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Directionality theory: a computational study of an entropic principle in evolutionary processes

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Analytical studies of evolutionary processes based on the demographic parameter entropy—a measure of the uncertainty in the age of the mother of a randomly chosen newborn—show that evolutionary changes in entropy are contingent on environmental constraints and can be characterized in terms of three tenets: (i) a unidirectional increase in entropy for populations subject to bounded growth constraints; (ii) a unidirectional decrease in entropy for large populations subject to unbounded growth constraints; (iii) random, non-directional change in entropy for small populations subject to unbounded growth constraints. This article aims to assess the robustness of these analytical tenets by computer simulation. The results of the computational study are shown to be consistent with the analytical predictions. Computational analysis, together with complementary empirical studies of evolutionary changes in entropy underscore the universality of the entropic principle as a model of the evolutionary process.

Keywords: evolution; entropy; fitness; computer simulation

1. INTRODUCTION

Evolutionary change in biological processes is characterized by a fundamental asymmetry. This property, which was recognized even before Darwin's time, pertains to a general tendency of morphological and phenotypic properties of a species over evolutionary time to undergo directional changes in complexity, contingent on environmental conditions. Complexity in this context can be parametrized in terms of morphometric properties such as body size. The dependency of trends in complexity on environmental constraints is illustrated by the horse clade, an example which has been extensively discussed in Forsten (1989) and Alberdi *et al.* (1995). Body size in the equid lineage during the Plio-Pleiostocene is described by a unidirectional increase in North America and a unidirectional decrease in Europe—two continents which differed significantly in climate and geographical structure during that epoch.

The problem of explaining directional trends (which, as the equid lineage indicates, may involve an increase or decrease in some property) in terms of a mechanistic model was one of the main impulses underlying Darwin's theory of evolution. The theory considered evolution as a two-step process. The first step is a variational dynamic in which new types are introduced in the population. The second step is a selective process in which the variant and the ancestral type compete for the available resources. Darwin introduced the term 'fitness' to characterize the capacity of the variant type to out-compete the ancestral type for the existing resources, and invoked this concept to explain the diversity of species and their adaptation to environmental conditions. Darwin's theory provided a mechanistic, albeit highly qualitative, explanation of the empirical observation of directional changes in morphological and phenotypic characteristics that describe the evolutionary process.

In Darwin's argument, fitness embodied primarily behavioural and morphological features. These features can assume an array of specific meanings according to ecological context: foraging ability if the subject of interest is finding resources; body size and shape if the issue is efficiency in removing or storing resources, or intimidating rivals in competition for mates; and visual acuity if the problem pertains to evading predators. When described in these contexts, fitness does not admit a simple operational description; consequently, the problem of translating Darwin's qualitative prescription into a quantitative model appeared intractable. The shift from a qualitative model to an operational scheme seems to have been first addressed by Fisher (1930), who recognized that any quantitative analysis of Darwin's theory must necessarily involve a demographic measure of competitive ability. Fisher (1930) considered the demographic variables fecundity and mortality, in view of their quantitative description, as the fundamental operational units, and inspired partly by Thomas Malthus' thesis on population growth, proposed the population growth rate, a function of the fecundity and mortality variables, as a measure of competitive ability. The significance of the population growth rate (the Malthusian parameter) as an index of Darwinian fitness rested on the Malthusian principle, whereby invasion of a mutant allele in an incumbent population is a deterministic process, which can be predicted by the population growth rate.

Since its enunciation in 1930, the Malthusian principle has become a cornerstone in both theoretical and empirical studies of population dynamics and evolutionary genetics. The Malthusian parameter now underpins most current efforts to explain the diversity of life history and to

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characterize directional change in evolutionary processes (Roff 1982; Stearns 1992; Charlesworth 1994).

Although the Malthusian tenet continues to exert a considerable influence on evolutionary studies, its significance as an explanatory model is considered questionable based on both empirical and theoretical investigations. Empirical studies of invasion in groups of vertebrates and invertebrates in Britain show that the population growth rate is not a valid predictor of invasion success (Lawton & Brown 1986). Theoretical studies of the dynamics of invasion show that the competitive interaction that underlies the process is a stochastic event, and that the Malthusian parameter does not in general predict its outcome (Demetrius & Gundlach 1999). Accordingly, the Malthusian parameter cannot provide the basis for a quantitative explanation of life-history diversity, and a parametrization of evolutionary change in natural populations. The question that now emerges is: Does there exist some function of the fecundity and mortality variables that will predict the outcome of competition between mutant and ancestral types and thus characterize Darwinian fitness?

The problem was resolved by recognizing that there are two distinct ways of counting the number of individuals in a population (Demetrius 1983). The first method simply enumerates the number of individuals in each age class and assigns the same weight, namely unity, to each group. This gives rise to what we call the 'census size'. The rate of increase of this census size is precisely the Malthusian parameter, which is given by the unique real root, denoted r, of the equation:

$$1 = \int_0^\infty \mathrm{e}^{-rx} l(x) m(x) \mathrm{d}x. \tag{1.1}$$

Here, $l(x)$ denotes the probability of surviving until age x, and $m(x)$ is the average number of offspring a female produces at age x. The product of $l(x)$ and $m(x)$, denoted by $V(x)$, is called the net-reproductive function at age x.

The second method of counting enumerates individuals in each age class and assigns weights according to the contribution that each class will make to future generations. This mode of counting gives rise to what we call an 'effective population size'. Note, however, that this effective population size is a purely demographic concept and is thus quite distinct from the effective population size used in population genetics. It was shown that the rate of increase of this demographic effective size is determined by the variability in the age at which individuals reproduce and die; a quantity we call entropy on account of its analogy with similar expressions that arise in statistical mechanics and information theory. Demographic entropy, denoted by H, is given by:

$$H = -\frac{\int_0^\infty p(x)\log(p(x))\mathrm{d}x}{\int_0^\infty xp(x)\mathrm{d}x} = \frac{S}{T}. \tag{1.2}$$

Here, $p(x) = \mathrm{e}^{-rx}V(x)$. The quantity $S = -\int_0^\infty p(x)\log(p(x))\mathrm{d}x$ is a measure of the uncertainty in the age of the mother of a randomly chosen newborn. The parameter $T = \int_0^\infty xp(x)\mathrm{d}x$ is a measure of the mean age at which individuals produce offspring (the generation time).

The function H has the dimension of inverse time and describes the rate of increase of an effective population size. The function S is a non-dimensional quantity. It is an information theoretic measure that describes the variability in the age at which individuals in the population reproduce and die. In terms of the function S, high entropy populations are described by late age of sexual maturity, small litter size and broad reproductive spread (Demetrius 2004), whereas low entropy populations are characterized by early age of sexual maturity, large litter size and narrow reproductive spread. The entropy functions H and S differ in terms of the normalizing constant, T, if generated by mutations with small effects. However, evolutionary changes in H and S are positively correlated (Demetrius 2001). Accordingly, the invasion criteria and the directionality theorems, which were established in terms of the entropy function H, will also be valid for the function S.

Entropy completely characterizes the demographic stability of the population, which is defined by the rate of decay of fluctuations in population numbers, caused by chance perturbations of the age-specific fecundity and mortality variables (Demetrius *et al.* 2004). Accordingly, entropy is positively correlated with 'demographic robustness', that is, the reduced sensitivity of any measurable property of the population with respect to perturbations in the parameters that affect its expression. Concomitantly, entropy will be negatively correlated with 'demographic flexibility', that is, the increased sensitivity of any measurable property with respect to perturbations of the individual demographic parameters. These dual properties of entropy underscore the ecological significance of this measure of fitness and its relevance in understanding the persistence and adaptation of a population under different environmental conditions.

The pertinence of entropy as a determinant of evolutionary change derives from the analytical fact that entropy predicts the outcome of competition between an invader and a resident population. This property can be qualitatively expressed in terms of the 'entropic principle' (Demetrius & Gundlach 1999; Demetrius 2001), whereby invasion dynamics in competing populations are stochastic processes whose outcomes are predicted by entropy.

The entropic criterion asserts that in 'equilibrium species', that is, species that spend the greater part of their life history in the stationary growth phase (bounded growth constraints), high entropy populations are more successful invaders than populations with low entropy. However, in 'opportunistic species', that is, populations which grow rapidly during spring and summer but are greatly reduced at the onset of winter (unbounded growth constraints), low entropy populations are the more successful invaders. When expressed in terms of criteria of demographic stability, the invasion condition asserts that in equilibrium species, increased robustness confers a selective advantage, whereas in opportunistic species increased flexibility enhances competitive success.

The entropic principle is a stochastic generalization of the Malthusian tenet. Analytical studies show that in populations of effectively infinite size, invasion is determined by the rate of increase of the census population size, which is the Malthusian parameter. Now, as the population size becomes very large, the different ways of counting by assigning weights to the different age classes converge to the same value and,

consequently, the entropic criterion for invasion based on the effective population size will reduce to the Malthusian criterion based on census size. Accordingly, the Malthusian tenet can be considered as the limit ($N \to \infty$, where N denotes population size) of the entropic principle (Demetrius 2001).

Evolutionary change is the result of a local invasion process in which new mutants are introduced in the population. Through a global selection process, the mutant types, together with the new array of genotypes generated by the Mendelian process, undergo changes in frequency subject to the ecological conditions determined by resources, predation or other external factors. Directionality theory describes the class of mathematical models that characterize this invasion–selection process. The models, which pertain to evolution in both constant environments (Demetrius 1992) and random environments (Arnold *et al.* 1994), analyse global changes in entropy as the composition of the population alters under the invasion–selection regime. The models predict that the changes in entropy are highly contingent on the ecological constraints (bounded or unbounded growth) and, hence, on the nature of the species (equilibrium or opportunistic) concerned. The evolutionary changes in entropy that ensue, as one population type replaces another, can be qualitatively expressed by the following principles (Demetrius 1992; Demetrius 1997):

(i) equilibrium species: a unidirectional increase in entropy;
(ii) opportunistic species, large population size: a unidirectional decrease in entropy;
(iii) opportunistic species, small population size: random changes of entropy.

Principle (i) asserts that, in the case of equilibrium species, evolutionary dynamics is a deterministic process. Principles (ii) and (iii) state that in the case of opportunistic species, the evolutionary trajectory is deterministic if the population size is large, and stochastic for small population size. The terms large and small in this context are not qualitative properties. They refer to quantitative entities which are functions of the demographic structure of the population (Demetrius & Gundlach 2000). Thus, the actual population numbers that define a small population size, and which will lead to random changes in entropy, will be different for small mammals and for insects, both opportunistic species, but described by quite distinct life histories.

The explanatory and predictive power of directionality theory have been documented in studies of a large variety of evolutionary phenomena including ecotypic patterns and trends in body size (Demetrius 2000), life-history distribution and the existence of mortality plateaus (Demetrius 2001) and scaling exponents in studies of allometric relations for metabolic rate (Demetrius 2003).

Empirical support for directionality theory has been provided using data from various species of plants (Ziehe & Demetrius 2005). This empirical study shows that in plants, a group of species with a high degree of phenotypic plasticity, the relation between ecological norms and directional trends in entropy is predicted by the entropic principles.

This article is concerned with the robustness of the entropic principles considered as analytically derived propositions describing the evolutionary process. We address this issue through a stochastic computational study of the dynamical system of invasion and selection. This computational study shows that the entropic principle is largely independent of the detailed ecological and genetic assumptions that underlie the analytic model. The computational study, together with the empirical analysis described in the companion article, argue for the universality of the entropic principle as important evolutionary tenet.

2. MODEL DESCRIPTION

The entropic principles are analytical statements derived from mathematical models which impose certain genetic, demographic and ecological constraints on the evolutionary process (Demetrius 1992; Arnold *et al.* 1994). The genetic assumptions, for example, were based on a diploid model and random mating with respect to both age and genotype. Ecological assumptions involve certain constraints on the density-dependent action on the age specific birth and death rates.

For the computer simulations, we consider an asexual population, a condition that excludes the Mendelian process considered in the analytical model. However, we will impose quite general conditions on the modes of growth of the equilibrium and opportunistic species. In effect, we will relax the specific kinds of density dependent constraints imposed by the analytical model. Accordingly, the analytical models and the computer simulation can be considered as complementary realizations of the evolutionary process.

The analytical model and the computational study provide two different views of the same problem and it can be very instructive to compare their results. If they differ, then it is important to investigate the reason for the discrepancy, since this often provides further insight into the structure of the problem or the assumptions that entered the analytical description. On the other hand, agreement between the results of the two approaches indicates that the entropic principle represents a largely model independent description of the underlying evolutionary process.

We will evaluate the predictions (i), (ii) and (iii) through a computer simulation of a population of genotypes that undergo mutation and selection. For this purpose, a C++ program was developed to numerically simulate populations that are based on the Leslie model. The population is divided into a number of discrete age classes, indicated by the boxes in figure 1*a*. Every year, individuals in each age class die with a probability $\mu(t)$, or otherwise move into the next higher age class with probability $1-\mu(t)$. Furthermore, an individual in age class i produces, on average, $m(i)$ offspring in the first age class. Finally, let $L(t) = \prod_{i=0}^{t} 1-\mu(i)$ denote the probability to survive from birth until the beginning of age t. Figure 1*b* shows the exact meaning of $L(t)$, $\mu(t)$ and $m(t)$ with respect to the simulation. It follows that $L(0) = 1$ and $\mu(0) = 0$, but $m(0)$ is not restricted in any way.

For the simulation, the genotype of an organism is completely defined by its survival, $L(t)$, and its fertility

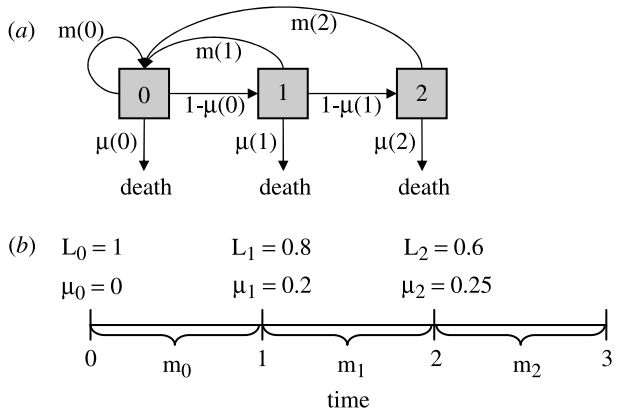

Figure 1. The population model used for the simulations is based on the Leslie model. (*a*) Life-history diagram of the population. Boxes represent age classes, $\mu(t)$ are mortality rates and $m(t)$ is the average number of offspring of an individual of age t. (*b*) Exact meaning of $L(t)$, $\mu(t)$ and $m(t)$ in this discrete time model. $L(t)$ is the probability of surviving from birth until the beginning of age t and thus $L(0)=1$ and $\mu(0)=0$.

function, $m(t)$. Since we are dealing with discrete time-steps, this reduces to two vectors of numbers. For the simulation, each individual is represented by an object that contains the survival and fertility vectors, as well as the current age of the organism. The simulation begins with a population of N wild-type individuals. Consecutive years of evolution are simulated by generating random numbers that decide whether each individual dies or survives to produce offspring.

For every iteration step (year), the following computations are performed (figure 2). For every individual of each genotype, a random number in the interval (0,1) is generated after increasing the individual's age by one. If this number is below the individual's current mortality probability (i.e. the mortality probability corresponding to the individual's new age), then the individual will die. Otherwise, it survives and produces a number of offspring specific to its age and genotype. The new individuals start with age zero. For each of these new individuals, a random number in the interval (0,1) is generated. If this random number is below the mutation rate, then this individual will be of a new mutant genotype.

The genotype of the wild-type is chosen such that its net-reproductive rate is larger than one, which results in a growing population. To test the predictions for equilibrium and opportunistic species, additional (although different) growth constraints have to be imposed. Equilibrium species are defined as populations with a roughly constant size. If the actual population size N exceeds the maximum population size (carrying capacity), an extrinsic mortality of $1-N_{\max}/N$ is applied in every iteration (year) to each individual, such that the population is reduced to the carrying capacity, $N_{\max}$. Since the realization of this mortality is again decided by a random process, the total population size, N, fluctuates around $N_{\max}$.

Opportunistic species are defined by a different life history. They expand in population size, unhindered for some time, until resources become depleted and the population collapses abruptly. The simulation mimics this behaviour. The population begins with an initial size N_{init}

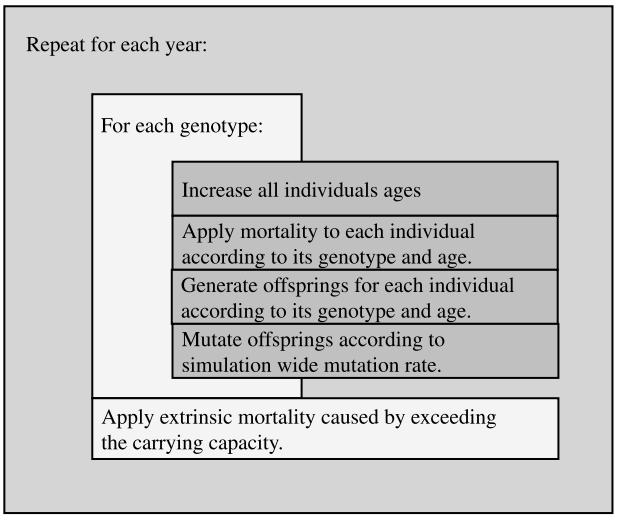

Figure 2. General overview of the simulation algorithm.

and grows exponentially for a certain period of time. After that, an extrinsic mortality $1-N_{\text{init}}/N$ is applied equally to all individuals to reduce the population size to N_{init}. In the scenario we have delineated, equilibrium species are analogous to the so-called *K*-selected organisms, while opportunistic species are analogous to *r*-selected organisms.

After each year, the dominant (most frequent) genotype of the simulation is determined and the entropy, H, is calculated using the demographic parameters for this genotype. This value for the entropy is then recorded and plotted for the whole time period of the simulation. It should be noted that this is only a monitoring process and thus the entropy is not used to manipulate the simulation in any way. Our model, however, incorporates the demographic structure of the population and can be considered a natural demographic generalization of the *r*–*K* model.

(a) *Mutations*

The ancestral type X is described by the net-fecundity function $V(x)$, and the mutant by $V^{\star}(x)$. In the analytical models which are used to represent mutations (Demetrius 1992), we assume that $V^{\star}(x)$ is a perturbation of the function $V(x)$ defined by $V^{\star}(x)=V(x)^{1+\delta(x)}$, where $\delta(x)$ is monotonic in x. The monotonicity condition is imposed to exclude mutations that could result in a net-fecundity function that is high at early and late ages, but low at intermediate age classes (which we regard as biologically unrealistic). Monotonicity derives from the notion that changes in the life-history variables are necessarily the result of enzymatic changes whose activity typically changes monotonically over time. A consequence of the monotonicity condition is that the relation between $V(x)$ and $V^{\star}(x)$ can be categorized in terms of the following four patterns.

Type 1*a* describes a mutation that corresponds to a decrease in the age of sexual maturity, and type 1*b* an increase in the age of sexual maturity. Both types are characterized by a translational shift of the net-fecundity function (figure 3). Type 2*a* and *b* correspond to mutations that cause a uniform increase or decrease in the net-fecundity functions.

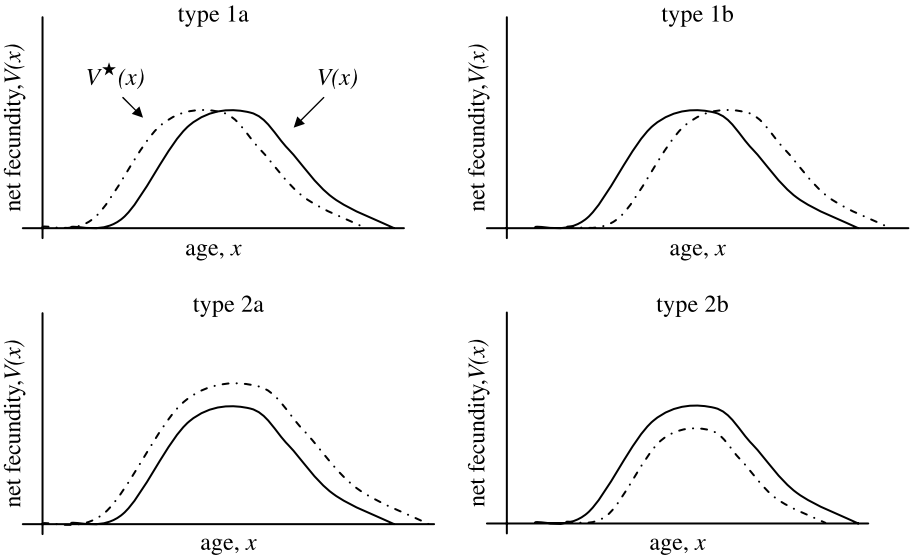

Figure 3. Possible effects of mutations on the net fecundity, $V(x)$. The net fecundity of a mutant genotype, $V^{\star}(x)$, can depart in two principal ways from the net fecundity of the ancestral type: either by a shift to earlier or later ages (type 1), or by an increase or reduction of the net fecundity (type 2).

In the computer simulation, mutations of the net-fecundity function, $V(x)$, are implemented by changing the underlying survival and fertility functions, since $V(x)^{1+\delta(x)} = l(x)^{1+\delta(x)} m(x)^{1+\delta(x)}$. For these changes, the most simple form of $\delta(x)$ was used, namely $\delta(x) =$ a random constant in the range ± 0.1.

The two categories of species that were termed equilibrium species and opportunistic species can also be distinguished more formally. This distinction can be defined in terms of a function called the reproductive potential, denoted by Φ, which is given by:

$$\Phi = \frac{\int_0^\infty p(x)\log(V(x))\mathrm{d}x}{\int_0^\infty xp(x)\mathrm{d}x} \equiv \frac{E}{T}. \qquad (2.1)$$

The quantity E is the net-reproductive function $\log(V(x))$, averaged over the probability distribution $p(x)$. The function E can assume negative or positive values depending on the distribution $V(x)$. From equations (1.2) and (2.1), we have the identity $\Phi = r - H$, so we note that

$$\Phi < 0 \Rightarrow r < H, \text{ and } \Phi > 0 \Rightarrow r > H.$$

Bounded growth corresponds to the condition $\Phi < 0$. This characterizes a population with a stationary growth rate, $r = 0$, or a growth rate which is exponentially increasing ($r > 0$), but bounded by entropy ($r > H$). The bounded growth condition is typical of what we have called equilibrium species, a species that spends the greater part of its evolutionary history in the stationary growth phase or with a population size that fluctuates around some constant value.

Unbounded growth corresponds to the condition $\Phi > 0$. This situation represents a population that is exponentially increasing with a population growth rate that exceeds entropy. The unbounded growth condition is typical of certain growth phases of opportunistic species that are subject to episodes of rapid exponential growth followed by brief periods of a decline in population numbers.

The reproductive potential, Φ, is the only point of interaction between the theoretical considerations and the simulation process. The sign of Φ decides if a genotype grows according to bounded ($\Phi < 0$) or unbounded ($\Phi > 0$) conditions. In principle, a mutation can change the sign of the reproductive potential. While this is a normal process that might happen in nature, for our simulations, we like to ensure that the population remains under the same growth conditions for the complete simulation. Whenever a mutant is generated, it is checked if it has a reproductive potential of the appropriate sign. If not, it is discarded. This control of the simulation process only ensures that the population remains under the same environmental condition. The intervention we impose does not influence the long-term behaviour of the entropy, H.

3. COMPUTATIONAL RESULTS: SELECTIVE OUTCOME

(a) *Condition I: bounded growth*

Principle (i) asserts that, in populations that spend the majority of their life history in a stationary growth phase, entropy increases under mutation and selection. This prediction is assessed by performing a long-term simulation with a population of 10 000 individuals (figure 4). The simulation begins with a homogeneous population consisting of only one genotype. A mutation rate of 10^{-5} leads to the occasional generation of rare mutants, as explained in §2. The diagram shows the entropy, H, of the most frequent (dominant) genotype in the population at a given time. At this mutation rate, only a few (up to five) different genotypes coexist in the overall population of approximately 10 000 individuals and the dominant genotype normally represents 70–100% of the population. The three different simulations shown were started with different founder genotypes. The empirical studies show that when condition I holds, rare mutants characterized by

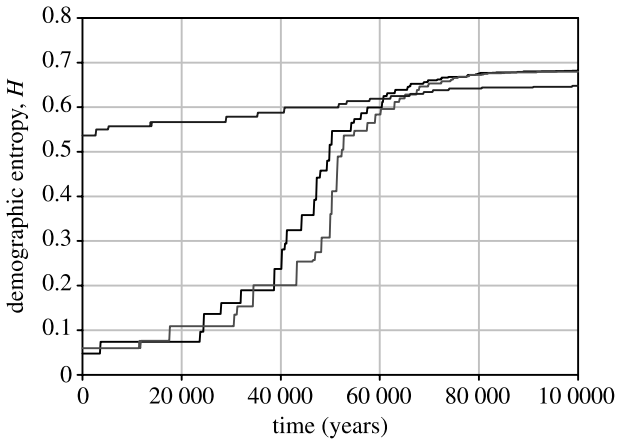

Figure 4. Computer simulation showing the change of entropy over evolutionary times for a large equilibrium species. The simulations were performed as explained in §2 with a total population size of 10 000, $\delta = 0.1$, and a mutation rate of 10^{-5} for a period of 100 000 years. The curves show the entropy of the most frequent mutant in the population. The three different curves show simulations for different starting genotypes.

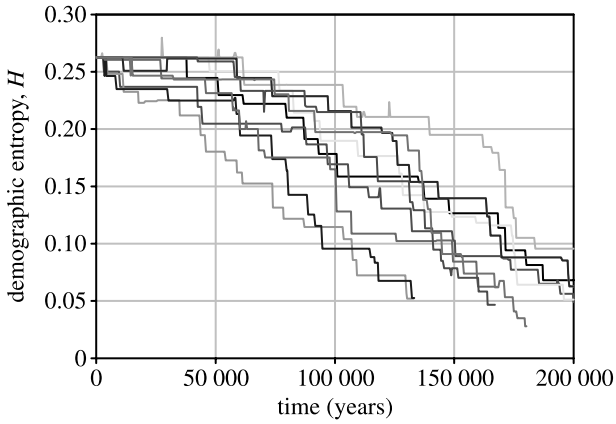

Figure 5. Computer simulation showing the change of entropy over evolutionary times for a large opportunistic species. The simulations were performed as explained in §2 with an initial population size of 200 that grows freely for 15 generations, $\delta = 0.1$, and a mutation rate of 10^{-4} for a period of 200 000 years. The curves show the entropy of the most frequent mutant in the population. The 10 different curves show different simulation runs for the same starting genotype.

a higher entropy will increase in frequency and displace the ancestral type. Hence, under bounded growth conditions, the population is described by a unidirectional increase in entropy.

(b) *Condition IIa: unbounded growth, large population*

Principle (ii) asserts that in large populations described by episodes of rapid population growth and decline (unbounded growth), entropy decreases over evolutionary time. The simulation conditions are slightly different from the bounded growth condition, and reflect the different growth trajectories of opportunistic and equilibrium species. The initial population starts with 200 individuals and can grow exponentially, without external mortality, for 15 generations. Then, a rapid population collapse is simulated by applying an external random mortality, such that the population is reduced to the initial 200 individuals. For these simulations, a mutation rate of 10^{-4} was used. The simulations show that when condition II*a* holds, the entropy decreases during evolutionary time. Rare mutants described by a lower entropy increase in frequency and displace the ancestral type. Figure 5 shows 10 repetitions of a simulation that lasted for 200 000 years. In all cases, the entropy decreases with time. In some cases, the simulation terminated because all individuals of the population died out. This problem aggravates with decreasing population sizes, and is described in more detail in §3*c*.

The previous simulations describe an evolutionary process under mutation and selection subject to two classes of ecological constraints: bounded growth (condition I) and unbounded growth for large population sizes (condition II*a*). The theory predicts that when subject to these two classes of constraints, the evolutionary process will be deterministic, leading to an increase of entropy for equilibrium species (bounded growth), and to a decrease for opportunistic species (unbounded growth).

The computational results are consistent with these predictions. However, the theory also predicts that in the case of unbounded growth and small population size, the evolutionary process should become stochastic with decreasing population size. This situation is described by condition II*b*.

(c) *Condition IIb: unbounded growth, small population*

Principle (iii) asserts that in small populations described by recurring episodes of rapid population growth and decline (unbounded growth), the long-term change in entropy is random. The initial population size used for this simulation is small and comprises only 50 individuals that can grow freely for five generations before the population re-collapses to the initial size. Mutants are generated at random intervals in the evolutionary history of the population with a probability of 10^{-4} per birth. Figure 6 shows 10 simulation runs over 10^6 years, each starting with the same genotype. The simulations show that the entropy is no longer guaranteed to decrease with time. Although the simulation time is much longer than in figure 5, there are several cases where the entropy develops randomly with time. However, there were also cases in which the entropy started to decrease and then the simulation stops because the population died out. This observation is consistent with the analytical studies described in Demetrius & Gundlach (2000). These studies indicate that the probability of extinction increases with demographic variance, the variance in the age at which individuals produce offspring. Since changes in the demographic variance and changes in entropy are negatively correlated (Demetrius 2001), we predict that the probability of extinction will increase with decreasing entropy.

The smaller the population size, the more likely the trajectory of entropy change will be described by a random walk. However, there are fundamental problems in using even smaller population sizes than we used. A small population needs to be simulated over a longer period of time because the small population size leads to a smaller

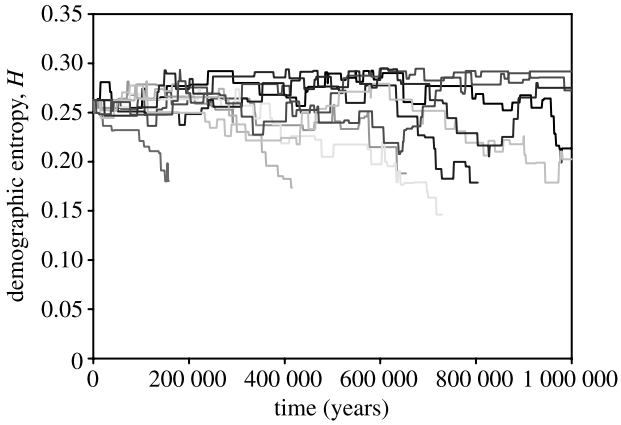

Figure 6. Computer simulation showing the change of entropy over evolutionary times for a small opportunistic species. The simulations were performed as explained in §2 with an initial population size of 50 that grows freely for five generations, $\delta = 0.1$, and a mutation rate of 10^{-4} for a period of one million years. The curves show the entropy of the most frequent mutant in the population. The 10 different curves show different simulation runs for the same starting genotype.

number of mutants that are generated per unit time. Unfortunately, at the same time, a smaller population size increases the risk that the whole population dies out because of random fluctuations in the birth and survival rates. This is a completely natural process, which effectively prevents the simulation of very small populations over extremely large time spans.

4. DISCUSSION

Darwin's theory of evolution is a mechanistic model that aims to explain the large diversity in phenotypic traits observed in natural populations in terms of processes acting at the individual level. In modern language, the theory postulates that the dynamical system, which describes the replacement of one population type by another, unfolds on two timescales. The first process, a mutation dynamic, acts on a short timescale and is the mechanism whereby new types are introduced in the population. The second process, natural selection, acts on a much longer timescale. This mechanism screens new types according to their capacity to survive and reproduce in competition with the ancestral type.

The issue of formalizing this process in terms of a dynamical model that provides a quantitative understanding of empirically observed trends in the evolutionary process has been central in theoretical evolutionary genetics for several decades. The problem can be characterized as follows: Is there some general population property that characterizes the direction of evolutionary change by natural selection?

This problem was originally addressed in the context of a general class of population genetics models, the so-called 'standard model' (Crow & Kimura 1970). These models essentially ignore the effect of ecological forces on the population dynamics. Populations are assumed to be demographically homogeneous with non-overlapping generations, and the gene frequency changes that occur under natural selection are assumed to derive from differences in the viability of genotypes. Fisher (1930), who was one of the main architects of the standard model, introduced the concept of mean fitness as a property that could quantify the direction of evolutionary change under natural selection. Fisher's fundamental theorem of natural selection, which predicts that mean fitness increases under natural selection, emerged as a unifying principle that has had considerable influence on evolutionary studies (e.g. Crow 2002). This influence derived partly from the qualitative insight the theorem yielded, and partly from Fisher's broader claim that the fundamental theorem is an analogue of the second law of thermodynamics and thus an evolutionary principle or universal natural law.

However, it is now generally conceded that the fundamental theorem of natural selection is a statement about the mean viability of genotypes subject to natural selection under constant environmental conditions (Maynard Smith 1989; Karlin 1992). Mean fitness in Fisher's model is a well-defined statistical property of a population calculated only from relative genotypic frequencies and dimensionless relative genotypic viabilities. This statistical property need not be related to the demographic property of the population as a whole. Accordingly, Fisher's theorem is not able to adequately explain the effects of changes in population properties over evolutionary times.

The class of models called directionality theory (Demetrius 1997) is a generalization of the standard model. Directionality theory studies long-term changes in the evolutionary process in terms of properties, which include both the demographic heterogeneity of the populations and the effect of environmental constraints on the demographic parameters.

Analytical studies of demographic models, based on the ergodic theory of dynamical systems, showed that the outcome of competition between a mutant and the ancestral type can be predicted in terms of a demographic parameter that was called entropy, on account of its formal analogy with concepts in statistical physics and thermodynamics (Demetrius 1997).

Analytical studies of changes in entropy under mutation and selection showed that these changes are constrained by the ecological conditions experienced by the population throughout its life history. These changes can be expressed in terms of two tenets:

(i) equilibrium species: a unidirectional increase in entropy;
(ii) opportunistic species: a unidirectional decrease in entropy for large population and random changes in entropy for small populations.

The computational study described in this article is designed to assess the robustness of the analytical results, and hence to specify the validity of principles (i) and (ii) as universal evolutionary propositions.

The computational analysis, which was intended to mimic critical features of real populations, provides strong support for the validity of the analytical results. The computational investigation of opportunistic species (that is, species subject to unbounded growth conditions) deserves further elaboration. In the case of large population size, the simulation shows that the evolutionary process is deterministic and described by a unidirectional decrease in entropy. We observe, however, that as the

population size decreases, a stochastic element enters. This is described by the random changes in entropy over evolutionary time. Thus, the simulation indicates that in the case of opportunistic species, the range of variation in the entropic changes will be highly variable. These patterns contrast sharply with our computational study of equilibrium species. In this case, our analysis indicates a unidirectional increase in entropy, which is largely deterministic and not subject to the influence of changes in population size.

The analytical result described in earlier studies, the empirical analysis described in a companion article (Ziehe & Demetrius 2005) and the computational model that this article develops suggest that the entropic principle has general validity and represents a largely model independent description of the underlying evolutionary process.

In view of this empirical and computational support, it is of interest to assess the predictive and explanatory range of directionality theory. We describe three phenomena that seemed to be intractable within the classical framework of evolutionary genetics, but which can now be elucidated in the context of directionality theory.

(i) *The evolution of body size*

Analytical studies show that evolutionary changes in entropy and body size are positively correlated (Demetrius 2000). We can therefore appeal to the entropic principles to delineate relations between certain ecological constraints and trends in body size. We predict a unidirectional increase in body size when bounded growth constraints prevail, a unidirectional decrease in body size under unbounded growth constraints and large population size and a random non-directional change when the population size is small (Demetrius 2000). The predictions underscore the empirical observation that evolutionary trends in body size are modulated by the ecological constraints that the species experience (Forsten 1989; Jablonski 1997). The predictions also explicate the empirical fact that trends over long term and trends in the short term have different statistical patterns. Evidently, the demographic condition described by small population size and unbounded growth can only prevail over short periods of time. Accordingly, we claim that random, non-directional changes in body size will only occur over short periods of a species' evolutionary history. Such patterns will be characteristic, for example, of small mammals that are opportunistic species. Large mammals, which are equilibrium species, spend the greater part of their evolutionary history with a population size that is either constant or varies around some constant value. Hence, lineages consisting of large mammals will be characterized by an increase in body size—a trend codified by Cope's rule.

(ii) *The existence of mortality plateaus*

In evolutionary models based on the Malthusian parameter as the index of Darwinian fitness, the intensity of natural selection is measured by the sensitivity of the long-run growth rate to changes in the age-specific fecundity and mortality variables (Hamilton 1966). This index of selective intensity declines with age, and entails that evolution will result in mortality rates that increase exponentially with age. This Gompertzian condition is now known to be inconsistent with empirical data for very advanced ages in several laboratory populations, and also for human populations in industrialized countries (Carey *et al.* 1992; Vaupel 1997). The analysis of the survivorship curves of large populations of medflies, nematodes and humans now indicates that a Gompertzian survivorship is not a universal property. In many instances, especially in industrialized human populations, the survivorship curve is non-Gompertzian, defined by a mortality rate that abates at advanced ages—a condition now called a 'mortality plateau'.

The evolutionary rationale for this diversity in survivorship curves can be resolved by invoking directionality theory. Darwinian fitness in the context of this theory is determined by entropy, and the intensity of selection is measured by the sensitivity of entropy to changes in the age-specific birth and death rates. This index of selective intensity is a convex function of age (Demetrius 2001). This implies that the response of entropy to changes in the life-table parameters will be relatively strong during the early and late stages of the reproductive process, but relatively weak during the intermediate stages. The evolutionary study of ageing in this model assumes that mutations have pleiotropic effects. This implies that allelic changes will not necessarily induce a phenotypic response localized at some particular age, but will generate effects that are global and expressed with varying intensity over the complete life cycle. The pleiotropic condition entails that natural selection, which acts only on individuals in the reproductive phase, may have effects on post-reproductives with an attendant change on the shape of the survivorship curve at advanced ages.

When integrated with the pleiotropic condition, directionality theory predicts that the shape of the survivorship curve will be contingent on the ecological constraints that the species endures. In equilibrium species, evolution increases entropy, whereas in opportunistic species, entropy may decrease or be subject to random, non-directional changes. Since the intensity of selection is a convex function of age, we can now predict that in equilibrium species the survivorship curve will be described by a mortality plateau, while in opportunistic species the typical condition will be a Gompertzian survivorship curve. Selection in opportunistic species has an inherent stochastic component given the effects of small size. Consequently, mortality plateaus may arise in this class of populations although the incidence of this life-history pattern will be rare.

(iii) *Scaling exponents for the metabolic rate*

The basal metabolic rate describes the rate of heat production of an organism at the resting state. Empirical studies of the relation between metabolic rate and body size show that the scaling exponent of the allometric relations is highly dependent on body size. Statistical analysis of the existing data argues against a universal value for the exponent (Dodds *et al.* 2001; White & Seymour 2003). The evidence supports a 3/4 scaling for large mammals and a 2/3 scaling in the case of small mammals and birds. Models based on an alleged fractal network have not been able to explain this variation in scaling exponents (West *et al.* 1997). A mechanism to explain the variation was proposed, based on processes of

energy transduction within biomembranes (Demetrius 2003). This class of models predicted that the metabolic rate, P, is given by $P = \alpha W^{(4\mu-1)/4\mu}$, where α denotes a proportionality constant which depends on certain physico-chemical properties of the biomembrane. The scaling exponent β is given by $\beta = (4\mu - 1)/4\mu$, where μ denotes the metabolic efficiency, the degree to which the electron transport process is correlated with ADP (adenosine diphosphate) phosphorylation.

Analytic studies of metabolic networks show that changes in metabolic rate and entropy are positively correlated (Demetrius 2003). We can thus appeal to directionality theory to predict that evolutionary changes in metabolic rate will satisfy principles similar to the directionality principles for entropy. We infer that equilibrium species (e.g. large mammals) will be described by metabolic networks which maximize metabolic rate, leading to a 3/4 rule ($\mu = 1$), whereas opportunistic species (e.g. small mammals) will be characterized by networks which minimize metabolic rates. The minimal metabolic rate, in the case of homeotherms, will be the rate that balances the rate of heat loss. This leads to a 2/3 rule for the scaling exponent, with $\mu = 3/4$.

Accordingly, the metabolic rate of organisms will be correlated with life-history distributions that are extremal states of entropy. Maximal rates are characteristic of equilibrium species whose life-history distributions maximize entropy, while minimal rates define opportunistic species whose life-history distributions minimize entropy.

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REFERENCES

Alberdi, M. T., Prado, J. L. & Ortiz-Janreguizar, E. 1995 Patterns of body size changes in fossil and living equini (Perissodactyla). *Biol. J. Linn. Soc.* **54**, 349–370.

Arnold, L., Demetrius, L. & Gundlach, V. M. 1994 Evolutionary formalism for products of positive random matrices. *Ann. Appl. Probab.* **4**, 859–901.

Carey, J. R., Liedo, P., Orozco, D. & Vaupel, J. W. 1992 Slowing of mortality rates at older ages in large medfly cohorts. *Science* **258**, 457–461.

Charlesworth, B. 1994 *Evolution in age-structured populations*. Cambridge: Cambridge University Press.

Crow, J. F. 2002 Perspective: Here's to Fisher, additive genetic variance, and the fundamental theorem of natural selection. *Evolution Int. J. Org. Evolution* **56**, 1313–1316.

Crow, J. F. & Kimura, M. 1970 *Introduction to population genetics theory*. New York: Harper & Row.

Demetrius, L. 1983 Statistical mechanics and population biology. *J. Stat. Phys.* **30**, 709–753.

Demetrius, L. 1992 Growth rate, population entropy and evolutionary dynamics. *Theor. Popul. Biol.* **5**, 220–243.

Demetrius, L. 1997 Directionality principles in thermodynamics and evolution. *Proc. Natl Acad. Sci. USA* **94**, 3491–3498.

Demetrius, L. 2000 Directionality theory and the evolution of body size. *Proc. R. Soc. B* **267**, 2385–2391.

Demetrius, L. 2001 Mortality plateaus and directionality theory. *Proc. R. Soc. B* **268**, 2029–2037.

Demetrius, L. 2003 Quantum statistics and allometric scaling of organisms. *Physica A* **322**, 477–490.

Demetrius, L. 2004 Caloric restriction, metabolic rate and entropy. *J. Geront.* **59A**, 902–913.

Demetrius, L. & Gundlach, M. 1999 Evolutionary dynamics in random environments. In *Stochastic dynamics* (ed. H. Crauel & M. Gundlach). New York: Springer-Verlag.

Demetrius, L. & Gundlach, V. M. 2000 Game theory and evolution: finite size and absolute fitness measures. *Math. Biosci.* **168**, 9–38.

Demetrius, L., Gundlach, V. M. & Ochs, G. 2004 Complexity and demographic stability in population models. *Theor. Popul. Biol.* **65**, 211–225.

Dodds, P. S., Rothman, D. H. & Weitz, J. S. 2001 Re-examination of the "3/4-law" of metabolism. *J. Theor. Biol.* **209**, 9–27.

Fisher, R. A. 1930 *The genetical theory of natural selection*. Oxford: Clarendon Press.

Forsten, A. 1989 Horse diversity through the ages. *Biol. Rev. Camb. Philos. Soc.* **64**, 279–304.

Hamilton, W. D. 1966 The moulding of senescence by natural selection. *J. Theor. Biol.* **12**, 12–45.

Jablonski, D. 1997 Body-size evolution in Cretaceous molluscs and the status of Cope's rule. *Nature* **385**, 250–252.

Karlin, S. 1992 R.A. Fisher and evolutionary theory. *Stat. Sci.* **7**, 13–33.

Lawton, J. & Brown, T. 1986 The population and community ecology of invading insects. *Phil. Trans. R. Soc. B* **314**, 607–617.

Maynard Smith, J. 1989 *Evolutionary genetics*. Oxford: Oxford University Press.

Roff, D. A. 1982 *The evolution of life-histories: data and analysis*. London: Chapman.

Stearns, S. C. 1992 *The evolution of life histories*. Oxford: Oxford University Press.

Vaupel, J. W. 1997 The remarkable improvements in survival at older ages. *Phil. Trans. R. Soc. B* **352**, 1799–1804.

West, G. B., Brown, J. H. & Enquist, B. J. 1997 A general model for the origin of allometric scaling laws in biology. *Science* **276**, 122–126.

White, C. R. & Seymour, R. S. 2003 Mammalian basal metabolic rate is proportional to body mass 2/3. *Proc. Natl Acad. Sci. USA* **100**, 4046–4049.

Ziehe, M. & Demetrius, L. 2005 Directionality theory: an empirical study of an entropic principle for life-history evolution. *Proc. R. Soc. B* **272**.

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