soma.

1.2.3 Measuring senescence

Senescence can be defined as a decline in physiological functioning with age that negatively affects the ability to survive and/or to reproduce. There is, however, no generally agreed upon measure of senescence.

One approach to measure senescence is to look at the change in mortality with age. In this case, senescence corresponds to an increase in mortality with age. This is a simple and widely accepted working definition (Finch, 1990, pg. 12).

Since mortality and fertility are closely linked, an ultimate measure of senescence should include both survival and reproduction. Partridge and Barton (1996) suggest using the reproductive value at age a to determine the state of senescence of an individual. The reproductive value captures the remaining reproductive contribution of an individual that is alive at age a. It was defined by Fisher (1930) as

$$v(a) = \frac{e^{r\,a}}{l(a)} \int_a^\infty e^{-r\,x}\, l(x)\, m(x)\, dx. \tag{1.1}$$

The survival function $l(x)$ indicates the probability of survival from birth (or conception) to age x and the maternity function $m(x)$ indicates age-specific reproduction. Age-specific survival and reproduction are weighted by the population

growth term $e^{-r\,x}$, which discounts future reproduction by the intrinsic rate of population increase r (see Appendix B). The integral sums up all reproductive contributions from age a onwards. Multiplication by $e^{r\,a}/l(a)$ accounts for the fact that the individual has already survived to age a.

Senescence in this framework corresponds to cases when the reproductive value declines with age, i.e. the derivative of $v(a)$ given in Equation 1.1 with respect to age is negative,

$$\frac{dv(a)}{da} \,<\, 0. \tag{1.2}$$

Applying the product and chain rule from basic calculus yields

$$\begin{aligned}\frac{dv(a)}{da} \,=\, r\,\frac{e^{r\,a}}{l(a)} \int_a^\infty e^{-r\,x}\,l(x)\,m(x)\,dx \\ -\,\frac{e^{r\,a}}{l^2(a)}\,\frac{dl(a)}{da} \int_a^\infty e^{-r\,x}\,l(x)\,m(x)\,dx \\ -\,\frac{e^{r\,a}}{l(a)}\,e^{-r\,a}\,l(a)\,m(a) \,<\, 0.\end{aligned} \tag{1.3}$$

Note that the probability of survival to age a, $l(a)$, is determined by the age-trajectory of mortality $\mu(x)$ from age zero to age a through the relation

$$l(a) \,=\, e^{-\int_0^a \mu(x)\,dx}. \tag{1.4}$$

Thus, Equation 1.3 can be simplified by substituting

$$\mu(a) \,=\, -\frac{\frac{dl(a)}{da}}{l(a)} \tag{1.5}$$

as well as substituting expression 1.1 for the reproductive value, which leads to

$$\frac{dv(a)}{da} \,=\, r\,v(a) \,+\, \mu(a)\,v(a) \,-\, m(a) \,<\, 0 \tag{1.6}$$

and after rearranging

$$v(a) \,<\, \frac{m(a)}{\mu(a)+r}. \tag{1.7}$$

Note that, if mortality and fertility do not change with age , i.e. $m(a) = m$ and $\mu(a) = \mu$, then the reproductive value is constant at the level

$$v(a) \,=\, \frac{m}{\mu+r} \tag{1.8}$$

for all ages a. Conditions 1.7 and 1.8 imply that senescence occurs if the reproductive value at age a is lower than it would be if both mortality and fertility remained constant from that age onwards. Clearly, if mortality and fertility are constant, then the organism does not senesce. Condition 1.7 implies that at least one of the two fitness components is adversely affected, which is intuitively appealing.

The change in reproductive value with age accounts for both the change in mortality and fertility, which is a favorable argument for its use as a measure of senescence. However, condition 1.7 takes into account the whole remaining life history. It seems more reasonable that the state of senescence of an individual at a certain age interval should be determined by changes in mortality and fertility at that specific age interval alone without any knowledge about the future. Furthermore, note that the population growth rate r enters the measure of senescence if reproductive value is used to account for the senescent state of an individual. But why should the population growth rate influence the definition of senescence? This issue disappears under the optimal equilibrium assumption since $r = 0$.

An alternative definition of senescence can be derived that accounts only for changes in the state of an individual at the current age interval, determined by mortality and fertility. Senescence corresponds to cases where mortality increases while reproduction is constant or decreases with age. The same is true if mortality does not change with age but fertility decreases. On the other hand, no senescence is observed if mortality decreases or remains constant and fertility increases or remains constant.

If mortality and fertility both increase, or both decrease, one has to be careful. If, for instance, fertility increases but mortality increases even more, then the loss in survival outweighs the gain in reproduction. If, on the other hand, mortality decreases, say, at a rate of -2% but fertility decreases even more, say, at a rate of -4%, then the gain in survival is more than erased by the loss in reproduction, i.e. $-4\% < -2\%$. In sum, senescence is conditioned by the fact that the change in mortality exceeds the change in fertility.

Formally, this can be expressed by comparing the relative change in mortality with the relative change in fertility. Relative changes are used to produce comparable quantities with the same units; change per time. The relative change in

mortality is given by

$$\frac{\frac{d\,\mu(a)}{da}}{\mu(a)} \equiv \acute{\mu}(a), \tag{1.9}$$

and the change in mortality over age relative to the current level of mortality is denoted by the short hand notation $\acute{\mu}(a)$. The same holds analogously for fertility $m(a)$.

In general, senescence is observed if the relative change in mortality is greater than the relative change in fertility at age a, i.e.

$$\acute{\mu}(a) > \acute{m}(a). \tag{1.10}$$

Table 1.1 summarizes the cases for senescence vs. non-senescence [2].

Tab. 1.1: Senescence or not

	$\acute{m}(a) > 0$	$\acute{m}(a) = 0$	$\acute{m}(a) < 0$
$\acute{\mu}(a) > 0$	sen if $\acute{\mu}(a) > \acute{m}(a)$ not if $\acute{\mu}(a) \leq \acute{m}(a)$	sen	sen
$\acute{\mu}(a) = 0$	not	not	sen
$\acute{\mu}(a) < 0$	not	not	sen if $\acute{\mu}(a) > \acute{m}(a)$ not if $\acute{\mu}(a) \leq \acute{m}(a)$

The burning question of my dissertation is whether the lower "triangle" in Table 1.1 is filled with life. Are there life histories that lack senescence which have been evolutionarily more successful than life histories with senescence? The first step on the way to answering this question is to determine how to measure "fitness", i.e. the evolutionary success of a strategy.

[2] Carey et al. (1992) point out that mortality patterns of medflies fluctuate up and down with age, which would correspond to "alternating periods of positive and negative senescence. It is questionable whether it is helpful to define the word senescence in this way." I agree that short-term fluctuations in mortality may not indicate positive vs. negative senescence. Consequently, in defining senescence as in 1.10, it is important to consider changes in mortality and fertility over reasonable age intervals, which should be determined relative to a species' lifespan.

1.2.4 Measuring fitness

The notion "fitness" captures the reproductive success of a genotype. Reproductive success results in population growth. Fitness is therefore often measured by the intrinsic rate of population increase, r, which is implicitly defined by the Lotka equation,

$$1 = \int_0^\infty e^{-r\,a}\, l(a)\, m(a)\, da. \tag{1.11}$$

From the beginning of life until the end, this integral sums up age-specific reproduction $m(a)$, which can only be realized if an individual is alive at age a, captured by $l(a)$. Furthermore, later-born offspring are discounted by population growth ($e^{-r\,a}$) because earlier-born offspring contribute relatively more to future generations. The value of r that uniquely satisfies this equation for given schedules of $l(a)$ and $m(a)$ is the intrinsic rate of population increase. An extensive treatment of the Lotka equation can be found in Appendix B.

Another frequently used measure of fitness is the net reproductive rate, R, given by

$$R = \int_0^\infty l(a)\, m(a)\, da. \tag{1.12}$$

Note that R counts the number of offspring produced per lifetime, accounting for survival. This measure of fitness is appropriate when the population size does not change. Otherwise, the intrinsic rate of population increase is more appropriate.

Both fitness measures hinge on the underlying assumptions of stable population theory. In his famous equation Lotka assumes a homogeneous population that is closed to migration. Either individuals are of one sex or individuals of only one sex determine r and R. Birth and death rates are constant over time and the environment is unchanging. There are no density effects. Intergenerational transfers such as parental care are neglected.

In the 1970s Brian Charlesworth, building on Haldane (1927) and Norton (1928), justified the use of r as a fitness measure. The results of Charlesworth (1973) show that in an age-structured, diploid, randomly mating population r can be associated with the fate of a rare, nonrecessive gene. In Charlesworth (1974) he gives approximations that are otherwise necessary. A comprehensive treatment can be found in Charlesworth (1994, Section 4.6.1), first published in 1980.

The use of the intrinsic rate of population increase, r, is accepted as a rea-

sonable working assumption (Charlesworth, 1994, 2000; Rose, 1991) for cases of constant and density-independent environments, but one must be aware of its restrictions (see Chapter 6).

1.2.5 Optimal life history

An optimal life history is captured by the age-trajectories of survival and reproduction that maximize fitness. Fitness can be measured by the intrinsic rate of population increase r and is determined by the schedules of survival and reproduction. In this context it is important to highlight that optimal life-history schedules depend, in turn, on the level of r (Goodman, 1982). If a population grows quickly, later births are devalued heavily and therefore a short generation time are favored. This strategy might differ substantially from a strategy that maximizes fitness in a non-growing, stationary population.

In my work, I will assume a population that is in long-term optimal equilibrium. I will not consider the evolutionary process of getting there and I will exclude the possibility that an equilibrium might never be reached. This is a simplified but reasonable assumption because, on an evolutionary time scale, any small deviation from $r = 0$ will have strong consequences: *"...any being, if it vary however slightly in any manner profitable to itself, under the complex and sometimes varying conditions of life, will have a better chance of surviving, and thus be naturally selected."* (Darwin, 1964, pg. 5). Many species have been around for a long time and, consequently, their life histories should be close to those in optimal equilibrium because otherwise the species would be ubiquitous or extinct.

Taylor et al. (1974) analytically proved that "*[m]aximizing the reproductive value at age zero is mathematically equivalent to maximizing the ultimate rate of increase*". Here r is referred to as the ultimate rate of increase in order to emphasize that this is the rate to which a population's growth rate will ultimately converge (see Appendix B). Discussion of the theorem was raised by Caswell (1980), who claimed that this would hold only under some very specific conditions. Yodzis (1981) clarified the issue and showed that Taylor et al. (1974) were generally right. However, he also pointed out the critical restrictions. First, maximizing the reproductive value gives only a local maximum of r. Second, the use of r as a fitness measure is an issue in itself. And third, the consequences of population regulation mechanisms, such as predation and density effects, are not

taken into account.

For $r = 0$ the reproductive value given in Equation 1.1 at age $a = 0$ equals the net reproductive rate R given in Equation 1.12, which is an alternative measure of fitness to r (see Section 1.2.4). Following Taylor et al. (1974)'s result, maximizing R is equivalent to maximizing r such that $r_{max} = 0$.

Maximizing life-time reproduction R with respect to any trait X can be formally expressed by the condition

$$\frac{d\,R}{dX} \;=\; 0. \tag{1.13}$$

If trait X is independent of age and affects both survival, $l(a, X)$, and reproduction, $m(a, X)$, at various ages, then together with Equation 1.12 this condition yields

$$\int_0^\infty \left(\frac{\partial l(a,X)}{\partial X}\, m(a,X) \;+\; \frac{\partial m(a,X)}{\partial X}\, l(a,X) \right) \, da \;=\; 0. \tag{1.14}$$

Extracting the product $l(a, X)\, m(a, X)$ and using the shorthand notation

$$\frac{\frac{\partial l(a,X)}{\partial X}}{l(a,X)} \;\equiv\; \acute{l}_X(a,X) \tag{1.15}$$

for the relative change in survival with respect to trait X and an analogous notation for the relative change in reproduction, the condition can be expressed as

$$\int_0^\infty \left(\acute{l}_X(a,X) \;+\; \acute{m}_X(a,X) \right) \, l(a,X)\, m(a,X)\, da \;=\; 0. \tag{1.16}$$

Finally, note that dividing by the life-time reproduction given in Equation 1.12 yields the average value (indicated by the bar) of the relative change (indicated by the acute accent) in survival,

$$\frac{\int_0^\infty \; \acute{l_X}(a,X)\, l(a,X)\, m(a,X)\; da}{\int_0^\infty \; l(a,X)\, m(a,X)\; da} \;\equiv\; \bar{\acute{l}}(a,X), \tag{1.17}$$

and analogously for reproduction. Consequently, condition 1.13 is equivalent to

$$\bar{\acute{l}}_X(a,X) + \bar{\acute{m}}_X(a,X) = 0. \tag{1.18}$$

The value of X that maximizes fitness corresponds to the point where the average relative change in survival plus the average relative change in reproduction with

respect to trait X equals zero.

If trait $X(a)$ only affects survival and reproduction at a specific age a, i.e. $l(x, X(a))$ and $m(x, X(a))$, then Equation 1.14 reduces to

$$\frac{d\,\mu(a,\,X(a))}{dX(a)}\,v(a) \;=\; \frac{d\,m(a,\,X(a))}{dX(a)}. \tag{1.19}$$

The value of $X(a)$ that maximizes fitness corresponds to the value where the change in mortality $\mu(a, X(a))$ with respect to trait $X(a)$ at age a times the reproductive value $v(a)$ at age a equals the change in reproduction $m(a, X(a))$ with respect to the trait at age a.

There are alternative ways to find the optimal schedule for a trait. Being optimal implies achieving the best life history strategy over the entire lifespan, which is equivalent to doing this at every age. Since the future does not influence the past, the optimal strategy at every age is to maximize

$$\textit{current reproduction} + \textit{survival to next age} \;\cdot\; \textit{remaining reproduction} \tag{1.20}$$

assuming the individual is alive at that age. Maximizing this quantity is equivalent to maximizing the current reproductive value given by Equation 1.1, which can be seen using the discrete-time formulation

$$v_a \;=\; \frac{e^{r\,a}}{l_a}\;\sum_{i=a}^{\infty}\; e^{-r\,i}\,l_i\,m_i. \tag{1.21}$$

Extracting the first term from the sum yields

$$v_a \;=\; m_a \;+\; \frac{e^{r\,a}}{l_a}\;\sum_{i=a+1}^{\infty}\; e^{-r\,i}\,l_i\,m_i.$$

Multiplying the sum by a factor of $1 = \frac{l_{a+1}e^{r}}{l_{a+1}e^{r}}$ and letting $p(a)$ be the probability of surviving from age a to $a+1$, $p(a) = l(a+1)/l(a)$, the nature of the general life history trade-off becomes apparent:

$$v_a \;=\; m_a \;+\; p(a)\,e^{-r}\,v_{a+1}. \tag{1.22}$$

The first term captures the profits obtained from current reproduction, m_a. The second term captures the future prospects. The future prospects depend on

the chance of getting there, i.e. surviving the age interval ($p(a)$, discounted by population growth e^{-r}) and future reproductive potential, which is reproductive value v_{a+1} at the next age (see Charlesworth (1994, Chapter 5) for review).

Current reproduction trades off with future survival and reproduction. On the one hand, this trade-off could be due to a direct negative effect of reproduction on survival. Mating activities, for instance, could be risky. Also, reproduction could cause damage that negatively affects future breeding attempts. Whereas this direct negative effect is not necessarily observed in all species, a negative indirect link becomes apparent if survival and reproduction are understood as distinct processes that compete for limited resources.

Schaffer (1983) stated that the *general life-history problem* is to allocate restricted resources between survival and reproduction in a way that maximizes an individual's fitness. To approach this problem Williams (1966) introduced the reproductive effort model, where reproductive effort is defined as the fraction of energy devoted to reproduction. Williams (1966) conjectured that, at every age, resources are allocated to maximize the remaining reproductive contribution of an individual that already survived to that age, i.e. the reproductive value. From Bellman's principle (see Bellman (1965) and Section 4.3 of this manuscript) we know that maximizing reproductive value at every age is equivalent to maximizing reproductive value at age zero. In that way Williams (1966) anticipated Taylor et al. (1974)'s result that "*[m]aximizing the reproductive value at age zero is mathematically equivalent to maximizing the ultimate rate of increase*". Extensive treatments of the evolution of optimal life histories can be found in Stearns (1992) and Roff (2002).

I want to emphasize how reproductive value emerges again and again as an important quantity. Not only was it proposed as a measure of senescence (Partridge and Barton, 1996) – it was also proved to be a measure of fitness (Taylor et al., 1974) and a central quantity for solving the general life-history problem (Williams, 1966).

1.2.6 Interesting recent developments

In Chapters 4 and 5, I will develop models to explain the evolution of senescence that focus on the age-patterns of mortality, fertility and growth using the concepts outlined above. Reproductive-effort models were developed in the 1970s

to understand when iteroparity (repeated breeding) is favored over semelparity (single breeding event, in which reproduction is fatal) (see Gadgil and Bossert (1970), Schaffer (1974) and Charlesworth and Leon (1976)). The shape of the age-trajectory of mortality itself attracted little interest. Instead, mortality was assumed to follow a particular pattern, for example to be constant, to be stepwise constant (distinguishing only between a juvenile and an adult period) or to follow an exponential pattern.

Some recent models of the evolution of senescence, however, do focus on the age-trajectory of mortality in conjunction with age-trajectories of growth, reproduction and transfers. These models draw heavily on the concept of allocation of restricted resources and on dynamic optimization techniques (see Bellman (1965) and Section 4.3).

Abrams and Ludwig (1995) develop a theoretical model based on the disposable soma theory (Kirkwood, 1981) and find that many different mortality trajectories can be optimal, an exponential increase being only one possible outcome. The model, however, does not allow for a decline in mortality with age.

Mangel and Bonsall (2004) also show that a diversity of optimal mortality trajectories is possible when mortality is viewed as a result of multiple physiological processes as well as when mortality is the consequence of growth and metabolism and associated damage. In their model, mortality can decrease over some ages before it ultimately increases. Another recent model by Mangel and Munch (2005) that focuses on compensatory growth derives mortality as result of growth and damage. The approach taken by Mangel and colleagues shows that optimal age-patterns of mortality can decrease if mortality is, at least in part, determined by physiological state. They point out the importance of "reunifying the connections between the biology of aging and demography" (Mangel and Bonsall, 2004, pg. 357).

Dynamic programming models that optimize resource allocation to growth, reproduction and repair of somatic damage based on the disposable soma theory of aging have been studied intensively by Kozlowski (1996), Cichon (1997), Kozlowski and Teriokhin (1999), Cichon and Kozlowski (2000) and Cichon (2001). Their models do not allow mortality to decline with age. Drenos and Kirkwood (2005) also describe a mathematical model based on the disposable soma theory. In their model the optimal level of investment in repair is always less than that required for non-senescence.

An approach that explicitly questions when senescence can be escaped is given by Gardner and Mangel (1997). They develop a stage-based model and find that the strength of selection can, under some circumstances, increase with age for clonal organisms.

Travis (2004) claims that, in a spatially structured population, a determinate lifespan can evolve with an optimal specific age of death, but in a freely mixing population with global dispersal evolution selects for individuals with ever-increasing lifespan. In a working paper, Doncaster and Seymour (2005) demonstrate that ever-extending reproductive life can be optimal in populations with density regulated recruitment, e.g., in the case of Bristlecone Pines. If seeds can be established only on a patch freed by the death of an adult, it pays to outlive your neighbors to ensure that your offspring can occupy the newly opened space.

Sozou and Seymour (2004) show that mortality does not necessarily have to increase, i.e. that non-senescence can be locally optimal, if the potential onset of deterioration is sufficiently rapid or early. Interestingly, they find that "for all forms of profile considered, conditions can be found for which a strategy involving no ageing is locally optimal".

In a recent paper, Chu and Lee (2006) study the conditions under which transfers from adult to offspring can be optimal. Applying dynamic optimization techniques and the idea of optimal resource allocation, they model the co-evolution of survival and transfers. A recent working paper by Robson and Kaplan (2005) derives a dynamic optimization model for the evolution of the human mortality pattern incorporating investment in quantity and quality of somatic capital and a budget constraint that reflects intergenerational transfers. These models can explain why mortality declines during development and why evolution licences a substantial period of post-reproductive life in humans.

With the models I am going to develop, I will not be focusing on a single species such as humans. I wish to understand more generally under what conditions what pattern of mortality can be expected. In particular, I want to study if and when non-senescence can be optimal. My dissertation is the first systematic attempt to find the characteristics that determine when senescence is optimal and when it is not. I will not focus on lifespan. A species with a short lifespan can still have a non-senescent life history. The length of life only reflects different time scales that different species live on. This would be a different question: When is

it optimal to live on what time scale? Instead I ask: When is it optimal to live under what qualitative mortality pattern?

My modeling strategy is to exploit the power of focused simplicity. The models will be kept as simple as possible, including only necessary ingredients that are chosen based on my particular question.

1.3 Orientation

In the following two chapters I discuss Hamilton's paper on the molding of senescence (Hamilton, 1966), disproving his dogmatic claim that senescence is inevitable and pointing out deficiencies of Hamilton's framework. Given the theoretical issues and empirical evidence, I come to the conclusion that life histories are likely to be shaped largely by optimization rather than by a burden of deleterious mutations, at least over ages where the bulk of life-time reproduction is realized.

In the subsequent two chapters, I develop optimization models to determine the optimal pattern of survival and reproduction over the life course of a species. The models in Chapter 4 are based on the state-variable size. The Chapter makes the case for negative senescence, i.e. the models show that, theoretically, senescence is not an inherent part of life. The model in Chapter 5 is built around the state-variable "vitality" and takes into account and addresses some of the deficiencies of the size-based models. The vitality model demonstrates that the space of optimal life histories is wide and covers a broad range of senescent and non-senescent strategies.

The final chapter, Chapter 6, emphasizes the need to connect the world of mutation accumulation and the world of optimization. I also suggest directions for future research on the evolution of senescence.

Part I

HAMILTON

2. HAMILTON'S INDICATORS OF THE FORCE OF SELECTION

2.1 Introduction

To quantify the force of selection, Hamilton derived expressions for the change in fitness with respect to age-specific mutations. Hamilton's indicators are decreasing functions of age. He concluded that senescence is inevitable: survival and fertility must decline with age. I show that an alternative parametrization of mutational effects leads to indicators that can increase with age. I then consider the case of deleterious mutations with age-specific effects. In this case, it is the balance between mutation and selection pressure that determines the equilibrium number of mutations in a population. In this balance the effects of different parameterizations cancel out, but only to a linear approximation. I show that mutation accumulation has little impact at ages when this linear approximation holds. When mutation accumulation matters, nonlinear effects become important and the parameterizations of mutational effects make a difference. The results also suggest that mutation accumulation may be relatively unimportant over most of the reproductive lifespan of any species.

Senescence can be defined as an increase in mortality and/or a decrease in fertility with age. Is senescence a universal characteristic of life? It is not obvious from an evolutionary perspective why it should be. Early in life, when individuals develop and grow, mortality falls and reproductive potential increases. Why is it that these age-patterns cannot persist, in some form, with mortality continuing to decline and reproductive capacity continuing to increase? George C. Williams (Williams, 1957, pg. 398) wrote:

" It is indeed remarkable that after a seemingly miraculous feat of morphogenesis a complex metazoan should be unable to perform the much simpler task of merely maintaining what is already formed".

William D. Hamilton's influential article on "The Moulding of Senescence by Natural Selection" (Hamilton, 1966, Hamilton, 1996) provides a reason why senescence "cannot be avoided by any conceivable organism". Hamilton combines insights about the evolution of senescence (Medawar, 1952, Williams, 1957) with concepts and models of population dynamics (Lotka, 1924). Hamilton asserts that " senescence is an inevitable outcome of evolution". Did Hamilton genuinely prove that senescence is theoretically inevitable?

2.2 Hamilton's derivations

How does a mutation that acts only at a specific age a influence the evolutionary success of an individual? Does it matter if this age is early or late in life? Hamilton (1966) built on the insight of Medawar (1952) that later-acting genes should be under weaker selection than earlier-acting ones due to the unavoidable decline in the number of survivors at higher and higher ages. A genetically-determined fatal disease that struck only at post-reproductive ages would be entirely out of reach of the force of selection.

2.2.1 The framework

To quantify the force of selection Hamilton considered age-specific, mutation-induced changes in fitness. Hamilton used the most widely-accepted measure of Darwinian fitness, the intrinsic rate of population increase r, implicitly defined by the discrete version of the Lotka equation

$$\sum_{x=0}^{\infty} e^{-r\,x}\, l_x\, m_x \;=\; 1. \tag{2.1}$$

The function l_x gives the chance of survival to age x. The function m_x measures the amount of reproduction at that age. If the population is stable, as assumed by Hamilton, then each combination of an age-specific maternity function m_x and an age-specific survival function l_x is associated with exactly one real r that satisfies Equation 2.1. The survival function l_x is defined as the product of the probabilities p_a of survival from age a to $a+1$:

$$l_x \;=\; p_0\, p_1\, \ldots\, p_{x-1}, \tag{2.2}$$

with

$$l_0 \;=\; 1.$$

The age-specific survival probabilities p_a depend on the instantaneous death rate μ_t, the force of mortality between age a and $a+1$, via

$$p_a \;=\; e^{-\int_a^{a+1} \mu_t\, dt} \;=\; e^{-\bar{\mu}_a}. \tag{2.3}$$

The cumulative mortality in the exponent reflects the average mortality during that time interval, denoted by $\bar{\mu}_a$.

2.2.2 Hamilton's indicator of survival

By taking the derivative of Equation 2.1 with respect to $\ln p_a$ and rearranging, Hamilton derived his basic result:

$$H^\dagger \equiv \frac{d\,r}{d\,\ln p_a} = \frac{\sum_{x=a+1}^{\infty} e^{-r\,x}\,l_x\,m_x}{\sum_{x=0}^{\infty} x\,e^{-r\,x}\,l_x\,m_x}. \tag{2.4a}$$

Note that Equation 2.3 implies that $H^\dagger$ can also be expressed as:

$$H^\dagger \equiv -\frac{d\,r}{d\,\bar{\mu}_a}. \tag{2.4b}$$

The value of $H^\dagger$ is a measure of the force of selection. It captures the change in fitness r induced by an increase in $\ln p_a$. An increase in $\ln p_a$ is equivalent to a reduction in average mortality $\bar{\mu}_a$ between age a and $a+1$. This sensitivity of fitness to changes in age-specific survival is captured by the ratio of remaining reproduction, the numerator in Equation 2.4a, to generation time, the denominator. Because $H^\dagger$ declines as age increases, Hamilton concluded that the force of selection must decline with age.

2.3 Alternative indicators

2.3.1 Different parametrization

Hamilton's conclusion hinges on the particular parametrization he chose for the nature of the effect of a mutation. Equally reasonable, alternative forms would have been dr/dp_a, dr/dq_a, $dr/d\ln q_a$ or $dr/d\ln\bar{\mu}_a$, where q_a is the probability of dying ($q_a = 1 - p_a$) and $\bar{\mu}_a$, as noted above, equals $-\ln p_a$. The results are as follows:

$$\frac{d\,r}{d\,p_a} = \frac{1}{p_a}\,H^\dagger, \tag{2.5a}$$

$$\frac{d\,r}{d\,q_a} = -\frac{1}{p_a}\,H^\dagger, \tag{2.5b}$$

$$\frac{d\,r}{d\,\ln q_a} = -\frac{q_a}{p_a}\,H^\dagger \tag{2.5c}$$

and

$$\frac{d\,r}{d\,\ln\bar{\mu}_a} \;=\; -\,\bar{\mu}_a\;H^{\dagger}. \tag{2.5d}$$

Strikingly, the expressions in Equation 2.5a-d can increase in absolute value with age – in contrast to $H^{\dagger}$, which always declines.

2.3.2 When selection pressure increases

Consider, for instance, Equation 2.5d. At pre-reproductive ages the value of $dr/d\ln\bar{\mu}_a$ is entirely determined by $\bar{\mu}_a$, as $H^{\dagger}$ is constant before maturity. At reproductive ages the change in fitness with respect to mortality increases from age a to $a+1$ if

$$\left|\frac{d\,r}{d\,\ln\bar{\mu}_a}\right| \;<\; \left|\frac{d\,r}{d\,\ln\bar{\mu}_{a+1}}\right|.$$

Substituting Equation 2.5d and 2.4a, and using the notion of reproductive value,

$$v_a = \frac{e^{r\,a}}{l_a}\;\sum_{x=a}^{\infty}\;e^{-r\,x}\,l_x\,m_x, \tag{2.6}$$

this inequality can be rearranged to give the following condition,

$$\left(\frac{\bar{\mu}_{a+1}\;-\;\bar{\mu}_a}{\bar{\mu}_{a+1}}\right)\frac{v_{a+1}}{m_{a+1}} \;>\; 1. \tag{2.7}$$

Hence, the value of $dr/d\ln\bar{\mu}_a$ will increase with age if $\bar{\mu}_a < \bar{\mu}_{a+1}$ and if future reproductive value is sufficiently large compared to fertility m_{a+1}. Taking into account the fact that Equation 2.1 must hold, the inequality in Equation 2.7 can be rearranged as

$$\left(\frac{\bar{\mu}_{a+1}\;-\;\bar{\mu}_a}{\bar{\mu}_{a+1}}\right)\frac{e^{r(a+1)}}{l_{a+1}}\left(1\;-\;\sum_{x=0}^{a}\;e^{-r\,x}\,l_x\,m_x\right) \;>\; m_{a+1}. \tag{2.8}$$

This inequality determines trajectories for m_{a+1} that lead to increasing sensitivity of fitness to changes in mortality over age given a specified, increasing path for $\bar{\mu}_a$. The survival and fertility functions plotted in Figure 2.1 and the resulting indicators $dr/d\ln\bar{\mu}_a$ and $dr/d\ln p_a$ plotted in Figure 2.2 provide an illustrative example.

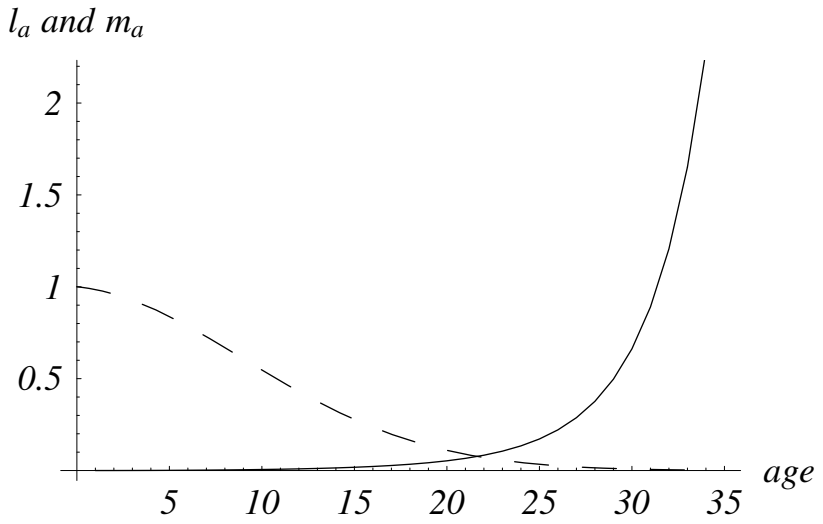

Fig. 2.1: **Example of survival and maternity functions l_a and m_a.** If age-specific survival probabilities p_a change according to $p_a = p_0^a$ with $p_0 < 1$, then the average force of mortality between age a and $a+1$ is given by $\bar{\mu}_a = -\ln p_0^a = -a \ln p_0$. Maternity m_{a+1} was chosen to be 0.01 units smaller than the left-hand side of the inequality in Equation 2.8, setting $r = 0$, $p_0 = 0.99$ and $m_0 = 0$. By age 34, survival falls to 0.25%. After age 34, I fixed age-specific survival p_a at its level of $p_{35} = 0.70$ corresponding to $\bar{\mu}_{35} = 0.35$ and adjusted m_a to a constant level of 133.265 such that Equation 2.1 is fulfilled.

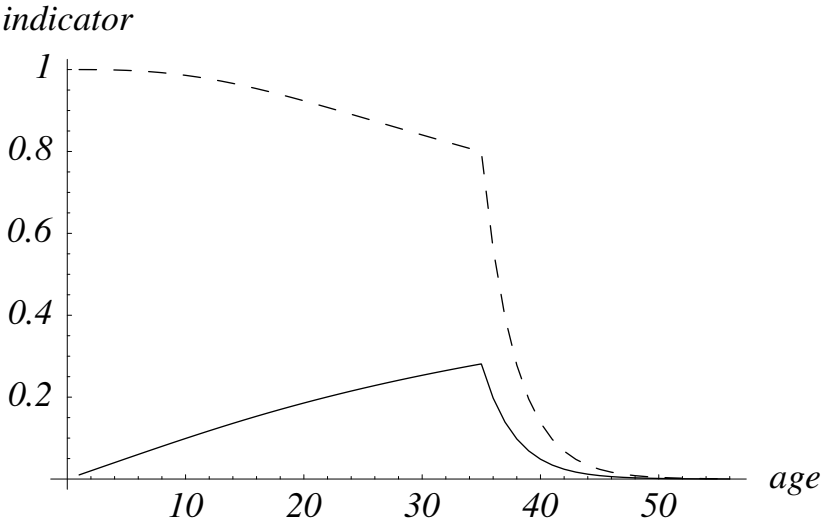

Fig. 2.2: **Comparison of $H^\dagger = \frac{dr}{d \ln p_a}$ (dashed line) with $\frac{dr}{d \ln \bar{\mu}_a}$ (solid line).** While Hamilton's indicator $H^\dagger$ declines, the alternative one increases until age 34. The increase would have continued if m_{a+1} had been further determined by the inequality in Equation 2.8. This, however, would result in a trajectory for m_a that would rise to enormous heights. Also note that Hamilton's indicator is greater than the alternative indicator, especially before age 35. This implies a considerably stronger force of selection on age-specific mutations that affect mortality.

Tab. 2.1: Various indicators of the force of selection in Hamilton's framework

Indicator	Change with age a
$\frac{d\,r}{d\,\ln p_a}$	$-$
$\frac{d\,r}{d\,p_a}$	$+$ or $-^*$
$\frac{d\,r}{d\,q_a}$	$+$ or $-$
$\frac{d\,r}{d\,\ln q_a}$	$+$ or $-$
$\frac{d\,r}{d\,\ln \bar{\mu}_a}$	$+$ or $-$
$\frac{d\,r}{d\,m_a}$	$-$
$\frac{d\,r}{d\,\ln m_a}$	$+$ or $-$

* "+ or −" means that the change with age can be positive or negative, depending on the trajectories of m_x and l_x.

2.3.3 *Fertility indicators*

The quantity Hamilton derived for the force of selection on age-specific mutations that affect fertility is

$$H^* \equiv \frac{d\,r}{d\,m_a} = \frac{e^{-r\,a}\,l_a}{\sum_{x=0}^{\infty} x\,e^{-r\,x}\,l_x\,m_x}. \tag{2.9}$$

Hamilton considered survival effects on a log scale: He could have done the same for reproduction, calculating

$$\frac{d\,r}{d\,\ln m_a} = m_a\,H^*. \tag{2.10}$$

Hamilton's indicator in Equation 2.9 necessarily declines with age but the alternative indicator in Equation 2.10 can increase with age, depending on the trajectory of m_a.

Table 2.1 summarizes the direction of changes over age of the various indicators of the force of selection. The differences in the dynamics are due to the nonlinearity of logarithmic and exponential transformations.

2.3.4 Are some indicators better?

Charlesworth (1994, p.191), who reconstructed Hamilton's results, suggested that "genetic effects on survival probabilities are more likely to be additive on a log scale." His conjecture implies that mutations have additive effects on mortality. Indeed, both of Hamilton's indicators $H^\dagger = -dr/d\bar{\mu}$ and $H^* = dr/dm$ can be interpreted as assuming that mutations additively affect average mortality $\bar{\mu}$ and fertility m. This is plausible because additive risk models are widely used, most commonly in evolutionary modeling (Caswell, 2001; Charlesworth, 2001). The indicators $\bar{\mu}H^\dagger$ and mH^* capture the effect of a proportional change in $\bar{\mu}$ and m. Proportional-hazard models in general and Cox proportional-hazard models (Cox, 1972) in particular are frequently used in demographic and epidemiological research.

Deleterious mutations influence the internal condition of an organism. Internal conditions are known to interact with the environment (Resznick et al., 2004; Williams and Day, 2003). These interactions affect mortality in a non-additive manner. The idea that traits are likely to combine non-additively is also supported by recent work by Promislow (2004) and Spencer and Promislow (2005) which concerns the network structure of genes and epistasis respectively.

Whether age-specific mutations act proportionally or additively has been a question for empirical research. Support for the preeminence of proportional hazards comes from *Drosophila*. The study by Promislow et al. (1996) of additive genetic variance favors proportional hazards. In Good and Tatar (2001) and Mair et al. (2003) change in current nutrient conditions affects mortality in a proportional manner. Furthermore, many mutants extend lifespan in *Drosophila* because they reduce mortality proportionally (Lin et al. (1998), Rogina et al. (2000) and Hwangbo et al. (2004)). An exception is the work on the mutant chico by Tu et al. (2002). Evidence for proportional hazards also comes from baboons (Bronikowski et al., 2002) and mice (Flurkey et al., 2001) [1].

Numerous demographic and epidemiological analyses of risk factors have found that proportional effects are more common than additive effects. In particular, the impact of genetic polymorphisms, such as ApoE 2, 3 and 4, on mortality has been modeled by proportional hazards (Gerdes et al., 2000). Empirical results

[1] I thank Marc Tatar for emphasizing the preeminence of proportional hazards and for pointing me to the relevant empirical evidence.

reviewed by Promislow and Tatar (1998) support the proportional-hazard assumption, suggesting that mutations act additively on log-mortality rather than log-survival. Hence, it seems plausible that the indicators $\bar{\mu}H^{\dagger}$ and mH^{*} will prove at least as valid as Hamilton's indicators.

2.3.5 Optimization vs. mutational burden

How mutations affect fitness is the focus of a vast literature (Bürger, 2000; Charlesworth, 1994; Crow and Kimura, 1970; Ewens, 1979; Haldane, 1937, 1957; Kingman, 1980). Since Medawar (1952) and Hamilton (1966), many biologists have considered the sensitivity of fitness with respect to age-specific changes in survival or fertility (Caswell, 2001) as an indicator of selection pressure. A key issue is whether age-patterns of mortality and fertility are molded by adaptive optimization processes or by the burden of non-adaptive mutations (Abrams, 1991; Charlesworth, 1994; Partridge, 2001; Partridge and Barton, 1993). Note that, in either case, an increase in mortality or a decrease in fertility is a byproduct of evolutionary processes. In the former case, senescence can arise as a side effect of an optimal balance between linked traits that effect fitness, and in the latter case senescence emerges as the weakening selection pressure is less and less successful in eradicating deleterious mutations.

Optimization models can be solved without using Hamilton's indicators (Vaupel et al., 2004). If the age-patterns mainly reflect the age-specific burden of mutations, then Hamilton's indicators are not sufficient. Age-specific levels of birth and death rates depend not only on the selection pressure but also on mutation rates. In the following section I analyze this balance.

2.4 Mutation-selection balance

How do the alternatives of parametrization in Table 2.1 affect the equilibrium number of deleterious mutations at each age? In particular, is the magnitude of mutation accumulation great enough to mold the trajectory of mortality?

The equilibrium number of mutations under mutation-selection balance can be approximated by the ratio of the total mutation rate ν (i.e., the hazard of a

mutation from a set of possible mutations) and the change in fitness r:

$$\bar{n} \approx \frac{\nu}{\frac{dr}{dn}}, \tag{2.11}$$

where n denotes the number of mutations and $\bar{n}$ denotes the equilibrium number (Charlesworth, 1994, pp. 125-126). The approximation holds if ν and $\bar{n}$ are small. Using the chain rule, the derivative in Equation 2.11 can be factored into the change in fitness with respect to survival or fertility and the effect on survival or fertility of having n mutations:

$$\frac{dr}{dn} = \frac{dr}{df}\frac{df}{dn}, \tag{2.12}$$

where f could be any of the denominators in Table 2.1.

2.4.1 Additive vs. proportional parametrization

Consider a mutation that has a small effect δ on mortality. Then f is equivalent to

$$\mu_a(n) = \mu_a(0) + n\,\delta \tag{2.13a}$$

in the additive case and

$$\ln \mu_a(n) = \ln \mu_a(0) + n\,\delta \tag{2.13b}$$

in the proportional case. From Eqs. 2.11, 2.12 and Table 2.1 it follows that

$$\bar{n} \approx \frac{\nu}{h_a^\dagger\,\delta} \tag{2.14a}$$

in the additive case and

$$\bar{n} \approx \frac{\nu}{\mu_a(0)\,h_a^\dagger\,\delta} \tag{2.14b}$$

in the proportional case. In these ratios $h_a^\dagger$ denotes remaining reproduction at age a of an individual with no deleterious mutations. It is related to Hamilton's indicator via $h_a^\dagger = H_a^\dagger T$, where T captures generation time.

Combining Eqs. 2.13 and 2.14 leads to the result

$$\mu_a(\bar{n}) \approx \mu_a(0) + \frac{\nu}{h_a^\dagger} \tag{2.15a}$$

in the additive case and

$$\mu_a(\bar{n}) \approx \mu_a(0) \exp\left(\frac{\nu}{\mu_a(0)\, h_a^\dagger}\right) \tag{2.15b}$$

in the proportional case. If mutations are rare, i.e. if $\nu/\mu_a(0)$ is small, then the formula for the proportional case can be approximated by

$$\mu_a(\bar{n}) \approx \mu_a(0)\left(1 + \frac{\nu}{\mu_a(0)\, h_a^\dagger}\right) = \mu_a(0) + \frac{\nu}{h_a^\dagger}. \tag{2.16}$$

Hence, if ν and $\bar{n}$ are small enough that the approximations in Equation 2.11 and Equation 2.16 hold, then mutation accumulation will result in about the same age-specific mortality regardless of whether mutations have additive or proportional effects.

2.4.2 A simple box model

If $\bar{n}$ is large, an alternative approach is necessary. Several helpful models have been developed (e.g. Kimura and Maruyama (1966), Ohta and Kimura (1973), Moran (1976), Moran (1977)); for a review see Bürger (2000) and Charlesworth (1994). A recent general model by Steinsaltz, Evans, and Wachter (2005) includes earlier models as special cases.

A solution based on a simple box model similar to that of Kimura and Maruyama (1966) can be readily developed. Assume a haploid, asexual population that is stationary in size. Further assume that mutations affect only one age class, to ensure that the equilibrium numbers of mutations are independent across ages. Focus on a single age a. Individuals are sorted into boxes according to their number of mutations at age a. Let $N(n)$ be the number of individuals in box n and let N be the total, constant population size at age a. In mutation-selection balance, the proportions $N(n)/N$ are fixed. Denote the lifetime reproduction of an individual in box n by $R(n)$. Let ν be the probability of passing on a new, additional mutation to the next generation. Assume that mutations occur successively, i.e. it is not possible to jump over boxes. Ignore back mutations. Mutations are deleterious, therefore $R(0) > R(1) > R(2)... > R(K)$, K being some maximum number.

The number of individuals $N(n)$ in box n is given by the inflow of individuals

minus the outflow per generation,

$$N(n) \;=\; N(n-1)\,R(n-1)\,\nu \;+\; N(n)\,R(n)\,(1-\nu). \tag{2.17}$$

It follows immediately that reproduction in box zero is

$$R(0) \;=\; \frac{1}{1-\nu}. \tag{2.18}$$

In the case of mutations that affect mortality, the lifetime reproduction of individuals in the n'th box is given by

$$R(n) \;=\; \sum_{x=0}^{a-1} l_x\, m_x \;+\; e^{\mu_a(0)\,-\,\mu_a(n)} \sum_{x=a}^{\infty} l_x\, m_x. \tag{2.19}$$

This result can be expressed as

$$R(n) \;=\; R(0) \;-\; \Delta(n)\, h_a^{\dagger}, \tag{2.20}$$

where $\Delta(n)$ is the fraction of remaining reproduction $h_a^{\dagger}$ that is lost due to carrying n mutations. In the additive case

$$\Delta(n) \;=\; 1 \;-\; e^{-\delta\, n} \tag{2.21a}$$

and in the proportional case

$$\Delta(n) \;=\; 1 \;-\; e^{-\mu_a(0)\,(\exp[\delta\, n]\,-\,1)}. \tag{2.21b}$$

It follows from 2.17 and 2.20 that

$$N(n) \;=\; \frac{N(0)}{\prod_{k=1}^{n} \Delta(k)}\, R(0)^{n+1} \left(\frac{\nu}{h_a^{\dagger}}\right)^{n} \prod_{k=1}^{n-1} (\, R(0) \;-\; \Delta(k)\, h_a^{\dagger}\,). \tag{2.22}$$

The equilibrium number of mutations is the average over all boxes, i.e.

$$\bar{n} \;=\; \frac{\sum_{n=0}^{K} n\, N(n)}{\sum_{n=0}^{K} N(n)}. \tag{2.23}$$

Figure 2.3 plots the equilibrium number of mutations over age in the additive versus proportional case for the example presented in Figure 2.1 and 2.2. As a

second example I consider female mortality, as given in the Swedish life table for 1778-82. Results are shown in Figure 2.4 and 2.5.

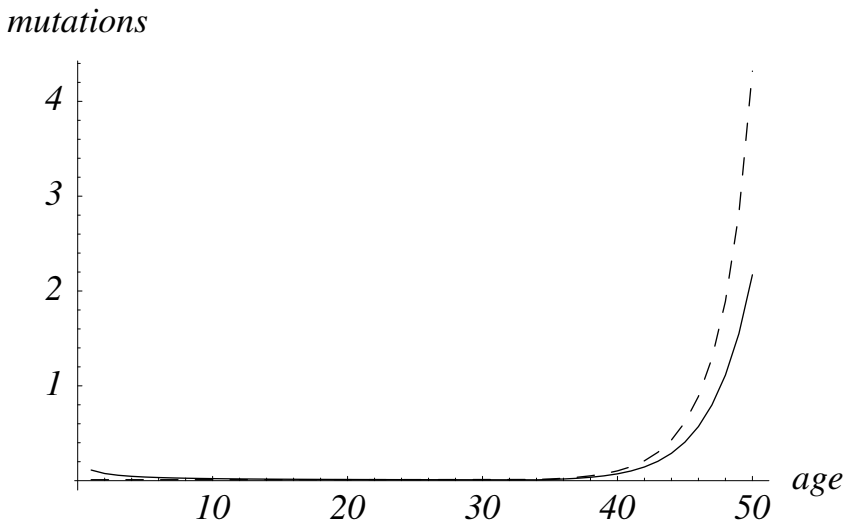

Fig. 2.3: **Equilibrium number of mutations: additive (dashed), proportional (solid).** I assume that mutation pressure $\nu = 0.001$. Furthermore, I assume that a mutation at any age reduces remaining reproduction by about ten percent in both the additive and proportional case. This refers to an average reduction in the proportional case since $\Delta(n)$ depends on the level of mortality at age a, as can be seen from Equation 2.21b. Specifically, $\delta = 0.1$ in 2.21a and $\delta = 0.35$ in 2.21b. While in the Hamiltonian case of an additive hazard the number of mutations remains low and then increases with age, proportional effects lead to an age-specific mutational load that declines at young ages. In the example only one quarter of one percent of individuals are alive at age 34. Before this age the mutational load is close to zero. After this age, however, the equilibrium number of mutations rises sharply.

The values of $h^\dagger$ that determine the number of mutations in Figs. 2.3 and 2.4 are calculated using specific *initial* fertility and mortality schedules. The mutations, however, will raise mortality, producing a new schedule that determines a new $h^\dagger$, as illustrated in Fig. 2.5. These dynamics are beyond the scope of this chapter. Note, however, that higher hazard rates would reduce the fitness costs of a change in age-specific mortality. Thus, more mutations would accumulate and the difference between additive and proportional parameterizations would be larger than predicted by my conservative estimate. A general treatment that takes into account interactions between ages is given by Steinsaltz, Evans, and Wachter (2005).[2]

[2] I thank Kenneth W. Wachter and Brian Charlesworth for helping me considerably with this section.

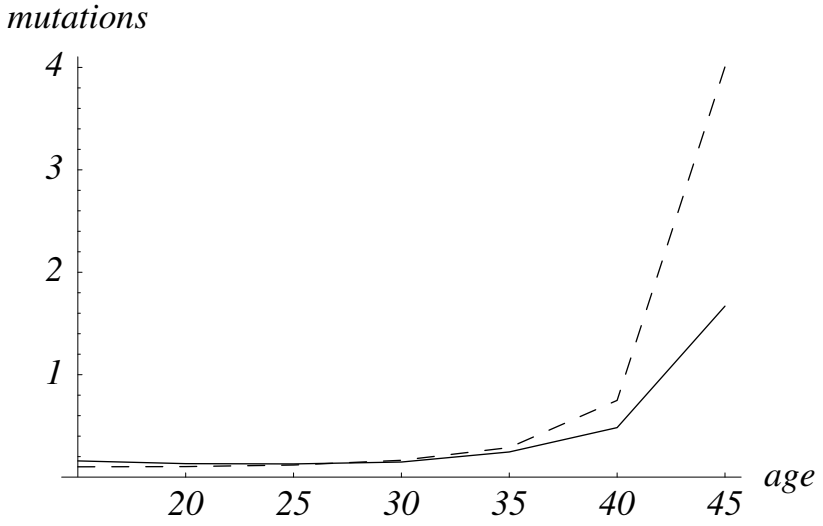

Fig. 2.4: **Equilibrium number of mutations: additive (dashed), proportional (solid).** The example is based on female mortality as given in the Swedish life table for 1778-82, for seven 5-year age-groups, beginning at age 15. Since the Swedish population was growing at that time, I normalized reproduction to ensure $R = 1.00$. I consider a deleterious mutation that reduces remaining reproduction at any age by about one percent, either in an additive or in a proportional way, i.e. $\delta = 0.01$ in Equation 2.21a and $\delta = 0.7$ in Equation 2.21b, and I assume a mutation pressure of $\nu = 0.001$. The difference between the additive and proportional case increases at higher ages, as levels of remaining reproduction decline. A slight decrease in the equilibrium number of mutations from the first to the second age-group can be observed.

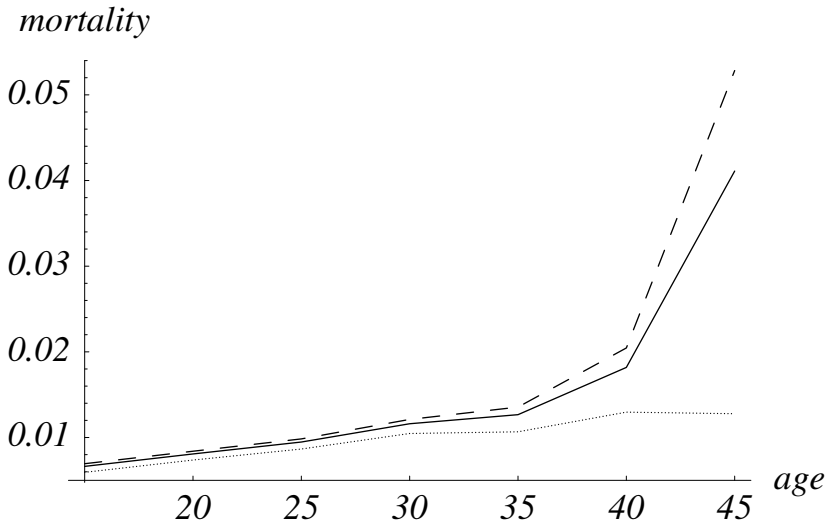

Fig. 2.5: **Mortality: additive (dashed), proportional (solid), initial mortality $\mu_a(0)$(dotted).** Initial mortality is from the Swedish life table for 1778-82, females, for seven 5-year age-groups, beginning at age 15.

2.5 The importance of mutation accumulation

The age-trajectory of mortality can be decomposed into three parts: one component is due to the accumulation of unfavorable mutations, another fraction results from selection processes that optimize the trade-offs necessitated by resource limitations, and the remaining fraction can be attributed to unavoidable, external risks of death. How strong is the influence of mutation accumulation?

The relative impact of mutation accumulation on the molding of the mortality trajectory is crucially determined by the ratio of mutation pressure ν to remaining reproduction $h_a^\dagger$, as indicated by Equation 2.14. The larger the value of ν, the more influential is mutation accumulation. But what is the magnitude of ν? Keightley and Charlesworth (2005) point out that the rate of deleterious mutations per haploid genome in *C. elegans* in protein coding genes is about 0.5 per generation. Kimura and Maruyama (1966) and Drake et al. (1998) suggest mutation rates per genome per generation of about 0.1 and between $0.1 - 100$, respectively. More recent publications estimate the genomic rate of deleterious mutations in humans to be at least 1.6 (Eyre-Walker and Keightley, 1999) or even 3 (Nachman and Crowell, 2000) per generation.

If the fraction of mutations that exclusively affect mortality at a specific age is low, then these values could be consistent with a value of $\nu = 0.001$. If ν is 0.001, then Figure 2.6 suggests that the influence of mutation accumulation is likely to be small over the major part of reproductive life. This remains speculation, however, until the magnitude of ν is estimated empirically. Abrams (1991) provides suggestive evidence that the importance of mutation accumulation is likely to be small relative to the importance of optimization among trade-offs. Partridge (2001) points out that little evidence can be found in favor of mutation accumulation but considerable evidence can be found to confirm the importance of trade-offs.

The conclusions drawn above and in the previous section were reached on the basis of a specific model of mutation accumulation. In general cases covered by the solutions given by Steinsaltz, Evans, and Wachter (2005), the form of the mutation-selection equilibrium depends on the extent of assumed genetic recombination. At both extremes, in the absence of recombination (equation 9 in their article) and in the presence of free recombination (equation 27), the parametrization of the mutational effect, i.e. whether the effect is additive or

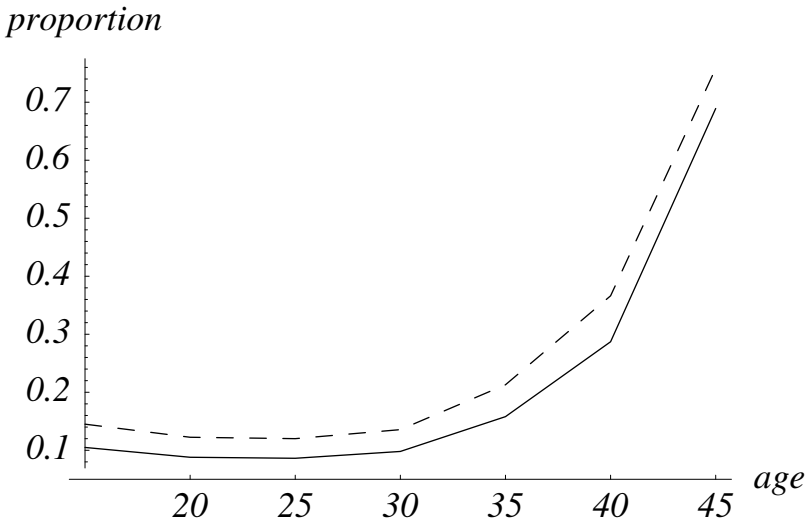

Fig. 2.6: **Proportion of mortality explained by mutation accumulation: additive (dashed) vs. proportional (solid) case.** The fraction $1-\mu_a(0)/\mu_a(\bar{n})$ indicates the proportion of equilibrium mortality that can be explained by the accumulation of mutations. For the example of Swedish females, when $\nu = 0.001$, mutation accumulation explains less than a third of total mortality. At ages 45-50, however, when mortality is high and fertility is low, mutation accumulation accounts for the bulk of total mortality. Note that this illustrative example does not pertain to actual Swedish mortality but to the hypothetical outcome of one round of mutation accumulation: see Section 3.1 for further discussion.

proportional, influences the mutation-selection equilibrium.

2.6 Conclusion

Hamilton stated that the force of selection inevitably has to decline with age, even "in the farthest reaches of almost any bizarre universe" (Hamilton, 1996). He concluded that the declining selection pressure would mold the age-pattern of mortality in a way that mortality is lowest at reproductive maturity and "trails upward indefinitely at the right ... roughly asymptotic to the age of the ending of reproduction" (Hamilton, 1996, pg. 119). Hamilton's claim about the inevitability of senescence has been generally accepted, but it can be disproved, even adopting his restrictive assumptions. As shown above, alternative indicators can be derived, within Hamilton's own framework, that can result, in some circumstances and over some age ranges, in an increasing force of selection with age, thus contradicting the basis for his claim.

The results of this chapter strengthen the view that demographic schedules of mortality and fertility appear to be shaped largely by optimization of trade-offs rather than by mutation accumulation. Only at ages when remaining reproduction is low does the influence of mutation accumulation appear to become predominant. At those ages, different parameterizations lead to different conclusions about the equilibrium number of mutations.

Some important empirical research questions are suggested by the theoretical findings of this chapter. Does the age-specific mutation rate ν change with age? If so, what is the age-trajectory of ν?

3. FURTHER CHALLENGES

Hamilton's claim of the inevitability of senescence can be disproved even within his own framework. Furthermore, his framework has several limitations. In this chapter theoretical and empirical issues that weaken his approach as the main explanation for the evolution of senescence will be discussed. Building on Medawar (1952) and Williams (1957), Hamilton wrote the pioneering *first* chapter on the moulding of senescence.

I draw two main conclusions.

- First, Hamilton's basic notion – that the age-pattern of mortality is an inverse function of the age-pattern of his indicator – is wrong. For both his indicator and the other indicators in Table 2.1 the relationship between the indicator and mortality is so complicated that sophisticated modeling is required.

- Second, several theoretical arguments as well as the bulk of empirical findings suggest that mutation accumulation is of secondary importance in molding the age-trajectories of mortality across the varied species of life. The primary force appears to be adaptation, i.e. the concept that patterns of aging are a byproduct of optimization of trade-offs. Hence, deep understanding of the evolution of aging requires optimization modeling.

3.1 General problem with all indicators

Because his indicator declines with age, Hamilton deduced that mortality must increase with age. The relationship between his indicator of selection pressure and the age-pattern of mortality is not a simple one, however. During development his indicator is constant, while mortality, for many and perhaps all species, is falling. At post-reproductive ages his indicator is zero, while mortality, at least in humans, rises and then slowly levels off. Although the mismatch between indicator and pattern was acknowledged by Hamilton himself, an inverse relation between his indicator and the age-pattern of mortality is commonly assumed. The main justification, from Hamilton onwards, appears to be that there is an inverse relation between his indicator and the age-trajectory of mortality at reproductive ages in humans.

It is well known among plant biologists that many plants are capable of reducing their hazard of death by continued growth after the onset of reproduction.

As discussed later in this chapter, various animals show negligibly increasing or declining mortality. I will show in Chapters 4 and 5 that optimization models can lead to strategies where mortality is constant or keeps on falling after reproductive maturity. Figure 3.1 compares these patterns to Hamilton's inevitably decreasing indicator. It is clear that mortality is not necessarily an inverse function of Hamilton's indicator.

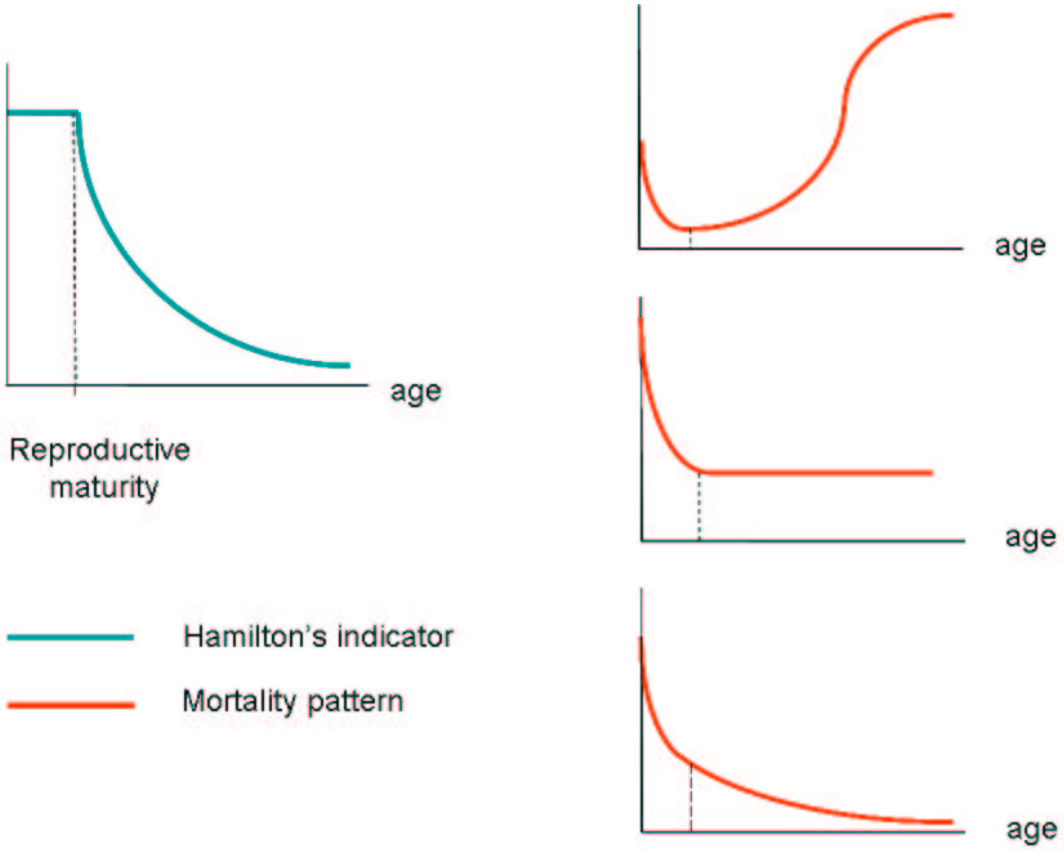

Fig. 3.1: The relation between Hamilton's declining indicator of selection pressure and three possible age-patterns of mortality.

The alternative indicator that I suggested for the force of selection can increase with age, but only if the hazard of death is increasing. The indicator, however, can also decrease when the hazard of death is increasing: whether the indicator increases or decreases depends on how fertility is changing. Furthermore, the indicator decreases if the hazard of death is decreasing. So, as with Hamilton's indicator, the alternative indicator is not necessarily inversely related to the age-pattern of mortality.

But then how are the indicators of the force of selection against senescence related to the shape of the age-pattern of mortality? Hamilton quantified the

selection pressure but he did not think carefully about the response to that pressure, although he acknowledges that "what way life schedules will be moulded by natural selection depends on what sort of genetical variation is available" (Hamilton, 1996, pg. 118). Lande (1982) emphasizes that the change in a phenotype is determined by selection pressure (i.e. the indicator) together with the response matrix (the so called G-matrix), which includes variances and covariances for all fitness-relevant traits. The matrix not only takes into account "genetical variation" but also trade-offs among traits. Hamilton ignored these trade-offs.

The indicator of selection pressure together with the response matrix yields information about *short* term evolutionary processes. The implications for the long term, however, cannot be readily assessed because the selection pressure is determined by what it shapes. The calculation of the indicator of selection pressure is based on the age-trajectories of mortality and fertility, and these trajectories depend on current levels of fitness-relevant traits. The entries in the G-matrix correspond to the variances and covariances at current levels of traits. But if, say, n traits are involved, then the indicator as well as the matrix take different values in an n-dimensional space. Evolution moves a species in this space at the speed and in the direction specifically determined by its position in that space. As position changes, speed and direction change.

In other words, as traits are shaped by evolution, they re-shape the selection pressure and possibly the G-matrix. It is not clear whether this process will ultimately converge and, if it does, to what evolutionary equilibrium. Since the force of selection is essential for evolutionary demographic theory, the implications of this feedback loop have to be understood. This requires modeling.

In sum, the quantities in Table 2.1 are *indicators* of the force of selection. They can provide an impression of the short-term direction and magnitude of the force of selection on age-specific survival and reproduction. But they are only one aspect of a multi-faceted story.

3.2 Theoretical arguments

3.2.1 Mutation-selection balance

If mutation accumulation were the main explanation for senescence, which Hamilton assumes is a trait that is common to all individuals in a population, then each

individual must be affected. For any particular deleterious mutation, mutation-selection balance implies that at least some individuals do not carry that mutation, namely those individuals in the zero-box. As long as selection pressure significantly exceeds mutation pressure, most individuals will be in the zero-box. Therefore, each individual would have to have his or her own set of deleterious mutations, being non-mutant for some genes and mutant for others. If genes had large and/or epistatic (non-linear) effects, a small set of genes could be sufficient. A population however, would then be highly heterogeneous, with some individuals suffering a rapid increase in mortality and others enjoying slow or postponed senescence. This does not appear to be the case, at least not for humans. Low variance in the age of senescent death requires the existence of many genes that have negative effects towards the end of reproductive life but no effects before that. Hamilton's theory assumes then that many genes have small effects that act additively. I will review the empirical evidence for age-specific, late-acting mutations in a subsequent section.

If there are few genes that have age-specific effects, then for mutation accumulation to be the main cause of senescence, these genes must be fixed in the population to lead to the phenomenon of senescence, which Hamilton claims to be universal. Fixation of a mutation implies that every individual in the population carries the same mutant allele for the gene in question. In this theoretical model this means that no individual is left in the zero box. The fixation of deleterious mutations at advanced ages poses a further challenge: unraveling.

3.2.2 Unraveling

Human mortality rises much more slowly than suggested by the results in Figure 2.5, consistent with an earlier, similar observation by Abrams (1991, pg. 357f). This leads to a problem we have not yet touched on. All the indicators in Table 2.1 imply that the force of selection drops to zero when reproduction ceases. Several authors have argued that recurrent, deleterious mutations that only effect post-reproductive ages would become fixed, yielding a black hole of death at the age when reproduction ends (Charlesworth and Partridge, 1997; Partridge, 1997; Tuljapurkar, 1997; Wachter, 1999). This could have been shown in all the figures above if the curves were drawn to higher ages. As $h_a^\dagger$ approaches ν, the equilibrium number of mutations steeply rises.

However, remaining reproduction $h_a^\dagger$ is calculated on the basis of a non-mutant life-history schedule. As $h_a^\dagger$ approaches zero, the equilibrium number of mutations rises to its maximum number at the age when $0 < h_a^\dagger << \nu$, even though a small fraction of reproduction is left. Hence, all bad genes after that age are fixed in the population and no individual is left with the non-mutant schedule. The disadvantage of carrying the mutation disappears, since every individual carries it. The fitness differential with respect to that mutation is gone. Therefore, a new $h_a^\dagger$ that falls more quickly near the end of reproductive life determines the selection pressure. Consequently, the point at which all mutations become fixed moves forward to a younger age. This process of unraveling would move the wall of death to younger and younger ages until it ultimately reaches maturity. Semelparity would be the only life-history strategy possible, which clearly is not the case.

Unraveling crucially depends on the age-trajectory of the mutation pressure. The age-window at the end of reproductive life, when selection pressure is weak and mutation pressure is strong, might be small. Let a be the first age when remaining reproduction is much smaller in magnitude compared to the mutation pressure, i.e. $0 < h_a^\dagger << \nu$, and A the age from which onwards remaining reproduction is zero, i.e. $h_A^\dagger = 0$. Unraveling will occur only if there are mutations whose effects become apparent inside but not before the age interval $[a, A]$. On the other hand, mutation accumulation will shape the age-pattern of mortality only if there are mutations that increase mortality at older ages, including within the interval $[a, A]$. Furthermore, such mutations cannot have major effects at ages where selection pressure is high.

In sum, there are many restrictions on the nature of the mutations that could permit mutation accumulation to shape aging, as discussed in this section and in the previous section. We will see in Section 3.3.1 below, that it is not clear that enough such mutations exist.

3.2.3 Variable environments

Hamilton assumes a constant environment but environments are – in fact – variable. Accounting for changing environments can weaken mutation accumulation considerably. As the environment switches between good and bad times, it becomes essential during bad periods (during droughts, for example) to survive a

long time in order to reproduce at all. Such a period would create a bottleneck. Only those individuals that were able to switch to a "survival mode", having no or very few bad mutations at higher ages, would constitute the gene-pool for all following generations, cleaning out any mutation accumulation.

Many species are able to switch between different life-history strategies depending on environmental conditions (Carey et al. (1998), Gardner et al. (2006), Amdam and Omholt (2002)). The same genome allows for strategies that can substantially differ in life expectancy. Given the short-lived strategy that might be optimal under average environmental conditions, mutations are predicted to accumulate at ages beyond the corresponding expected end of life. These mutations would raise mortality, preventing a substantial extension of lifespan, i.e. switching to the long-lived strategy. For species with alternative short and long-lived strategies, an increase in mortality with age in the short-lived strategy cannot be explained by mutation accumulation.

This reasoning only holds if mutations are assumed to be age-specific, i.e. time counting. Probably, however, gene expression is state-specific rather than age-specific. In this case a deleterious mutation could hide in the genome if the respective gene is not expressed in survival mode.

State- or condition-specific mutations could also explain results from an experiment conducted in Linda Partridge's laboratory. Mair et al. (2003) show that dietary shifts can lead to switching between two different trajectories of mortality, one for the line on a restricted diet and one for the unrestricted line. The possibility of immediate shifts between a higher and a lower mortality curve in both directions, up and down, cannot be explained by simple mutation accumulation, especially since the shifts can occur at both younger and older ages. Such shifts and other kinds of plasticity in the age-pattern of mortality can, however, be explained by optimization models, as I discuss in Chapter 6.

Let me also note that the influence of unpredictable, stochastic environments (and in this regard also finite population sizes, finite time, and neutral theory) cannot be neglected when explaining the evolution of senescence (Orzack and Tuljapurkar (1989), Tuljapurkar (1990)). I will return to these points in Chapter 6.

3.2.4 Other mechanisms

Variable environments are one counter-mechanism against mutation accumulation. Other mechanisms that can reduce the amount of mutations accumulating are synergistic epistasis and the occurrence of beneficial mutations (Schultz and Lynch, 1997; Whitlock and Bourguet, 2000). In the former case, the force of selection prevents the accumulation of mutations more strongly, because mutational effects magnify each other. In the latter case, the beneficial effect of some mutations offsets the deleterious effect of other mutations and therefore prevents an increase in mortality. Note that optimization of age-patterns of mortality, fertility and other traits results from the selection of beneficial mutations.

Hamilton pointed out that his results cannot explain the decline in mortality during development nor the existence of a post-reproductive period. Hamilton hypothesized that parental care is a missing piece in his framework that could account for both decreasing juvenile mortality as well as life after the end of reproduction. Parental care is a special form of resource transfer from parents to offspring. Lee (2003), Chu and Lee (2006) and Robson and Kaplan (2005) argue that intergenerational transfers that are made before, at and after birth can significantly influence the evolution of life-history schedules and, in particular, could explain the U-shaped trajectory of mortality in humans.

3.3 Empirical evidence

3.3.1 Testing preconditions for mutation accumulation

Three important preconditions for Hamilton's approach are:

- The existence of genes with effects confined to particular ages, especially to later ages.
- Mutations in these genes have small, deleterious effects.
- Effects of mutations do not interact with each other.

These preconditions have been tested empirically with an emphasis on the first condition.

To test the first precondition for the theory of mutation accumulation two large demographic studies in *Drosophila* have been conducted. Pletcher et al.

(1998) used inbred lines and found only weak evidence for the existence of mutations with deleterious effects confined to higher ages. The mutational load at later ages of their lines, however, might have been effectively saturated because of inbreeding depression (Yampolsky et al. (2001), see also Sgrò and Partridge (2000)). Negative epistasis at such a high mutational load could explain the results of Pletcher et al. (1998). Yampolsky et al. (2001) conducted experiments with outbred lines of *Drosophila* and found clear evidence for age-specific effects after 10 and 20 generations. This evidence, however, decreased after 30 generations.

Evidence from Pletcher et al. (2002) (for *Drosophila*) and Golden and Melov (2004) (for *C. elegans*), who tested age-specific gene-expression levels, supports the existence of genes with age-specific effects, whereas Landis et al. (2004) found a small tendency towards down-regulation of energy metabolism genes in *Drosophila* over adult ages. As a general pattern for both *Drosophila* and *C. elegans*, McCarroll et al. (2004), found gene expression levels to be higher at younger ages than at later ages.

The second precondition of mutation accumulation is that mutations have small effects. Some mutations may, however, have major effects. It has been shown that the lifespan can be strongly effected by single mutations in *C.elegans* (Johnson and Wood (1982), Lithgow et al. (1995)) and *Drosophila* (Lin et al. (1998), Parkes et al. (1998), Clancy et al. (2001), and Tatar et al. (2001)).

Hamilton's third precondition is that aging-related genes should effect mortality in a linear, i.e. non-epistatic, manner. It has been shown, however, that genes effecting the lifespan of flies and worms interact (Shook et al. (1996), Leips and Mackay (2000)) and their expression depends on their genetic background (Spencer et al., 2003). Recently, Spencer and Promislow (2005) showed for *Drosophila* that gene $\times$ genetic background interactions not only affect lifespan as a whole, but they also affect mortality in an age-specific manner. They conclude that aging-related traits could, to a significant extent, be shaped by age-specific epistasis. This possibility has not been considered so far in the evolutionary theories of senescence. The epistatic action of aging-related genes is further supported by Promislow (2004), who shows that proteins associated with senescence interact more strongly than would be expected by chance.

If mutation accumulation were the main cause of senescence, the empirical evidence should be abundant and clear. The evidence, however, suggests that two

out of three preconditions may be violated and evidence for the first precondition is not unambiguous.

3.3.2 Checking predictions from mutation accumulation

If mutation accumulation were at work, then a main prediction is that there will be an increase in genetic variation and inbreeding effects with age. The evidence for an increase in genetic variation is mixed. Some evidence supports such an increase (Hughes and Charlesworth (1994), Hughes (1995)) whereas others report an increase in genetic variance early in life followed by a decline in later life (Promislow et al. (1996), Tatar et al. (1996)). The strongest support for the mutation accumulation theory is given by Hughes et al. (2002), who show a marked increase in both genetic variation and inbreeding effects in *Drosophila* with age. The authors emphasize that the increase in inbreeding effects is expected only under mutation accumulation, not under antagonistic pleiotrophy (Charlesworth and Hughes, 1996). Caution should be exercised regarding evidence of increasing inbreeding depression with age because old flies may just be more enfeebled and hence susceptible to the effects of inbreeding.

On the basis of his results, Hamilton made predictions about the age-pattern of mortality. He inferred that mortality should be lowest at reproductive maturity and "trails upward indefinitely at the right ... roughly asymptotic to the age of the ending of reproduction" (Hamilton, 1996, pg. 119), i.e. the theory of mutation accumulation would rule out the existence of a post-reproductive period. Mortality trajectories at older ages, however, have been found to level off and, in some studies, to decline for humans and various species kept in protected environments (Carey et al. (1992), Curtsinger et al. (1992), Charlesworth and Partridge (1997), Vaupel et al. (1998), and Partridge and Mangel (1999)). Several species studied in the laboratory have been shown to enjoy an extended period of post-reproductive life.

The level of extrinsic mortality determines the age beyond which remaining reproduction ($h_a^\dagger$) becomes negligible in the wild. This is the age at which Hamilton predicts a steep increase in mortality. The higher the extrinsic risk of death, the earlier the age at which mutations could accumulate. Hence, animals kept in laboratories, zoos, or other protected environments should suffer senescence at ages few of them would reach in the wild. Their lifespans should not exceed

maximum lifespan in the wild. Many lab and zoo animals, however, live much longer than in the wild (Carey et al. (1992) and Carey and Judge (2000)).

Furthermore, when kept protected from extrinsic hazards, a steeper rise in mortality with age is predicted for populations from high risk environments than for populations from lower risk environments. However, guppies from high risk pools showed a slower pace of senescence than guppies from lower risk pools when brought into the laboratory (Resznick et al., 2004), contrary to the prediction of mutation accumulation theory. Differences in phenotypic development under high and low density conditions is one explanation for this phenomenon. Abrams (2004) discusses this and several other explanations for the guppy puzzle. To explain long lives in protected environments, alternatives to the theory of mutation accumulation, e.g., alternatives based on optimization approaches, have to be found.

3.3.3 Empirical evidence for non-senescence

According to Hamilton senescence should be a ubiquitous characteristic of life histories, and mortality should start rising when reproductive maturity is reached. Three well-known gerontologists (Comfort, 1956; Strehler, 1977; Finch, 1990) emphasized, however, that "certain animals and plants do not manifest increases of mortality rate or other signs of senescence" (Finch, 1990, p. 221). In particular, Finch (1998, 1990), Finch and Austad (2001) and Ottinger et al. (2003) have prepared the way for studies of non-senescence by focusing research on species with " negligible senescence", i.e., species for which death rates rise very slowly, if at all, with age. Caswell (2001, p. 39) discusses increases in fertility as well as decreases in mortality with size (and therefore with age) and provides numerous examples and references.

The strongest evidence for non-senescence in animal species comes from studies of corals. Babcook (1991) shows in three coral species (*Goniastrea aspera, G. favulus, and Platygyra sinensis*) that mortality is inversely related to colony size and age. Furthermore, the total fecundity of the three species increases steeply with size and age, "due to a combination of increased polyp fecundity and increased surface area"(Babcook, 1991). Grigg (1977) presents comparable results for two other corals, *Muricea californica* and *Muricea fruticosa*.

Like the massive reef-building corals, some plants develop into large clonal

clusters (Finch, 1990, Table 4.2, p. 229). The quaking aspen (*Populus tremuloides*) grove studied by Kemperman and Barnes (1976) covered 81,000 square meters and was estimated to be at least 10,000 years old. It seems likely that the bigger such a clonal cluster is, the lower is its chance of death.

Other species that are candidates for non-senescence include the wild leek *Allium tricocum* (Nault and Gagnon, 1993), brown algae *Ascophyllum nodosum* (Aberg, 1992), the forest tree *Garcinia lucida* (Guedje et al., 2003), the neotropical tree *Cecropia obtusifolia* (Alvarez-Buylla and Martinez-Ramos, 1992) and the cushion plant *Limonium delicatulum* (Hegazy, 1992).

Strong evidence for a period of parallel increase in age-specific survival and fertility in non-modular animals can be found for some species of molluscs. Fertility often increases by ten-fold or so as individuals grow following reproductive maturity, and mortality decreases sharply (e.g., for the marine gastropods *Umbonium costatum* (Noda, 1991; Noda et al., 1995) and *Littorina rudis* (Hughes and Roberts, 1981) and the bivalve *Yoldia notabilis* (Nakaoka, 1994, 1996)). There is also evidence of non-senescence for echinoderms such as sea urchins (Ebert and Southon, 2003). Hydra species (Martinez, 1998) are likely candidates as well.

Some vertebrates may possibly enjoy non-senescence. Finch (1990) summarizes suggestive data on rockfish, hagfish and various other species. For some reptiles, death rates decline somewhat after the age of reproductive maturity is reached, e.g., for *Sceloporus graciosus* (Tinkle et al., 1993), some populations of *Sceloporus undulatus* (Tinkle and Ballinger, 1972) and some populations of *Lacerta vivipara* (Heulin et al., 1997)[1].

Kohler et al. (2005) analyze data sets for various species living in zoos and aquaria worldwide. They state that "there are several groups for which the age-pattern of mortality is nearly level". Comparing survival probabilities from the first decade of life (age 1 to 10, i.e. excluding juvenile death) with the second decade of life the evidence shows that raptors and crocodiles enjoy better survival in the second decade of their lives than in the first decade. Ratites show no signs of decrease in survival probability from their first to their second decade of life.

Non-senescent life histories cannot be explained by mutation-accumulation.

[1] I thank my colleague Martin Doelling for his substantial help in gathering the references regarding evidence of non-senescent species.

3.4 Conclusion

The empirical evidence together with the theoretical arguments presented in this chapter indicate that mutation accumulation theory does not provide the fundamental explanation for the evolution of age-patterns of mortality. Together with my results from Chapter 2 they cast doubt on the assertion that senescence is inevitable.

It seems likely that the variety of possible age-trajectories of mortality is broad.

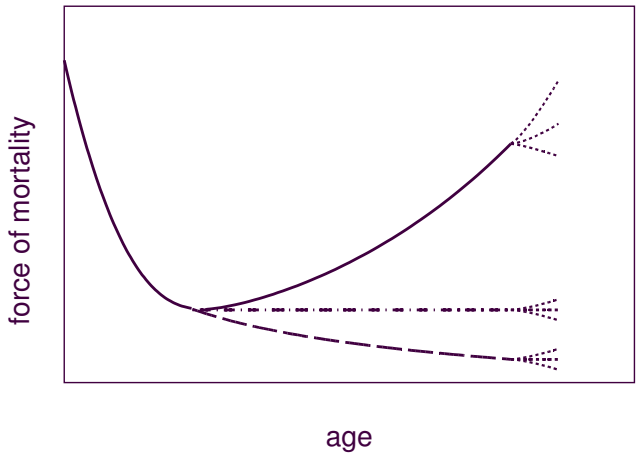

Fig. 3.2: Different hypothetical mortality trajectories.

Figure 3.2 summarizes various possibilities. During the first phase of life, development, mortality declines. During the second phase, mortality may increase, it may remain roughly constant, or it may decline. Then late in life, when most adults are dead, mortality may increase, level off or decline.

The age that marks the start and end of the different phases might be influenced strongly by growth patterns. For some species, growth ceases at reproductive maturity and marks the age when mortality starts rising. As noted above, however, individuals from many species continue to grow after the onset of reproduction and mortality may continue to fall until the age when growth

stops. Models are needed to study which of these hypothetical age-patterns are theoretically possible. I will derive such models in the following two chapters.

Note that the age-pattern of mortality reflects the average mortality in the population. The frail tend to die first. Hence, as individuals die, average mortality successively approaches the individual mortality trajectory of the most robust ones. The more heterogeneous a population is, the stronger is this effect. Therefore the age-pattern of mortality might exhibit a leveling and even a decline in mortality although the underlying individual age-pattern is still increasing (Vaupel et al. (1979), Vaupel and Yashin (1985), Vaupel and Carey (1993), Charlesworth and Partridge (1997) and Partridge and Mangel (1999)).

The evidence suggests that mortality and fertility over the bulk of reproductive life are shaped by mechanisms other than mutation accumulation. Theories based on trade-offs might explain the existence of non-senescent life-history strategies (Partridge and Barton (1993), Partridge (2001), Partridge and Gems (2002)). It is not clear whether mutation accumulation plays a significant role in the evolution of senescence. If it turns out that mutation accumulation is an important mechanism for some species at older ages, then models of mutation accumulation need to be combined with trade-off models of the evolution of senescence to clarify the dynamics of demographic schedules (Abrams (1991), Vaupel et al. (2004)). In the following two chapters, I develop trade-off models and explore their implications for the evolution of the age-patterns of mortality.

Part II

OPTIMIZATION MODELS

4. OPTIMIZATION MODELS BASED ON SIZE

4.1 Size matters

Hamilton did not prove that senescence is inevitable. Furthermore, it seems likely that the age-trajectory of mortality is largely shaped by optimization: only at advanced ages, when the bulk of total lifetime reproduction has been realized, might mutation accumulation play a role. So the question arises: could it be optimal for a species not to follow a senescent life-history strategy?

As Caswell argues, for many organisms " the age of an individual tells little or nothing about its demographic properties" (Caswell, 2001, p. 39). Often what is important is size or stage of development. He concludes that " [s]ize-dependent demography is probably the rule rather than the exception and is especially pronounced in species with a large range of adult body size as a result of indeterminate adult growth."

Trees, for example, continue growing over an extended period of their life, gaining strength, becoming more robust and thereby reducing their susceptibility to death. (If trees at sites exposed to wind are too tall, then their susceptibility to damage and death might increase: this, however, is a special case.) A larger size (tall, thick stem, more leaves, longer roots) lowers the risk of death and enables better access to resources (light, water, nutrients). Larger trees produce more seeds than smaller trees.

The same is true for some species of fish. For instance, in some species the young adult fish, still small, has only a few progeny and is the prey of bigger fish. Over time the fish grows large enough to become a predator itself, increasing its level of resources and lowering its own risk of death.

Small alligators are prey to a variety of predators including raccoons, otters, wading birds, and fish. But most dangerous to small alligators probably are predators of their own kind, the larger alligators. Large alligators also die of cannibalism and fight with each other (see http://myfwc.com/gators/facts.htm). An individual alligator's size and strength determines whether it receives or becomes an additional ration of food.

In this chapter, I hypothesize that candidate species for non-senescent life histories are species that continue to grow substantially after the onset of reproduction and for which size is strongly associated with continued survival and reproductive success. This appears to be the case for the plant *Plantago lanceolata* after seasonal effects are removed (Roach and Gampe, 2004). The study of

Plantago lanceolata was the particular motivation for me to develop a general life-history model based on size rather than age to understand whether non-senescence is theoretically possible.

Evidence for size-dependent mortality is reported for herbaceous plants in general (Harper (1977), Solbirg (Solbirg), Cook (1980), Sarukhán et al. (1984)), thistles in particular (Rees et al. (1999), Rose et al. (2002)), trees (Jimenes and Lugo, 1985), corals (Hughes and Jackson, 1985) and fish (Peterson and Wroblewski (1984), Moss et al. (2005)). Sauer and Slade (1987) also document the effect of body mass on reproduction and survival in vertebrates.

For some species mortality may not decrease as size increases: there may be no relation, or mortality may increase with size. In addition, it is important to note that, for some species, larger size may not *cause* lower mortality. Larger size may have co-evolved with lower mortality, both resulting from some other aspect of the species' life history. For some species, for instance species like *Drosophila*, which exhibits discrete developmental stages rather than continuous growth, size may not be a key determinant of mortality. So a size-based model can shed light on the life history of only some species. But these species are "conceivable organisms" and may show non-senescent life-history strategies.

Size is the central state variable in the models I will develop in this chapter. Size determines mortality and fertility. Age enters the models only insofar as it takes time to grow – age itself does not matter. Using size as the state variable in these kinds of models is a first step to understanding whether *any* life history could be non-senescent. Note that the state variable size can be understood not only as physiological size but more generally as "size and strength". In Chapter 5, I develop a new model that is based on "vitality" rather than size.

4.2 A size-based life-history model

An optimal life history maximizes lifetime reproductive success. Accordingly, the energy available to an organism, which is always limited, has to be distributed among the basic processes of life: reproduction, maintenance and growth. How evolution solves this allocation problem determines the optimal trajectory of growth and thereby the optimal trajectories of the main demographic schedules, mortality and fertility.

All forms of life have to deal with damage. Damage occurs all the time and is

discarded or repaired continuously, sometimes fully, sometimes partially. Models that take into account the influence of damage on mortality and fertility can do so on the occurrence and/or on the disposal and repair side. Energy allocation problems imply that disposal and repair of damage decreases when more energy is allocated to reproduction and therefore less energy remains for processes of maintenance and growth. Models based on the concept of energy allocation do not necessarily account for where the damage comes from. Reproduction itself, for instance, can be a direct cause of damage. For simplicity, the model I am going to develop in this chapter will focus on the energy allocation trade-off between reproduction, on the one hand, and maintenance and growth on the other. That is, I treat growth and repair as elements of the same general process and I do not explicitly model damage resulting from reproductive activities. I assume that the occurrence of damage increases proportionally with size.

Models based on the concept of optimal energy allocation over the life cycle represent a fundamental approach in life history modeling. Early applications of this concept were developed more than three decades ago, for example by Cole (1954), Gadgil and Bossert (1970), Schaffer (1974), Taylor et al. (1974), and Leon (1976). More recent examples of the application of the concept of optimal energy allocation include Charlesworth (1990), Perrin (1992), Perrin and Sibly (1993), Kozlowski (1996), Cichon (1997), Teriokhin (1998), Charnov et al. (2001), Mangel and Stamps (2001), Kaplan and Robson (2002), Chu and Lee (2006) and Charnov and Gillooly (2004).

Generally, such life-history models are driven by the trade-off between reproduction and growth. Depending on the particular research focus, growth is sometimes further differentiated into growth of acquisition structure, storage structure, defense structure, reproductive structure and/or cognitive functioning. The central quantity of interest is the fraction of energy allocated to reproduction, the reproductive effort of an individual.

Life history models based on the concept of reproductive effort have been studied intensively (for a review see Charlesworth (1994, Section 5.3.4.)). Common to these models is the assumption of a direct, inverse relation between survival and reproduction, which is mediated by reproductive effort. One outcome of these models is that reproductive effort should increase with age (Gadgil and Bossert (1970), Schaffer (1974)). However, Fragen (1972) produced some counter-examples and Charlesworth and Leon (1976) derived conditions that would lead

to a decreasing reproductive effort with age, i.e. to an increase in survival with age. These results illuminate the general pattern of how reproductive effort should change with age. But, as Charlesworth (1994, pg 214) put it: "The problem of solving for the optimal life history with this model is a formidable one."

My research aim is to study the variety of qualitative patterns of mortality and fertility over age. In particular, I wish to understand whether it can be optimal for mortality to be constant or to fall over an extended period of life after the onset of reproduction. Interestingly, optimal patterns of mortality and fertility were commonly found to be flat in numerical studies by Charlesworth (1990). In these studies, reproductive effort increased so slowly, that it appeared to be virtually constant.

The examples given in the previous section suggest that, for some species, mortality decreases with size and fertility increases with size. For species with continued growth that follow this pattern, constant or falling mortality after the onset of reproduction seems to be optimal, at least for some period of the lifespan. Consequently, the models developed in this chapter are designed to capture this simple pattern based on the state variable size.

In contrast to previous reproductive effort models, the link between survival and reproduction will be mediated by size. The important implication of this assumption is that an increase in reproductive effort not necessarily leads to a decrease in survival, and a decrease in reproductive effort not necessarily leads to an increase in survival. I will emphasize this point in Section 4.2.2.

Every organism has to cope with the ubiquitous processes of deterioration. This means that some of the energy invested in "growth" is needed to repair damage. Only what is left after the requirements of maintenance have been met can be used to increase current size. Size changes according to the balance between repair and damage. Thus, size in this framework can increase, decrease or remain constant and, consequently, mortality can increase, decrease or remain constant. Whether mortality increases or decreases is an outcome of the model and not an assumption. This is a crucial feature, which distinguishes this model from previous models.

The importance of size is generally recognized (Caswell, 2001, pg. 39). A state-based model that assumes an inverse relation between state and mortality has been developed before (Perrin, 1992). However, Perrin implicitly assumes a non-senescent life history because mortality cannot increase in his model. Perrin's

approach does not account for the occurrence of damage and its possible repair. A model that incorporates damage and repair was developed by Kozlowski (1996), Cichon (1997) and Cichon and Kozlowski (2000). However, in their framework mortality does not depend on state but on accumulated damage and can, at best, remain constant. Complete repair of current damage is realized only if all energy is invested in repair, i.e. at the cost of zero reproduction. Otherwise mortality rises at a pace determined by reproductive effort. An increase in mortality is inevitable.

An innovative feature of the approach I will be taking is that I combine the inverse relation of mortality and size with the possible accumulation of damage and its repair. My research builds on and further develops Vaupel et al. (2004). Mangel and colleagues (Mangel and Bonsall (2004) and Mangel and Munch (2005) have recently developed other models in which mortality is the consequence of growth and metabolism and associated damage.

4.2.1 The general optimization problem

The general optimization problem can be formalized as follows. Let $\xi(a)$ denote the size (and strength) of an individual at age a. Let $\pi(a)$ denote the fraction of energy allocated to growth at that age. Assume that the change in size over age depends on investment $\pi(a)$ and size $\xi(a)$ but not on age a itself, i.e. that the trajectory of $\xi(a)$ is determined by the autonomous first-order differential equation

$$\frac{d\,\xi}{d\,a} \equiv \dot{\xi} = g(\xi(a), \pi(a)). \tag{4.1}$$

Note that the dot indicates a change over age. Initial size is given by $\xi(0)$. From that size onwards, the age-trajectory of $\pi(a)$ determines the age-trajectory of $\xi(a)$.

The optimal trajectory of $\pi(a)$ over the life course is assumed to be the strategy that maximizes Darwinian fitness, measured as lifetime reproductive success, a functional of the form

$$\max R = \int_0^\infty f(\xi(a), \pi(a))\, da, \tag{4.2}$$

where $f(\xi(a), \pi(a))$ depends on the age-trajectories of mortality and fertility and hence on the age trajectories of $\xi(a)$ and $\pi(a)$. The age horizon is potentially

infinite, but non-zero mortality insures that every individual has a finite lifespan.

The general optimization problem is described by the objective as given in Equation 4.2 and the autonomous first-order differential equation as given in Equation 4.1, which determines the change in size over age.

4.2.2 The specific optimization problem

The change in size is determined by the fraction of energy invested in growth, $\pi(a)$. Energy is allocated between growth and maintenance on the one hand, and reproduction on the other hand. The fraction of energy allocated to reproduction, the reproductive effort, is captured by $1 - \pi(a)$, since in this model maintenance and growth are assumed to be paid out of the same budget. In accordance with the literature, the change in size is assumed to be inversely related to reproductive effort.

Larger size implies higher complexity, which is more costly to maintain. The rate of occurrence of new damage will be assumed to increase proportionally with size (Koojiman, 2000; West et al., 2001). A simple way of modeling deterioration is to assume a linear relation with size, i.e.

$$\delta(\xi(a)) \;=\; \delta_0 \;+\; \delta_1\, \xi(a), \tag{4.3}$$

where $\delta_0 > 0$ and $\delta_1 > 0$ are constant parameters.

Size is assumed to change proportionally to the level of current size $\xi(a)$. This implies the assumption that available resources are proportional to size, an assumption also made by Charlesworth and Leon (1976), Gadgil and Bossert (1970) and Leon (1976). Furthermore I assume that the change in size is proportional to the difference between investment $\pi(a)$ and deterioration $\delta(\xi(a))$. Growth only occurs if investment exceeds the current rate of deterioration. Therefore, the change in size can be specified as

$$\frac{d}{da}\,\xi(a) \;=\; k\,(\pi(a) \;-\; \delta(\xi(a)))\,\xi(a) \tag{4.4}$$

where $k > 0$ is a constant scaling parameter. Initial size can be normalized by setting $\xi(0) = 1$. Substituting (4.3) into (4.4) yields the following logistic

differential equation

$$\frac{d\xi(a)}{da} = k\,(\pi(a) - \delta_0 - \delta_1\,\xi(a))\,\xi(a). \tag{4.5}$$

This equation captures the change in size and specifies the general function $g(\cdot)$ of Equation 4.1.

Life starts off with growth. Then at some age some energy is invested in reproduction. This age at onset of reproduction (reproductive maturity) α is determined by the age when $\pi(a) < 1$ for the first time. Figure 4.1 depicts the age-trajectory of size during development. The curve is given by the solution to Equation 4.5, namely

$$\xi(a) = \left(\frac{\delta_1}{1-\delta_0} + \left(1 - \frac{\delta_1}{1-\delta_0}\right) e^{-k\,(1-\delta_0)\,a}\right)^{-1}, \tag{4.6}$$

taking into account that investment is constant at $\pi(a) = 1$ over that period and $\xi(0) = 1$. This logistic function has an upper limit of $(1-\delta_0)/\delta_1$, which reflects the size an organism would eventually approach if it continues to spend all available resources on maintenance and growth. In size-based approaches,

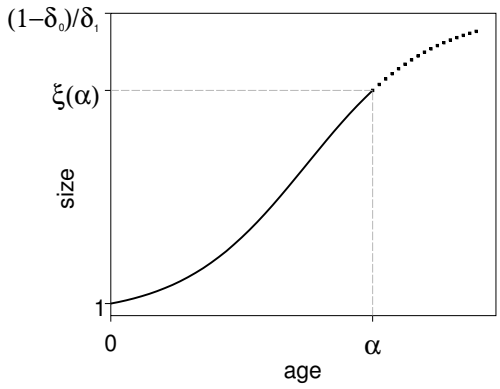

Fig. 4.1: Size $\xi(a)$ as a function of age a according to Equation 4.5.

growth functions that have an upper bound, such as the logistic function or the von Bertalanffy growth function, are frequently used, since size cannot increase indefinitely.

To ensure that the initial investment of $\pi_0 = 1$ actually leads to growth an

additional restriction on the parameters in (4.3) is necessary. From (4.5) one gets

$$\left.\frac{d\xi(a)}{da}\right|_{a=0} = k\,(\,1 - \delta_0 - \delta_1) > 0$$

and hence

$$\delta_0 + \delta_1 < 1. \tag{4.7}$$

This inequality concurrently guarantees that $\delta(\xi) < 1$.

The general function $f(\cdot)$ given in Equation 4.2 can be specified by the product of the probability of surviving to age a, $l(a)$, and the amount of reproduction at that age, $m(a)$. The objective function is then specified by

$$\max\, R = \int_0^\infty l(a)\, m(\,\xi(a),\, \pi(a)\,)\; da. \tag{4.8}$$

The survival function $l(a)$ is determined by the trajectory of mortality up to age a via

$$l(a) = e^{-\int_0^a \mu(\xi(t))\,dt}. \tag{4.9}$$

The age-specific force of mortality, denoted by $\mu(a)$, is assumed to be inversely proportional to $\xi(a)$. As discussed in Section 4.1, I focus on species for which growth enhances future survival. A simple way to model mortality in this case is to let

$$\mu(a) = \frac{b}{\xi(a)} + c. \tag{4.10}$$

The constant parameter $b \geq 0$ captures the size-dependent, "intrinsic" component of death and the constant parameter $c > 0$ captures the size-independent, "extrinsic" component of death.

The model implies that, if no energy is allocated to growth, then size deteriorates exponentially and therefore mortality increases exponentially. However, whether it is optimal to invest all available energy in reproduction is an outcome of the model. An exponential increase in mortality is not a built-in property of the model. If mortality increases, it can do so at any pace, exponential being the extreme case. In the exponential case, the mortality function is the same as the Gompertz-Makeham function. Exponentially increasing mortality ("Gompertz Law") is frequently assumed in the literature, based on various empirical observations. The general structure of the mortality function is the same as that used by Perrin (1992) (except for an exponent to size).

In accordance with the literature, I assume reproduction to be proportional to available resources (which are proportional to $\xi(a)$) and to the reproductive effort (in this model $(1 - \pi(a))$). A simple way to specify reproduction is to assume a linear relation with reproductive effort; this approach was taken by Charlesworth (1990), Perrin (1992), Kozlowski (1996), Cichon (1997) and Cichon and Kozlowski (2000). The maternity function, denoted by $m(a)$, is thus given by

$$m(a) \;=\; \varphi\,(1 - \pi(a))\,\xi(a). \tag{4.11}$$

Note that the constant, positive parameter φ can be adjusted to ensure that the optimal strategy yields a net reproductive rate $R = 1$. This implies that population density is assumed to affect lifetime reproductive success in a proportional manner. Note further that fertility and mortality are written as functions of age for purposes of brevity only. To be precise, $m(a) = m(\xi(a), \pi(a))$ and $\mu(a) = \mu(\xi(a))$.

The pleiotropic effects of size can be summarized as

$$\frac{d}{d\xi}\,\mu(\xi) \;<\; 0, \qquad \frac{\partial}{\partial\xi}\,m(\xi,\pi) \;>\; 0, \qquad \frac{d}{d\xi}\,\delta(\xi) \;>\; 0. \tag{4.12}$$

A larger size implies a lower risk of death, a higher reproductive potential but also a higher level of deterioration, which increases the costs of maintenance. Recall that the mediating effect of size between mortality, fertility and damage constitutes an important difference to previous models of reproductive effort, as emphasized at the beginning of this chapter. Equations 4.3, 4.4, 4.10 and 4.11 imply that an increase in reproductive effort $(1 - \pi(a))$ does not necessarily lead to a reduction in survival. As long as the level of $\pi(a)$ does not fall below the level of damage $\delta(\xi(a))$, size does not shrink and therefore mortality does not increase. Conversely, a declining investment in reproduction does not lead to improved survival as long as the level of investment $\pi(a)$ is below the level of damage $\delta(\xi(a))$.

4.3 An optimization model that leads to non-senescence

The optimal solution is a trajectory over age. Therefore, this is a dynamic rather than a static optimization problem. Two main approaches can be distinguished: Bellman's dynamic programming approach (Bellman, 1965) and Pontryagin's

Maximum Principle (Pontryagin, 1962). Comprehensive treatments of dynamic programming methods applied to biological problems are given in Mangel and Clark (1988) and Clark and Mangel (2000) as well as Bulmer (1995). The Appendix to Mangel (1987) shows how to connect dynamic state variable modeling with the ideas of classical demography and life history models.

4.3.1 The state ratchet

Bellman's general way of thinking implies a feedback loop strategy. In any particular given state, make the best possible decision. This decision will steer the state to some subsequent level. Again, given this subsequent state, do the best you can do. An optimal trajectory of decisions can be found by beginning at the last possible state and working backwards. The most important precondition for this strategy is that decisions only depend on the current state and potential future gains and losses but not on the past.

In particular, at each size $\xi(a)$ the amount of energy invested in growth $\pi(\xi(a))$ at that size determines whether size increases, decreases or is maintained. Depending on this decision, size changes over age according to Equation 4.2. The optimal trajectory of energy allocation to growth determines the optimal trajectory of size over age, which in turn determines the optimal age-trajectories of mortality and fertility.

Following Bellman's way of reasoning, the general nature of the optimal strategy can be understood intuitively. Assume each size is associated with a unique level of optimal investment and size changes continuously over age. Then each $\xi(a)$ is associated with a single $\pi^*(a)$ (the star indicating 'optimal') that determines whether size increases, decreases or is maintained.

Assume at a particular size $\xi(a)$ that the optimal investment results in an increase in size to $\xi(a^+) > \xi(a)$ at age $a^+ > a$. Assume further that, at the subsequent bigger size, it would be optimal to shrink. Then size would shrink to some lower value $\xi(a^{++}) < \xi(a^+)$ at age $a^{++} > a^+$. However, size is a continuous variable. In order to grow from $\xi(a)$ to $\xi(a^+)$ it must have been optimal to grow at each intermediate size between $\xi(a)$ and $\xi(a^+)$. Shrinking again from $\xi(a^+)$ to $\xi(a^{++})$) would imply that this optimality is violated at each level of size between $\xi(a^+)$ and $\xi(a^{++})$. Each intermediate size would be associated with two optimal strategies instead of one, which is a contradiction.

This line of reasoning leads to an important result, which I will call "the state ratchet". If, for the optimization problem formulated above, an optimal solution exists and each state is associated with exactly one optimal strategy, then any continuous, optimal state trajectory must be a monotonic function over age. Consequently, if the state variable initially increases, it will never decrease and if the state variable initially decreases it will never increase. Since maintenance implies that state does not change, the optimal strategy, which is bound to state only, will not change over age. Therefore, if, for any finite interval, it is optimal to maintain the current state, it will be maintained forever.

The state ratchet has important consequences for any optimal life history in this framework. Since life begins with growth it can never be optimal to shrink. Size can only increase and then be maintained at some point. Since mortality is assumed to be inversely related to size, mortality can never increase. Senescence is impossible. Intriguingly, this simple approach challenges Hamilton's postulate of inevitable senescence. It is possible to overcome the state ratchet, as I will discuss in a later section of this chapter, but only by making the model more complicated. Let's first consider the basic model.

4.3.2 The Maximum Principle

Pontryagin's way of thinking involves planning the whole future at time zero, in contrast to Bellman's backward step-by-step approach. Optimizing all future decisions at time zero requires knowledge about how decisions, the "control variable(s)", influence the change in the state variable(s) over time. The change in state(s) over time is determined by the so called "equation(s) of motion", i.e. first order differential equations that capture the change in any state variable over age. For my particular problem the control variable is the investment in growth, $\pi(a)$. One state variable is size, $\xi(a)$. Equation 4.5 determines the corresponding equation of motion, the change in size over age.

As in Bellman's approach, there is an important precondition. The optimal decision at any age a should only depend on the current state and potential future gains and losses but not on previous ages. However, survival to age a, as given in Equation 4.9, depends on the trajectory of mortality between age zero and age a. Therefore, survival must be treated as an additional state variable. Note that

survival changes over time according to

$$\frac{d}{da}\, l(a) \;=\; -l(a)\, \mu(a) \tag{4.13}$$

with initial condition $l(0) = 1$. Equation 4.13 depicts the equation of motion for the second state variable, survival.

Pontryagin's Maximum Principle (Pontryagin, 1962) associates a specific function with the optimal control problem stated above, the "Hamiltonian"

$$\begin{aligned} H(\,\xi, l, \pi, \lambda_1, \lambda_2\,) \;=\;& \; l(a)\, m(\xi, \pi) \\ & + \lambda_1(a)\, [\, k\,(\,\pi(a) \;-\; \delta_0 \;-\; \delta_1\, \xi(a)\,)\, \xi(a)\,] \\ & - \lambda_2(a)\, l(a)\, \mu(\xi). \end{aligned} \tag{4.14}$$

The first term is the contribution of the objective function (given in Equation 4.8 at age a: This term captures the current gains from a decision $\pi(a)$ at states $\xi(a)$ and $l(a)$. The remaining terms are the weighted sum of the change in the state variables. The factors $\lambda_1(a)$ and $\lambda_2(a)$ are costate variables. Costate variables capture the values of a hypothetical additional unit of $\xi(a)$ and $l(a)$ respectively at age a, the "shadow price" of size and survival.

Conditions for an optimum

The Maximum Principle requires that an optimal solution necessarily fulfills the following criteria:

- The Hamiltonian function is maximized with respect to the investment strategy. In general, if $H(\cdot)$ is differentiable, then

  $$\frac{d}{d\pi}\, H(\cdot) \;=\; 0. \tag{4.15}$$

  In particular

  $$H_\pi(\cdot) \;=\; l(a)\, m_\pi(\xi, \pi) \;+\; \lambda_1(a)\, k\, \xi(a) \;= 0, \tag{4.16}$$

  the subscript π indicating the partial derivative. Clearly, if the Hamiltonian is linear in the control variable, then the maximum is attained at the boundaries of the feasible set for the control. Note that the last term dropped

out. The shadow price of survival does not influence the maximum of the Hamiltonian.

- Furthermore the "adjoint equations"

$$\frac{d}{d\xi} H(\cdot) = -\frac{d}{da} \lambda_1(a), \quad \text{and} \quad \frac{d}{dl} H(\cdot) = -\frac{d}{da} \lambda_2(a) \tag{4.17}$$

must hold. The change in the shadow price of a state variable must equal the negative change in the Hamiltonian with respect to that state. More specifically, the adjoint equations associated with size and survival, respectively, are given by

$$\dot{\lambda}_1 = -H_\xi(\cdot) = -l\, m_\xi(\xi, \pi) - \lambda_1 k\,(\,\pi - \delta_0 - 2\,\delta_1\,\xi\,) + \lambda_2\, l\, \mu_\xi(\xi) \tag{4.18}$$

and

$$\dot{\lambda}_2 = -H_l(\cdot) = -m(\xi, \pi) + \lambda_2\, \mu(\xi). \tag{4.19}$$

- As age approaches infinity the values of an additional unit of size and survival, as captured by λ_1 and λ_2, respectively, have to approach zero. This is reflected in the transversality conditions, given by

$$\lim_{a\to\infty} \lambda_1(a) = \lim_{a\to\infty} \lambda_2(a) = 0. \tag{4.20}$$

Note that the state, control and costate variables are all functions of age. However, for brevity they are written as ξ, π, λ_1 and λ_2 wherever no confusion arises.

Solution

Taking into account that

$$k\,(\pi - \delta_0 - 2\,\delta_1\,\xi) = \frac{\dot{\xi}}{\xi} - k\,\delta_1\,\xi \tag{4.21}$$

the solution to the differential Equation in 4.18 gives the shadow price of an additional unit size at age a,

$$\lambda_1(a) = -\frac{1}{\xi(a)} \int_a^\omega e^{-k\,\delta_1 \int_a^t \xi(\tau)\, d\tau}\, \xi(t)\, l(t)\, (\lambda_2(t)\, \mu_\xi(t) - m_\xi(t))\, dt. \tag{4.22}$$

Equation 4.19 can be solved as

$$\lambda_2(a) \;=\; \frac{1}{l(a)} \int_a^{\omega} \; l(t)\, m(t)\, dt. \tag{4.23}$$

The shadow price of survival at age a is equivalent to the reproductive value at that age. Inserting 4.23 into Equation 4.18 leads to

$$\begin{aligned} \lambda_1(a) \;=\; & \tfrac{1}{\xi(a)} \textstyle\int_a^{\omega} \; e^{-k\,\delta_1 \int_a^t \xi(\tau)\, d\tau}\, \xi(t) \\ & \cdot \left(l(t)\, m_\xi(t) \;-\; \mu_\xi(t) \textstyle\int_t^{\omega} \; l(\tau)\, m(\tau)\, d\tau \right) \; dt. \end{aligned} \tag{4.24}$$

To find an explicit expression for size, Equation 4.5 can be solved, resulting in

$$\xi(a) \;=\; \frac{\exp\left\{ \int_0^a \; k\,(\pi(t) \;-\; \delta_0)\, dt \right\}}{\frac{1}{\xi(0)} \;+\; \int_0^a \; k\,\delta_1 \, \exp\left\{ \int_0^t \; k\,(\pi(\tau) \;-\; \delta_0)\, d\tau \right\} \; dt}. \tag{4.25}$$

It can be seen that the state variable size increases in a logistic manner.

Result

With the state ratchet I showed that size must follow a monotonic path. The same result can be proved applying optimal control theory. For an infinite horizon autonomous optimal control problem with a single state variable, the optimal state path must be monotone (Kamien and Schwartz (1991, p. 179) and Léonard and Van Long (1992, p. 294)). Recall from Equation 4.11 that fertility is linear in π. Therefore, the Hamiltonian function is linear in π, which results in solutions at the boundaries of the feasible set of investment strategies π, i.e. either one or zero.

Initially, $\pi_0 = 1$ and π remains at one until maturity. At maturity, a boundary solution implies that $\pi = 0$. If this were so, size would decrease, contradicting the state ratchet. Therefore, one expects what is called a "singular solution" in control theory. A singular solution requires that

$$\dot{H}_\pi \;=\; 0 \;=\; \dot{l}\, m_\pi^* \;+\; \dot{\lambda}_1\, k\, \xi^* \tag{4.26}$$

has to be satisfied. It would be natural if $\pi = \delta(a)$ were the singular solution required. Since size is constant in maintenance mode, the optimal solution would stay on the singular path forever. It turns out that $\pi = \delta(a)$ is the singular

solution, as discussed below.

Since a logistic increase in size implies an upper limit to growth, there must be an age a^* at which size is finally maintained,

$$\pi \;=\; \delta(\xi), \qquad \forall\, a \;\geq\; a^*. \tag{4.27}$$

Consequently $\xi(a^*) = \xi^*$, $m(a^*) = m^*$ and $\mu(a^*) = \mu^*$ will be constant. If size is constant the reproductive value is simply given by the quotient of m^* and μ^*. Since the reproductive value of an individual at age a is captured by the costate variable $\lambda_2(a)$, this costate will be constant as well.

Assume $\pi = \delta(a)$ from age a^* onwards. Taking into account that

$$l(a) \;=\; l(a^*)e^{-\mu^*\,(a\,-\,a^*)}, \tag{4.28}$$

it follows from (4.24) for all $a \geq a^*$ that

$$\lambda_1(a) \;=\; \frac{l(a)\,m^*}{(k\,\delta_1\,\xi^* \;+\; \mu^*)} \left(\frac{m^*_\xi}{m^*} \;-\; \frac{\mu^*_\xi}{\mu^*}\right). \tag{4.29}$$

This expression combined with condition (4.26) leads to an equation that determines the size at which the optimal investment should switch to maintenance mode,

$$\frac{m^*_\pi}{m^*} \;=\; \frac{k\,\xi^*}{k\,\delta_1\,\xi^* \;+\; \mu^*} \left(\frac{\mu^*_\xi}{\mu^*} \;-\; \frac{m^*_\xi}{m^*}\right). \tag{4.30}$$

The relative change in reproduction with respect to the investment in growth must equal the weighted difference between the relative changes in mortality and reproduction with respect to size. Note that this condition does not depend on age: (4.26) will be zero for all ages $a > a^*$ once maintenance mode is reached.

In this model fertility is given by Equation 4.11. From (4.30) it follows that a singular solution is determined by

$$\frac{\mu(\xi^*_a)}{k} \;=\; (1 \;-\; \delta_0 \;-\; 2\,\delta_1\,\xi^*_a) \;+\; \frac{(1 \;-\; \delta_0 \;-\; \delta_1\,\xi^*_a)\,b}{\mu(\xi^*_a)\,\xi^*_a}. \tag{4.31}$$

The individual will grow at full speed until its size satisfies Equation 4.31[1].

Substituting $\mu(\xi) \;=\; b\,/\,\xi \;+\; c$ yields a cubic polynomial with three roots. Generally, these roots can be real and complex. Viable strategies correspond

[1] I thank Anatoli Michalski for his explanations regarding optimal control theory.

to real, nonnegative roots. The optimal size at maturity corresponds to the root that maximizes life-time reproduction. Strategies can be determined numerically; I used MATHEMATICA™ to calculate the solution.

4.3.3 An alternative derivation

The state ratchet implies that if there is a single state variable, then the optimal investment strategy of an organism has to be growth, possibly followed by maintenance, i.e. the feasible set of $\pi(a)$ is

$$\pi(a) \in [\,\delta(a),\, 1\,]. \tag{4.32}$$

A valuable hint follows from Pontryagin's Maximum Principle. Since the Hamiltonian is linear in $\pi(a)$ the optimal investment maximizes the Hamiltonian function at the boundaries of the feasible set (4.32). The upper limit $\pi(a) = 1$ is associated with full growth and no reproduction. The lower limit $\pi(a) = \delta(a)$ switches the organism to maintenance mode with constant, nonzero fertility and mortality.

In this case the integral in (4.8) can be solved explicitly. The switching age, when $\pi(a)$ drops to $\delta(a)$, marks the onset of reproduction, age α. It follows that

$$R \,=\, l(\alpha)m(\alpha) \int_\alpha^\infty \exp\left\{-\int_\alpha^a \mu(t)\,dt\right\} da \,=\, l(\alpha)\,\frac{m(\alpha)}{\mu(\alpha)}\,, \tag{4.33}$$

where $m(\alpha)$ and $\mu(\alpha)$ are the constant levels of fertility and mortality in maintenance mode after α.

The age α at which reproduction starts is determined by the value ξ_α that maximizes R in (4.33). Using the fact that from age zero to α there is a one-to-one correspondence between age a and size ξ, one can express (4.33) as a function of ξ_α. Inverting the logistic growth function $\xi = L(a)$ given in (4.6) leads to

$$a = L^{-1}(\xi) = \frac{1}{k\,(\,1\,-\,\delta_0)}\,\ln\left(\frac{1\,-\,\frac{\delta_1}{1-\delta_0}}{\frac{1}{\xi}\,-\,\frac{\delta_1}{1-\delta_0}}\right). \tag{4.34}$$

Thus, by substituting $\alpha = L^{-1}(\xi_\alpha)$ in (4.33) one can express $R = R(\xi_\alpha)$ as a function of size at reproductive maturity ξ_α. The optimization problem now can

be solved by setting the derivative of $R(\xi_\alpha)$ with respect to ξ_α equal to zero, i.e.,

$$l_{\xi_\alpha}\,\frac{m}{\mu}\,+\,m_{\xi_\alpha}\,\frac{l}{\mu}\,-\,\mu_{\xi_\alpha}\,\frac{l\,m}{\mu^2}\,=\,0\,. \tag{4.35}$$

Because

$$l_{\xi_\alpha}\,=\,\frac{d}{d\xi_\alpha}\,l(\xi_\alpha)\,=\,\frac{d}{d\xi_\alpha}\,\exp\left\{-\int_1^{\xi_\alpha}\,\mu(\xi)\,\left[k\,(\,1\,-\,\delta_0\,-\,\delta_1\,\xi)\,\xi\right]^{-1}\,d\xi\right\}$$

$$=\,-l(\xi_\alpha)\,\mu(\xi_\alpha)\,\left[k\,(\,1\,-\,\delta_0\,-\,\delta_1\,\xi_\alpha)\,\xi_\alpha\right]^{-1}\,,$$

optimal size at maturity is given by

$$\frac{\mu(\xi_\alpha)}{k}\,=\,(\,1\,-\,\delta_0\,-\,2\,\delta_1\,\xi_\alpha\,)\,+\,\frac{(\,1\,-\,\delta_0\,-\,\delta_1\,\xi_\alpha\,)\,b}{\mu(\xi_\alpha)\,\xi_\alpha}\,. \tag{4.36}$$

This equation is equivalent to 4.31. Using calculus and static optimization and applying Bellmann's way of thinking with a hint from Pontryagin leads to the same result as using dynamic optimization applying Pontryagin's Maximum Principle.

4.3.4 The simplest model leads to sustenance

In the simplest case of size-independent mortality, i.e. $b\,=\,0$, an explicit solution for the optimal size at maturity can be derived:

$$\xi_\alpha\,=\,\frac{(\,1\,-\,\frac{c}{k}\,-\,\delta_0\,)}{2\,\delta_1}\,. \tag{4.37}$$

Results for three illustrative parameter combinations are shown in Figure 4.2. Equation 4.37 implies

$$\frac{d\xi_\alpha}{dc}\,<\,0\,,\,\frac{d\xi_\alpha}{d\delta_0}\,<\,0\,,\,\frac{d\xi_\alpha}{d\delta_1}\,<\,0\;\text{ and }\;\frac{d\xi_\alpha}{dk}\,>\,0. \tag{4.38}$$

Furthermore, (4.37) and (4.34) imply

$$\frac{d\alpha}{dc}\,<\,0\;\text{ and }\;\frac{d\alpha}{d\delta_1}\,<\,0\,. \tag{4.39}$$

Increasing extrinsic mortality reduces age and size at maturity. Changes in α with respect to k and δ_0 depend on the parameter combination in a rather complicated

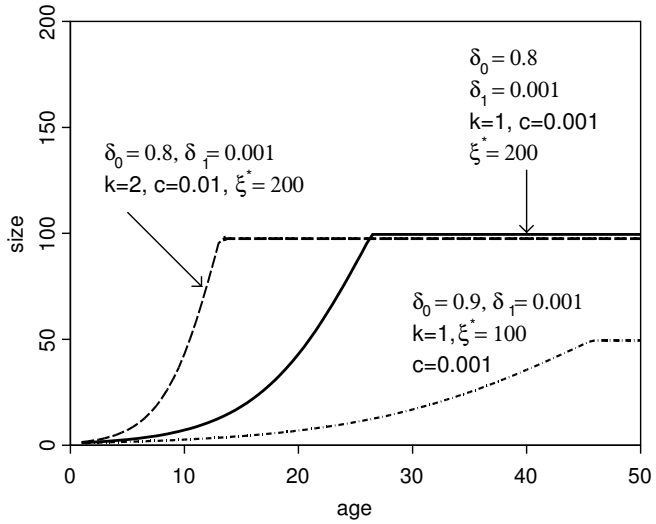

Fig. 4.2: Size $\xi(a)$ for three selected parameter combinations. Note that ξ^* denotes maximum possible size.

way. For very small maximum attainable sizes and very slow speed of growth, α can increase with increasing k and decrease with increasing δ_0. Usually, however, an increase in k will lead to a decline in α while an increase in δ_0 will lead to a decrease in α.

If $b > 0$ in (4.10), then mortality declines as size increases. Hence for positive but small b

$$\xi_\alpha \,|_{b>0} > \xi_\alpha \,|_{b=0} \,. \tag{4.40}$$

If, however, b is large then the increased risk of death may make it optimal to start reproducing at a smaller size. Some illustrative results are shown in Table 4.1. If b gets too large then the resulting solutions are nonviable strategies: the species cannot survive because mortality is too high. Such nonviable strategies correspond to roots of Equation 4.31 that are complex or negative.

In sum, the simplest model in which a single state variable determines the optimal strategy and reproductive effort affects fertility in a linear way can only lead to sustenance, i.e. a period of development followed by maintenance. Senescence is impossible and all there is to be optimized is the age at maturity. From this age onwards the individual maintains its state forever. Complications have to be added to the simple model to get optimal strategies that are more flexible than this basic strategy. Note that flat mortality and fertility profiles were found

Tab. 4.1: Optimal size ξ_α and age α at the start of reproduction for size-dependent mortality ($b > 0$) according to Equation 4.31.

ξ_α	α	ξ_{max}	$l(\alpha)$	b	c	k	δ_0	δ_1
62.26	50.96	100	0.005	0.5	0.001	1	0.9	0.001
53.46	47.34	100	$1.1 \cdot 10^{-9}$	2	0.001	1	0.9	0.001
60.02	50.02	100	0.00003	1	0.001	1	0.9	0.001
25.68	17.66	100	0.0012	1	0.1	2	0.9	0.001
56.86	24.36	100	0.0045	1	0.01	2	0.9	0.001
64.06	25.87	100	0.0056	1	0.000001	2	0.9	0.001
127.66	29.31	200	0.006	1	0.001	1	0.8	0.001
129.18	14.74	200	0.08	1	0.001	2	0.8	0.001

to be very common in numerical studies by Charlesworth (1990).

4.3.5 Introducing nonlinearity can lead to supersustenance

Supersustenance – a sustenance strategy that includes a period of parallel growth and reproduction after the initial period of development and before the terminal period of maintenance – is precluded by the linearity in $\pi(a)$ of Pontryagin's Hamiltonian. To allow supersustenance a model specification has to be found which results in a Hamiltonian that is nonlinear in $\pi(a)$.

To solve such an optimization problem the Bellman principle of dynamic programming can be used. Because the size ratchet precludes an organism from returning to previous states, the optimal trajectory of the allocation strategy can be found by a backward algorithm starting at the maximum attainable size at which maintenance is the only possible strategy. I developed such an algorithm (see appendix C), which produced results that were consistent with the analytic solution in the case of fertility being linear in $\pi(a)$. This algorithm can be readily applied to the following nonlinear fertility function:

$$m(a) = \varphi\, \pi(a)\, (1 - \pi(a))\, \xi(a) = \varphi\, (\pi(a) - \pi^2(a))\, \xi(a). \tag{4.41}$$

The second term in the product, $\pi(a)$, can be interpreted as the efficiency of converting size $\xi(a)$ into reproduction $m(a)$. As $\pi(a)$ approaches zero, i.e. as resources are largely directed to fertility rather than growth and maintenance, this efficiency declines.

Figure 4.3 shows an illustrative result. For the parameters used in this model, reproduction starts when the organism grows to about 25% of its potential maximum size. Then, until maintenance mode is eventually reached at age 250, there is an extended period of supersustenance.

This still simple model leads to optimal strategies of development followed by a period of parallel growth and reproduction followed by maintenance. In addition to the age at maturity, the age at maintenance as well as the path of investment between maturity and maintenance need to be optimized. However, senescence is still not an option. Any decline in size (i.e. an increase in mortality) is precluded by the state ratchet. To arrive ultimately at a framework where senescence is a possible optimal outcome the basic model has to be complicated even further.

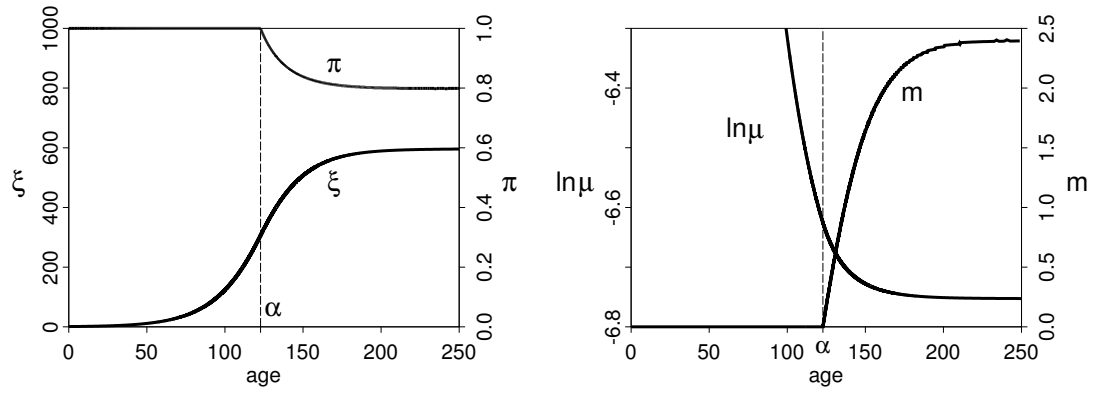

Fig. 4.3: Supersustenance for model variant (4.41). Parameter values were $k = 0.1$, $\delta_0 = 0.5$, $\delta_1 = 0.0005$, $b = 0.1$, $c = 0.001$, $\varphi = 0.02$. The force of mortality before age 100 is very high and rapidly falling.

4.4 An optimization model that leads to senescence

The state ratchet implies that any single-state life-history model along the general lines described above will always yield growth, declining mortality and increasing fertility followed by maintenance mode. Even if an exogenous event reduces ξ to some lower level ξ^-, then the individual would simply resume growth with the π-strategy previously followed at ξ^-.

In this kind of model, the single variable size ξ determines the capability of an individual to gather resources, to produce progeny and to avoid death. This spectrum might be too broad to be captured by size alone. Size can be measured by weight, length, number of cells, number of modular units or some similar index. While body size is determined by the number of cells and may remain constant, the functioning of cells may decline due to insufficient investment in maintenance because each cell is subject to continuous wear and tear. Therefore, it seems reasonable to distinguish between quantity and quality of cells. Functioning can be captured by a second state variable denoted by the Greek letter υ, which can take values between one and zero. The "vitality" of an individual can then be modeled as the product of ξ times υ, size weighted by functioning. Adding a second state variable to the model is a way to escape the state ratchet.

The model can be reformulated as follows. Fertility is given by

$$m(a) \;=\; \varphi\,(\pi(a) \;-\pi^2(a))\;\xi(a)\,\upsilon(a), \tag{4.42}$$

and mortality is given by

$$\mu(a) = \frac{b}{\xi(a)\,\upsilon(a)} + c. \tag{4.43}$$

Note that both fertility and mortality now depend on the product of size and functioning, $\xi(a)\,\upsilon(a)$, which captures vitality. The particular nonlinearity in fertility was retained.

This model can lead to determinate growth. Let a^* be the age at which growth is completed. Then $d\xi/da = 0$ for all $a > a^*$, where $\xi(a^*) = \xi^*$ denotes the size attained at the end of the determinate growth period. For $a < a^*$, functioning does not change, i.e. $\upsilon(a) = 1$. If investment falls below maintenance level, i.e. $\pi(a^*) < \delta_0 + \delta_1\,\xi(a^*)$ at a^*, functioning starts to deteriorate exponentially at the rate $\acute{\upsilon} = \kappa\,(\pi(a) - \delta_0 - \delta_1\,\xi^*)$ with initial condition $\upsilon(a^*) = 1$. If $\pi(a^*)$ is chosen to equal the deterioration at that age, the individual maintains its current functioning: this corresponds to the case of determinate growers with sufficient repair or replacement of tissues to escape senescence. The age a^* is not necessarily identical to age at reproductive maturity α, although for many determinate growers the two approximately coincide. The parameter combinations I used in the algorithm led to strategies for which $a^* = \alpha$.

Growth in ξ is positive until determinate size is attained and zero afterwards:

$$\frac{\frac{d\xi(a)}{da}}{\xi(a)} = \begin{cases} k\,(\pi(a) - \delta_0 - \delta_1\,\xi(a)) & \text{if } \pi(a) > \delta_0 + \delta_1\,\xi(a) \\ 0 & \text{otherwise,} \end{cases} \tag{4.44}$$

where $\xi(0) = 1$. Functioning is constant at one until determinate size is reached and then declines:

$$\frac{\frac{d\upsilon(a)}{da}}{\upsilon(a)} = \begin{cases} 0 & \text{if } a < a^* \\ \kappa\,(\pi(a) - \delta_0 - \delta_1\,\xi^*) & \text{if } a \geq a^* \end{cases} \tag{4.45}$$

where $\upsilon(0) = 1$. Note that $\pi(a) - \delta_0 - \delta_1\,\xi^* < 1$. The parameters k and κ

determine the speed of increase in size and the speed of decline in functioning, respectively.

Figure 4.4 exemplifies the optimal trajectories of $\pi(a)$, $\xi(a) \cdot \upsilon(a)$, $\mu(a)$ and $m(a)$ for determinate growth for this model. The results were obtained numerically. The maximum attainable size is $\xi = 25$; this size is almost reached at age of reproductive maturity α.

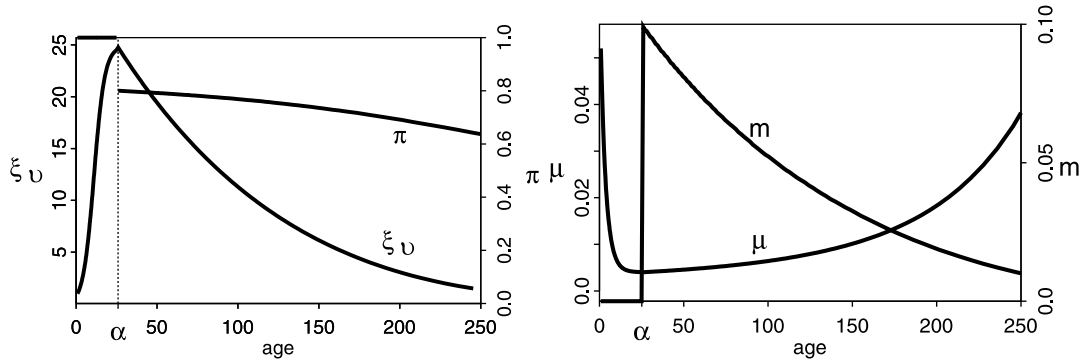

Fig. 4.4: $\xi(a) \cdot \upsilon(a)$, force of mortality μ and fertility m resulting from optimal strategy $\pi(a)$ as a function of age a, for model with parameters $k = 3$, $\delta_0 = 0.9$, $\delta_1 = 0.004$, $\kappa = 0.05$, $b = 0.05$, $c = 0.002$, $\varphi = 0.02$.

In this model, the state variable that effectively determines the strategy switches from size to functioning at age a^*. Before age a^* size is the only effective state variable, since functioning is constant. After age a^* functioning is the only effective state variable, since size is constant. Therefore, the state ratchet applies and functioning cannot increase again once it has fallen below one. The switch between size and functioning is assumed to occur only once. Growth cannot be resumed.

Another possibility for overcoming the state ratchet, but keeping a model that is essentially based on a single state, is to introduce a switch variable, which is a binary indicator that determines whether the organism is in up or down mode. The switch itself does not affect survival or reproduction. To jump the maintenance barrier, the switch needs to change from up into down mode. In this case the optimality of the strategy is not violated, as the smaller state is now associated with a different value of the switch. Depending on whether the switch is triggered once or several times, internally or externally, different state trajectories can emerge. Any repeated trajectories of increase and decrease have to be identical. This line of reasoning will be taken further in the next chapter.

4.5 Discussion

The first, simplest, model developed above led to sustenance as the only possible life-history strategy. The function describing reproduction had to be made nonlinear to get divergence from this prototype life history. The slightly more complex model led to a variety of possible life-history strategies between sustenance and supersustenance. But senescence could still never be optimal.

To arrive at senescent strategies the state of the individual had to become more complicated, now being, effectively, a product of two variables, size and functioning. The product of size and functioning can be interpreted as reflecting the vitality of the individual. Vitality and not size determines mortality and fertility. Consequently it is possible that individuals might maintain about the same body weight, length or cell number over an extended period of life but suffer a decline in vitality due to wear and tear and lack of repair.

Although the eventuality was not considered here, size could increase over an extended period of life with this growth counterbalancing forces of deterioration and functional decline. In such species the ability to escape mortality, as captured by ξ times υ, may remain roughly constant—resulting in non-senescence.

Note the distinction between senescence, on the one hand, and deterioration and functional decline, on the other. The term senescence is used only with regard to entire organisms, not parts of organisms. In this model deterioration is captured by $\delta(a)$ and decline in functioning by a decrease in $\upsilon(a)$. A tendency for existing body parts to deteriorate and to require repair or replacement to maintain functioning may possibly be a "fundamental, universal, and intrinsic" property of living organisms (Arking et al., 1991); senescence, as defined here, is not.

The theoretical results of this chapter and the empirical evidence presented in Section 3.3.3, suggest the following hypotheses:

- Senescence characterizes individuals in species that attain a size at reproductive maturity that is close to maximum size. Such determinate-growth species include mammals, birds, insects and some other species including the nematode worm *C. elegans*. The main model species studied by gerontologists are mammals (including humans, rats and mice), insects (especially *Drosophila* but also Medflies and some other insect species), *C. elegans*, and yeast. All of these species fall into this determinate-growth category. Many

determinate-growth species also have fixed oocyte stocks or are otherwise limited with regard to reproductive capacity. Species that experience declines in fertility with age or that have limited fertility seem likely to suffer senescence.

- Non-senescence characterizes individuals in species that attain a size at reproductive maturity that is less than maximum size and that gain reproductive capacity as they grow. Such species with indeterminate growth include most trees, many other perennial plants, many modular animals such as corals and perhaps sponges, some kinds of algae, many fish, reptiles and amphibians, and probably various nonmodular invertebrates such as some mollusks and some echinoderms.

Species falling into the second category are not typically model organisms in gerontological research. This might be one reason why the universality of senescence was accepted as gerontological dogma.

Many biologists would agree that, for many species, stage is what determines mortality and fertility rather than age. If age itself matters at all, this line of thinking leads to the conjecture that biological age may be better captured by the "average age" of an individual — i.e., by some appropriate measure of the average age of the organs, body parts or cells of an individual — than by the chronological age of the individual. In indeterminate-growth species, continuing increases in size keep average age below chronological age. Furthermore, organisms that can repair, replace or rejuvenate body parts may show, over chronological time, slow increases or even decreases in average age. For instance, trees that replace their leaves annually, that develop new roots and new branches to replace damaged or lost ones, and that continue to grow may be of an average individual age that remains roughly constant and may even decline with chronological age. For some species of plants and animals, there can be a complete turnover of body parts over a time interval: for these species, average individual age can be much lower than chronological age and can decline over time if the individual grows and its component parts continue to renew themselves with time.

A remarkable example is Hydra (Martinez, 1998). Most species as small as hydra have a short life expectancy. Hamilton's reasoning would imply that hydra should senescence quickly after having lived past its typical lifespan in the wild. Contrary to this prediction, mortality is constant and has been effectively zero for

hydras kept in the laboratory of Daniel Martinez for four years. Because there is rapid turnover of a hydra's cells, this example directs attention to considering not only size, i.e. quantity of cells, but also quality of cells. The first two models developed in this chapter consider size only, while the third model is a first attempt to incorporate not only quantity but also quality of cells. The model I develop in the following chapter accounts for both quantity and quality of cells.

This chapter has shown that non-senescence is a life-history strategy that is theoretically possible. Senescence can be avoided by "conceivable" organisms, namely by species with size-dependent vital rates. This finding together with the empirical evidence presented in Section 3.3 leads me to the hypothesis that non-senescence may indeed be a life history followed by some and maybe many plant and animal species. In the following chapter I develop a more general model to further study the evolution of senescence vs. non-senescence.

4.6 Next steps

A critical examination of the model developed above indicates several directions to explore.

- If the intrinsic mortality component b is large, then strategies could become nonviable because initial mortality would be too high. To get around this pitfall one could allow for a variable size at birth. This adds a further question to be answered: what is the optimal size at birth?

- The nonlinearity in fertility was introduced by means of efficiency of reproduction. Is there a more elegant way to incorporate efficiency?

- Reproduction and growth relate directly to size. This implicitly assumes that available resources are proportional to size. Is there a more realistic way to model resources?

- The vitality of an organism was modeled as a product of the two states size and functioning, in order to develop a model that can lead to non-senescent as well as senescent life-history strategies. The resulting model specifications seem rather complicated. Furthermore this model is not able to capture a simultaneous increase in size with a decrease in functioning.

Size and deterioration were assumed to remain constant once functioning starts to decline. An idea for getting around this complication was suggested in Section 4.4.

The following chapter will take these points into account.

5. AN OPTIMIZATION MODEL BASED ON VITALITY

The models developed in Chapter 4 show that non-senescence can be optimal. Size constitutes the central state variable in this framework. Mortality falls with increasing size and reproductive potential rises. The case of determinate growth, however, poses a challenge to this framework. Determinate growers, such as humans, often reach their final size at about the age of maturity. While size remains constant after the onset of reproduction, mortality steadily rises. This is incompatible with the strict size-dependence of mortality. A new model can be developed to address the deficiencies of the size-based model. To capture changing mortality at a constant size, the quality of size will be considered. The approach is rationalized in the following way. Even if size remains unchanged, all cells progressively accumulate damage over time and deteriorate. *Vitality*, defined as an individual's size adjusted for the functioning of body cells, can decline and therefore mortality can increase despite a constant body size. This notion was introduced in Section 4.4, where vitality was defined as the product of two functions, size and functioning. Here, vitality captures the accumulated functioning of all body cells, i.e. if a cell has been damaged and only works at 80 % of the capacity of an undamaged cell, this cell will account for 0.8 units of total vitality.

Facing ubiquitous decay, life is sustained by processes of regeneration and rejuvenation. The continuous creation of new, undamaged cells counterbalances deterioration. This balance determines whether or not vitality declines. The level of rejuvenation and repair depends on the trade-offs between reproduction on the one hand and growth and maintenance on the other. The optimal schedule of resource allocation determines the optimal trajectory of vitality. Increasing vitality raises reproductive potential and lowers mortality. Reproduction results in offspring but entails slower growth or even decline in vitality. The trajectory of vitality over age determines the age-trajectories of fertility, mortality and growth. The following evolutionary-demographic model sheds light on the fundamental questions of life-history theory based on the single state variable, vitality.

Anderson (2000) developed a model based on the variable vitality. Anderson defines vitality as a randomly varying component of mortality which leads to death if vitality ever reaches zero. The use of the state variable vitality, as defined here, constitutes a new approach to life history modeling.

5.1 The vitality model

Survival is a function of mortality. In accordance with the size-based models it seems natural to model mortality as an inverse function of vitality, denoted by ψ. A simple function for the force of mortality, μ, is

$$\mu(\psi) = \frac{b}{\psi} + c, \tag{5.1}$$

where b and c are constant parameters. The intrinsic parameter b captures all causes of death an individual can escape from by increasing its vitality, while the extrinsic parameter c captures the always prevalent, non-zero risk of death. Note that "extrinsic" and "intrinsic" refer to vitality-dependent vs. vitality-independent mortality.

Reproduction and growth depend on the level of available energy. In the size-based models, energy was simply proportional to size. However, energy production is not equivalent to size but has been found to scale allometrically with it (Lavigne, 1982). A sound theoretical basis for a particular relation between size and net energy available was given by West et al. (2001), their Equation (3). This formula captures the difference between energy created by cell metabolism and energy required for it, based on an allometric relation between size and energy production.

The model developed in this chapter uses Equation (3) from West et al. (2001) to determine the available resources of an individual at its current level of vitality. The formula of West et al. (2001) is based on the variable size. The link between vitality and size is assumed to be tight enough to justify the substitution of vitality for size in this equation for this specific model. Net energy production, denoted by $\epsilon(\psi)$, depends on the difference between build-up and break-down processes at current vitality,

$$\epsilon(\psi) = k\,\psi^{0.75} - \kappa\,\psi, \tag{5.2}$$

where k and κ are constant parameters. Anabolic, build-up processes are directly linked to metabolic output, which is assumed to be proportional to vitality to the power 0.75. Catabolic, break-down processes are assumed to be proportional to vitality to the power one.

The exact value 0.75 for anabolic processes was thought to be a so called life-

history invariant (Charnov, 1993). The method of calculating these life-history invariants has recently been called into question (Nee et al. (2005), De Jong (2005)). The particular value of 0.75 might therefore not be invariant across species. The qualitative results of my model, however, do not depend on the particular value 0.75 but only require the existence of such an allometric relation.

Energy production is maximal at vitality ψ_ϵ

$$\psi_\epsilon = \left(\frac{3}{4}\frac{k}{\kappa}\right)^4. \tag{5.3}$$

As in the size-based model, growth and maintenance are paid out of the same budget. Part of the energy available must be used to offset the declining functioning of cells. The change in vitality is given by the difference between the fraction of resources allocated to growth (newly built cells) and the unavoidable deterioration of functioning of current cells at a constant rate δ. Damage is proportionally to vitality and integrates naturally into the structure of West et al.'s equation. Consequently, vitality ψ changes over time according to

$$\dot{\psi} = \pi(\psi)^{\eta_g}\,\epsilon(\psi) - \delta\,\psi, \tag{5.4}$$

where $\pi(\psi)$ denotes the fraction of energy allocated to growth, as in the models in Chapter 4. In contrast to those models, $\pi(\psi)$ can now have a nonlinear effect on the change in state depending on the value of the constant parameter η_g (g for growth). In the extreme case of no energy allocation to growth and maintenance, vitality deteriorates exponentially and, as in the size-based model, mortality rises exponentially. Note that η_g has no effect if $\pi(\psi)$ equals either zero or one. The reasoning behind the incorporation of this parameter will be given below.

The level of $\pi(\psi)$ that corresponds to maintenance of current vitality can be derived from Equation 5.4. Denoting the level of $\pi(\psi)$ at $\dot{\psi} = 0$ by π_0 and inserting Equation 5.2 yields

$$\pi_0 = \left(\frac{\delta}{k\,\psi^{-0.25} - \kappa}\right)^{\frac{1}{\eta_g}}. \tag{5.5}$$

Vitality cannot increase indefinitely. An upper limit to ψ, denoted by Ψ, is

reached at maximum investment $\pi(\psi) = 1$ and $\dot{\psi} = 0$,

$$\Psi \equiv \left(\frac{k}{\kappa + \delta}\right)^4. \tag{5.6}$$

Available energy must be nonnegative. This implies that

$$\psi \leq \left(\frac{k}{\kappa}\right)^4 \tag{5.7}$$

must hold. This is always true since Equation 5.7 implies that ψ cannot exceed maximum attainable vitality Ψ, as given by Equation 5.6.

In the initial size-based model (Section 4.3) reproductive effort and reproductive output are related linearly. As explained in Section 4.3.2, it turns out that this assumption restricts optimal solutions to energy allocation exclusively to either growth or reproduction. To develop a model that permits a broad scope of possible investment strategies, a nonlinear influence of investment needs to be incorporated that still includes the possibility of exclusive allocation. This is the technical argument that motivates the introduction of parameter η_g in Equation 5.4. The biological motivation for introducing nonlinear effects is the following.

Growing a human arm requires considerable effort and is so difficult that, if the arm is lost, no new arm can regrow. In contrast, growing a branch of a tree can be done readily to increase size or replace broken branches. The growth apparatus in humans and trees is inherently different. In the former case, it might be very costly and even impossible to keep or rebuild the machinery that would allow the regrowth of a lost arm. In the latter case, maintenance is cheap because existing machinery can be used to maintain the organism without much additional cost.

Parameter η_g captures the nature of the growth and maintenance apparatus of a species. When η_g exceeds one, the investment function π^{η_g} in Equation 5.4 is convex. The marginal benefits in outcome become larger as π approaches one. Note that the convexity favors exclusive investment strategies. When η_g is below one, the investment function π^{η_g} is concave. The marginal benefits in output become smaller as investment approaches one. Note that concavity favors intermediate investment strategies. The parameter η_g in Equation 5.4 captures the returns to scale in growth and maintenance investment. The parameter can also be interpreted as the efficiency of the growth system. Values of η_g below one

correspond to efficient, i.e. cheap growth, and values of η_g above one correspond to inefficient, i.e. costly growth.

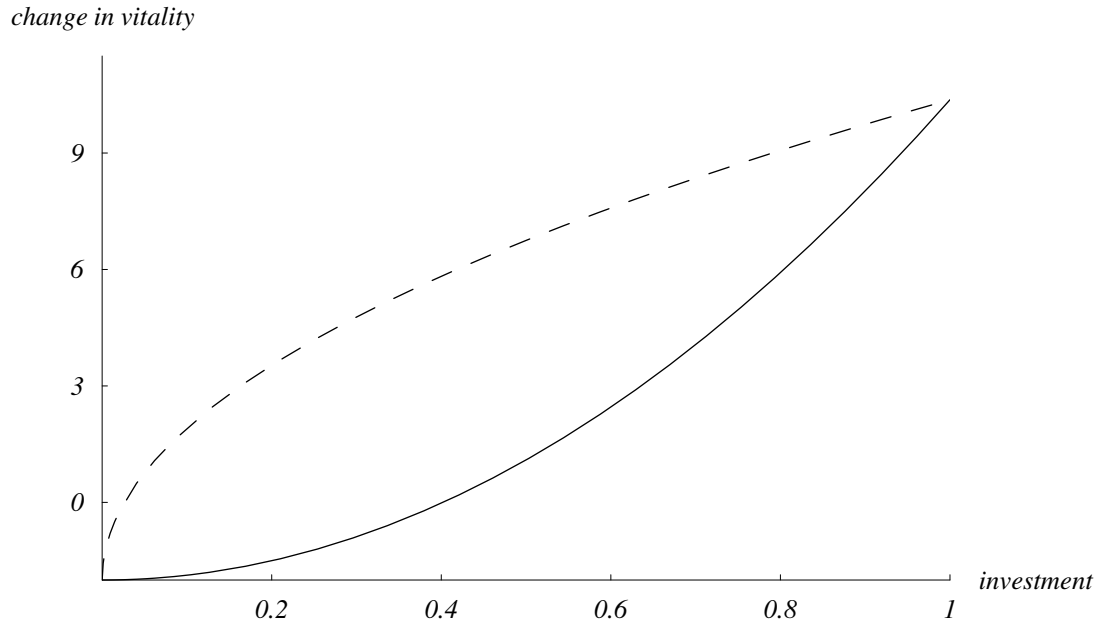

Fig. 5.1: The influence of η_g via investment π on the change in vitality as specified by Equation 5.4. The dashed line exemplifies values of η_g below one, in particular $\eta_g = 0.5$. The solid line exemplifies values of η_g above one, in particular $\eta_g = 2$. In both cases $\psi = 20$, $k = 3$, $\kappa = 0.8$ and $\delta = 0.1$.

Figure 5.1 illustrates the influence of parameter η_g via investment π on the change in vitality. Note that the change in vitality is always larger for a given level of investment π when η_g is below one as opposed to being above one. Likewise, any particular level of change in vitality requires a smaller investment, given that η_g is below one rather than above one. Note further that values of η_g below one imply a concave shape, while values above one correspond to a convex shape of the change in vitality with increasing investment.

In the modified size-based model (Section 4.4) an arbitrary attempt was made to introduce nonlinearity with respect to reproductive effort. Here, nonlinearity in reproductive effort is captured by the parameter η_r (r for reproduction), which captures the efficiency of reproduction, analogous to η_g.

In the size-based model, offspring are born at size one. This initial offspring size determines the initial mortality rate, the amount of energy necessary to create one offspring and therefore the number of offspring produced. If offspring could be born at larger sizes, they would be more robust and therefore would have

higher survival chances from the very beginning of life. On the other hand, larger offspring require more energy per offspring. In this way, offspring size effects the optimal energy allocation strategy and is a variable expected to be optimized by the trade-off between quantity and quality of offspring.

In the vitality model, the maternity function is specified as

$$m(\psi) \;=\; \varphi\,[\,1 \;-\; \pi(\psi)\,]^{\eta_r}\,\frac{\epsilon(\psi)}{\psi_0^{\eta_j}}. \tag{5.8}$$

In accordance with the size-based models, fertility is proportional to available energy, in this model $\epsilon(\psi)$, and reproductive effort, $1-\pi(\psi)$. Available energy is divided by the initial vitality of offspring, ψ_0. The constant parameter $\eta_j > 1$ (j for juvenile) accounts for energy that is needed to create one offspring but that does not accumulate in the vitality of an offspring. Contrary to the parameters η_r and η_g, parameter η_j captures the level of "wastage" rather than "efficiency". The wastage parameter η_j does not influence the optimal trajectory of investment over the life course. As a constant, $\psi_0^{\eta_j}$ can be taken outside the integral that accumulates life-time reproduction. Optimal offspring size can be determined once the optimal path of energy allocation over the life course is found. Perrin (1992) incorporated offspring size in a similar manner, without the exponent, but in Perrin's approach offspring size was a given constant, not a variable to be optimized. The constant φ is a scaling parameter set to the value that ensures that optimal lifetime reproduction is equal to one and, hence, $r_{max} = 0$.

The manner in which nonlinearities are incorporated in the present chapter is biologically and technically motivated. The approach makes use of the well-known concept used in economics of the Cobb Douglas production function. Each input factor to the production function is raised to a power reflecting how efficient each factor, in economics labor and capital, is in producing output. Two new parameters (that influence the optimal trajectory of investment) enter the model as exponents of investments. Power functions have previously been used to introduce nonlinearities into life-history models (Gadgil and Bossert (1970), Schaffer (1974), Cichon and Kozlowski (2000), Cichon (1997), Charlesworth (1990); see Charlesworth (1994, Section 5.3.4.) for review). In particular, the importance of the shape of the investment function for the optimal life history strategy has been recognized. In their reproductive effort models, Gadgil and Bossert (1970) and Schaffer (1974) found that concave investment functions favor iteroparous

strategies (repeated breading, i.e. intermediate reproductive effort) while convex investment functions favor semelparous strategies (a single breeding event, in which reproduction is fatal, i.e. exclusive investment).

George E. P. Box said: "All models are wrong, but some are useful." (Box, 1979) Models are wrong because they simplify the complexity of life. But without this simplification, patterns can hardly be observed and understood. A useful model captures the most important aspects of reality, reveals general patterns and provides a source for hypotheses that could explain basic processes of life. Such a model, although necessarily wrong, enhances our understanding of nature.

Adding efficiency and offspring size to the size-based model increases complexity but it also considerably broadens the model's potential for predicting various life-history strategies. The non-linearities capture cases in nature when parallel investment in growth and reproduction is optimal. Therefore, these extensions to the model can be justified as a useful complication to a still simple model.

5.1.1 The parameters

k, κ and δ

Parameter k captures the speed of growth of vitality (Equations 5.2 and 5.4). Faster growth implies a rapid fall in mortality (Equation 5.1) and reduces the time of development. Furthermore, higher values of k decrease maintenance costs (Equation 5.5) and increase maximum vitality (Equation 5.6). Parameter κ is inversely related to maximum vitality. Elevating κ slows growth, increases maintenance costs (Equation 5.5) and decreases maximum vitality (Equation 5.6). Parameter δ determines the rate of decline in vitality (Equation 5.4). Higher δ increases maintenance costs (Equation 5.5) and decreases maximum vitality (Equation 5.6).

If all available energy is allocated to reproduction, then δ determines the constant rate of increase in mortality (Equation 5.1). A decline in vitality implies not only a reduction in survival but also in reproductive potential. Therefore, larger values of δ will tend to increase the investment of resources in growth in order to slow down the deterioration process.

Parameters k and κ determine the shape of the energy trajectory over vitality (Equation 5.2). If $\kappa < 3\delta$, then energy is an increasing function of vitality because the maximum attainable vitality is smaller than the level of vitality that

maximizes energy, $\Psi < \psi_\epsilon$. Otherwise, if $\kappa > 3\delta$, then the trajectory of energy is hump-shaped with respect to vitality. The influence of the relation between κ and δ on the energy trajectory over vitality is visualized in Figure 5.2. Note that an increase in vitality beyond the threshold given by Equation 5.3, which corresponds to the peak of energy, can only be optimal if the corresponding reduction in mortality offsets the loss in available resources, i.e. in growth and reproductive potential.

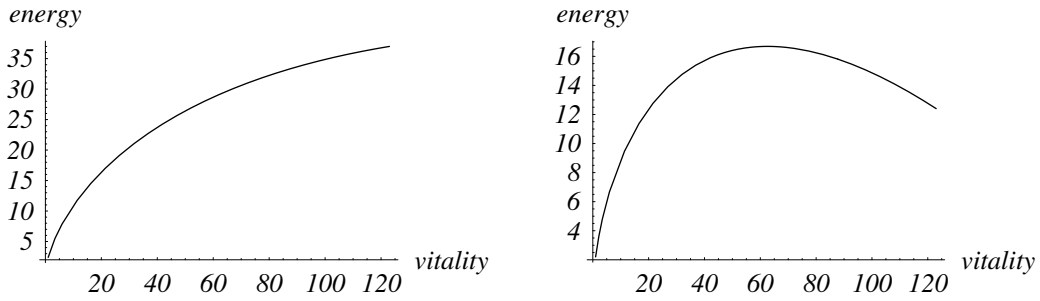

Fig. 5.2: Comparison of trajectories of energy over vitality for two parameter combinations that lead to a maximum attainable vitality of $\Psi = 123$ but imply different shapes: left: $k = 3$, $\kappa = 0.6$, $\delta = 0.3$; right: $k = 3$, $\kappa = 0.8$, $\delta = 0.1$.

The parameters k, κ, and δ set the speed of growth and decay and can therefore be used to determine the time and size scale of the strategy. Getting a handle on measurable quantities like time and size in this model is one future project that naturally follows from my dissertation (see Chapter 6).

b and c

Parameters b and c determine the overall level of mortality (Equation 5.1). Parameter b captures the state-dependent, intrinsic component of mortality, i.e. b determines how important it is to attain and maintain a high level of vitality. The value of b determines the minimum level of state-dependent mortality, b/Ψ, which also depends on maximum vitality Ψ. Since b/ψ_0 determines infant mortality, the magnitude of b also influences the optimal vitality at birth. Parameter c captures the state-independent, extrinsic mortality component. The overall level of infant mortality is given by $b/\psi_0 + c$ and the minimum mortality that can be attained is given by $b/\Psi + c$.

The influence of extrinsic and intrinsic mortality in this model is investigated below (see Section 5.4.1).

η_r and η_g

Parameter η_r captures the intrinsic costs of reproduction (Equation 5.8). It determines the propensity to share resources between reproduction and growth. Clearly, if an organism follows an exclusive strategy, i.e. either reproduction or growth and repair, then π equals one or zero and an exponent will have no influence. However, if energy is shared between processes, then larger values of η_r reduce the reproductive output that could have been achieved with the same level of investment at lower values of η_r. Values below one favor parallel investment in growth and reproduction.

Parameter η_g captures the intrinsic costs of growth and determines the maintenance costs of a certain level of vitality (Equation 5.5). A large value of η_g implies higher maintenance costs at each level of vitality. Therefore, low values of η_g favor non-senescence strategies. During periods of parallel growth and reproduction, higher η_g implies a reduced speed of growth.

Both parameters η_r and η_g capture the efficiency of energy use and determine how advantageous it is to specialize in growth and reproduction, i.e. how costly it is to run a growth and reproduction system in parallel. The costs of reproduction and maintenance are expected to crucially determine the optimal energy allocation between reproduction and growth. In this chapter I will investigate whether or not this expectation is fulfilled.

5.2 Solution

The solution to this life-history problem consists of two distinct optimization procedures. First, the optimal path of investment is determined in a dynamic optimization procedure. The term $\varphi/\psi_0^{\eta_j}$ in Equation 5.8 is a constant and does not influence the optimal trajectory of investment. The value of this constant is then determined in the subsequent, second part of the solution. It is a simple maximization.

In addition to the state variable "vitality" I introduce a second, binary state variable – the "growth mode". The state of an individual is now described by the pair of state variables (*vitality, growth mode*). The "growth mode" can take on two values: "up" and "down". In up mode, vitality is not decreasing (i.e., it is increasing or constant). In down mode, vitality is not increasing. This two-

state optimization problem can lead to optimal solutions of vitality patterns that are not confined to monotone state trajectories (see Section 4.3.1). Note that, for a fixed value of the growth mode, the logic of the state ratchet still applies. Independently of when and how often the growth mode switches, any repeated trajectories of increase and decrease have to be identical.

To solve the dynamic optimization problem I applied a dynamic programming approach by developing an algorithm (see Appendix D), following a backward procedure and assuming stepwise constant vitality (Bellman, 1965). Crucial to Bellman's approach is that the optimal decision does not depend on the past, but is based solely on the current state. The state determines possible current and future payoffs. An essential requirement for this backward optimization to work is the knowledge of an ultimate state with known payoffs, the ultimate future expectation. The procedure starts at this ultimate state and then works backwards along the state trajectory. If the growth mode can switch back and forth, then such an ultimate state cannot be identified and the problem becomes intractable with Bellman's approach. Therefore I assume that the switch can only occur once. Since life necessarily starts off with growth, the switch is initially in up mode and can optionally change into down mode.

The state trajectory is assumed to be stepwise constant. The time it takes to change from vitality ψ to vitality $\psi \pm \Delta$ ($\Delta > 0$, step size) is given by the step time

$$\tau(\psi, \pi) \;=\; \frac{\Delta}{\dot{\psi}}, \tag{5.9}$$

where $\dot{\psi}$ is defined in Equation 5.4. Note that, if vitality falls, then $\tau(\psi, \pi) = -\Delta/\dot{\psi}$ and if vitality is maintained then $\tau(\psi, \pi) = \infty$.

At each level of vitality the algorithm maximizes remaining reproduction, given by

$$R(\psi) \;=\; \int_0^{\tau} e^{-\mu(\psi)\,a}\, m(\psi, \pi)\, da \;+\; e^{-\mu(\psi)\,\tau(\psi,\pi)}\, R(\psi_{next}). \tag{5.10}$$

Since vitality is constant over the time interval τ the integral in Equation 5.10 can be solved, yielding

$$R(\psi) \;=\; \frac{m(\psi, \pi)}{\mu(\psi)} \left[1 \;-\; e^{-\mu(\psi)\tau(\psi,\pi)}\right] \;+\; e^{-\mu(\psi)\,\tau(\psi,\pi)}\, R(\psi_{next}). \tag{5.11}$$

Remaining reproduction is given by current reproduction weighted by the chance of dying in that interval and remaining reproduction at the subsequent level of vitality weighted by the probability of surviving the time interval.

The algorithm to determine the optimal investment trajectory $\pi^*(\psi)$ (the star indicates "optimal") has two parts, one for each mode. For this application, the ultimate state corresponds to a vitality of $\psi = 0$ and therefore to a mortality that is infinite and remaining reproduction of zero. Consequently, the first part of the algorithm begins in down mode at the end of possible state trajectories, i.e. at the last level of vitality $\psi > 0$ when the switch is in down mode. It is convenient to choose $\psi = 1$. Then, the initial step is to find $\pi_d^*(1)$ and the corresponding $R_d^*(1)$ (the d indicates "down mode") using Equation 5.11:

$$\begin{aligned} \pi_d^*(1)) &= \max_{\pi\,\epsilon\,[0,\,\pi_0]} R_d(1) \qquad (5.12) \\ &= \max_{\pi\,\epsilon\,[0,\,\pi_0]} \frac{m(1,\pi)}{\mu(1)} \left[1 - e^{-\mu(1)\tau(1,\pi)}\right] + 0 \\ &= \max_{\pi\,\epsilon\,[0,\,\pi_0]} \frac{(1-\pi)^{\eta_r}(k-\kappa)}{b+c} \left[1 - e^{-(b+c)\,\Delta\,/\,(\pi^{\eta_g}\,(k-\kappa)-\delta)}\right]. \end{aligned}$$

Note that the second state variable constrains investment π to values between zero and π_0, limiting the trajectory of vitality to being non-increasing.

The procedure is repeated working backwards for all levels of vitality up to the maximum attainable vitality $\psi = \Psi$, determined by Equation 5.6. For each level of vitality the optimal investment is found by

$$\pi_d^*(\psi) = \max_{\pi\epsilon[0,\,\pi_0]} \frac{m(\psi,\pi)}{\mu(\psi)} \left[1 - e^{-\mu(\psi)\tau(\psi,\pi)}\right] + e^{-\mu(\psi)\,\tau(\psi,\pi)}\, R_d^*(\psi-\Delta). \quad (5.13)$$

This part of the algorithm gives an optimal decision for each level of vitality in down mode. [1]

Maximum attainable vitality Ψ gives the ultimate state for the second part of the algorithm. If the switch is in up mode and vitality is at its maximum attainable level Ψ, then the decision is whether to either stay in up mode and maintain maximum vitality or to switch into down mode and follow the already

[1] Note that I have imposed one restriction. I assume symmetric division of cells. This implies that if a cell has been damaged, then all its copies will inherit this damage. If $\pi = 0$ is optimal at any time, then no copies are made from currently undamaged cells. Each cell suffers some damage and no undamaged copies are left to make new cells from. Therefore π has to remain zero. This assumption restricts the scope of possible life histories. One can readily relax this assumption and I plan to do so in future research.

calculated optimal investment in down mode:

$$\pi_u^*(\Psi) = \begin{cases} \pi_0(\Psi) \quad \text{if} \quad R_u^*(\Psi) = \frac{m(\Psi,\pi_0)}{\mu(\Psi)} > R_d^*(\Psi) \\ \\ \pi_d^*(\Psi) \quad \text{otherwise.} \end{cases} \tag{5.14}$$

Note that if mortality μ and fertility m are constant, then remaining reproduction is given by m/μ.

Then vitality is followed backwards, down to the smallest level of vitality $\psi = 1$. [2] At each level of vitality the optimal investment is found by

$$\begin{aligned} \pi_u^*(\psi) &= \max_{\pi \epsilon [\pi_0, 1]} R_u(\psi) \\ &= \max_{\pi \epsilon [\pi_0, 1]} \frac{m(\psi,\pi)}{\mu(\psi)} (1 - e^{-\mu(\psi)\tau(\psi,\pi)}) \\ &\qquad + e^{-\mu(\psi)\,\tau(\psi,\pi)}\, R_u^*(\psi + \Delta) \end{aligned} \tag{5.15}$$

if $R_u^*(\psi) > R_d^*(\psi)$ and otherwise $\pi_u^*(\psi) = \pi_d^*(\psi)$. The second part of the algorithm gives an optimal strategy for each level of vitality in up mode.

The optimal strategy over the life course can be found by connecting the results from part one and two of the algorithm in the following way: Results are saved in the form of a vector

$$\begin{pmatrix} \textit{remaining reproduction} \\ \textit{direction of change} \\ \textit{vitality} \\ \textit{investment} \\ \textit{time} \end{pmatrix} = \begin{pmatrix} R^*(\psi) \\ G,\ S \textit{ or } M \\ \psi \\ \pi^*(\psi) \\ \tau^*(\psi) \end{pmatrix} \tag{5.16}$$

Note that the variable "direction of change" takes on the value G for growth if

[2] Vitality in the model is treated as a dimensionless variable, assuming that vitality is normalized by dividing through with a reasonable base unit ($\psi_0 = \psi_{base}/\psi_{base} = 1$). For the sake of simplicity, functioning at birth is assumed to be perfect. Therefore ψ_{base} is equal to the number of cells (corresponding to the minimum size) at birth. In order to establish the real vitality scale from the algorithm, vitality has to be multiplied by ψ_{base}.

vitality increases, S for shrinkage if vitality decreases and M for maintenance if vitality remains constant. For each level of vitality, the optimal vector is saved in a list. The optimal solution can be found from this list by connecting the vectors in the right order. The only logical succession of vectors regarding the direction of change are $(G, \ldots, G, M)$, $(G, \ldots, G, S, \ldots, S, M)$ and $(G, \ldots, G, S, \ldots, S)$. Trivially, vectors need be be nested according to subsequent levels of vitality.

The second optimization procedure attempts to find the optimal vitality at birth. Note that the vitality an individual is endowed with at birth can be seen as a transfer from parent to offspring before birth. In order to solve this problem knowledge about the expected lifetime reproduction at each level of vitality is necessary. The remaining reproduction at each level of vitality $R^*(\psi)$ is given by the succession of first entries in each vector of the list, the result of the first optimization procedure. Taking into account Equation 5.8, lifetime reproduction is given by

$$R^* = \varphi \frac{R^*(\psi_0)}{(\psi_0)^{\eta_j}}. \tag{5.17}$$

Consequently, optimal vitality at birth can be calculated solving

$$\psi_0^* = \max_{\psi \epsilon [1, \Psi]} \frac{R^*(\psi)}{(\psi)^{\eta_j}}. \tag{5.18}$$

Finally, the constant parameter φ can be used to adjust R^* to be equal to one. This implies that density effects achieve population stationarity by reducing lifetime offspring production (Charlesworth (1973), Mylius and Diekmann (1995)).

5.3 The eight varieties of life histories

Eight different types of optimal strategies can be found to result from this model. Strikingly, the variety of strategies is broad and includes senescent as well as non-senescent life histories. In this section, I will describe these eight strategies with the help of illustrative examples. Then, in the following section, I will analyze under what conditions each strategy can be optimal.

Strategies are classified with respect to the specific trajectory of π. From birth to maturity, $\pi(\psi) = 1$ and vitality increases. The age of and vitality at maturity are defined as the age and vitality when $\pi(\psi)$ drops below one for the first time. After maturity, vitality might be maintained, increase or decrease. Once maintenance of vitality is optimal, it will be optimal at all subsequent ages.

Each description of a strategy begins at maturity. Note that the function $\pi(\psi)$ captures the trajectory of actual investment, whereas the function $\pi_0(\psi)$ determines the level of investment that would be necessary to maintain the current level of vitality ψ.

5.3.1 Strategies with senescence

The definition of senescence I suggest in Chapter 1 is based on both mortality and fertility. For the sake of simple classification let us define senescence, in this framework, as an increase in mortality with age.

Exponentially increasing mortality is often assumed and exponential curves are often fitted to empirical data on mortality. Whether mortality increases exponentially or at a different pace, however, is dependent on the particular life history. The following two strategies capture cases where mortality increases exponentially from a certain age onwards. Interestingly, the two subsequent strategies capture cases where a slower than exponential increase in mortality is optimal.

Gompertzian Senescence

Gompertzian Senescence corresponds to a strategy of $\pi = 0$ at the moment of maturity and thereafter. Vitality decreases exponentially at a rate of δ. Senescence captures the familiar case of Gompertzian mortality, with mortality and fertility patterns being similar to those of many mammals, birds, and other species. Reproduction is initiated and mortality rises exponentially when investment switches

from one to zero. An example is illustrated in Figure 5.3 with the parameter combination

$$\eta_r = 2,\ \eta_g = 2,\ b = 0.3,\ c = 0.01,\ k = 3,\ \kappa = 0.8,\ \delta = 0.1. \tag{5.19}$$

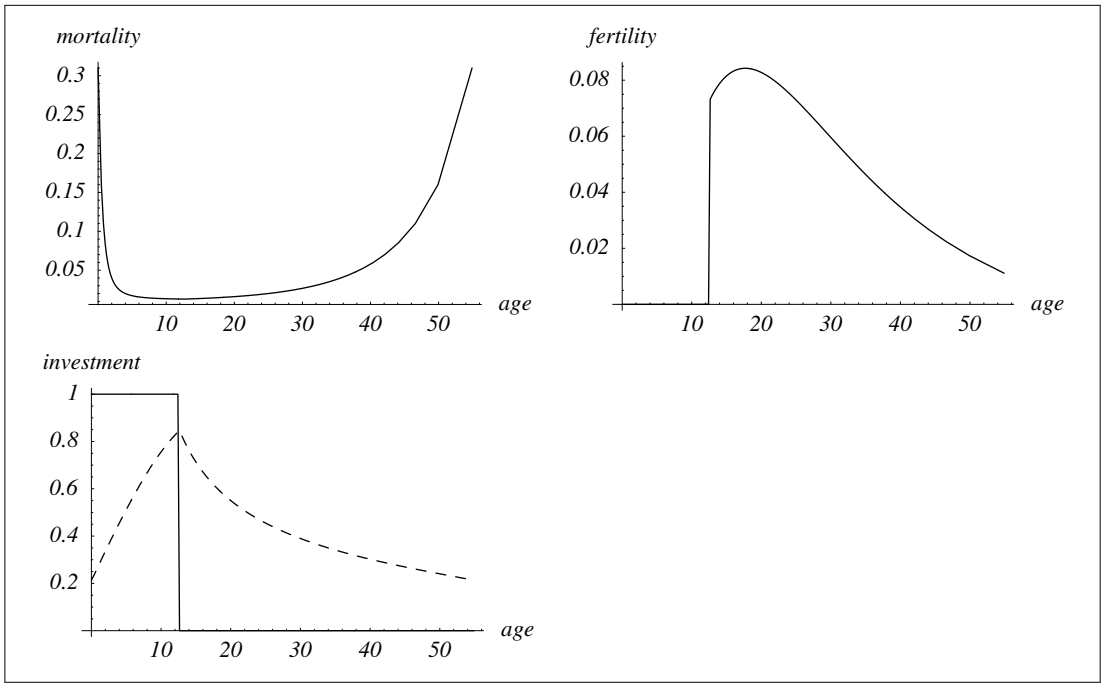

Fig. 5.3: Example of Gompertzian Senescence. (Dashed line: π_0, level of investment required for maintenance)

Delayed Senescence

Delayed Senescence corresponds to a strategy of $\pi > \pi_0$ followed by $\pi = 0$. Vitality first increases and then decreases exponentially at a rate of δ. After an early age of maturity a larger reproductive potential is striven for and established during a period of parallel growth and reproduction. Fertility increases while mortality decreases. Then, in a second reproductive peak, the reproductive potential is harvested at the cost of deterioration of the individual. Mortality increases exponentially. An example is illustrated in Figure 5.4 with the parameter combination

$$\eta_r = 0.5,\ \eta_g = 2,\ b = 0.2,\ c = 0.1,\ k = 3,\ \kappa = 0.8,\ \delta = 0.1. \tag{5.20}$$

Note that investment in growth and maintenance increases slightly before it falls to zero. This pattern emerged for all parameter combinations I used that resulted in a Delayed Senescence strategy. It is unclear, however, whether this bump in the investment trajectory is generally optimal for this strategy.

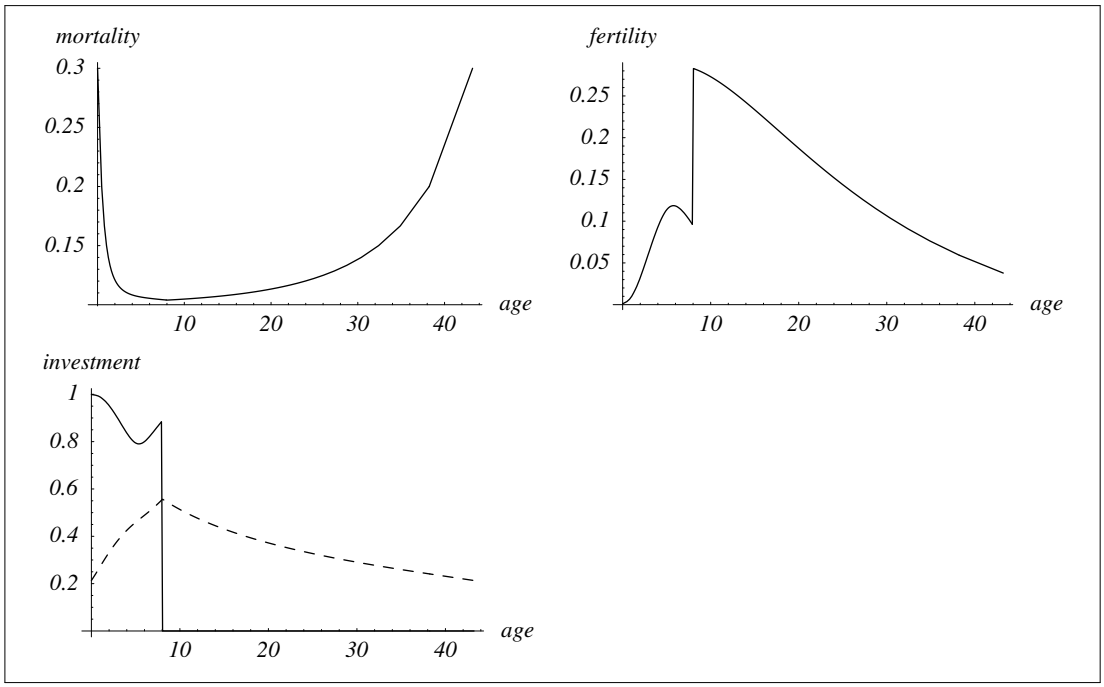

Fig. 5.4: Example of Delayed Senescence. (Dashed line: π_0, level of investment required for maintenance)

Subsustenance

Subsustenance corresponds to a strategy of $0 < \pi < \pi_0$, where $\pi \approx \pi_0$. Vitality slowly decreases. The missing fraction of energy that would be necessary to truly maintain vitality is used to increase reproductive output. An example is illustrated in Figure 5.5. Life expectancy at birth is only 13, and, at reproductive maturity $\alpha = 8$, it is about 31. Investment after maturity falls just slightly below maintenance level, as indicated by the dashed line. Note that the increase in mortality is retarded in such a way that the strategy is almost equivalent to real maintenance[3]. The corresponding vitality trajectory is shown in Figure 5.6. The example pertains to the parameter combination

$$\eta_r = 2,\ \eta_g = 0.5,\ b = 1,\ c = 0.001,\ k = 3,\ \kappa = 0.8,\ \delta = 0.1. \tag{5.21}$$

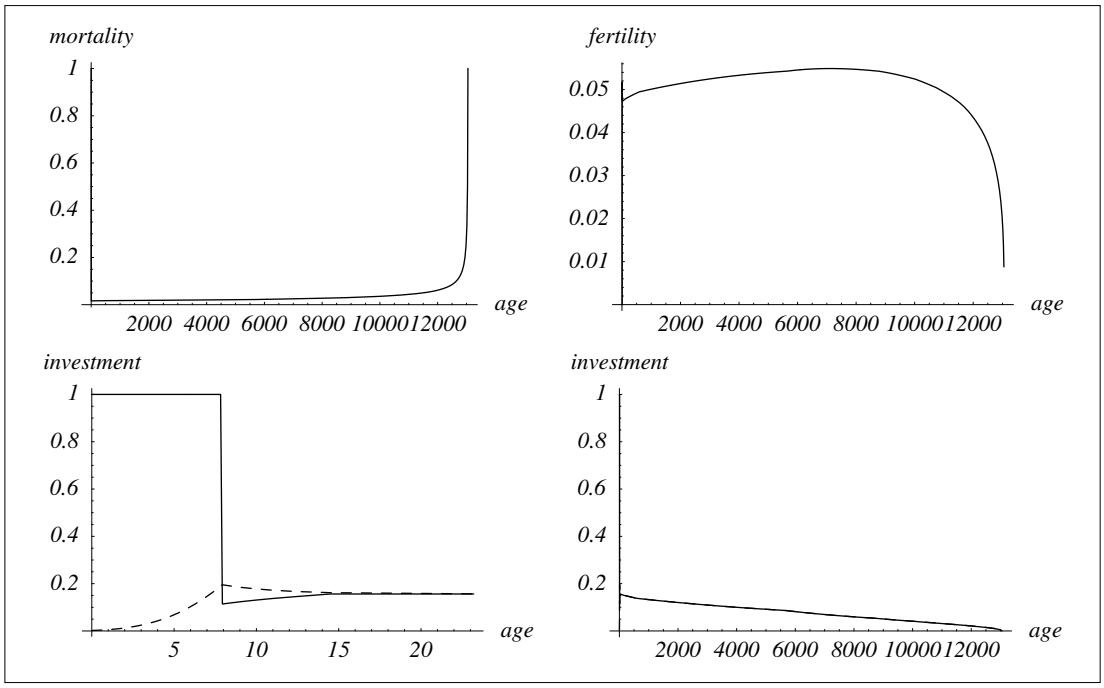

Fig. 5.5: Example of Subsustenance. (Dashed line: π_0, level of investment required for maintenance.) Note that in the lower right graph the trajectories of π and π_0 overlap, because π falls just slightly below π_0.

[3] The strategy seems so close to maintenance that it may be an artefact of the numerical approximation methods I used. I am in the process of carefully checking into this. Similar potential difficulties may apply to two other strategies described below: Delayed Subsustenance and Delayed Partial Senescence.

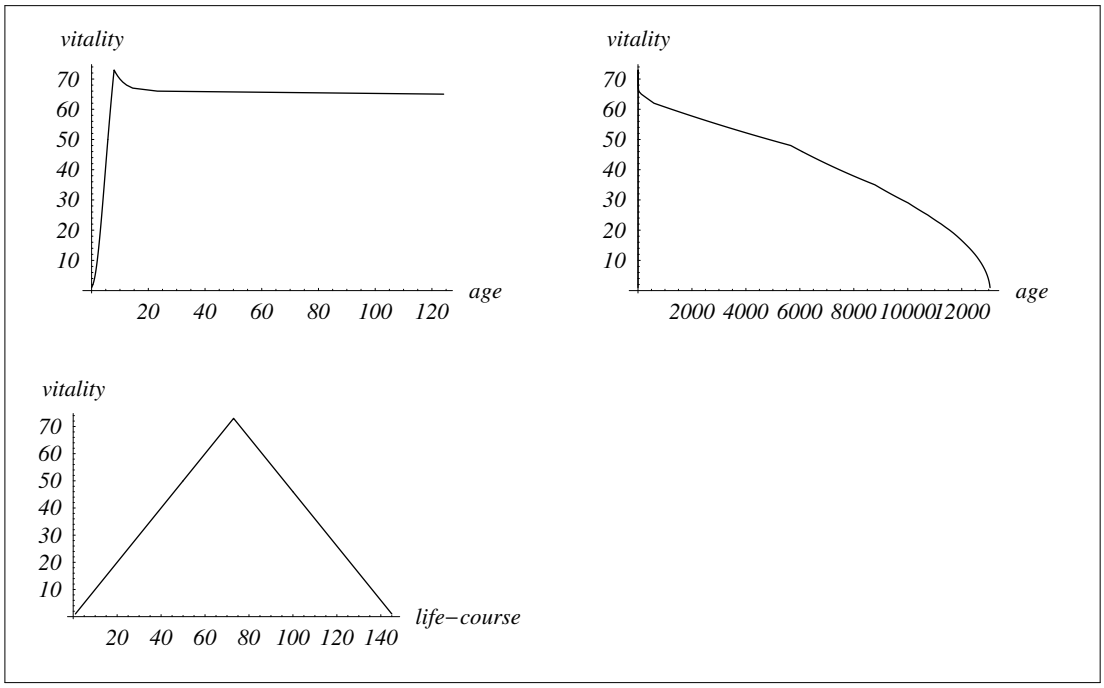

Fig. 5.6: Example of Subsustenance. (Life course: measures the number of one unit changes in vitality.) Vitality trajectory.

Delayed Subsustenance

Delayed Subsustenance corresponds to a strategy of $\pi > \pi_0$ followed by $0 < \pi < \pi_0$, where $\pi \approx \pi_0$. Vitality first increases and then decreases at a very slow pace. An example is illustrated in Figures 5.7 and 5.8 with the parameter combination

$$\eta_r = 1,\ \eta_g = 0.5,\ b = 0.1,\ c = 0.02,\ k = 3,\ \kappa = 0.7,\ \delta = 0.2. \tag{5.22}$$

In contrast to the case of Subsustenance where investment suddenly drops (Figure 5.5), investment falls smoothly from one down to just below maintenance level in Figure 5.7. The slow deterioration in vitality in the case of Delayed Subsustenance (Figure 5.8) is preceded by a period of parallel growth and reproduction. In the case of Subsustenance (Figure 5.6) this period is missing: vitality falls markedly after the onset of reproduction before a further decrease in vitality is retarded more strongly. To understand the difference between Subsustenance and Delayed Subsustenance, note in particular the difference between the lower left-hand graphs in Figure 5.5 and Figure 5.7.

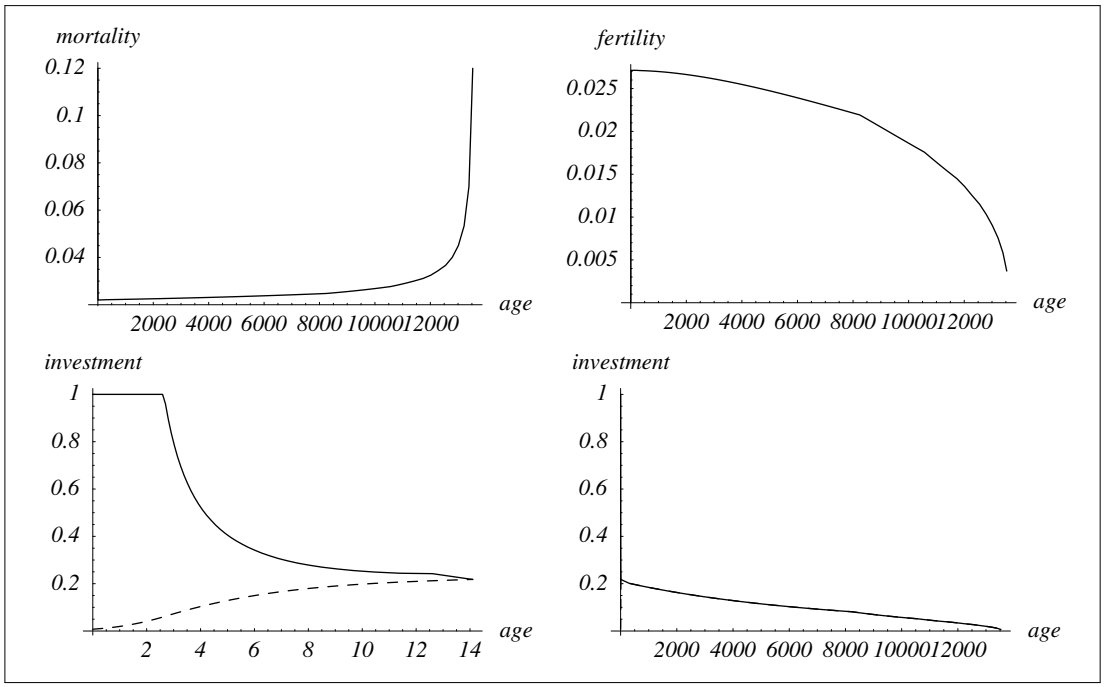

Fig. 5.7: Example of Delayed Subsustenance. (Dashed line: π_0, level of investment required for maintenance.) Note that in the lower right graph the trajectories of π and π_0 overlap, because π falls just slightly below π_0.

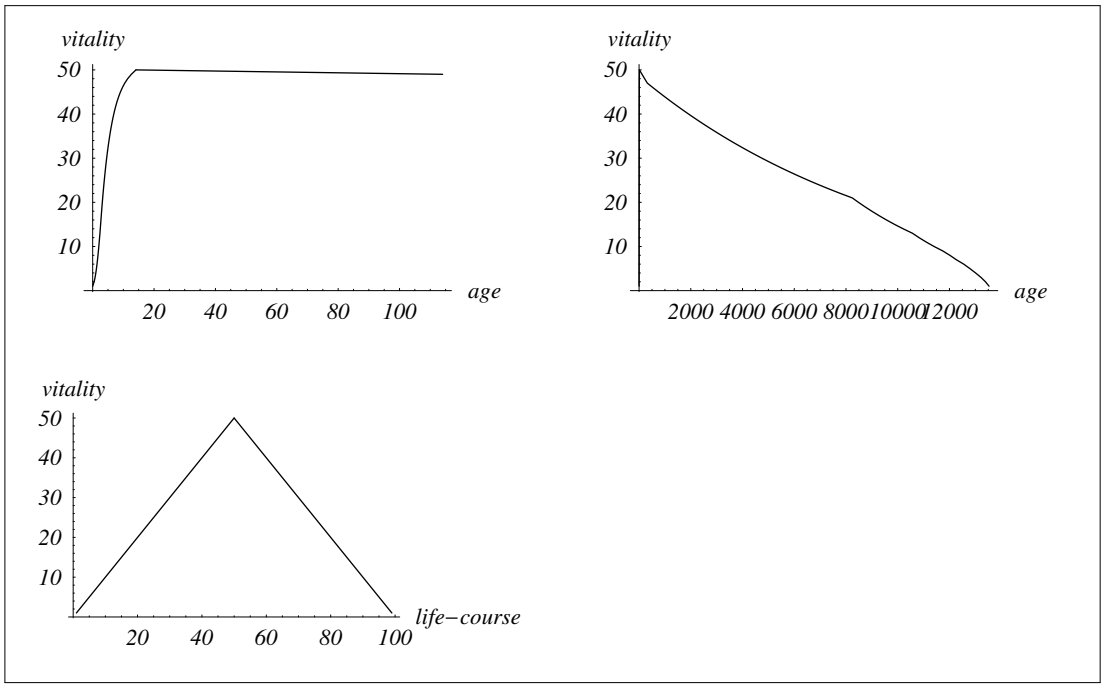

Fig. 5.8: Example of Delayed Subsustenance (Life course: measures the number of one unit changes in vitality). Vitality trajectory.

5.3.2 Strategies with sustenance

The following two strategies capture cases where senescence is never optimal, i.e. mortality never increases. The parameter combinations are not peculiar nor extremely different from the previous cases. Non-senescence and senescence, in this model, can be found to coexist in contiguous neighborhoods of the parameter space.

Sustenance

Sustenance corresponds to a strategy of $\pi = \pi_0$ immediately after the period of development. Vitality is maintained. The case of Sustenance is illustrated in Figure 5.9. At the age of maturity, investment drops down to maintenance level. Reproduction starts and both mortality and fertility remain at non-zero, constant levels. This example pertains to the parameter combination

$$\eta_r = 2,\ \eta_g = 2,\ b = 0.2,\ c = 0.001,\ k = 3,\ \kappa = 0.8,\ \delta = 0.1. \tag{5.23}$$

Note that this parameter combination differs from the example in Figure 5.3 only by the level of mortality, where senescence is optimal. Lowering mortality at the boundary can shift a strategy from senescence to non-senescence. This remarkable, surprising result merits further theoretical attention and empirical investigation.

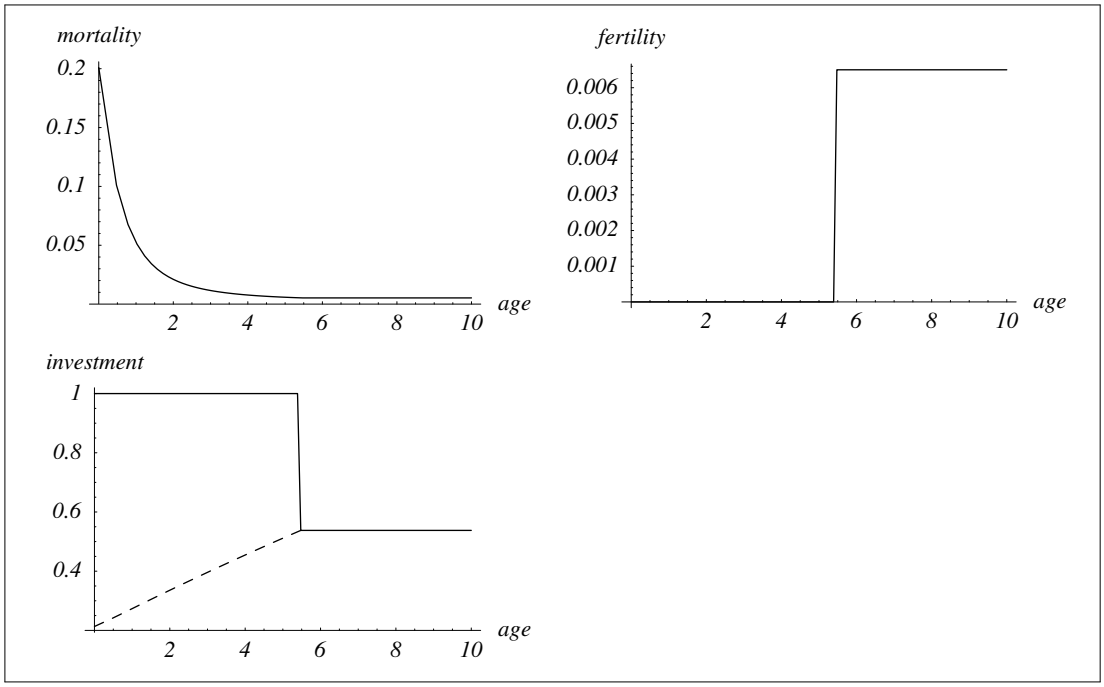

Fig. 5.9: Example of Sustenance. (Dashed line: π_0, level of investment required for maintenance.)

Supersustenance

Supersustenance corresponds to a strategy of $\pi > \pi_0$ followed by $\pi = \pi_0$. Vitality first increases and then is maintained. The case of Supersustenance is illustrated in Figure 5.10. Investment falls smoothly from one down to maintenance level. Mortality decreases while fertility increases until the trajectories reach a constant level. This example pertains to the parameter combination

$$\eta_r = 0.5,\ \eta_g = 0.5,\ b = 0.2,\ c = 0.004,\ k = 3,\ \kappa = 0.8,\ \delta = 0.1. \tag{5.24}$$

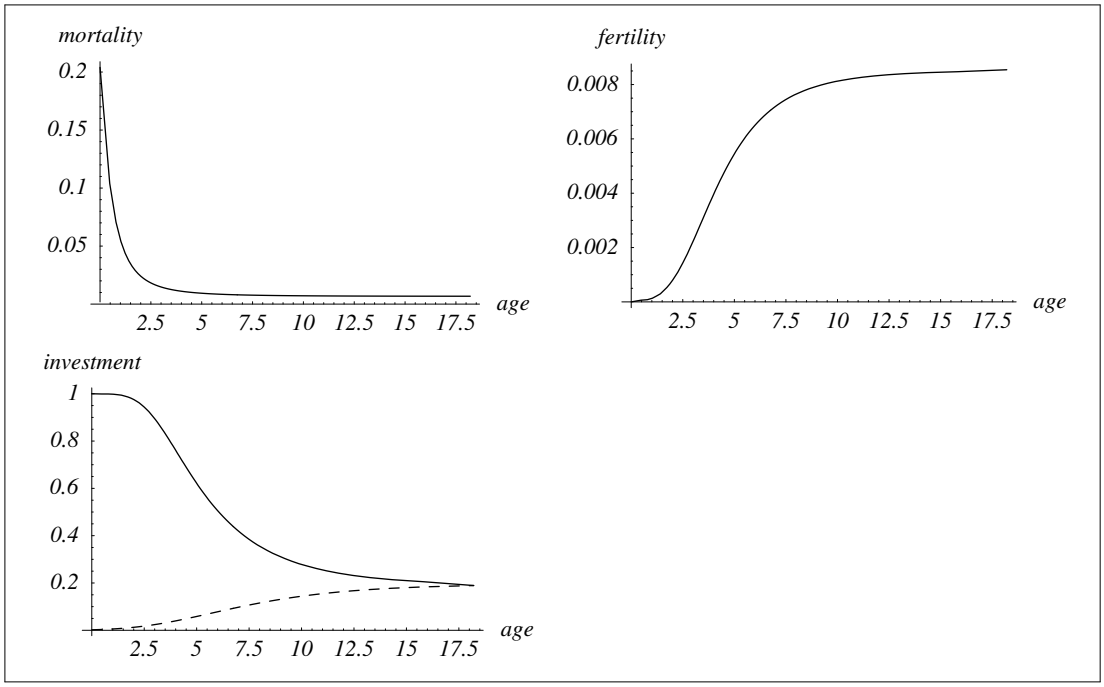

Fig. 5.10: Example of Supersustenance. (Dashed line: π_0, level of investment required for maintenance.)

5.3.3 Strategies with both senescence and sustenance

Life does not have to be "either/or" but can be "both/and". The subsequent two strategies illustrate life histories where senescence and non-senescence characterize different portions of the life course.

Partial Senescence

Partial Senescence corresponds to a strategy of $\pi < \pi_0$ followed by $\pi = \pi_0$. Vitality decreases and then is maintained. The case of Partial Senescence is very interesting. A high reproductive potential is built up during development and then harvested at the cost of falling vitality until a level of vitality is reached that is sufficient to keep mortality at a low level. An example is illustrated in Figure 5.11 with the parameter combination

$$\eta_r = 2,\ \eta_g = 0.5,\ b = 0.2,\ c = 0.004,\ k = 3,\ \kappa = 0.7,\ \delta = 0.2. \tag{5.25}$$

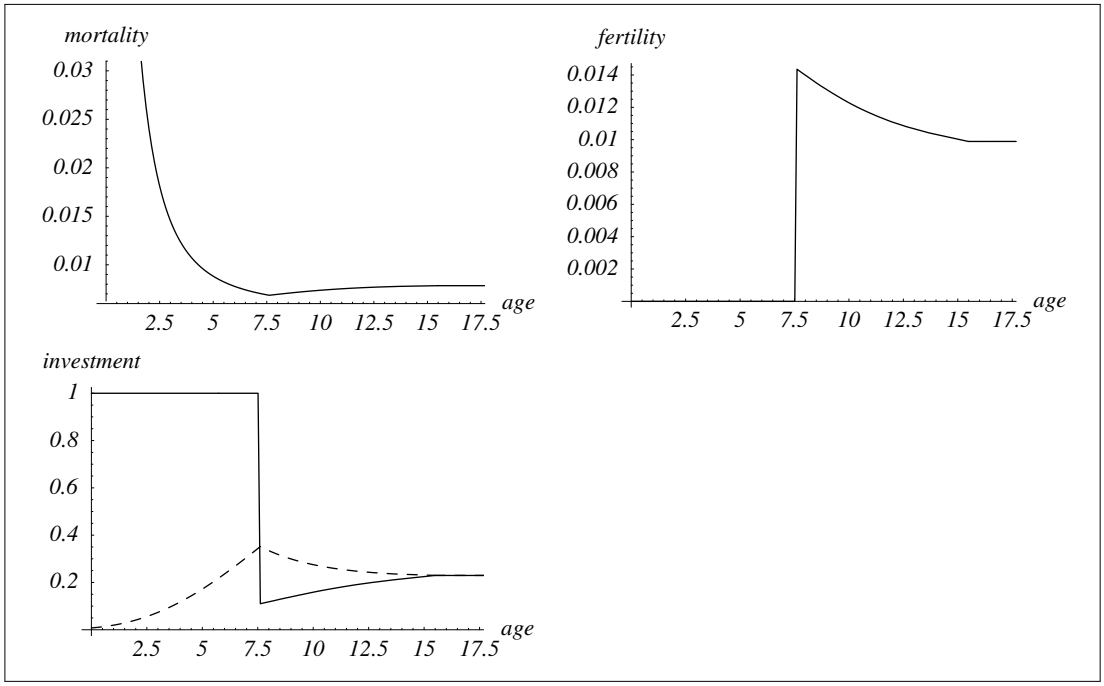

Fig. 5.11: Example of Partial Senescence. (Dashed line: π_0, level of investment required for maintenance.)

Delayed Partial Senescence

Delayed Partial Senescence corresponds to a strategy of $\pi > \pi_0$, followed by $0 < \pi < \pi_0$, followed by $\pi = \pi_0$. Vitality continues to increase after the onset of reproduction, then decreases and then is maintained. A period of parallel growth and reproduction precedes a long period of life when the organism deteriorates at a slow pace before a lower level of vitality is eventually maintained. An example is presented in Figures 5.12 and 5.13. Note that investment is not only plotted over age but also over the life course to clarify the strategy. Each step of the life course corresponds to a one unit change in vitality. Vitality increases after the age of maturity $\alpha = 4$ until it reaches a peak of about 60 at age 14. Then vitality starts to fall. The period of decline in vitality is slowed down to such an extent that the corresponding changes in mortality and fertility are negligible over the main part of life (life expectancy at maturity $e^0(\alpha) = 22$). The example pertains to the parameter combination

$$\eta_r = 1,\ \eta_g = 0.5,\ b = 0.3,\ c = 0.01,\ k = 3,\ \kappa = 0.7,\ \delta = 0.2. \tag{5.26}$$

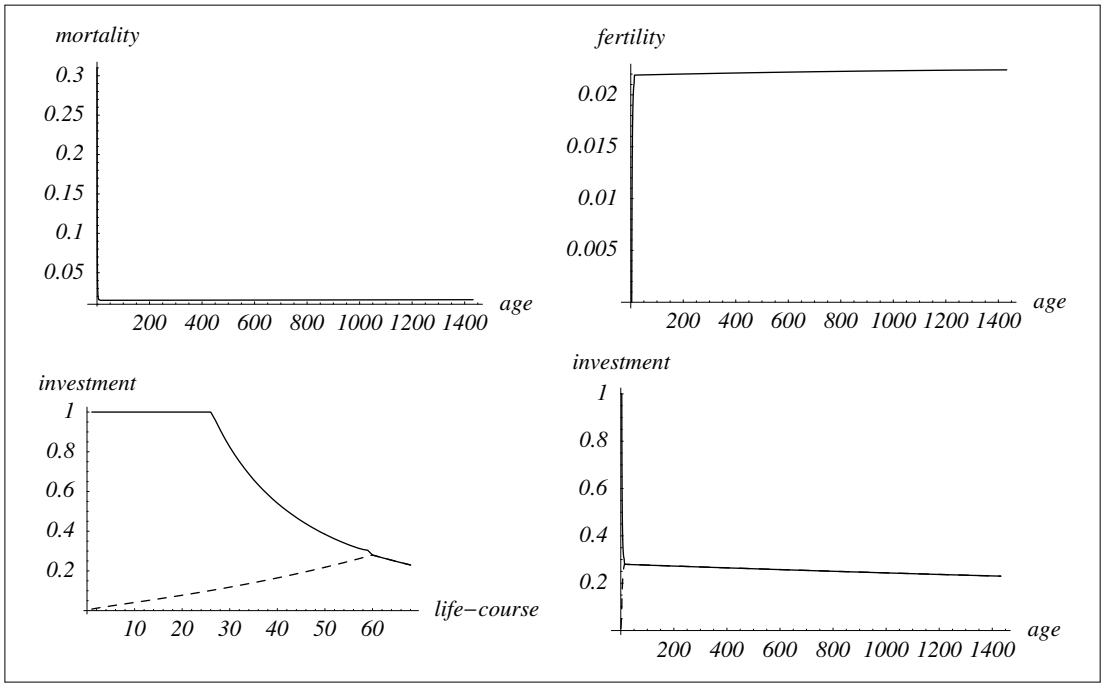

Fig. 5.12: Example of Delayed Partial Senescence. (Dashed line: π_0, level of investment required for maintenance. Life course: measures the number of one unit changes in vitality.) Note that in the lower right graph the trajectories of π and π_0 overlap, because π falls just slightly below π_0.

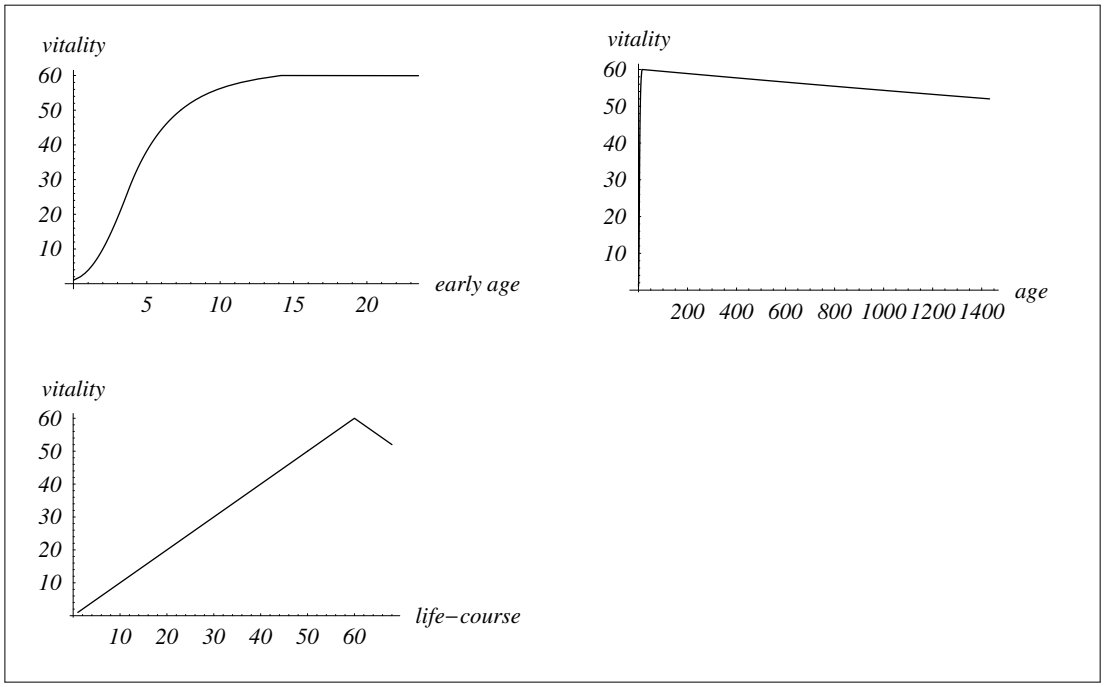

Fig. 5.13: Example of Delayed Partial Senescence (Life course: measures the number of one unit changes in vitality.) Vitality trajectory.

5.4 When senescence is optimal and when it is not

The model sheds light on the characteristics that determine whether senescent or non-senescent life histories are optimal. Several of the strategies exemplified above show mortality patterns that increase over some part of reproductive life but decrease or remain constant over other parts of reproductive life. My suggestion for a definition of senescence in Chapter 1 applies to particular age-groups, but what criteria should be used to label a complete life-history strategy "senescent" or "non-senescent"? In the following, one way of approaching such a classification is suggested.

Whether a particular life history is classified as senescent or non-senescent can be determined by the proportion of lifetime reproduction that is realized at ages when mortality rises, i.e. when $\pi < \pi_0$. This indicator of senescence, S, is given by

$$S = \frac{\sum_{x=0}^{\infty} J_x \, l_x \, m_x}{\sum_{x=0}^{\infty} l_x \, m_x}, \tag{5.27}$$

where $J_x = 1$ if investment in growth is below maintenance level ($\pi(\psi(x)) < \pi_0(\psi(x))$) and $J_x = 0$ if investment is greater than or equal to the amount required for maintenance of vitality. If $S = 1$, the strategy is fully senescent and if $S = 0$, the strategy is fully non-senescent. All values in between describe mixed strategies. For the eight strategies discussed above, the "Gompertzian Senescence" and "Subsustenance" strategies are fully senescent, the "Sustenance" and "Supersustenance" strategies are fully non-senescent, and the other strategies are mixed.

After running the algorithm for many different parameter combinations, I found that the efficiencies η_r and η_g and the mortality parameters b and c are the most influential for the qualitative differences in mortality patterns. Therefore, I studied the interplay between high and low levels of efficiencies and mortality parameters in more detail. Figure 5.14 illustrates the degrees of senescence indicated by S for the combinations of η_r and η_g, given the specific parameter combination $k = 3, \kappa = 0.8$ and $\delta = 0.1$. The surfaces span over different mortality conditions determined by b and c. The words "falling" and "constant" pertain to cases where mortality is decreasing or does not change over reproductive ages. The words "slow" and "exponential" pertain to cases where, if mortality rises, it does so either very slowly or at an exponential pace. The values of the indicator

of senescence S are determined by the underlying life-history strategies. Table 5.1 contains the detailed strategies corresponding to the colors in Figure 5.14.

Together, Figure 5.14 and Table 5.1 summarize the results of the vitality model. Several main features are noteworthy:

The implications of costly reproduction

Low costs of reproduction ($\eta_r < 1$, row one in Figure 5.14 and Table 5.1) correspond to non-senescent strategies over a broad range of intrinsic and extrinsic mortality. When reproduction is cheap the dominant color is blue in Figure 5.14, meaning the indicator of senescence is equal to zero. Efficient reproduction implies a high propensity for parallel investment in reproduction and growth. Consequently, a period of parallel reproduction and growth is optimal and therefore the prevalent strategy is Supersustenance. In the cases I investigated, an efficient mode of reproduction leads to at least some period of reproductive life when mortality falls after the onset of reproduction. After that period the level of mortality determines whether it is optimal to withstand deterioration (Supersustenance) or not (Delayed Subsustenance or Delayed Senescence). Fully senescent strategies (S=1, color=red) are suboptimal if reproduction is cheap.

High costs of reproduction ($\eta_r > 1$, row two in Figure 5.14 and Table 5.1) mainly result in senescent life histories. When reproduction is expensive the dominant color is red in Figure 5.14, meaning the indicator of senescence is equal to one. The more η_r exceeds one, the greater deviations from exclusive investment in reproduction ($\pi = 0$) are penalized. In order to reproduce successfully the individual cannot afford to reproduce and maintain its state simultaneously unless repair is sufficiently cheap. Therefore, over a broad range of mortality conditions, strategies where mortality increases over reproductive life are optimal.

5.4.1 The mortality paradox

To fully understand the optimal patterns of mortality, the influence of the costs of maintenance, captured by the columns in Figure 5.14 and Table 5.1, has to be taken into account. Interestingly, the left and right columns appear to be roughly mirrored, a fact which demands attention. Clearly, low and high costs of maintenance imply opposite effects of changes along the horizontal axis, i.e. of changes in the extrinsic hazard of death.

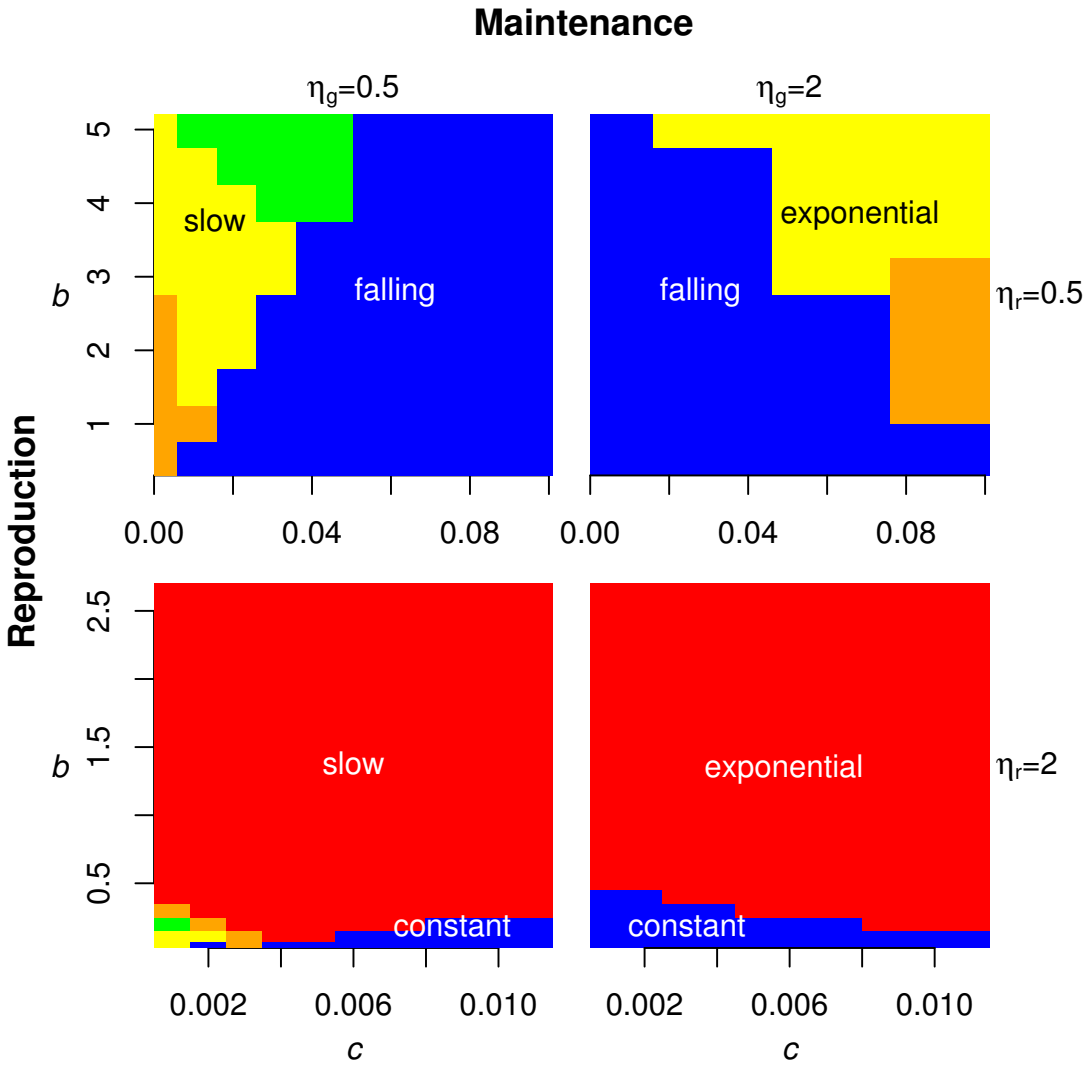

Fig. 5.14: Senescence surfaces: *Red* = Senescence ($S = 1$), *Blue* = Non-senescence ($S = 0$), *Green* = Mixed ($0 < S < 0.35$), *Yellow* = Mixed ($0.35 < S < 0.65$), *Orange* = Mixed ($0.65 < S < 1$). Rows: $\eta_r = 0.5, \eta_r = 2$, Columns: $\eta_g = 0.5, \eta_g = 2$. In all cases $k = 3, \kappa = 0.8, \delta = 0.1$. The words "falling" and "constant" pertain to cases where mortality is decreasing or does not change over reproductive ages. The words "slow" and "exponential" pertain to cases where, if mortality rises, it does so either very slowly or at an exponential pace.

Tab. 5.1: Strategies for cheap versus costly reproduction and maintenance for low and high intrinsic and extrinsic hazard of death.

	$\eta_g = 0.5$				$\eta_g = 2$			
$\eta_r = 0.5$		4.2	*del sub*	*del sub*	*super*	4.2	*super*	*del sen*	*del sen*
	b	2.2	*del sub*	*super*	*super*	b 2.2	*super*	*super*	*del sen*
		0.2	*super*	*super*	*super*	0.2	*super*	*super*	*super*
		c	0.001	0.041	0.081	c	0.001	0.041	0.081
$\eta_r = 2$		2.2	*sub*	*sub*	*sub*	2.2	*sen*	*sen*	*sen*
	b	1.2	*sub*	*sub*	*sub*	b 1.2	*sen*	*sen*	*sen*
		0.2	*part*	*sub*	*del sub*	0.2	*sust*	*sust*	*sen*
		0.1	*part*	*del part*	*sust*				
		c	0.001	0.005	0.009	c	0.001	0.005	0.009

sen: Gompertzian Senescence, del sen: Delayed Senescence, sub: Subsustenance, del sub: Delayed Subsustenance, sust: Sustenance, super: Supersustenance, part: Partial Senescence, del part: Delayed Partial Senescence

In the case of low costs of maintenance ($\eta_g < 1$, first column in Figure 5.14 and Table 5.1), non-senescence is favored more strongly, the greater the extrinsic hazard. This is striking. Exactly the opposite has generally been stated – that a high risk of extrinsic death should favor senescence (Williams, 1957). But my model predicts that this hypothesis is not true for species with low costs of maintenance. What could explain this unexpected and seemingly paradoxical result?

It is a well-supported (Stearns (1992) and Roff (2002)) and intuitively appealing fact that a high extrinsic hazard of death favors early reproductive maturity. A short juvenile period reduces the time available for development and hence the time to attain a certain vitality. Vitality, however, determines the level of energy available and therefore the potential to reproduce. If individuals have to mature early because of a very risky environment, their reproductive potential might be small. Therefore, depending on the costs of reproduction, a small potential should be maintained (Sustenance) and, if possible, further increased (Supersustenance) since maintenance costs are low.

If, on the other hand, life is safe the individual can afford to spend a long time building up a high level of vitality, i.e. a large reproductive potential. Instead of paying the price of maintaining a high level of vitality, it may be evolutionarily advantageous to harvest this potential at the cost of a loss in functioning. The crucial point is that the age at which this loss in functioning truly becomes apparent can be postponed to the extent that the decline in vitality is almost equivalent to real maintenance, facilitated by the efficient repair system. This strategy (Subsustenance) has the benefit that more energy can be allocated to reproduction, which is particularly important if reproduction is expensive.

An interesting strategy, namely Partial Senescence, is optimal at low levels of mortality, when maintenance is cheap but reproduction is expensive. The propensity to share resources between reproduction and growth is small due to costly reproduction. Therefore exclusive investment is desirable. Low maintenance costs, on the other hand, favor the preservation of vitality rather than decay, which implies sharing of resources. Since mortality is low the individual can afford to mature late, attaining a high reproductive potential. However, maintaining this level of vitality would be strongly penalized in terms of reduced reproduction. Instead, the individual harvests the large potential and mortality increases after reproductive maturity. But when vitality has fallen to a level that can be pre-

served without too much penalty, any further deterioration is suboptimal. The individual maintains its state and mortality is constant.

In sum, for low costs of maintenance, an increase in the extrinsic hazard of death shifts the strategy from virtual maintenance to real maintenance of vitality. Note that it might be hard to distinguish Subsustenance from Sustenance in reality as sample sizes in empirical data might be too small to detect an increase in mortality. Further note that virtual maintenance, i.e. Subsustenance, was a very common outcome in numerical studies by Charlesworth (1990).

Williams (1957) conjectures that low levels of extrinsic mortality should be associated with slow-senescent strategies and high levels of extrinsic mortality should be associated with fast-senescent strategies. His hypothesis is in accordance with the results from previous reproductive effort models (for a review see Charlesworth (1994, Section 5.3.4.)). Higher extrinsic risk tends to increase reproductive effort, which implies higher levels of mortality. In this section I have shown that my results predict under some circumstances not only the opposite effect of an increase in parameter c but also that non-senescent strategies can be optimal. A theory based on optimization of trade-offs can account for constant or declining age-patterns of mortality while a theory based on mutation accumulation cannot explain these patterns. In Section 6.4.1 I will discuss the concept of extrinsic mortality and return to Williams's hypothesis (see Section 6.3.1 and Section 6.4.3).

5.4.2 Further results

High costs of maintenance ($\eta_g = 2$, second column in Figure 5.14 and Table 5.1) imply that a strong extrinsic hazard of death favors senescence and a weak extrinsic hazard favors non-senescence, which is in line with the general way of thinking. Any attempt to retard deterioration is expensive. The levels of vitality that correspond to viable reproductive potentials cannot be preserved due to the high costs of maintenance. Instead, reproductive potential is built up and subsequently harvested using all energy available and no energy is allocated to maintenance. In this case, any decay is exponential.

If both reproduction and growth are costly, $\eta_r > 1$ and $\eta_g > 1$, then exponentially increasing mortality (Gompertzian Senescence) is optimal unless mortality is sufficiently low, in which case sustenance is the optimal strategy.

Generally, low levels of intrinsic mortality favor non-senescence. If reproduction is cheap, then the non-senescent strategy is Supersustenance. If reproduction is costly, then the non-senescent strategy is Sustenance.

As long as maintenance and/or reproduction are cheap it can be optimal to precede any period of decay by a period of parallel investment in growth and reproduction (Delayed Subsustenance, Delayed Partial Senescence, Delayed Senescence). Note that parallel growth and reproduction simultaneously allows for an early age at maturity (at still low vitality) to ensure at least some reproduction in high risk environments but also for a further build-up of reproductive potential.

5.5 The humanesque case

The example in Figure 5.3 corresponds to a senescent strategy ($S = 1$). Mortality falls until the age of maturity at about 13. Thereafter, mortality rises exponentially at a constant rate $\delta = 0.1$. Reproduction follows a hump-shaped curve. Note that the simple model does not capture menopause. Life expectancy at birth as well as life expectancy at maturity equal 25. If the time units correspond to years this setting of parameters captures the main features of ancient human life history. However, vitality in humans is only partly determined by the functioning of body cells. What makes humans a special case is the large brain with the capacity to learn and to acquire human capital (Kaplan and Robson, 2002). Still, the "humanesque" case can be used to understand which parameter crucially affects the boundary between senescence and non-senescence. Results are shown in Tables 5.2 and 5.3.

5.5.1 Changes in efficiency

The effects of deviations in the efficiency parameters from the humanesque case are shown in Table 5.2. (The humanesque case is given in the first row and again in the sixth row).

Decreasing η_g at constant η_r shifts the strategy between five (!) different categories, ranging from Senescence to Supersustenance. This is a striking finding. The alternating pattern between senescent and non-senescent strategies is remarkable. As discussed in Section 5.4.1 this phenomenon can be explained by shifts between virtual and real maintenance. The important point, emphasized

Tab. 5.2: Changes in efficiencies

Cost of Reproduction η_r	Cost of Maintenance η_g	S	Strategy
2.0	2.0	1	Senescence
2.0	1.0	0	Sustenance
2.0	0.6	1	Subsustenance
2.0	0.45	0.87	Delayed subsustenance
2.0	0.4	0	Supersustenance
2.0	2.0	1	Senescence
1.0	2.0	0	Sustenance
0.4	2.0	0	Supersustenance

$k = 3$, $\kappa = 0.8$, $\delta = 0.1$, $b = 0.3$, and $c = 0.01$

by the results in Table 5.2, is that the costs of maintenance crucially affect a species' characteristic age-pattern of mortality.

Decreasing η_r at constant η_g shifts the strategy between three different categories, ranging from Senescence to Supersustenance. Changes in the costs of reproduction have a strong influence on the age-patterns of mortality.

In sum, the costs of maintenance, η_g, are a crucial determinant of a species' characteristic age-pattern of mortality. The costs of reproduction, η_r, are of almost equal importance to the optimal age-patterns of mortality. The humanesque life history is at one end of two key life-history dimensions determined by the costs of maintenance and reproduction.

5.5.2 Changes in mortality

Reduction in the mortality parameters, either b (from 0.3 to 0.1) or c (from 0.01 to 0.004), can change the strategy from senescence (Gompertzian Senescence) to non-senescence (Sustenance), as shown in Table 5.3. The optimal humanesque

life history can be shifted from exponential increasing mortality to constant, non-humanesque mortality patterns by a reduction in mortality. Extrinsic causes of death have been reduced considerably over human history. Does this result suggest that the human life history could possibly evolve towards non-senescence? Probably not, because, as I will show in the following, the impact of mortality changes is constrained by the magnitude of η_g and η_r.

Note that the strategy of Gompertzian Senescence corresponds to a strategy of $\pi = 1$ followed by $\pi = 0$ at maturity. One and zero to any power of $\eta_g > 0$ and $\eta_r > 0$ will remain one and zero. In this specific example I chose values of 2. The true values for the costs of maintenance and reproduction, however, are unknown. Maybe values of 3 or 4 or 10 or even 100 are more appropriate for the humanesque case? It turns out that even an efficiency value of 3 can prevent the shift from senescence to non-senescence. Table 5.3 illustrates that the ultimate reduction of either intrinsic or extrinsic mortality to zero still implies that senescence is the optimal life history in the humanesque case. The efficiencies of the growth and reproductive systems restrict life histories in their adaptation to changing mortality conditions. If humanesque efficiency parameters were at the level of 2, then the model suggests that evolutionary forces could promote non-senescence in humans. If humanesque efficiency parameters are larger than 2, then senescence is inevitable in humans, at least in my model.

5.5.3 Influence of changes in mortality on age and vitality at maturity

For $\eta_r = \eta_g = 2$, the effects of changes in mortality on age and vitality at maturity, life expectancy and the indicator of senescence can be seen in Figures 5.15 and 5.16. Generally in this model, higher extrinsic mortality c reduces age and vitality at maturity. This is also true for intrinsic mortality b, as long as the strategy is senescent. A higher value for b for non-senescent strategies increases age and vitality at maturity. Remarkably, there is a pronounced bifurcation between Gompertzian Senescence and Sustenance. For Gompertzian Senescence strategies it is important to initially build up a large reproductive potential that subsequently can be harvested at the cost of a loss in functioning. Sustenance relies on a small but persistent potential that is harvested from an early age onwards.

Figures 5.15 and 5.16 exemplify the narrow line between senescence and non-

Tab. 5.3: Interaction between efficiencies and mortality

Cost of Reproduction η_r	Cost of Maintenance η_g	Intrinsic Mortality b	Extrinsic Mortality c	Age of Maturity α	Vitality at Maturity ψ_α	Strategy
2	2	0.3	0.01	13	104	senescent
2	2	0.3	0.004	6	51	non-senescent
2	2	0.1	0.01	3	21	non-senescent
3	2	0.3	0	20	120	senescent
3	2	0	0.01	13	106	senescent
2	3	0.3	0	19	119	senescent
2	3	0	0.01	13	106	senescent

$k = 3$, $\kappa = 0.8$, and $\delta = 0.1$

senescence. Close to the bifurcation, the characteristic differences in age and vitality at maturity for $\eta_r = \eta_g = 2$ become apparent. Non-senescent life histories correspond to an early age at maturity and a low but constant reproductive potential, whereas senescent life histories correspond to a late age at maturity and a high but decreasing reproductive potential. This can also be seen in Table 5.3.

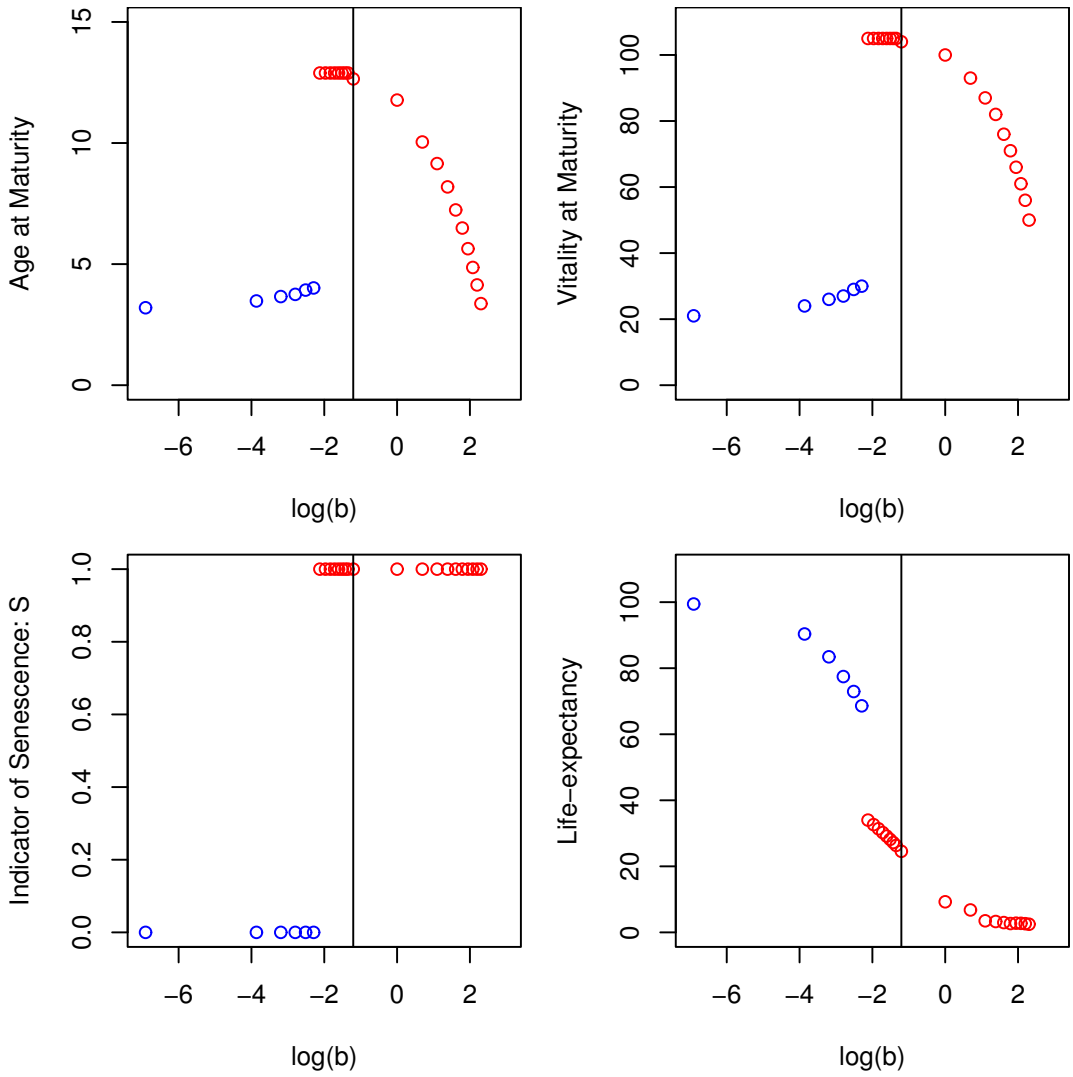

Fig. 5.15: Impact of deviations of intrinsic mortality (b) on a log scale from the humanesque case marked by the vertical line ($b = 0.3$). (red = senescence, blue = sustenance)

The values of k, κ, and δ are of no direct importance to the boundary between non-senescence and senescence. Their influence on the strategy by changing the

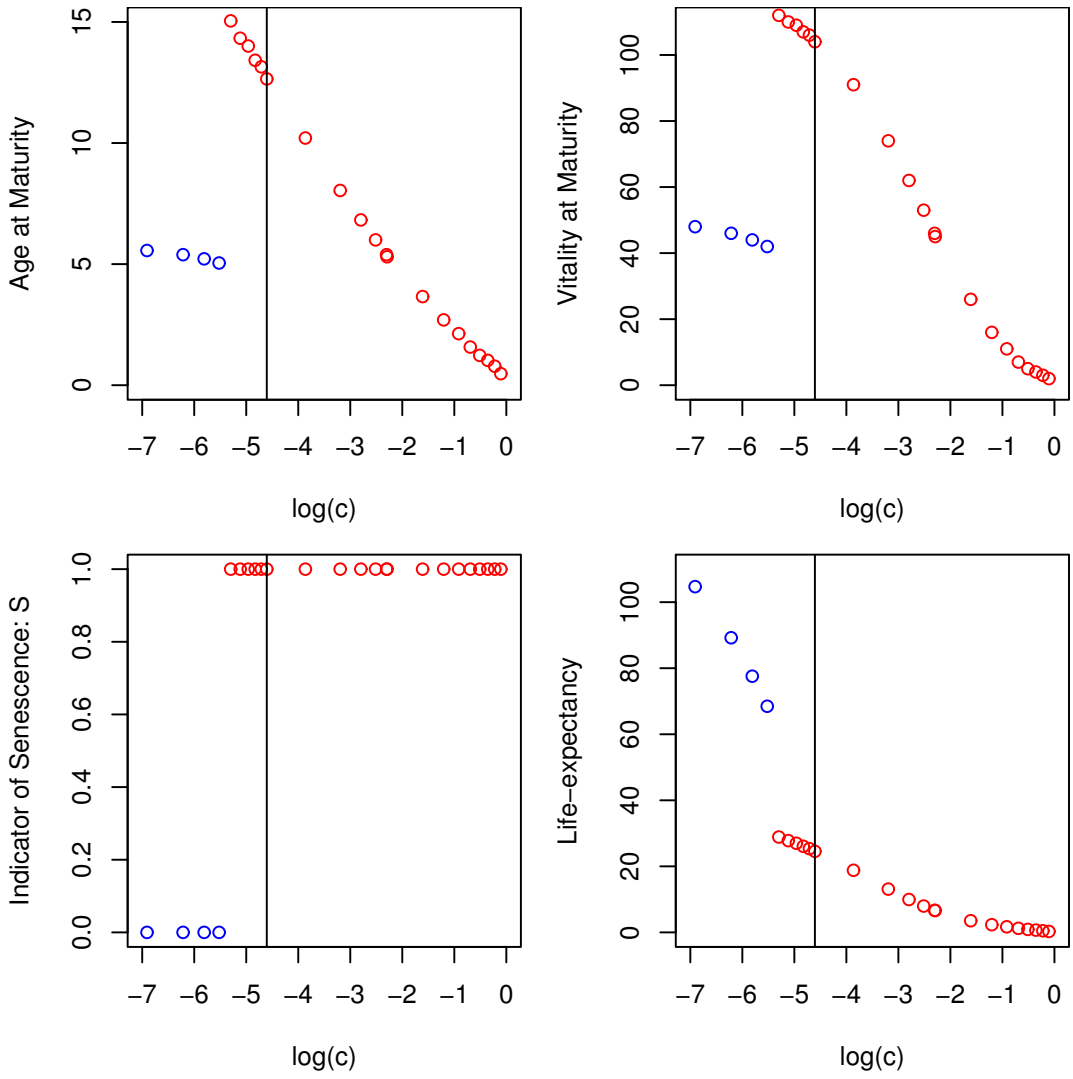

Fig. 5.16: Impact of deviations of extrinsic mortality (c) on a log scale from the humanesque case marked by the vertical line ($c = 0.01$). (red = senescence, blue =sustenance)

level of maximum vitality Ψ can be offset by changes in intrinsic mortality b.

5.6 Summary

The simple model developed in this chapter captures the main features of life - mortality, reproduction, development, growth and maintenance. The results show that the range of optimal life histories is wide.

The costs of growth and maintenance fundamentally determine whether an optimal life history follows a non-senescent strategy or a senescent strategy. Of almost equal importance are the costs of reproduction. The influence of mortality conditions on the boundary between non-senescence and senescence can be strong. This influence, however, is constrained by the costs of maintenance and reproduction. If the costs are too high, even reduction of either intrinsic or extrinsic mortality to zero cannot shift a senescent strategy to a non-senescent one.

An increase in the extrinsic hazard of death promotes non-senescent strategies if costs of maintenance are low and senescent strategies if the costs of maintenance are high. Clearly, the influence of changes in mortality on a species' characteristic pattern of aging can only be understood in light of the levels of efficiency of reproduction and maintenance.

Generally, a low level of intrinsic mortality favors non-senescent strategies. Both intrinsic and extrinsic mortality influence details of a life history, i.e. optimal age and vitality at maturity as well as life expectancy, but they are less crucial in determining senescence versus non-senescence. The boundary between senescence and non-senescence is narrow and implies a sharp shift in the optimal age and vitality at maturity.

Gompertzian Senescence, i.e. exponentially increasing mortality, is the prevalent optimal strategy only if both reproduction and maintenance are costly. If maintenance is cheap, then Gompertzian Senescence is never optimal. If maintenance is costly but reproduction is cheap then Gompertzian Senescence is only optimal at high levels of extrinsic and intrinsic mortality.

Efficient maintenance and growth systems favor maintenance strategies after growth is completed while efficient reproductive systems favor strategies of parallel growth and reproduction.

The model suggests that life-history categories may be largely determined by

the efficiencies of growth and reproductive systems.

Part III

FUTURE

6. DIRECTIONS FOR RESEARCH

6.1 Orientation

The models and analyses of the preceding chapters have shown that senescence is not inevitable. Much more research is needed to understand why in some species mortality increases after maturity while in others it does not. My results raise an important new question for aging research: when does senescence vs. sustenance evolve?

The study of the evolution of the age-patterns of mortality and fertility is still a wide-open field of research waiting for exploration. In this chapter, I summarize my thoughts about which part of the field I want to explore next and then what I think are the most interesting and important additional directions to take.

6.2 Direct extensions of my models

In this section I will describe several directions for research that follow naturally from my dissertation.

6.2.1 Linking burden & optimization

Whether senescence is due to a burden of deleterious mutations or is a byproduct of optimization among trade-offs has been and still is the subject of intense discussion. In the following, I will outline my ideas of how linking both approaches could help to resolve the debate.

My next project

My next research project is to develop a model that combines mutational burden and optimization. Using the model developed in Chapter 5, this could be done by including a mutational load term in the mortality function. Initially, the mutational load would be equal to zero. The optimal mortality and fertility patterns, given zero mutational load, can then be used to calculate selection pressure. The selection pressure plus assumptions about the magnitude and possible age-pattern of the mutation rate will determine the new mutational load. Given the new mutational load, a new round of optimization could be done. With this approach one would be able to analyze what proportion of mortality is due to optimization and what proportion is due to mutational load.

The question is whether the procedure converges. If decreasing selection pressure allows deleterious mutations to accumulate and leads to a rising mortality pattern, then the new selection pressure would fall more quickly, allowing still more mutations to accumulate. As more mutations accumulate, mortality would start rising earlier and earlier. Therefore, this model could shed light on whether the feedback loop between traits and evolution can lead to an unraveling of the life history.

Theoretical attempt

Optimization models can lead to life histories that show non-senescence. Non-senescence cannot be explained by Hamilton's declining indicator. Could the alternative, increasing indicator I suggested in Section 2.3 be consistent with the predictions of optimization models?

An increase in the alternative indicator is conditioned on an increase in mortality with age. Furthermore, future reproductive potential as captured by reproductive value has to be large compared to current reproductive contribution. Therefore, although mortality increases, fertility has to increase even more. Following my definition, senescence pertains to cases where the change in mortality exceeds the change in fertility. Consequently, an increase in the alternative indicator implies that the life history shows non-senescence at that age. This line of reasoning is supported by an analytical proof I derive in Appendix A. Given that selection pressure increases from age a to $a+1$, an optimal life history must be non-senescent at that age. Note that the proof hinges on using my definition of senescence given in Chapter 1.

My proof only pertains to the special case when a change exclusively affects a certain age a. This is a very restrictive assumption but it is in line with Hamilton's framework. Contrary to Hamilton's approach, I allow both mortality and fertility to change at that age. The proof, although limited, shows a first attempt to connect the idea of declining selection pressure with the idea that life histories are optimal.

6.2.2 Measurable quantities and testable hypotheses

Evolutionary demographic theory is based on models. Each model is based on assumptions that simplify reality. A set of models can form a theory that illumi-

nates a broad range of the real world because different simple models shed light on different, specific aspects of reality. Some models generate general insights, other models lead to testable hypothesis, and still other models make both contributions. I have developed simple models that contribute general insights to evolutionary demographic theory. In the future I plan to rethink and maybe reformulate my models to get a handle on measurable quantities to derive testable hypotheses from them.

This effort is a direct extension of my work. The parameters k, κ, and δ in the vitality model can be used to set a time and size scale. What is needed is an explicit expression that links vitality and size. This relationship hinges on knowledge about the rate at which cells are lost.

The η-parameters capture the costs of maintenance and reproduction and have a major influence on the results of the model. Therefore it is important to understand how to root them in reality. What are the magnitudes of the η-parameters for different types of species? This question has to be answered to generate testable hypotheses from the model.

The assumption of symmetric cell division in my model should be relaxed, especially since asymmetric cell division is very likely to be the rule rather than the exception (Kirkwood (2005), Stewart et al. (2005)). In particular, a damaged mother cell can give rise to an undamaged successor. In this case, strategies are feasible that switch from zero investment in maintenance (implying that all mother cells have some damage) to non-zero again. I excluded this possibility in the models I developed in this dissertation. In the future I plan to explore cases when my models can lead to age-patterns where a period of exponentially increasing mortality is followed by plateaus of either constant or slowly increasing mortality.

6.2.3 The diversity of aging

My dissertation can be viewed as a theoretical exploration of the inter-species diversity of aging, i.e., of how varied aging can be for different species and what factors determine whether a species' strategy involves sustenance or senescence. I believe that the models I developed can also be usefully applied, if somewhat refocused, to studies of intra-species variability of aging patterns resulting from environmental cues or conditions. A further research project that derives from

my dissertation is to develop this kind of application of my models.

As an example, consider the important article by Mair et al. (2003). This group, from Linda Partridge's laboratory, explored two kinds of phenotypic plasticity of aging in genetically-identical lines of *Drosophila*. They manipulated diet and demonstrated that flies shifted to a restricted diet experienced, for the rest of their lives, the same trajectory of lower mortality as flies kept on the restricted diet all their lives. In terms of my vitality model, this effect is most simply explained by a shift in the parameter b. The "vitality" of a fly is unchanged by the dietary shift: the shift influences how vitality determines mortality. In contrast, Mair et al. (2003) show that a reduction in temperature slows the pace of mortality increase with age. This effect can be captured in my model by a change in the deterioration parameter δ, or by a more general change in all the "scale" parameters k, κ, and δ or by a change in the strategy π. Which of these possibilities best captures reality? Collaborative theoretical and empirical research might answer this intriguing question.

A variety of other researchers, including James Carey, Thomas Johnson, James Curtsinger and Marc Tatar, have conducted laboratory studies of how some environmental change alters subsequent age-patterns of mortality and, in some cases, fertility. It may be possible to interpret the results of such studies in terms of changes in the parameters of my models – and this might shed light on mechanisms that underlie the phenotypic plasticity of aging.

6.2.4 The characteristics of senescent vs. non-senescent species

Species can be classified according to various characteristics. A challenging direction for future research is to identify the characteristics that distinguish senescent from non-senescent species.

The results of my size-based models in Chapter 4 suggest that species with the capability of continued growth after the onset of reproduction are candidates for non-senescent life-history strategies. The results of my vitality-based model of Chapter 5 suggest that the costs of growth and maintenance (as captured by parameter η_g) and to an almost equal extent the costs of reproduction (as captured by parameter η_r) are the major determinants of senescence vs. sustenance. Developing a theory that identifies the relevant traits in reality that correspond to low vs. high values of η_g and η_r is a promising direction for future research

opened up by my dissertation.

In this regard, modularity might prove to be an important trait that can be associated with inexpensive growth and maintenance. The ability to reproduce clonally from segregated body parts, i.e. vegetative propagation, might prove to be associated with inexpensive reproduction. More thought is needed to come up with other plausible hypotheses about characteristics that correspond to particular values of η_g and η_r.

The results of Chapter 5 further suggest that the parameters for intrinsic (i.e. state-dependent) and extrinsic (i.e. state-independent) mortality conditions (as captured by parameters b and c respectively) can influence the typology of senescence vs. sustenance, albeit constrained by the values of η_g and η_r. What characteristics in a species determines the level of b and c? Williams (1957) provides one hypothesis of how mortality conditions should influence the patterns of senescence. Research on this question has been done, e.g. by Ricklefs (1998) and Ricklefs and Scheuerlein (2002), but further research is needed to understand the influence of mortality components on the evolution of aging.

Mapping typologies of species into a typology of aging would be a major step towards understanding the evolution of senescence vs. sustenance. The simplest typology of aging would distinguish between species with strategies of senescence vs. sustenance. A more elaborate typology could be based on the eight age-patterns of mortality and fertility discussed in Chapter 5. In addition to classifying species according to the shape of age-patterns of mortality and fertility, species could also be classified by their time scale: is life measured in hours, days, weeks, months, years, decades or centuries? Similarly, size-scale could be used: is size measured in nanometers, micrometers, millimeters, centimeters, decimeters or meters? As discussed above, other possible classifications could be growth mode, i.e. determinate vs. indeterminate growth, or the structure of the body plan, i.e. modular vs. non-modular structure.

6.2.5 Alternative applications

The vitality model is a very general model that could also shed light on other aspects of life that influence successful survival and reproduction. One important aspect is learning. If the single state variable in my models is interpreted as including the level of knowledge or cognitive ability, then the change in state can

be due to learning or loss in cognitive ability. If more experience and knowledge imply a lower risk of death and more reproductive success, then my model can be extended to apply to the evolution of learning.

6.3 Other modeling extensions

In this section, I discuss several other directions for research for developing evolutionary demographic models. Over the past three years, there has been a spate of stimulating research in this area and I cite some pathbreaking recent advances.

6.3.1 Density effects

Trees do not move. To live they need space to stand on. Therefore population density is crucial in a forest. If all patches are taken, no seedlings can establish themselves. This is true not only for trees in a forest but for many plants in many environments. In a recent working paper, Doncaster and Seymour (2005) show that this density effect can explain the evolution of the great longevity of Bristlecone Pines. If seeds can only root themselves on a patch freed by the death of an adult, then longer lived trees have an evolutionary advantage. Their offspring will occupy the space opened by the death of the shorter lived trees whose offspring will not have found space to successfully establish themselves. The density effect favors the evolution of longevity.

Density is not only important for trees. The abundance of individuals in a population can significantly influence the evolution of life-history traits in general. If density effects play a role, then Lotka's intrinsic rate of population increase r is not an appropriate measure of fitness. Charlesworth (1973) suggests using the number of individuals in the so called critical age group instead. Mylius and Diekmann (1995) analyze what fitness measure to use, given the specific way density constrains population dynamics. The fitness measure used in the models I developed in Chapters 4 and 5 is in accordance with the results of Mylius and Diekmann (1995, pg. 4). In my models, density affects fertility via the multiplicative parameter φ for all ages equally.

Abrams (1993) analyzes theoretically how extrinsic mortality should affect senescence, given different scenarios of density dependence. Williams (1957) hypothesized that individuals living under more hazardous conditions should exhibit faster senescence and thereby lower survival than individuals living under more

benign conditions. Abrams (1993) shows that Williams' hypothesis will not always be valid if density effects alter population dynamics.

Density could also affect the optimal phenotype in a population. This could help to explain a puzzle recently noted by Resznick et al. (2004). They observe that, for a population of guppies living under two different mortality regimes in the wild, individuals from the high-risk environment show better survival when brought into the laboratory than individuals from the low-risk environment, contrary to William's hypothesis. However, because fewer individuals survive in the dangerous habitat, density is lower than under safer conditions. Therefore, the optimal high-risk phenotype develops when resources are more abundant, while the low-risk phenotype develops when resources are scarce. If more abundant resources allow for better growth and development and if this influences adult mortality, then the high-risk phenotype can be more robust than the low-risk phenotype. This density effect as well as several other possible explanations for the guppy-puzzle are discussed by Abrams (2004).

Bronikowski and Promislow (2005) emphasize that, depending on how senescence is defined and what kind of condition-dependent mortality is prevalent, different long-term effects on the evolution of senescence can be expected.

6.3.2 Intergenerational transfers

Resources are scarce. Therefore, the age-trajectory of resources available to an individual over the life course constrains the evolution of optimal life histories. In this regard, resource flows among individuals are a crucial fitness component. The common fitness measures R and r do not include intergenerational transfers and, in particular, parental care. This can seriously distort results for species with significant periods of offspring dependence. Indeed, the degree of independence and the level of mortality at birth both reflect initial parental investment in offspring. From this perspective, size at birth relative to size at reproductive maturity is an important quantity. Lee (2003) points out that the act of giving birth in itself can be interpreted as a transfer from mother to child. Therefore transfers should generally be captured by any measure of fitness.

Chu and Lee (2006) and Robson and Kaplan (2005) study conditions under which transfers from adult to offspring can be optimal: they model the coevolution of longevity and transfers in human populations. Modeling efforts along

these lines could explain the decline in mortality during development as well as the modest rather than steep increase at post-reproductive ages.

6.3.3 Environmental fluctuations

Environmental fluctuations are certain over the life course of nearly all species. But their timing and magnitude can be highly uncertain. Natural selection needs time to work. If the environment changes faster than it takes selection to be effective, then chance plays a major role in favoring one species over another from one moment to the next. Populations can keep on fluctuating and might not reach a stable age-distribution. In variable environments the intrinsic rate of population increase is a poor measure of fitness because it assumes a stable population. Instead, the stochastic growth rate should be used to measure fitness (Orzack and Tuljapurkar (1989), for a review see Tuljapurkar (1990)). In a changing environment, the intrinsic rate of population increase r can be negative at every point in time but the stochastic growth rate can be positive: r does not capture real population dynamics.

Ripley and Caswell (2005) demonstrate that an indicator of selection pressure – namely the relative change in the stochastic growth rate induced by changes in adult growth and survival of soft-shell clams – is strongly dependent on the amount of uncertainty in the recruitment of baby-clams. This state-dependent analysis implies that their indicator of selection pressure can increase with age if this uncertainty is large.

The development of phenotypes depends on the environment. Environmental cues can switch life histories between alternative age-trajectories of mortality and fertility most suitable to current conditions; some phenotypes can have prolonged life expectancy (Carey et al. (1998), Amdam and Omholt (2002) and Gardner et al. (2006)). If life is harsh, nematode worms, for instance, can enter a state of very low metabolic activity, called the dauer state, that enables the worm to survive long periods of drought. Switching strategies require survival and reproductive patterns to be highly plastic.

In a recent issue of *Science*, Kussell and Leibler (2005) offer a new method for approximating long-term reproductive success in fluctuating environments. Organisms can switch phenotypes according to the prevalent environment. Switching rates turn out to mimic the rate at which the environment is fluctuating.

Furthermore, two extreme strategies of switching are compared – responsive vs. stochastic switching. Kussell and Leibler (2005) show that switching strategies will be responsive or stochastic, depending on whether the costs of sensing the environment match the gains in reproductive success. An important determinant of this decision is the speed at which environments fluctuate. The information content of the environment (entropy) appears explicitly in the optimal solution, pointing to a deep connection between population biology and information theory.

6.3.4 Population dynamics

It is useful to assume optimal equilibrium when studying whether non-senescence could be optimal at all. Research is needed to relax this assumption to better understand the domain of non-senescence vs. senescence. Given within-species dynamics like frequency dependence, could a non-senescent strategy be invaded by an alternative, senescent variant?

Survival is heavily influenced by the ability to resist diseases. A more or less costly immune system is necessary to fight the threats from the fast-evolving micro world. Given across-species dynamics like the co-evolution of the micro and macro world, how does the never-ending battle with parasites influence the evolution of senescence? More generally, some species are prey and other species are predators. Almost all species compete with other species for food and other resources. How does the competition among species influence age-patterns of mortality and fertility?

6.3.5 Summary

The models developed in this dissertation were designed to shed light on whether non-senescent life-history strategies could be optimal. Further research can deepen and extend evolutionary demographic theory in various directions. In the previous sections I have highlighted the directions that I think are of most immediate interest and importance. In particular, I laid out several research projects that directly derive from my dissertation, namely:

- Integrating optimization and the burden of deleterious mutations in a single model,

- Reformulating my models such that the parameters are measurable and testable hypotheses can be derived,
- Focusing my models so that they can be used to understand how a species responds to changes in laboratory conditions, such as dietary or temperature manipulations,
- Mapping typologies of species into typologies of aging, and
- Applying the general model to alternative questions such as the co-evolution of longevity and learning.

In addition I have outlined five other directions for further evolutionary-demographic modeling, involving

- Density effects,
- Intergenerational transfers,
- Fluctuating environments,
- Intra-species population dynamics, and
- Inter-species population dynamics.

6.4 Prospects for evolutionary demography

Evolutionary Demography is an interdisciplinary area of research that has been newly evolving in recent years. In the following sections I highlight three lines along which the field could move forward. First, some canonical ideas need to be rethought. Second, new data, methods and measures are needed. Third, aging – the processes of change over age – can only be understood in the light of both senescence and sustenance together.

6.4.1 Moving beyond the burden of "deleterious fixations"

The phrase "deleterious fixations" is meant to emphasize that research on aging has been and still is influenced by long-held "truths" that channel thinking into directions that are limited and might even be wrong.

One of these fixations has successfully been rethought. For a long time, lifespan was believed to be strictly limited and specific to a species, i.e. nothing could be done about aging. The origin of the species-specific, limited lifespan paradigm can be traced back to Aristotle and Buffon. But over the past two decades gerontology has experienced a paradigm shift. Many experiments on flies, worms, yeast, rodents and other species led to the discovery that dietary restriction can prolong survival, helping shape the newly emerging insight that lifespan is not limited but plastic. Vaupel et al. (1998) present age-patterns of mortality based on large sample sizes that do not increase steeply but instead level off or even decline at later ages for several species, thereby disproving the limited lifespan paradigm. Research on nematode worms, starting with Klass and Hirsch (1976) and Johnson and Wood (1982), demonstrates that changes in single genes can radically alter longevity.

One of the most remarkable examples of the plasticity of aging is presented in a paper by Mair et al. (2003) that shows that changes in diet enable switching up and down between different mortality curves in *Drosophila*. Vaupel et al. (2003) point out that similar patterns of switches have been observed in humans. Vaupel and colleagues show that mortality is plastic in humans even at advanced ages. One illustration is the convergence of mortality patterns in East and West Germany after reunification.

Indeed, a lot can be done about aging. The shift from the limited to the plastic lifespan paradigm is a major step forward in understanding senescence, exemplifying the importance of moving beyond a "deleterious fixation".

In the following, I list some other recalcitrant concepts that have channeled thinking on aging.

- Universal senescence

  Hamilton made the dogmatic claim that the force of selection inevitably declines, thus postulating the universality of senescence. This has restricted creative thinking about possible age-patterns of mortality.

  How universal is senescence?

- Gompertz Law

  It is widely believed that the age-pattern of mortality follows Gompertz law, but is it a law? We do not know what species exhibit this pattern over

what range of age.

How universal is an exponentially increasing hazard of death?

- No senescence in the wild

  It is often asserted that senescence is not experienced in the wild because individuals do not live long enough due to a high extrinsic hazard of death. This conjecture is intuitively appealing but it might be wrong, as pointed out by Nesse (1988) and Carey and Gruenfelder (1997). Carey and Gruenfelder summarize information available on the role of the elderly in primates, elephants and whales. Furthermore, Carey's recent observation of supine behavior in medflies – flies approaching death start lying on their backs, taking a rest once in a while over the remaining days of their lives – indicates that interesting patterns of senescence may be open to study.

  Is there senescence in the wild? What are the age-patterns of mortality in the wild compared to those of creatures in captivity?

- Extrinsic hazard of death

  Is it useful to distinguish between "extrinsic" and "intrinsic" hazards of death? The "intrinsic" hazard depends on age or, more generally, on an individual's state or condition. Are there "extrinsic" hazards that are independent of age or condition?

  Extrinsic mortality is sometimes understood to be captured by the difference in mortality patterns of animals in the wild compared to patterns of those in captivity. However, animals kept in the zoo cannot pursue their natural behavior, for instance running long distances. The lack of exercise and of other behaviors performed in natural environments might distort mortality patterns in artificial habitats. Therefore, extrinsic mortality is not captured simply by the difference between mortality patterns in the wild and in captivity.

  Probably most causes of death are condition-dependent. Natural catastrophes that kill all members of a group independently of condition could be seen as extrinsic risk, but such catastrophes may be rare.

  What causes of death are truly condition-independent for a particular species?

6.4.2 The need for data, methods, and measures

Future theories of the evolution of aging should rest on scientific evidence. So far, the empirical evidence available on the age-trajectories of mortality and fertility for most species is based on small sample sizes (Finch (1990), Promislow (1991), Tatar et al. (1993) and Wilson (1994)). Meaningful age-patterns of demographic schedules, however, need to be based on large numbers of individuals, especially when studying senescence, because the size of the "interesting", later age-groups is progressively diminished by death. Vaupel (1997) and Vaupel et al. (1998) review the current empirical evidence of age-trajectories of mortality for species that are based on large sample sizes. These species include humans, *Drosophila*, medflies, three other species of fruit flies, a parasitoid wasp, the nematode worm *C. Elegans*, and yeast.

Serious study of the process of aging requires knowledge about actual patterns across a wide range of very different species. Biologists interested in different species collect a large amount of data on their particular species to answer their particular questions. It would be useful to obtain knowledge about what data are out there and whether people would be willing to contribute their data to a large database that allows for broad comparative studies of life-history patterns. A comparative study of the qualitative age-trajectories of mortality and fertility including candidates from the whole range of species with sufficiently large sample sizes is essential for developing theories of the evolution of aging.[1]

Methods need to be developed and applied that allow extraction of as much information as possible from the data available. Combining information from different data sources can lead to more conclusive results (Yashin et al. (1999), Yashin et al. (2000)). An important step has recently been taken by Carey and colleagues (Müller et al., 2004): they developed a method for constructing life tables for captured cohorts of unknown age.[2] Their method circumvents the necessity to follow individuals longitudinally in the wild from birth onwards.

[1] The Max Planck Institute for Demographic Research in Rostock has started to collect datasets on patterns of mortality, fertility and growth for non-human species, in captivity and in the wild, from several researchers who have done large-scale experiments or field studies. Other researchers, including Shripad Tuljapurkar and Steven Orzack, and Susan Alberts and Tim Coulson, are also in the process of building databases on age-trajectories of mortality, fertility, and growth. The ISIS (International Species Information System) provides data for species kept in zoos which have recently been used to calculated comparative life tables for selected species of captive animals (Kohler et al. (2005), unpublished).

[2] This became necessary because the capture-recapture approach is not feasible for some species, including the medflies studied by Carey.

In addition to the strong need for new data and methods, it is important to develop a deeper understanding of how to measure senescence and sustenance. I suggest defining senescence as was discussed in Chapter 1: i.e., senescence occurs if but only if the relative change in mortality with age exceeds the relative change in fertility. When gathering data to get comparative evidence it is absolutely essential to agree upon what is to be measured and compared.

Even though the ultimate interest of evolutionary demography is focused on patterns over age, the deeper causal link is more than likely with stage and not age. Models should be based on stage and incorporate a biologically justified link from stage to age. Empirical observations and theoretical insights should be used to identify the crucial stage-variables that determine mortality and fertility patterns of a species. These variables need to be measured and included in the data sets.

6.4.3 A new burning question

A major and very important focus of research over the last decades has been testing which of the two leading theories, mutation accumulation vs. antagonistic pleiotropy, has more power to explain the evolution of senescence. Half a century after Medawar, Williams and Hamilton, evidence has been published both for and against mutation accumulation and antagonistic pleiotropy. The debate has still not been settled. Recent contributions include Charlesworth and Hughes (1996), Charlesworth (2001), Hughes et al. (2002), Partridge and Barton (1993), Partridge (2001) and Steinsaltz et al. (2005).

This dissertation shows that senescence and sustenance are two sides of the process of aging. One cannot be deeply understood without the other. The new burning question that arises from my work is: when does senescence vs. sustenance evolve? An overarching theme that could guide theoretical and empirical work is: to what extent are age-schedules shaped by adaptive vs. non-adaptive processes? What I have done in this dissertation is to broaden the focus from

- mutation accumulation vs. antagonistic pleiotropy to explain senescence to
- adaptive vs. non-adaptive theories to explain senescence vs. sustenance.

Medawar, Williams and Hamilton developed the basic ideas of the evolutionary theories of aging. The broadened focus suggested here allows us a wider perspective.

Adaptive

Adaptive theories explain aging as a byproduct of evolutionary optimization. Such theories are based on models of optimization constrained by trade-offs. Antagonistic pleiotropy and the disposable soma theory are adaptive theories of senescence. Senescence, which in itself is always a maladaptive process, is selected for because the trade-offs that constrain the life history are such that the benefits in fitness outweigh the costs due to senescence.

Reliability theory (LeBras (1976), Gavrilov and Gavrilova (1991), Vaupel (2003), Horiuchi (2003)) is another adaptive approach to explain senescence. Individuals are adapted to functioning over a sufficient period to guarantee the transmission of their genes. The subsequent senescent process is a byproduct that is determined by the preceding adaptive pattern.

If senescence and sustenance, i.e. aging, is explained by adaptive processes, then understanding is needed of the factors that have a strong impact on selection pressure vs. the factors that change selection pressure only slightly. Identification of the "strong forces" vs. "weak forces" of selection would provide a priority list of factors for understanding what shapes the age pattern of demographic schedules and its underlying variables[3]. For instance, Smith et al. (2005, p. 1042, Fig. 5) show that environmental conditions can radically change stage- (and thereby age-) specific selection pressure. That is, the factor "environment" changes the importance of the different life-history transitions among states. This means that the variability of the environment is a strong force of selection. Note that, for this example (a threatened floodplain plant), selection pressure is highly state- but not age-dependent.

The list of valuable extensions to evolutionary demographic models given above in Section 6.3 is, likewise, a list of strong forces of selection, i.e. variability of the environment, density dependence, resource transfers, dynamics within and across species and probably more. Clearly, these components could interact with each other. Such interactions together with trade-offs among life-history traits at different ages can lead to dynamics that are not captured by the simple age-specific changes assumed in the indicators for the force of selection discussed in Chapter 2.

[3] I am grateful to Marc Tatar and Daniel Promislow for discussions about this.

Non-adaptive

A non-adaptive theory is all about what the force of selection cannot achieve. From the viewpoint of a non-adaptive theory, senescence exists because evolution is not strong enough to eradicate it. Sustenance, on the other hand, cannot be explained by non-adaptive theories. Only adaptive approaches have the potential to fully explain the aging process, while non-adaptive theory can partially account for the senescent side of the story. This indicates that adaptive approaches will be more powerful in explaining the aging process, although non-adaptive approaches could still play some role in explaining senescence.

The theory of mutation accumulation is a non-adaptive theory. The successive weakening of the force of selection for or against mutations implies that these mutations become increasingly neutral. Neutral theory explains the fate of a gene due to genetic drift and this drift strongly depends on population size. In this regard, assumptions about the time-horizon (infinite vs. finite) and the rate at which mutations occur at different ages are crucial to the conclusions from any mutation-accumulation model.

Over the last few years mounting knowledge about the human genome has been accumulating. Sufficient data are now available to check for age-specific gene-expression patterns in humans and also in other species such as *Drosophila*. It is possible to compare the fraction of individuals exhibiting neutral versus non-neutral mutations at young versus old ages. Evolutionary theories of senescence predict that falling selection pressure should make non-neutral mutations look more and more like neutral mutations as age increases. So if the fraction of individuals exhibiting non-neutral age-specific mutations becomes more similar over age to the fraction with neutral mutations, then this would be evidence for senescence being influenced by a non-adaptive process.

Evolution is constrained by phylogenetic history. A species can exhibit a non-adaptive age-pattern because a particular evolutionary path channels traits to a limited, possibly sub-optimal range. These phylogenetic channels could only be overcome in the very long run. So both mutation accumulation and phylogeny are non-adaptive forces shaping aging.

Further thoughts

Creative thinking about alternative approaches to explain aging is needed. What are possible factors that shape the age-trajectories of mortality and fertility? Williams's hypothesis suggests the crucial importance of the extrinsic hazard of death. His hypothesis has been tested and evidence has been found for and against it. The contradictory evidence shows that this single factor is not enough to explain the pace of senescence. Williams identified one important variable that now needs to be put into perspective with other possible candidates.

What combination of these candidates leads to what qualitative age-pattern? In particular, when does senescence evolve and when sustenance? Clear, testable hypotheses need to be derived from theoretical models and empirical observations for what qualitative patterns of mortality and fertility are expected and when. My models in Chapters 4 and 5 are a first systematic contribution to answering this question. My findings suggest that attention should be given to the costs of maintenance and reproduction.

An equally interesting and related question is how plastic the process of aging can be. For instance, studies of human twins have shown that the same genome can be associated with different patterns of senescence due to phenotypic plasticity. Only 25 % of the variation among twins in life expectancy can be attributed to genetic variation (McGue et al. (1993), Herskind et al. (1996)). So, how heterogeneous are species with respect to aging? What species have high plasticity, what species have low plasticity, what characteristics determine the degree of plasticity? Understanding the plasticity of senescence and sustenance would provide a strong tool in steering our own process of aging in the most advantageous way, i.e. towards a long and healthy life.

6.5 Conclusion

Senescence and sustenance are described by the age-trajectories of mortality and fertility. The age-trajectories of mortality and fertility are the fundamental demographic schedules: they determine the dynamics and structures of populations. In particular, they determine a population's genetic structure and size. Evolution can be viewed as change in genetic structure and size of populations over time. Changes in genetic structure lead to changes in age-trajectories. Therefore, evo-

lution molds and is molded by demographic schedules of mortality and fertility. To understand the evolution of life it is crucial to study these schedules. Mortality and fertility are deeply interconnected with each other and in particular with the age-schedule of growth. The models developed in this dissertation shed new theoretical light on the evolution of the age-schedules of mortality, fertility and growth and their interconnections.

My models suggest that a remarkable variety of patterns may be optimal under different circumstances. The limited empirical data available suggests that species may exhibit a rich diversity of age-schedules of mortality, fertility and growth. Current understanding of the biology of aging is largely based on laboratory studies of a restricted range of species. Getting reliable data on a wide variety of species is a crucial research need.

The evolutionary demographic theory of aging should aim at illuminating senescence vs. sustenance through the study of the age-patterns of mortality, fertility and growth. In particular, the research should explain why some species have a quickly or slowly increasing hazard of death and why others have a constant or falling hazard of death. The models I have developed are a first step towards gaining a deeper understanding of the evolution of senescence vs. sustenance. They lead to the general insight that the costs of maintenance and reproduction are the major determinants shaping these patterns.

In addition to exploring alternative qualitative patterns, evolutionary demographic theory should shed light on questions such as why some species live on short time scales and others on long ones, why some species grow large and others stay tiny and why some species produce numerous small progeny while others produce only few large progeny compared to adult body size. Thinking about scales of time and size could aid in the understanding of what kinds of species exhibit senescence vs. sustenance.

These species can be classified according to several characteristics. How such typologies map onto the typologies of senescence vs. sustenance will undoubtedly be a stimulating direction for future research.

Senescence is not inevitable. Life provides an alternative strategy: sustenance. Sustenance can theoretically be an optimal life-history strategy and is empirically observed for some species. Sustenance may be the strategy for a great many species in which mortality appears to fall or be constant over age, at least over an extended period of life after reproductive maturity. More extensive empirical

evidence is needed for a broad range of species beyond humans, rodents, flies, nematodes and yeast. My thesis, the central insight of this dissertation, is: to deeply understand why some species senesce, it is necessary to understand why other species do not.

APPENDIX

A. PROOF

A.1 Selection pressure & optimization

Assume age-specific mortality μ_a and fertility m_a to be stepwise constant (indicated by the lower script a) over small time intervals of length τ. Then reproductive value, given by

$$v(a) \;=\; \frac{1}{l(a)} \int_a^{\infty} \; l(x)\, m(x)\; dx, \tag{A.1}$$

can be written as

$$v(a) \;=\; \frac{1}{l(a)} \int_a^{a+\tau} \; l(a)\, e^{-\mu_a x}\, m_a\; dx \;+\; \frac{e^{-\,\mu_a \tau}}{l(a)} \;\int_{a+\tau}^{\infty} \; l(x)\, m(x)\; dx \tag{A.2}$$

and solving the integral

$$v(a) \;=\; \frac{m_a}{\mu_a} \left(1 \;-\; e^{-\,\mu_a \tau}\right) \;+\; \frac{e^{-\,\mu_a \tau}}{l(a)} \;\int_{a+\tau}^{\infty} \; l(x)\, m(x)\; dx. \tag{A.3}$$

If remaining reproduction at age a is denoted by

$$h(a) \;=\; \int_a^{\infty} \; l(x)\, m(x)\; dx, \tag{A.4}$$

then we have

$$h(a) \;=\; l(a)\, v(a) \tag{A.5}$$

and

$$h(a+\tau) \;=\; l(a)\, e^{-\,\mu_a \tau}\, v(a+\tau) \tag{A.6}$$

Selection pressure on mortality increases if [1]

$$\mu_a\, h(a) \;<\; \mu_{a+\tau}\, h(a+\tau), \tag{A.7}$$

assuming a proportional hazard model.

Substituting expression A.5 for $h(a)$ and expression A.6 for $h(a+\tau)$ in condition A.7 and rearranging leads to the condition

$$m_a \left(1 \;-\; e^{-\,\mu_a \tau}\right) \;<\; e^{-\,\mu_a \tau}\, v(a+\tau)\, (\mu_{a+\tau} \;-\; \mu_a). \tag{A.8}$$

[1] Note that $h(a) = H^{\dagger}(a) \cdot T$ and T denotes generation time. (see section2.3 equation 2.5d and inequality 2.7)

Assume further that an optimal change in age-specific mortality and fertility is sought such that reproductive value at age a is maximized. Mortality and fertility at all other ages are assumed to be unaffected by this choice. Reproductive value at age a is maximized if

$$\begin{aligned}\frac{dv(a)}{da} &= \frac{\dot{m}_a}{\mu_a}\,(1 - e^{-\mu_a\tau}) \\ &\quad - \frac{m_a}{\mu_a^2}\,(1 - e^{-\mu_a\tau})\,\dot{\mu}_a \\ &\quad + \frac{m_a}{\mu_a}\,e^{-\mu_a\tau}\,\dot{\mu}_a\,\tau \\ &\quad - e^{-\mu_a\tau}\,\dot{\mu}_a\,\tau\,v(a+\tau) \\ &\quad - e^{-\mu_a\tau}\,m(a+\tau) \\ &= 0,\end{aligned} \tag{A.9}$$

where the dot indicates a change over age.

To take into account inequality A.8 imposed by increasing selection pressure, Equation A.9 can be rearranged to

$$\begin{aligned}&\frac{\dot{m}_a}{\mu_a}\,(1 - e^{-\mu_a\tau}) \\ -\ &\frac{m_a}{\mu_a^2}\,(1 - e^{-\mu_a\tau})\,\dot{\mu}_a \\ +\ &\frac{m_a}{\mu_a}\,e^{-\mu_a\tau}\,\dot{\mu}_a\,\tau \\ -\ &e^{-\mu_a\tau}\,m(a+\tau) \\ =\ &e^{-\mu_a\tau}\,v(a+\tau)\,(\mu_{a+\tau} - \mu_a).\end{aligned} \tag{A.10}$$

Note that the right-hand side of Equation A.10 equals the right hand side of inequality A.8

The change in mortality over age is captured by

$$\dot{\mu}_a = \frac{\mu_{a+\tau} - \mu_a}{\tau} \tag{A.11}$$

and analogously the change in fertility over age is captured by

$$\dot{m}_a = \frac{m_{a+\tau} - m_a}{\tau}. \tag{A.12}$$

Using these two equations and substituting inequality A.8 into Equation A.10

yields

$$(\acute{m}_a - \acute{\mu}_a) \left[\frac{(1 - e^{-\mu_a \tau})}{\mu_a} - e^{-\mu_a \tau} \tau \right] > 1, \tag{A.13}$$

where the acute accent abbreviates relative changes, i.e. $\dot{\mu}_a/\mu_a$ and $\dot{m}_a/m_a$. If selection pressure increases at age a an optimal life history has to fulfill condition A.13 under the assumptions made above. Could such a life history show senescence at that age?

The condition for senescence derived in Chapter 1 is given by

$$\acute{\mu}_a > \acute{m}_a. \tag{A.14}$$

Therefore, the first term in expression A.13 is negative. For condition A.13 to be true this implies that

$$\left[\frac{(1 - e^{-\mu_a \tau})}{\mu_a} - e^{-\mu_a \tau} \tau \right] < 0 \tag{A.15}$$

must hold. This requires that

$$e^{\mu_a \tau} < 1 + \mu_a \tau. \tag{A.16}$$

Let $\varepsilon > 0$ denote a constant. The exponential function can be written using Taylor's approximation and the inequality becomes

$$e^{\mu_a \tau} = 1 + \mu_a \tau + \varepsilon < 1 + \mu_a \tau \tag{A.17}$$

which is a contradiction. Therefore

$$\acute{\mu}_a \leq \acute{m}_a \tag{A.18}$$

which is non-senescence. Q.E.D.

B. STABLE POPULATION THEORY

B.1 The Basic Idea

Stable population theory was born in 1760 when Leonard Euler put forward his "Hypothesis of mortality" (Euler, 1760). Euler intended to infer missing population parameters from incomplete empirical data sets. Already in 1748 Euler had calculated a simple population projection assuming a constant survival and fertility schedule. This approach led him to the important discovery that such a population would increase over time in geometric progression, i.e. the ratio of births between two successive times t and $t+1$ would approach a constant value as t approaches infinity. Euler gave this projection to Johann P. Süssmilch as a contribution to "Die göttliche Ordnung" (Süssmilch, 1761).

Motivated by his finding in 1748 Euler (1760) assumed that births of the present year multiplied by a constant would determine births in the following year and that the survival schedule was fixed given a one-sex population that is closed to migration. This approach enabled Euler to explicitly calculate the multiplicative constant, λ, he already had found to exist. Euler's contribution was the igniting spark of what later would become "stable population theory". The actual birth of stable population theory was achieved after an incubation of 147 years by Alfred James Lotka.

Alfred James Lotka (1880-1949) was a chemist and physicist who published in 1907 a short article in Science that laid the foundation for stable population theory (Lotka, 1907). Lotka was looking for a mechanism that drives the dynamics and structure of a population over time. This mechanism should link a population's current size and structure to its past. The inflow and outflow of individuals of a population is determined by the age-specific mortality and fertility rates. Applying those rates to a population of known size in the past should give the population size in the future. As done by Euler, Lotka considered a one-sex population that is closed to migration.

B.2 The Lotka Equation

Let's follow Lotka's derivations: Assume a population with a constant age-structure over time. The age-structure is captured by the age-specific fractions $c(a)$ of the total population $N(t)$ at time t. The number of individuals between

age a and $a + da$ is given by

$$N(a,t) \;=\; N(t)\, c(a)\, da, \tag{B.1}$$

where da captures the width of an age group. The value of $N(a,t)$ can also be expressed changing the perspective to the past. Individuals of age a at time t have been the babies born a years ago, $B(t-a)$, who survived. If the probability to survive to age a is $l(a)$, then $N(a,t)$ can be calculated applying

$$N(a,t) \;=\; B(t-a)\, l(a)\; da. \tag{B.2}$$

Equating both expressions and rearranging yields

$$c(a) \;=\; \frac{B(t-a)}{N(t)}\, l(a). \tag{B.3}$$

Since the age-distribution $c(a)$ is assumed to be independent of time the per capita birth and death rates, b and d, do not change and the rate of increase, $r = b - d$ will be constant. Then, Lotka argued, the population size will increase like a capital stock with annual interest rate r, i.e.

$$B(t-a) \;=\; B(t)\, e^{-ra}. \tag{B.4}$$

Substitution into Equation B.3 results in

$$c(a) \;=\; \frac{B(t)}{N(t)}\, e^{-ra}\, l(a) \tag{B.5}$$

Noting that $B(t)/N(t)$ equals the constant per capita birth rate b, it follows that

$$c(a) = b\, e^{-ra}\, l(a). \tag{B.6}$$

Since the sum over all fractions $c(a)$ has to equal one, integration and rearrangment leads to Lotka's first basic result,

$$b = 1/\int_0^\infty e^{-ra}\, l(a)\; da. \tag{B.7}$$

This equation determines the per capita birth rate, b. However, Equation B.7 does not account for the fact that the per capita birth rate b is a condensed expression

of age-specific reproductive events, captured by the so called maternity rates, $m(a)$.

Sharpe and Lotka (1911) explicitly incorporated an age-specific reproduction schedule. If each mother aged a gets $m(a)$ children, the number of babies for that age group is $B(t-a)\,l(a)\,m(a)\,da$. Summing over all age classes it follows that

$$B(t) = \int_0^\infty B(t-a)\,l(a)\,m(a)\,da. \tag{B.8}$$

This equation is called the *Renewal equation*. Assuming that births are growing exponentially, $B(t) = e^{rt}$, Equation B.8 can be written as

$$1 = \int_0^\infty e^{-ra}\,l(a)\,m(a)\,da. \tag{B.9}$$

In this form Equation B.9 is generally known as the Lotka equation or the Euler-Lotka equation, sometimes also as the characteristic equation. This equation determines the intrinsic rate of population growth, r. The adjective "intrinsic" emphasizes that each combination of birth and death schedules is associated with a particular r.

Note that this approach assumes a continuous flow of fertility. The term $m(a)\,da$ denotes the probability that a women aged a will give birth to a (girl)child before age $a + da$, i.e. a women will get $m(a)\,da$ of a child in time interval da. Depending on the framework the Lotka equation can equally well be stated in discrete time,

$$1 = \sum_{x=0}^{\infty} e^{-rx}\,l_x\,m_x, \tag{B.10}$$

where $l_0 = 1$.

Sharpe and Lotka (1911) discovered an important characteristic of populations confronted with constant vital rates. They show that the age-distribution of a population can be variable in some reasonable range due to irregularities, but that there exists an underlying stable form, the stable population, to which the age-distribution will ultimately converge. Hence, independently of the initial distribution, the final composition of the population is solely determined by its rate of growth, intrinsic to its constant birth and death schedule. It should be emphasized that in a stable population not the absolute numbers, but the age-specific rates of births and deaths remain constant over time. A special case of a

stable population is the *stationary* population, which pertains to the case of zero population growth, i.e. $r = 0$.

The phenomenon that populations "forget their past" once confronted with constant demographic parameters is known as *strong ergodicity*, following Hajnal (1958). If vital rates are changing over time but are the same for two (or more) different populations, those populations will resemble each other in structure after sufficient time has past by. Their crude birth and death rates will be the same. This property is known as *weak ergodicity* and was first derived by Norton (1928). It was also conjectured by Coale and again demonstrated by Lopez (1961).

That each population will almost always tend to its fixed form was graphically proven by Lotka (1922) himself. Lotka shows that only if the fertility schedule depends on the age-structure and if the reproductive age-classes are so sparsely occupied that births are not sufficient to keep the population alive, his claim would not hold. Lotka's insights were not accepted without criticism until William Feller gave a rigorous mathematical proof (Feller, 1941). Since then the Lotka equation has been accepted.

The expressions (B.6), (B.7), (B.8) and (B.9) are the basic equations of stable population theory and most fundamental and important to demography and its applications in various neighboring sciences. Lotka's work rests on the shoulders of Euler, but Lotka did not give any credit to Euler. Nevertheless Lotka's contributions to stable population theory went far beyond Euler.

B.3 Discovering the Roots of the Lotka Equation

The intrinsic rate of population increase is implicitly defined by an integral equation. In the following it will be shown that, indeed, there is a unique real root that satisfies the Lotka equation.

Assume that sufficient time has past such that the founding population does not contribute to population growth. Note that Equation B.8 constitutes a homogeneous integral equations with the following properties: First, any solution multiplied by a constant c remains a solution. Second, adding solutions to each other yields a solution. If $B_1(t)$ and $B_2(t)$ solve the integral, so does $c_1B_1(t) + c_2B_2(t)$. Since Lotka anticipated e^{rt} as a solution for $B(t)$ he formulated a general expres-

sion for a solution to Equation B.8:

$$B(t) = Q_1\, e^{r_1 t} + Q_2\, e^{r_2 t} + ... \tag{B.11}$$

Substituting this into (B.8) yields

$$1 = \int_0^\infty e^{-r_n a}\, l(a)\, m(a)\; da$$

for $n = 1, 2, 3, ...$, where the r_n's are determined by the roots of

$$1 = \int_0^\infty e^{-r a}\, l(a)\, m(a)\; da.$$

Since the product $l(a)\, m(a)$ will always be positive, this is a strictly monotonically decreasing function in r. For $r \to +\infty$ the integral converges to zero and for $r \to -\infty$ it approaches infinity. Consequently there is exactly one single real root, say ρ, for which the integral equals unity. The root of $r = 0$ defines the net reproduction rate, given by

$$R_0 = \int_0^\infty l(a)\, m(a)\; da. \tag{B.12}$$

This value is the ratio of births between two successive generations and reflects the increase or decrease in the number of births from one generation to the next, i.e. the life-time expectation of offspring for a female. The sign of the real root is determined by the following rule:

$$\rho \gtreqless 0 \text{ as long as } R_0 \gtreqless 1.$$

What does a value of $R_0 = 1$ mean? It means that each mother replaces herself with exactly one baby girl, the population is stationary and the growth rate equals zero. Values above one imply that mothers produce more offspring than necessary to replace themselves and by that the population is growing at a rate $\rho > 0$. If the net reproduction rate is below one, then the population will shrink in size.

Besides real roots, complex solutions have to be considered. Any complex root of the equation is of the form $u + iv$. Following Euler's theorem it is true

that

$$e^{-ra} = e^{-ua - i\,va} = e^{-ua}[cos\,(va) - i\,sin\,(va)].$$

Since the integral has to equal 1 (a real number) the imaginary part must vanish. Only the factor $cos(va)$ remains. This cosine will never exceed unity. For values of the cosine smaller than one the term e^{-ua} must outbalance this factor by taking larger values to fulfill Equation B.9, hence u has to be smaller than the real root ρ (Keyfitz, 1968, 103). Keyfitz (1968, 103) also notes that in practice u will always be negative. The solution (B.11) will be dominated by its real root for sufficiently big t in the series (B.11). The real root will determine the intrinsic rate of growth for the stable age-distribution. But on the way from the initial age-structure of the population towards its stable form, the complex roots will influence the population dynamics through gradually diminishing oscillations in the path of births towards stability.

Why is it not sufficient to simply calculate the crude growth rate of a population from its crude birth $(B(t)/N(t))$ and death rates $(D(t)/N(t))$ instead of dealing with an integral equation? Clearly, if vital rates have remained constant in a population over a long time period, the crude growth rate and the intrinsic growth rate will be identical. However, if vital rates have fluctuated considerably during the recent history of a population, then a discrepancy between these rates can be observed. This discrepancy provides a means of evaluating how stable the population under consideration actually is. Furthermore, the solution to Equation B.9 stands for the intrinsic *capacity* of multiplication of a population. In comparison, the crude birth and death rates, varying with the observed values, are only a picture of the moment without any message about the underlying potential of growth of the population.

B.4 Calculation of the Real Root

The intrinsic rate of population increase, r, is implicitly defined by an integral equation. To calculate the real root of this equation Lotka applied the expansion of the exponential function and the concepts of moments and cumulants. Considering only the first two terms of the expansion Lotka derived a very good approximation for r in terms of the first two cumulants (Lotka, 1934). A far easier way of calculating r is given by Coale (1957) substituting a rather rough

approximation of r into Equation B.9, adjusting r in a particular way depending on the divergence of the integral from 1 and iteratively repeating this process.

To find a reasonable starting value for this iteration Coale took into account the fact that $B(t)/B(t-T) = R_0$, where T is the length of one generation. Assuming exponential growth, $B(t)$ equals e^{rt} and it follows that

$$R_0 = e^{r\,T}.$$

This equation relates the rate of increase per generation, R_0, to the annual rate of increase of the population, r. It states that the time a population, growing at a rate r, would need to increase by a factor R_0, is T. The range in which T can vary for humans is rather narrow, namely between 26 and 33. Most commonly it takes values around 29. Therefore for humans a good starting value for r can be calculated from $r_1 = ln(R_0)/29$.

Substituting r_1 into the Lotka equation (Equation B.9) gives a result slightly different from one, say $1+\delta$. The next step is to infer δ from (B.9). Taking the derivative with respect to r leads to

$$\frac{dy}{dr} = -\int_0^\omega a\,e^{-ra}\,l(a)\,m(a)\;da = -A\,y, \tag{B.13}$$

where y is the Lotka integral and A is the average age of childbearing in the stable population, given by

$$A = \frac{\int_0^\omega a\,e^{-ra}\,l(a)\,m(a)\;da}{\int_0^\omega e^{-ra}\,l(a)\,m(a)\;da} = \frac{T}{y}.$$

Since for $r = \rho$, y will equal one, the change in y with respect to r at this point will equal $-A$, hence the total difference, δ, will equal this change times the deviation of r from its real value, $-A\Delta r$ and it follows

$$\Delta r = -\delta/A.$$

Comparing the mean length of generation, T, and the mean age of childbearing, A, the difference between those two values is not very large. Dublin and Lotka (1925) note that the average age of childbearing A will not differ from T more than 0.6 of a year. Therefore it is reasonable to choose 29 also as an approximation for A. The next value for r is found by adding $\delta/29$ to r_1. Being even more correct

Coale adjusts for the error which occurs by assuming that A equals 29 and uses

$$r = r_1 + \frac{\delta}{29 - \delta/r_1}$$

for his calculations. With this approximation Coale is able to recompute Lotka's results in excellent agreement. Only in the case of unusual high T Lotka's results are slightly better, but the error for Coale's result is still less than three-tens of one percent of the correct value.

Generally, a solution to the Lotka equation can be found numerically applying the Newton-Raphson method. Today, with Mathematica and other software, the exercise is easy.

B.5 Extensions

Preston and Coale (1982) and Arthur and Vaupel (1984) generalized Lotka's results by dropping the stability assumptions. Mortality and fertility can change with time. Therefore, age-groups no longer have to grow at the same rate but do so at particular age-specific rates $r(a)$. Let's briefly sketch the basic derivation.

Multiplying Equation B.5 by total population size $N(t)$ at time t gives the expression for the number of individuals aged a, denoted by $N(a)$,

$$N(a) \;=\; B\, l(a)\, e^{-ra}, \tag{B.14}$$

omitting the index for time for convenience now and in the following. The probability of surviving up to age a, $l(a)$, is given by

$$l(a) \;=\; e^{-\int_0^a \mu(x)\, dx},$$

where the exponent captures the cumulated age-specific mortaltiy rate $\mu(x)$ from birth to age a. Differentiating both sides of Equation B.14 with respect to age and dividing by $N(a)$ leads to

$$\frac{1}{N(a)} \frac{dN(a)}{da} \;=\; -\mu(a) \;-\; r.$$

Note that the relative change in survival $l(a)$ equals the negative force of mortality $\mu(a)$ at that age.

To relax the stability assumption let r depend on age, i.e.

$$\frac{1}{N(a)}\frac{dN(a)}{da} = -\mu(a) - r(a).$$

Taking into account that

$$\frac{1}{N(a)}\frac{dN(a)}{da} = \frac{d\,log\,N(a)}{da},$$

integration leads to the following result:

$$N(a) = N(0)\,e^{-\int_0^a r(x)\,dx - \int_0^a \mu(x)\,dx} \tag{B.15}$$

$$= B\,e^{-\int_0^a r(x)\,dx}\,l(a). \tag{B.16}$$

Preston and Coale (1982) derived the basic equations that characterize any population closed to migration by its age-specific birth, death and growth rates,

$$c(a) = b\,e^{-\int_0^a r(x)\,dx}\,l(a) \tag{B.17}$$

$$b = 1/\int_0^\infty e^{-\int_0^a r(x)\,dx}\,l(a)\,da \tag{B.18}$$

$$1 = \int_0^\infty e^{-\int_0^a r(x)\,dx}\,l(a)\,m(a)\,da. \tag{B.19}$$

Lotka's system of equations as given in Eqs. B.6 B.7 and B.9 covers a special case in which $r(a)$ is the same for all ages.

For a population that is open to migration Preston and Coale (1982) show that the population size at age a is determined by

$$N(a) = N(0)\,e^{-\int_0^a r(x)\,dx}\,e^{-\int_0^a e(x)\,dx}\,l(a), \tag{B.20}$$

assuming that the population changes continuously over time. The term $e(x)$ captures the net out-migration. Net in-migration is implicitly included as a reduction in mortality. Migration affects a population in a way similar to mortality. People are added (lives saved) and taken away (lives lost).

Clearly, it is possible to consider any form of entering and leaving any kind of specified group. As long as the duration of membership (analogous to age) in this group can be exactly defined the formulas are applicable. There could be μ_i different attrition rates for i different factors that can change the size of

the group, additional to the force of mortality. Under the condition that each attrition factor is a continuous function of age the last equation can be generalized to

$$N(a) \;=\; N(0)\, e^{-\int_0^a r(x)\,dx} e^{-\sum_i \int_0^a \mu_i(x)\,dx}, \tag{B.21}$$

where again the time index has been omitted for all variables. From this formula, it is possible to get back to the corresponding stationary population by simply multiplying by $e^{\int_0^a r(x)\,dx}$.

C. ALGORITHM: SIZE

Note: this algorithm is written in Mathematica. For discussion of the model see Chapter 4.

```
Needs["Utilities`MemoryConserve` "]

(*----parametersetting----------*)
γ = .004;
δ0 = .9;
b = 0.05;
k = 3;
κ = 0.05;
c = 0.002;
ξmax = ((1 - δ0) / γ) - 0.0001
ξ0 = 1;
φ = 0.02;
Δ = 0.25;
j = 0.001;

(*---------Functions-------------*)
δ[ξ_] := δ0 + γ ξ;
μ[ξ_] := b / ξ + c;
m[ξ_, p_] := φ ((1 - p) - (1 - p)^2) ξ;
xi[a_] := ((γ / (1 - δ0)) + (1 / ξ0 - γ / (1 - δ0)) Exp[-k (1 - δ0) a]) ^ (-1);
α[ξ_] := -Log[(ξ^-1 - γ / (1 - δ0)) / (1 / ξ0 - γ / (1 - δ0))] / (k (1 - δ0));
Sur[a_] := Exp[- NIntegrate[b / xi[t] + c, {t, 0, a}]];
τ[ξ_, p_] := Δ / (k (p - δ[ξ]) ξ);
Initialize[ξ_] := (
   p = δ[ξ];
   Rmax = m[ξ, p] / μ[ξ];
   a = α[ξ];
   tao = 0;
   R = Sur[a] Rmax;
   OSG = {{R, M, ξ, a, p, tao}});

(*-----Initialization----------*)
Initialize[ξmax];
```

```
(*-------Growth algorithm--------------*)
Do[(
   ξ = ξmax - n;
   p = δ[ξ];
   RM = m[ξ, p] / μ[ξ];
   RG = RM;
   a = α[ξ];
   L = Sur[a];
   tao = 0;
   help = {RG, M, ξ, a, p, tao};
   Do[(
     test = m[ξ, pi] (1 - Exp[- μ[ξ] τ[ξ, pi]]) / μ[ξ]
                          + Exp[-μ[ξ] τ[ξ, pi]] Rmax;
     If[test > RG, (RG = test; tao = τ[ξ, pi];
       help = {RG, G, ξ, a, pi, tao}), RG = RG]
    ), {pi, δ[ξ] + (1 - δ[ξ]) / 100, 1, (1 - δ[ξ]) / 100}];
   Rmax = help[[1]];
   OSG = Prepend[OSG, help]
  ), {n, Δ, ξmax - 1, Δ}];
i = 1;
resultG = {OSG[[i]]};
help = OSG[[i]];
While[help[[2]] == G, (i = i + 1;
       resultG = Append[resultG, OSG[[i]]];
       help = Last[resultG])];
```

```
(*---------Shrink Algorithm-----------*)

τ[ξ_, p_, d_] := -Δ / (κ (p - d) ξ);
ξmin = 0;
OSStotal = {{{0, 0, 0, 0, 0, 0}}};

Do[(
   ξhelp = ξmin + nl;
   d = δ[ξhelp];
   a = α[ξhelp];
   L = Sur[a];
   OSS = {{0, 0, 0, 0, 0, 0}};
   Rmax = 0;

   Do[(
     ξ = ξmin + n2;
     p = d;
     RM = m[ξ, p] / μ[ξ];
     RS = RM;
     tao = 0;
     help = {RS, M, ξ, a, p, tao};
     Do[(
       test = m[ξ, pi] (1 - Exp[- μ[ξ] τ[ξ, pi, d]]) / μ[ξ]
                        + Exp[-μ[ξ] τ[ξ, pi, d]] Rmax;
       If[test > RS,
        (RS = test;
         tao = τ[ξ, pi, d];
         help = {RS, S, ξ, a, pi, tao}),
        RS = RS]
      ), {pi, 0, d - (1 - δ[ξ]) / 100, (1 - δ[ξ]) / 100}];
     Rmax = help[[1]];
     OSS = Prepend[OSS, help];
    ), {n2, Δ, ξhelp, Δ}]; OSStotal = Prepend[OSStotal, OSS]),
  {nl, Δ, ξmax, Δ}];
```

```
(*---------Prepend growth period---------*)

τ[ξ_, p_, d_] := Δ / (k (p - d) ξ);
OStotal = {resultG};

Do[(
   OSG = {{0, 0, 0, 0, 0, 0}};
   Rmax = OSStotal[[s, 1, 1]];
   ξmax = OSStotal[[s, 1, 3]];
   Do[(
     ξ = ξmax - n;
     a = α[ξ];
     tao = 0;
     RG = 0;
     help = {RG, G, ξ, a, pi, tao};
     Do[(
       test = m[ξ, pi] (1 - Exp[- μ[ξ] τ[ξ, pi]]) / μ[ξ]
                                  + Exp[-μ[ξ] τ[ξ, pi]] Rmax;
       If[test > RG,
        (RG = test; tao = τ[ξ, pi];
         help = {RG, G, ξ, a, pi, tao}),
        RG = RG]
      ), {pi, δ[ξ] + (1 - δ[ξ]) / 100, 1, (1 - δ[ξ]) / 100}];
     Rmax = help[[1]];
     OSG = Prepend[OSG, help]
    ), {n, Δ, ξmax - 1, Δ}];
   OSG = Drop[OSG, -1];
   OSGS = OSG;
   Do[OSGS = Append[OSGS, OSStotal[[s, i]]],
    {i, 1, Length[OSStotal[[s]]] - 1}];
   OStotal = Append[OStotal, OSGS]
  ), {s, 1, Length[OSStotal] - 1, 1}];
test = 0;
Do[If[test < OStotal[[q, 1, 1]],
    (test = OStotal[[q, 1, 1]];
     strategy = OStotal[[q]]),
    test = test], {q, 1, Length[OStotal]}];
```

D. ALGORITHM: VITALITY

Note: this algorithm is written in Mathematica. For discussion of the model see Chapter 5.

```
Needs["Utilities`MemoryConserve` "]
<< Graphics`MultipleListPlot`

φ = 1;
ϕ0 = 1;
η2 = 0.75;
η3 = 1.2;
Δ[x_] := (x - 1) / 1000 // N;
ϕmax[k_, κ_, δ_] := IntegerPart[((k/(δ + κ))^4)];
μ[ϕ_] := b / ϕ + c;
m[ϕ_, x_] := φ (1 - x)^η1 (k ϕ^η2 - κ ϕ) / (ϕ0)^η3;
τ[ϕ_, x_] := Δ[ϕmax[k, κ, δ]] / (-δ ϕ + x^η3 (k ϕ^η2 - κ ϕ));
p0[ϕ_] := (δ ϕ / (k ϕ^η2 - κ ϕ))^(1/η3);
OSS = {};

Do[
 (OSS = {};
  Rmax = 0;
  n = ϕmax[k, κ, δ];
  psi = ϕmax[k, κ, δ];
  BigR = 0;
  i = 0;
  While[n >= ϕ0 - 0.5,
   (ϕ = ϕmax[k, κ, δ] - n + ϕ0;
    p = p0[ϕ];
    RM = m[ϕ, p] / μ[ϕ];
    RS = RM;
    tao = 0;
    help = {RS, M, ϕ, p, tao};
    Do[(
      test = m[ϕ, pi] (1 - Exp[μ[ϕ] τ[ϕ, pi]]) / μ[ϕ]
                    + Exp[μ[ϕ] τ[ϕ, pi]] Rmax;
      If[test > RS, (RS = test; tao = -τ[ϕ, pi];
        help = {RS, S, ϕ, pi, tao}), RS = RS]),
     {pi, 0, p - p / 1000, p / 1000}];
```

```
  If[help[[4]] == 0,
   (OSS = Take[OSS, -i];
    Rmax = BigR;
    i = i + 1;
    n = psi;
    ϕ = ϕmax[k, κ, δ] - n + ϕ0;
    p = p0[ϕ];
    test = m[ϕ, 0] (1 - Exp[ μ[ϕ] τ[ϕ, 0]]) / μ[ϕ]
                  + Exp[μ[ϕ] τ[ϕ, 0]] Rmax;
    help = {test, S, ϕ, 0, -τ[ϕ, 0]};
    Rmax = help[[1]];
    OSS = Prepend[OSS, help];
    BigR = OSS[[1, 1]];
    psi = psi - Δ[ϕmax[k, κ, δ]];
    n = n - Δ[ϕmax[k, κ, δ]];
   ),
   (Rmax = help[[1]];
    OSS = Prepend[OSS, help];
    n = n - Δ[ϕmax[k, κ, δ]])]
 ]];
OSG = {OSS[[1]]};
Rmax = OSG[[1, 1]];
j = 2;
Do[
 (ϕ = ϕmax[k, κ, δ] - y;
  p = p0[ϕ];
  RM = m[ϕ, p] / μ[ϕ];
  RG = RM;
  tao = 0;
  help = {RG, M, ϕ, p, tao};
```

```
  Do[(
    test = m[ϕ, pi] (1 - Exp[- μ[ϕ] τ[ϕ, pi]]) / μ[ϕ]
                    + Exp[-μ[ϕ] τ[ϕ, pi]] Rmax;
    If[test > RG, (RG = test; tao = τ[ϕ, pi];
      help = {RG, G, ϕ, pi, tao}), RG = RG]),
   {pi, p + (1 - p) / 1000, 1, (1 - p) / 1000}];
  If[OSS[[j, 1]] > help[[1]],
   (Rmax = OSS[[j, 1]]; OSG = Prepend[OSG, OSS[[j]]]),
   (Rmax = help[[1]]; OSG = Prepend[OSG, help])];
  j = j + 1
 ), {y, Δ[ϕmax[k, κ, δ]], ϕmax[k, κ, δ] - ϕ0, Δ[ϕmax[k, κ, δ]]}];
(*-------calculate optimal investment path, Oinvest------*)
v = 1;
For[v = 1, OSG[[v, 2]] == S, v = v + 1];
If[v > Length[OSG], Print["nonviable"],
 (
  For[y = v, OSG[[y, 2]] == G, y = y + 1];
  Ogrow = Take[OSG, y];
  If[MemberQ[Last[Ogrow], M],
   (Oinvest = Ogrow),
   (Oshrink = Take[OSS, -(y - 1)];
    v = 1;
    If[MemberQ[First[Oshrink], M],
     (Oshrink = {First[Oshrink]}),
     (For[v = 1, (MemberQ[Oshrink[[v]], S]
         && v < Length[Oshrink]), v = v + 1];
      Oshrink = Take[Oshrink, v])];
    Oinvest = Join[Ogrow, Oshrink])];
  (*-----calculate optimal vitality at birth, Psi0 -------*)
  remrep = {};
  For[j = 1, j < Length[Oinvest], j = j + 1,
   (remrep = Append[remrep, Oinvest[[j, 1]] / Oinvest[[j, 3]]^γ3])]
  posi = Position[remrep, Max[remrep]][[1, 1]];
  optPsi0 = Oinvest[[posi, 3]];
  PsiOinvest = Take[Oinvest, {posi, Length[Oinvest]}];
  If [MemberQ[First[PsiOinvest], S], Print["nonviable"],
```

```
(
 (*-----calculate age trajectories -------*)
 age = {0};
 help = 0;
 v = 1;
 For[v = 1, v < Length[PsiOinvest],
  (help = help + PsiOinvest[[v, 5]];
   age = Append[age, help]; v = v + 1)];
 pii = Table[PsiOinvest[[i, 4]], {i, 1, Length[PsiOinvest]}];
 xii = Table[PsiOinvest[[i, 3]], {i, 1, Length[PsiOinvest]}];
 pmaint = Table[p0[xii[[i]]], {i, 1, Length[xii]}];
 mpsi = Table [m[xii[[i]], pii[[i]]], {i, 1, Length[xii]}];
 mupsi = Table [μ[xii[[i]]], {i, 1, Length[xii]}];
 piage = Table[{age[[h]], pii[[h]]}, {h, 1, Length[xii]}];
 pOage = Table[{age[[h]], pmaint[[h]]}, {h, 1, Length[xii]}];
 mage = Table[{age[[h]], mpsi[[h]]}, {h, 1, Length[xii]}];
 muage = Table[{age[[h]], mupsi[[h]]}, {h, 1, Length[xii]}];
)])]
), {ηl, 2, 2, 10}, {ηg, 2, 2, 10}, {k, 3, 3, 1}, {κ, 0.8, 0.8, 1},
{δ, 0.1, 0.1, 2}, {b, .3, .3, 1.2}, {c, 0.01, 0.01, 0.2}];
```

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