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Interim Report **IR-11-014**

A simple fitness proxy for structured populations with continuous traits, with case studies on the evolution of haplodiploids and genetic dimorphisms

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Approved by

Ulf Dieckmann
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June 2011

To appear in Journal of Biological Dynamics

A simple fitness proxy for structured populations with continuous traits, with case studies on the evolution of haplo-diploids and genetic dimorphisms

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Abstract

For structured populations in equilibrium with everybody born equal $\ln(R_0)$ is a useful fitness proxy for ESS and most adaptive dynamics calculations, with R_0 the average lifetime number of offspring in the clonal and haploid cases, and half the average lifetime number of offspring fathered or mothered for Mendelian diploids. When individuals have variable birth states, as is *e.g.* the case in spatial models, R_0 is itself an eigenvalue, which usually cannot be expressed explicitly in the trait vectors under consideration. In that case $Q(Y \mid X) := -\det\left(\mathbf{I} - \mathbf{L}(Y \mid X)\right)$ can often be used as fitness proxy, with $\mathbf{L}$ the next-generation matrix for a potential mutant characterised by the trait vector Y in the (constant) environment engendered by a resident characterised by X. If the trait space is connected, global univadability can be determined from it. Moreover it can be used in all the usual local calculations like the determination of evolutionarily singular trait vectors and their local invadability and attractivity.

We conclude with three extended case studies demonstrating the usefulness of Q: the calculation of ESSes under haplo-diploid genetics (I), of Evolutionarily Steady genetic Dimorphisms with a priori proportionality of macro- and micro-gametic outputs (an assumption that is generally made but the fulfilment of which is a priori highly exceptional) (II), and of ESDs without such proportionality (III). These case studies should also have some interest in their own right for the spelled out calculation recipes and their underlying modelling methodology.

Key words: Fitness, fitness proxy, haplo-diploid ESS, Evolutionarily Steady genetic dimorphism, Evolutionarily Stable genetic dimorphism, Ideal Free genetic dimorphism, Evolutionarily Steady Polymorphism, Evolutionarily Stable Polymorphism, Ideal Free Polymorphism.

0. Methodological preamble

This paper is about an efficient tool for analysing relatively complicated eco-evolutionary models. Models are mathematical structures plus interpretation rules; theories are rules for constructing and analysing models. Theoretical evolutionary biology aims to predict the properties of organisms from evolutionary considerations. Therefore we want our population dynamical model formulations to be interpretable at the level of individuals. This makes the natural framework for our discourse that of the theory of structured populations, which is fundamentally different from the classical ODE and discrete time formalisms. The only individual level parameters that are well represented in the latter formalisms are migration rates. In other aspects but few organisms satisfy the assumptions implicitly made in the construction of discrete time models with non-overlapping generations, and no organism comes close to the life histories implicitly assumed in ODE population models.

Example: *Logistic population growth*. With the individual-oriented concept of environment espoused in the theory of structured populations, the classical logistic equation with n the spatial density of individuals can be rewritten as $\mathrm{d}n/\mathrm{d}t = r(E)n$, with $E = n/K$ and $r(E) = r_0(1-E)$, to bring out that the non-constancy of r should be due to a reaction of the individuals to their surrounding environment. To delve a little deeper in this reaction, r should be decomposed into a sum of per capita birth and death rates, $r(E) = b(E) - d(E)$, as these two contributions represent radically different modes in which individual level mechanisms can affect r. We leave open the somewhat awkward question of how the E-dependence of r should be thought of as being derived from an E-dependence of b and d (this dependence easily becomes complicated since negative birth rates are not allowed). Instead we go for the microscopic perspective. To this end consider a thought experiment in which E is kept artificially constant, e.g. by harvesting or adding individuals, depending on whether n is larger or smaller than K. In that case b and d become constants. For the deaths this means that individuals die at random, for the births this means that young are born in clutches of average size c (with possibly $c = 1$) that are produced in a Poisson process with rate b/c. There exist no organisms with this life history. □

Classical ODE population models can be very useful for generating ideas about what real population models might do. However, their parameters are basically phenomenological and any relations with individual level parameters are at best fudged. This lack of sufficiently clear-cut interpretation rules to a matching biological reality makes that they cannot be considered models in the strict sense of the word and should rather be called metaphors or toy models.

Although in their immediate interpretation the epistemological status of classical discrete time population models fares but a little better than that of the ODE models, they are further saved by the fact that at equilibrium the birth rate of a structured population generally satisfies an equation equal to the equilibrium equation for the population densities of a discrete generation model with matching expected lifetime offspring numbers. Under the assumption of random mating this statement also extends to the models of classical population genetics. Not only that, also the invasion of a new type into an existing equilibrium, if looked at on a generation as opposed to a real time basis, is described by equations that match those of familiar discrete time models. So although throughout we use the language of structured population models, you may in the concrete examples first read the interpretation of the various symbols only cursorily before turning to the equations to regain your sense

of familiarity, and thereafter reread the definitions to acquaint yourself with the structured population perspective.

Dealing with the dynamics of structured population models often leads to uncomfortably heavy mathematical formalism. Luckily the subject of this paper lets us restrict ourselves to population dynamical equilibria and generation-wise argument, where the equations simplify to more familiar ones, only interpreted with a more proper attention to biological reality (Diekmann et al. 2003).

1. The concepts of invasion fitness and fitness proxies

Ecologically, fitness can be defined as the hypothetical asymptotic time-averaged rate of exponential growth $\rho(Y,E)$ which results from a thought experiment in which one lets a clone of type Y grow in an ergodic environment E (see *e.g.* Metz *et al.*, 1992; Metz, 2008). Here the term "environment" is, in the tradition of the theory of structured populations (*e.g.* Metz & Diekmann 1986; Diekmann *et al.* 2001, 2003), supposed to refer to everything, whether biotic or abiotic, outside an individual that has the potential to influence its population dynamically relevant behaviour. If, as depicted in Figure 0, the environment is determined by the attractor of a resident population, $E = E_{attr}(X)$, one speaks of invasion fitness (or invasion exponent, Rand *et al.*, 1994). Another name is dominant transversal Lyapunov exponent, or in the special case that the environment is constant, dominant transversal eigenvalue (Hofbauer and Sigmund, 1998). Invasion fitness is the main tool for dealing with long term Darwinian evolution, with mutants in the role of (prospective) invaders.

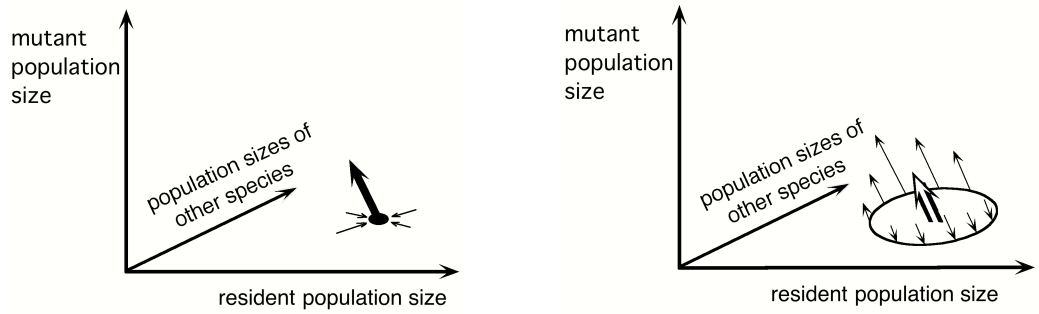

Figure 0: Illustration of the idea of transversal eigenvalue and Lyapunov exponent. In the special case of a scalar population state the transversal Lyapunov exponent can be calculated as the time average of the mutant growth rates at the community attractor.

One reason for using the adjective "hypothetical" in the opening sentence is that most populations of interest do not reproduce clonally but follow some Mendelian pattern. Part of the mental construction of hypothetical clonal individuals out of diploid Mendelian ones is to diminish the average offspring number of a biological individual by a factor one half to make up for the fact that it transmits only half of its alleles to each of its offspring. Hence, the fitness of a diploid phenotype is defined as the asymptotic time-averaged relative growth rate of the so diminished number of descendants, in a thought experiment where these descendants all have the same life history parameters as their ancestor. These parameters include mating propensities while mating opportunities are considered a component of the environment. This construction works, at least for most of the ecological scenarios considered so far, in that by means of this fitness concept one arrives at the same evolutionary predictions for phenotypes as by working through the full intricacies of Mendelian inheritance (*e.g.* Metz 2008). Be aware though that when it comes to calculating polymorphic evolutionary outcomes in the presence of genetic constraints,

and also for some complicated sexual interactions (Eshel, 1991), this shortcut no longer works, and there is no alternative but to go back to the basics and calculate the invasion fitness of alleles on loci potentially affecting the traits under consideration to arrive at the correct prediction.

Only in the simplest cases it is possible to find explicit formulas for the invasion fitness. However, for some of the simpler ecological scenarios there exist good proxies (which unfortunately often are incorrectly referred to as just fitness). With proxy we mean here a quantity that is not on all occasions quantitatively equal to fitness, yet can be substituted for it in some evolutionary calculations. In this paper we will derive one further proxy, or rather an even simpler proxy for a commonly used proxy, that should ease evolutionary calculations for a large class of complicated ecological and population genetical scenarios.

What quantities can be used as fitness proxy depends on the use one wants to make of fitness. The main use of invasion fitness is in ESS theory and adaptive dynamics, such as the calculation of Pairwise Invasibility Plots (PIPs), a convenient tool for analysing ESSes and their evolutionary stability properties for scalar traits (see Figure 1; we shall interpret the abbreviation ESS here as Evolutionarily Steady, *i.e.* uninvadable, Strategy since the definition of the ESS concept does not imply that ESSs are evolutionarily stable). For those particular uses often all one needs is a quantity that is sign equivalent to fitness: sign(*proxy*) = sign(ρ).

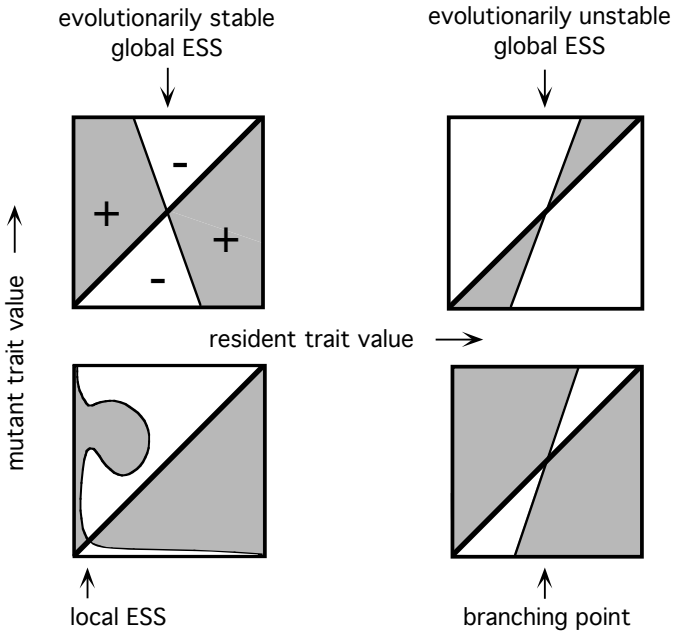

Figure 1: Pairwise Invasibility Plots: sign, as indicated in the upper left panel, of the fitness of potential mutants as a function of the mutant and the resident traits. The four panels show some alternative possible configurations, indicative of correspondingly different evolutionary phenomena. The abbreviation ESS stands for Evolutionarily Steady Strategy. The upper right panel explains our use of Steady instead of the still more common Stable as interpretation for the middle symbol in ESS.

The main type of ecological scenario where a good deal of biological detail can be incorporated and yet a good fitness proxy is available, is where the community state converges to an equilibrium point giving rise to a correspondingly non-fluctuating environment. In that case the appropriate, for easily interpretable and if all

individuals are born equal easily calculable, fitness proxy is $\ln(R_0)$, the logarithm of the average lifetime offspring number, or basic reproduction ratio, R_0.

Throughout this paper we consider only non-fluctuating resident environments. A second assumption is that the demographic parameters, and hence R_0 and ρ, are smooth in the traits (*c.f.* Ferrière and Gatto, 1995).

In general, individuals can be born in more than one possible state, as is for example the case in spatially distributed populations which have to be dealt with by taking spatial location on board as a component of the *h(eterogeneity)-state* of individuals, which then consists of a location and a physiological state, plus possibly a marker of social status, *etc., etc.*. Due to our assumption of environmental constancy the physiological state can be replaced by a proxy state consisting of age together with the state at birth. Integrating out over age gives the next-generation operator **L**. R_0 corresponds to the dominant eigenvalue of this operator. As spelling out the general argument in mathematical as opposed to heuristic terms requires the introduction of technical mathematics that is not germane to the message of this paper, we only give two examples showing the essentials in the simplest possible case. The mathematical details of the definition and calculation of R_0 in the general case may be found in Diekmann *et al.* (1990, 2003), with the latest generalisation in Thieme (2009).

Example: *Finite h-state spaces and clonal reproduction.*
The growth of a population of finite state individuals in continuous time is given by

$$\frac{\mathrm{d}}{\mathrm{d}t}N = (\mathbf{R}+\mathbf{T})N\,,$$

N the vector of spatial densities of individuals in different states. (In our present context N refers to the mutants. To keep the notational burden low we suppress dependences on the trait vector of the mutants and resident environment.) The matrices **R** and **T** are built up from per capita rates. The off-diagonal components of **T** equal the transition rates between the corresponding h-states, the diagonal components equal minus the overall rates of state transitions from the h-states minus the h-state dependent death rates. The components of **R** equal the average pro capita birth rates in dependence on the h-state of the parent split according to the h-state of the offspring. The invasion fitness ρ corresponds to the rightmost eigenvalue of **R**+**T**.

Arguing on a generation basis from births to births is possible only for constant environments. The reason for choosing the births as reference points is that usually the set of birth states is considerably smaller than the full complement of states necessary to describe how an individual passes through its life. The first components of N will refer to the birth states. To step back and forth between a population state and a birthrate based formalism we need a matrix **K** injecting the vector of birth rates into the space of changes in densities of all individuals, young and old alike:

$$\mathbf{K}^{\mathrm{T}} = \begin{pmatrix} 1 & 0 & \cdots & 0 & 0 & \cdots & \cdots & 0 \\ 0 & \ddots & \ddots & \vdots & \vdots & & & \vdots \\ \vdots & \ddots & \ddots & 0 & \vdots & & & \vdots \\ 0 & \cdots & 0 & 1 & 0 & \cdots & \cdots & 0 \end{pmatrix}.$$

As can be seen from this formula, $\mathbf{K}^{\mathrm{T}}$ projects the space of population rates onto the space of birth rates.

The Diekmann-Gyllenberg-Metz birthrate based approach to structured populations is to put individuals center-stage. In the present case the state of an

individual moves according to a Markov chain with killing, and the probability that individuals born in certain birth states at age a are alive and reside in certain states is given by the matrix $\mathrm{e}^{a\mathbf{T}}\mathbf{K}$. Hence the average birth rate at age a split out according to the birth state of the parent and that of the kids is $\mathbf{\Lambda}(a) = \mathbf{K}^{\mathrm{T}}\mathbf{R}\mathrm{e}^{a\mathbf{T}}\mathbf{K}$. This expression shows that given the mechanism as embodied in the matrices **R**, **T** and **K** it is possible to calculate the average birth rate of an individual. Hence, age and birth state together are a proxy state for the goal of calculating the average birth rates of individuals over their life.

The vector of population birth rates satisfies a matrix version of Lotka's integral equation

$$B(t) = \int_0^{t+\tau} B\big(t-a\big)\mathbf{\Lambda}(a)\mathrm{d}a + \mathbf{K}^{\mathrm{T}}\mathbf{R}\,\mathrm{e}^{(t+\tau)\mathbf{T}}\,N(-\tau)$$

which for $\tau \to \infty$ reduces to

$$B(t) = \int_0^{\infty} B\big(t-a\big)\mathbf{\Lambda}(a)\mathrm{d}a\,.$$

Substitution of an exponential trial solution $\mathrm{e}^{\rho a}U$ gives that the invasion fitness ρ can be calculated from $\mathbf{\Lambda}$ by solving characteristic equation:

$$\text{dominant eigenvalue of } \tilde{\mathbf{\Lambda}}(\rho) = 1\text{, with } \tilde{\mathbf{\Lambda}}(z) := \int_0^{\infty} \mathrm{e}^{-za}\mathbf{\Lambda}(a)\mathrm{d}a$$

and that U equals the eigenvector with eigenvalue 1 of $\tilde{\mathbf{\Lambda}}(\rho)$. The general theory of renewal equations tells that for $\tau \to \infty$ indeed $B(t)$ will grow like $\mathrm{e}^{\rho a}U$. From the fact that also $B(t) = \mathbf{K}^{\mathrm{T}}\mathbf{R}N(t)$ it follows that the ρ found in this manner also satisfies $\det(\mathbf{R}+\mathbf{T}-\rho\mathbf{I}) = 0$.

For this model

$$\mathbf{L} := \int_0^{\infty} \mathbf{\Lambda}(a)\mathrm{d}a = \tilde{\mathbf{\Lambda}}(0) \quad \text{and} \quad R_0 = \text{dominant eigenvalue of } \mathbf{L}\,.$$

Since all components of $\tilde{\mathbf{\Lambda}}(z)$ are positive and decrease with z, also its dominant eigenvalue decreases with z. Hence, ρ is positive when $R_0 > 1$ and is negative when $R_0 < 1$.

Finally, the following argument shows that this R_0 rightfully can be interpreted as an average lifetime offspring number. The average lifetime numbers of offspring by individuals born in different states equals $\mathbf{1}^{\mathrm{T}}\mathbf{L}$, where **1** is a vector that has all its components equal to 1. The natural probability distribution to average these numbers over is the stationary distribution generated by the generation process itself, *i.e.,* the right eigenvector U of **L** corresponding to R_0, normalised such that $\mathbf{1}^{\mathrm{T}}U$=1. Doing so gives $\mathbf{1}^{\mathrm{T}}\mathbf{L}U = \mathbf{1}^{\mathrm{T}}R_0U = R_0\mathbf{1}^{\mathrm{T}}U = R_0$. □

Example: *Mendelian diploids with everybody born equal, but potentially for a distinction between males and females.*

In the case of diploid hermaphrodites with but a single birth state, R_0 equals half the sum of the average numbers of offspring fathered or mothered. The factor one half again comes from the wish to define R_0 such that the outcome from naive evolutionary calculations based on this "offspring number" for individuals matches the outcome from more detailed genetically based calculations.

When the sexes are separate, the sex difference comes on top of the physiological structure. So in the simplest case the h-state equals the pair (sex, physiological state). In diploids, if everybody is born equal but for their sex, the corresponding next-generation operator is

$$\mathbf{L} = \tfrac{1}{2}\begin{pmatrix} \ell_{\mathrm{ff}} & \ell_{\mathrm{fm}} \\ \ell_{\mathrm{mf}} & \ell_{\mathrm{mm}} \end{pmatrix},$$

with ℓ_{ff} the lifetime number of daughters of a female, ℓ_{fm} the lifetime number of daughters of a male, ℓ_{mf} the lifetime number of sons of a female, and ℓ_{mm} the lifetime number of sons of a male, all for the mutant, as they happen to occur in the environmental and genetic background provided by the resident population. The simplest case is when the sex determination is independent of the locus in which the mutant differs from the resident as then we can write $\ell_{\mathrm{ff}} = p_{\mathrm{f}} f$, $\ell_{\mathrm{mf}} = p_{\mathrm{m}} f$, $\ell_{\mathrm{fm}} = p_{\mathrm{f}} m$, $\ell_{\mathrm{mm}} = p_{\mathrm{m}} m$, with m and f the numbers of offspring fathered and mothered over a lifetime, and p_{m} and p_{f} the probability of being born a male or a female. In that case $\mathbf{L}$ has rank one and

$$R_0 = \tfrac{1}{2}\left(p_{\mathrm{f}} f + p_{\mathrm{m}} m\right).$$

This result could also have been obtained more directly by observing that everybody is born stochastically equal, having exactly the same probability of being born male or female. We then get R_0 by just averaging over the possibilities.

As a curiosity we mention that when the locus on which the mutant differs has an influence on the sex determination we can still end up with the same formula by defining p_{m} and p_{f} to be the asymptotic probabilities of being born a male or a female, *i.e.*, by choosing for p_{m} and p_{f} the components of the right eigenvector U of $\mathbf{L}$, and defining m and f again as the number of offspring fathered or mothered over a lifetime, *i.e.*, $f = \ell_{\mathrm{ff}} + \ell_{\mathrm{mf}}$, $m = \ell_{\mathrm{fm}} + \ell_{\mathrm{mm}}$. Then, by using $R_0 = \mathbf{1}^{\mathrm{T}}\mathbf{L}U$, exactly the same formula for R_0 is obtained. Only the similarity of the expressions is pleasing: to calculate p_{m} and p_{f} we first have to calculate R_0.

An other matter is that when it comes to considering trait evolution we will have to account for the fact that, contrary to the situation in hermaphrodites, the developmental patterns of separate sexes are necessarily different. Hence, trait vectors will generally consist of two components, the traits of the male, Y_{m} or X_{m}, and those of the female, Y_{f} or X_{f}. In general these two sex-dependent trait vectors do not evolve independently as they are coupled by their genetic covariance (or mutational covariance, depending on whether one focuses on intermediate term evolution starting with enough accessible genetic variation, or on evolution starting from a genetically impoverished population or going on for so long that it runs out of the initial variation). Only in the extreme case that the covariances between male and female traits are all zero the female and male co-evolve as if they were separate species. In the other extreme case, $X_{\mathrm{m}} = G(X_{\mathrm{f}})$, the standing and mutational variation in the male and female trait vectors is fully correlated, and we can speak of a single evolutionary trait vector, expressed differently in males and females (except when G is equal to the identity, in which case we have just a single trait vector). □

In general, that is, if they do not reduce to a matrix with some special convenient structure, next-generation operators do not allow explicit expressions for their dominant eigenvalue. Hence, there is a need for a next layer of proxies, this time for R_0.

The main theorem of the paper, telling how the characteristic polynomial of the next-generation matrix evaluated at 1 can be used to decide about global uninvadability, is stated and proved in section 3. In section 2 we sketch the essential geometrical nature of the result for the special case of 2×2 matrices, as this is the only case allowing neat pictures. In section 4 we summarise local calculation recipes which can *i.a.* be used for the determination of (local properties of) Evolutionarily Singular Points, that is, points X where $[\partial\rho/\partial Y](X,E_{\text{attr}}(X)) = 0$ (the derivative being taken for the first argument of ρ, written as Y when ρ was first introduced, after which the resulting function is evaluated at $(X,E_{\text{attr}}(X))$). These two lines of argument culminate in Section $4\frac{1}{2}$ in the introduction of the new fitness proxy $Q(Y \mid X)$. In sections 5 to 7 we present three case studies of how the abstract results can be put to good use.

2. The R_0–criterion for invasion and its extension for nonnegative 2×2 matrices

The result that we are after is basically topological in nature. In this section we lay bare the underlying structure for the case of 2×2 matrices, where everything can easily be visualised. This also allows us to show how the general fitness proxy to be described in the next section can be seen as a natural extension of the $R_0 < 1$ non-invasion criterion for Leslie matrices. The general result is described in section 3. The proof there makes no use of the ideas developed in this section. If you are mainly interested in applications or in the general proof, you may just as well directly move to that section. This section is only meant for those who get motivated by seeing how different results connect.

To keep our arguments relatively uncluttered we shall couch them in the form of the derivation of estimates for the sign of the invasion fitness for simple discrete time models in matrix form. The insights thus obtained apply without change to estimating the sign of $\ln(R_0)$ in more complicated models that allow the next-generation operator of the linearised mutant dynamics to be represented as a matrix.

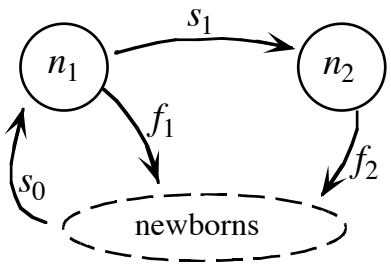

Figure 2: Simple life history used to illustrate how R_0 can be interpreted as 1-P(1).

Consider the life history graphically represented in Figure 2, with the survival probabilities $0 \le s_0, s_1 \le 1$ and fertilities $f_1, f_2 \ge 0$, determined by the environment set by the community as well as by a potentially evolving trait vector. (To avoid clutter, we shall in this section hide the ever-present arguments $(Y \mid X)$.) Time is supposed to run in steps and the indices 1 and 2 of the population sizes n_i refer to age expressed in number of time steps. The population recurrence corresponding to this life history is

$$N' = \mathbf{A}N \quad \text{with} \quad N = \begin{pmatrix} n_1 \\ n_2 \end{pmatrix}, \qquad \mathbf{A} = \begin{pmatrix} s_0 f_1 & s_0 f_2 \\ s_1 & 0 \end{pmatrix}.$$

The characteristic equation for a mutant in a constant environment set by a resident community is

$$P(\lambda) := \lambda^2 - f_1 s_0 \lambda - f_2 s_1 s_0 = 0,$$

and

$$\rho = \ln(\lambda_d),$$

λ_d the corresponding dominant eigenvalue (*i.e.* $\lambda_d \geq |\lambda_i|$). There is only a single birth state, so

$$R_0 (= \mathbf{L}) = f_1 s_0 + f_2 s_1 s_0.$$

By rewriting the characteristic equation as

$$1 = f_1 s_0 \lambda^{-1} + f_2 s_1 s_0 \lambda^{-2}$$

it is easy to see (Figure 3) that

$$R_0 \gtrless 1 \quad \Leftrightarrow \quad \rho \gtrless 0.$$

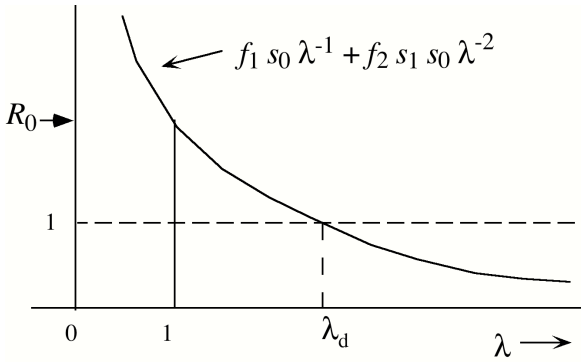

Figure 3: Relation between R_0 and λ_d fot the life history of Figure 1.

In this example

$$P(1) = 1 - R_0.$$

Therefore

$$P(1) \gtrless 0 \quad \Leftrightarrow \quad \rho \lesseqgtr 0.$$

However, unfortunately the latter result does not extend to more general models lacking the crucial zero in the matrix **A**.

Figure 4 depicts the usual criteria for when the modulus of the dominant eigenvalue of a 2×2 matrix is smaller than 1. If we indicate in the same picture the realisable values of the trace and determinant for 2×2 Leslie matrices (Figure 5), it becomes clear why for such matrices this complicated combination of criteria can be replaced by the simple R_0-criterion.

If we then also look which regions in the (trace , det)-plane can be realised by general non-negative matrices (Figure 6), it becomes clear why the $P(1) > 0$ criterion does not extend to general non-negative 2×2 matrices. The trouble comes from the right upper region between the line $P(1) = 0$ and the parabola det = $\frac{1}{4}$ trace^2 in which also the second eigenvalue is larger than one.

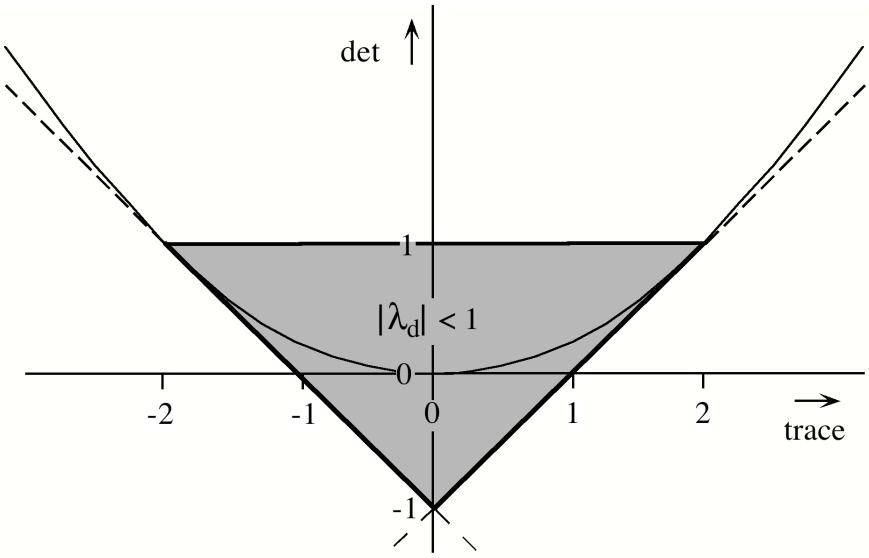

Figure 4: The values of the trace and determinant of a 2×2 matrix for which its dominant eigenvalue is smaller than 1. The parabola separates the regions with real and with complex eigenvalues. On the line det = trace -1 a real eigenvalue crosses 1, on the line det = - trace -1 a real eigenvalue crosses -1, and for complex eigenvalues crossing the line det = 1 corresponds to their modulus crossing 1. Some further details about the location of the real eigenvalues are given in Figure 7.

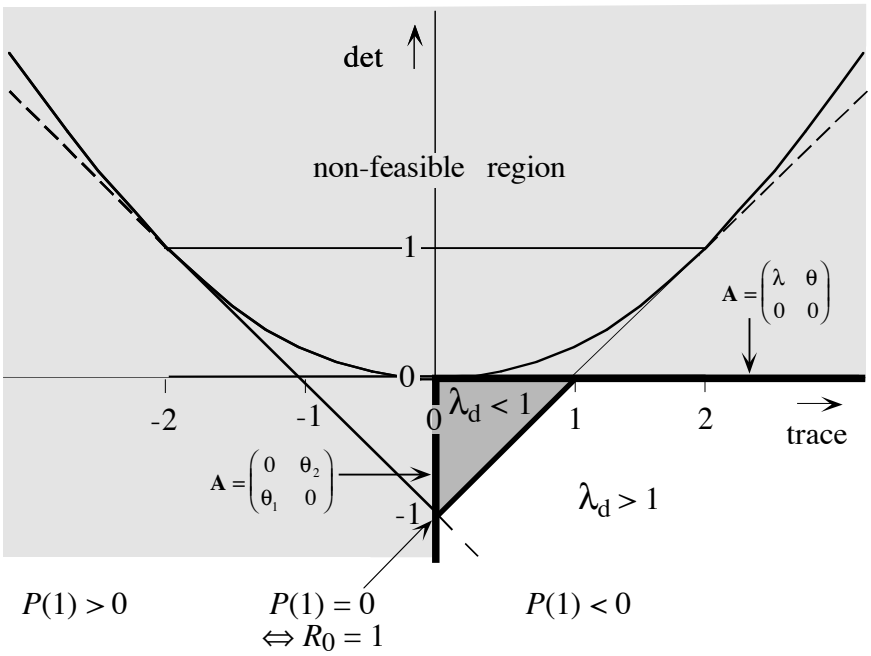

Figure 5: The values of the trace and determinant that can be realised by 2×2 Leslie matrices **A**. The formulas correspond to the generic form of **A** on the curve indicated by the arrow, with λ and (the) $\theta(_i)$ free parameters. Note that $P(1) = 1 - \text{trace} + \det$. For Leslie matrices $\begin{pmatrix} a & b \\ c & 0 \end{pmatrix}$, P (1) = 1 – a – bc.

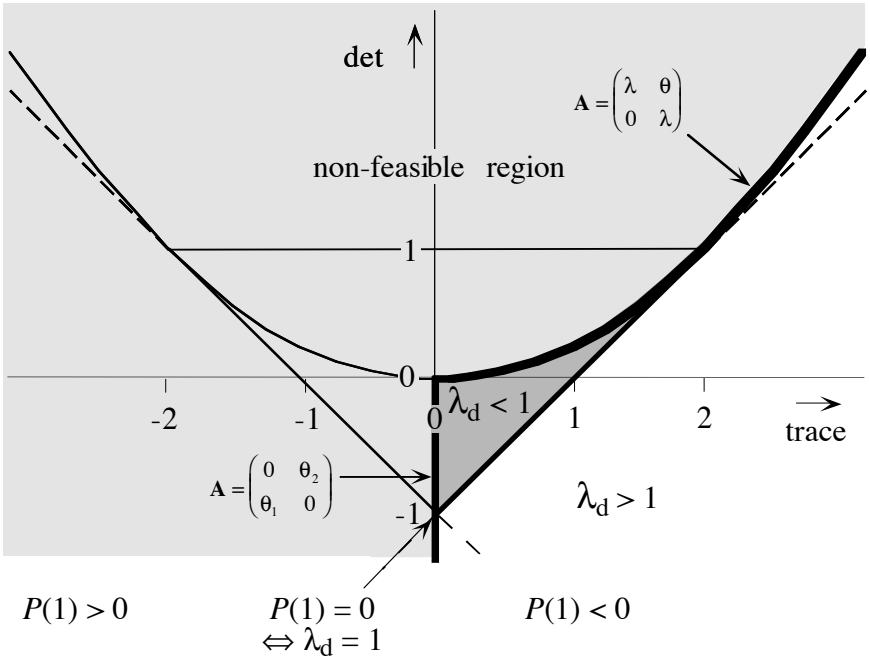

Figure 6: Stability region for a general non-negative 2×2 matrix **A**. The formulas correspond to the generic form of **A** on the curve indicated by the arrow, with λ and (the) $\theta(_i)$ free parameters.

Figure 6 also suggests how one may still put the $P(1) > 0$ criterion to good use even when the underlying population dynamics leads to more general 2×2 matrices as basis for the calculation of the needed invasion fitnesses: any resident, including any prospective ESS, has invasion fitness zero. Hence, any mutant equal to the resident finds itself on the line segment from (trace,det) = (0,-1) to (trace,det) = (2,1). We shall assume first that at the resident phenotype $\text{trace}^2 \neq 4\,\det$. (This condition is guaranteed when for the resident **A** is irreducible.) Assume now that the strategies under consideration are characterised by a trait vector from some $\mathbb{R}^n$. If the life history parameters depend continuously on the trait vector, any continuous curve in trait space will map to a continuous curve in (trace,det)-plane. If for no alternative strategy the corresponding point in (trace,det)-plane ever lies in the region $P(1) \leq 0$, then the troublesome region can never be reached by following a continuous path in trait space starting from the resident. Hence, no strategy can invade that is connected to it by a continuous path in trait space. The conclusion is that if for all strategies but a prospective ESS $P(1) > 0$, then no strategy that can be connected continuously to this prospective ESS can invade. Hence, under these conditions if the trait space is connected the prospective ESS is indeed uninvadable.

Now consider the case where for the resident $\text{trace}^2 = 4\,\det$. Since the population is at equilibrium, **A** then has the form $\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$ instead of the more general form indicated in Figure 6 for matrices with $\text{trace}^2 = 4\,\det$. As an example you may think of a population living in two patches with the strategy parameter being the migration rate between those patches and no migration for the prospective ESS. In that case the previous argument goes through on the condition that close to the prospective ESS det < 1, or equivalently trace < 2.

In the following section we shall extend the above result for 2×2 matrices to general $n \times n$ matrices. As a preparation Figure 7 shows more details of how in the 2×2

case the location of the characteristic polynomial, and hence of its roots, changes with trace and det.

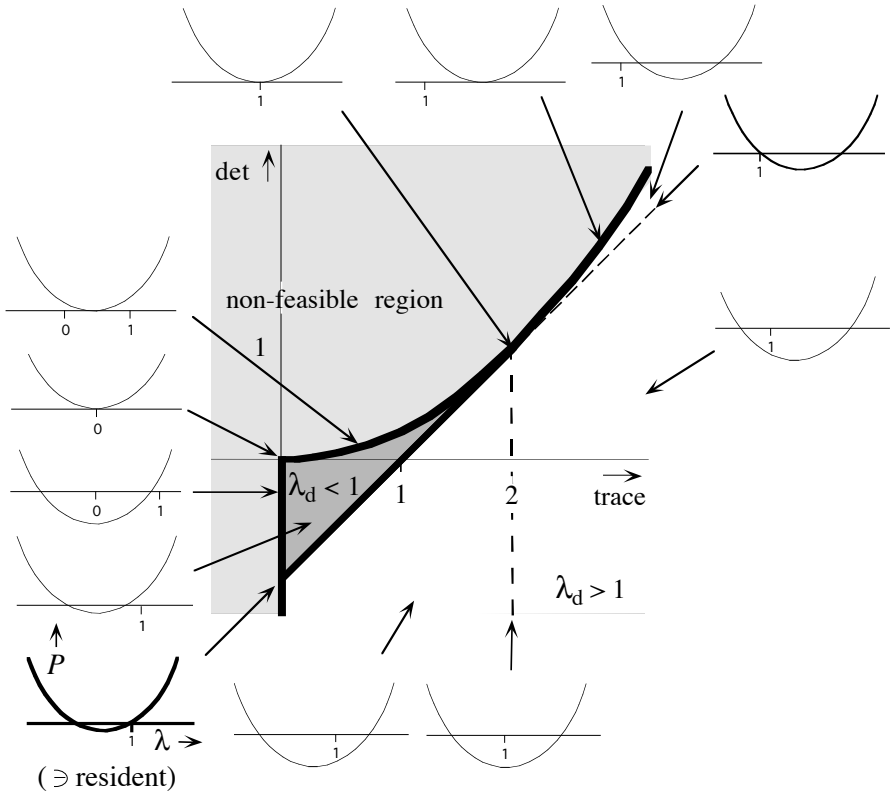

Figure 7: Location of the characteristic polynomial in dependence on trace and det.

3. The $P(1) > 0$ criterion for general $n \times n$ matrices

Let $P(\lambda; Y|X) := \det(\lambda \mathbf{I} - \mathbf{L}(Y|X))$ denote the characteristic polynomial of the next-generation matrix of the linearised dynamics of a Y mutant in an X resident community (expressed so that the leading coefficient is positive).

Theorem: The resident X is uninvadable if (i) the demographic parameters depend continuously on the trait, and (ii) the trait space is connected, and (iii)

$$P(1; Y|X) > 0 \text{ for all } Y \neq X,$$

and (iv) $\frac{\partial P}{\partial \lambda}(1; X|X) \neq 0$ (which is always the case if $\mathbf{L}(X|X)$ is irreducible) or $\frac{\partial P}{\partial \lambda}(1; X|X) = 0$ and $R_0 < 1$ for Y close to X (the latter condition is guaranteed *e,g.* by $\frac{\partial^2 P}{\partial \lambda^2}(1; X|X) \neq 0$ and $\frac{\partial P}{\partial \lambda}(1; Y|X) > 0$ for Y close to X).

On the other hand if

$$P(1; Y|X) < 0 \text{ for some } Y,$$

then that Y can invade X.

Proof: Invasion fitness and R_0 are continuous in the demographic parameters and hence in the traits. R_0 of the resident equals 1. By assumption all alternative strategies can be reached from the resident by following a continuous path through trait space. Therefore, only values of R_0 can occur that can be reached through bifurcations compatible with R_0 being the dominant eigenvalue of a non-negative matrix and the assumption that $P(1; Y|X) > 0$. The existence of such an eigenvalue is guaranteed by the Perron-Frobenius theorem. The assumptions of non-negativity make the dominant eigenvalue non-negative real and hence a continuous function of the demographic parameters and of the traits. (Eigenvalues are smooth functions except for an indeterminacy where they cross; given that the dominant eigenvalue is always real it is necessarily continuous, although not smooth, over such a crossing.) The assumption that $P(1; Y|X) > 0$ makes that the dominant eigenvalue is not allowed to move continuously to above 1 in the manner indicated in the lower left panel of Figure 8.
For the second part, if $P(1; Y|X) < 0$ for some Y there must be some real $\lambda > 1$ such that $P(\lambda; Y|X) = 0$. Since this λ is an eigenvalue and since $R_0(Y|X)$ is dominant, either $R_0(Y|X) = \lambda > 1$ or $R_0(Y|X) > \lambda > 1$. □

(For general polynomials P with positive leading term there is also a way to produce a positive real root above 1 from a starting situation where there are no such roots while all the time keeping $P(1; Y|X) > 0$, to wit through the bifurcation depicted in the lower right panel of Figure 8. However, for non-negative matrices this bifurcation is ruled out by observing that just before such a bifurcation would occur there have to exist complex eigenvalues with modulus larger than the non-negative real dominant eigenvalue, which would contradict its dominance.)

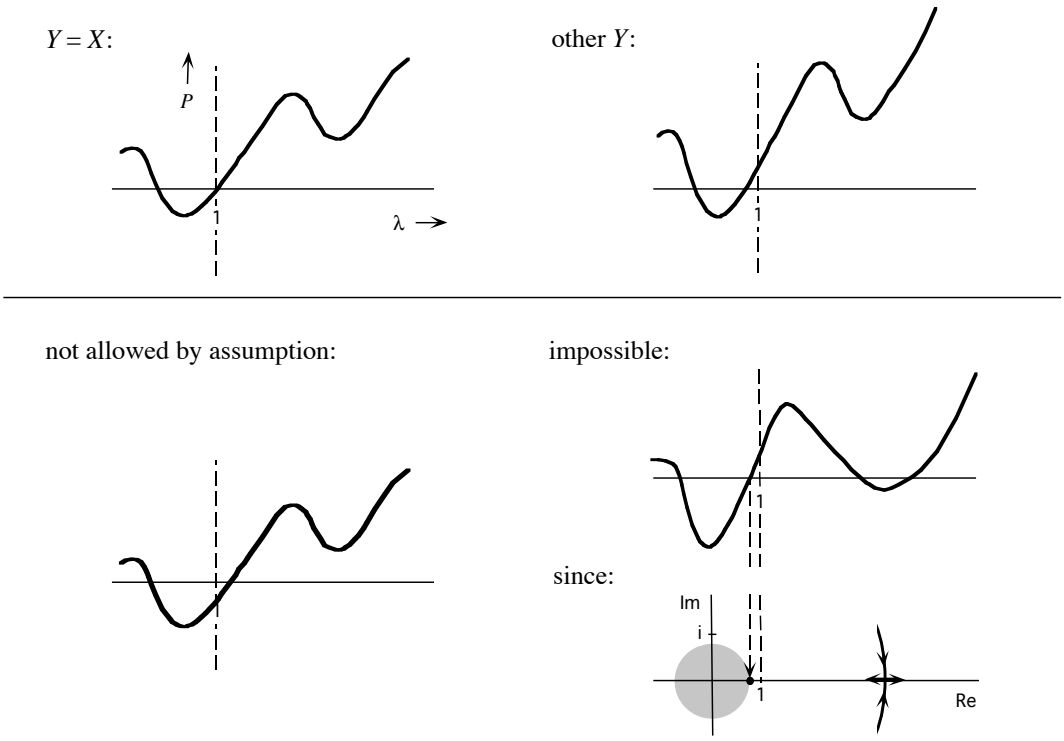

Figure 8: Starting from a situation where the dominant eigenvalue equals 1 certain bifurcations of the root pattern of the characteristic polynomial of a positive matrix are excluded by the assumption that $P(1; Y|X) > 0$.

In the next section we shall consider in more detail the toolbox for higher dimensional trait spaces, which is based largely on local calculations. Here we only discuss the implications of the above Theorem for the drawing of PIPs.

For the calculation of PIPs one can largely concentrate on solving for Y in $P(1; Y|X) = 0$. See Figure 9. If one in addition knows some point in the (X,Y)-plane for which the invasion fitness is negative, then the invasion fitness is also negative in all points that connect to this point by a continuous path that does not cross one of the solution curves of $P(1; Y|X) = 0$. As soon as such a curve is crossed, the fitness changes from negative to positive. Similarly, if one knows a point for which invasion fitness is positive, then invasion fitness is also positive in all points that connect to this point by a continuous path that does not cross one of the solution curves of $P(1; Y|X) = 0$. Since in this case also some other eigenvalue may pass through 1 when a solution curve is crossed, fitness may or may not change sign there.

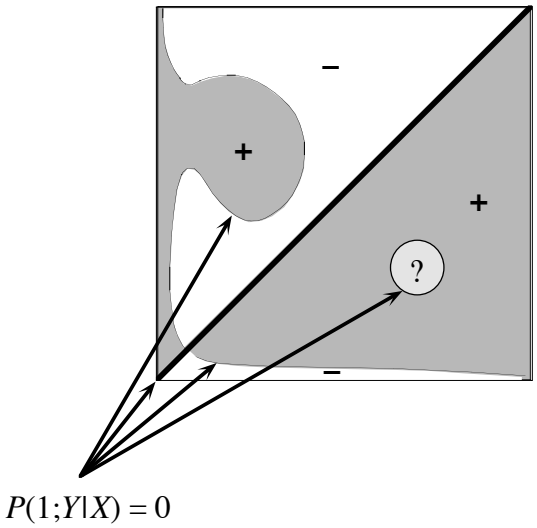

Figure 9: The information given by the solutions of the equation $P(1; Y|X) = 0$ in the (X,Y)-plane about the signs of the invasion fitness.

4. Local theory

The general theory of Section 3 is dependent only on the connectivity of the trait space, but its application is subject to constraints. In particular, simple graphical tools like PIPs require the traits to be scalar. Therefore for higher dimensions, and for most numerical work, local calculations dominate the trade.

As far as we are aware, the first authors to derive local invadability properties directly from the characteristic polynomial of the linearised invasion dynamics were Taylor and Bulmer (1980). Their calculations were taken further by Courteau and Lessard (2000). As these techniques are extremely useful in applications we summarise here their extension to higher dimensional trait spaces.

To keep the calculations simple we shall throughout this section assume that the next generation matrix is always irreducible.

Let

$$s(Y|X) := \rho(Y|E_{\text{attr}}(X)).$$

Points in trait space where $[\partial s/\partial Y](Y|X) = 0$, are called Evolutionarily Singular (Metz *et al*. 1996, Geritz *et al*., 1998). Examples are all the special points indicated in Figure

1. The goal of this section is to calculate ESPs and to derive indicators for their local invadability and attractivity from the characteristic polynomial.

As before we assume that $E_{\mathrm{attr}}(X)$ does not fluctuate. Since all calculations below are local, it pays first to write out a number of relations that hold good locally for the characteristic polynomial of the next-generation matrix and for invasion fitness and R_0:

$$P\big(R_0(Y\,|\,X);Y\,|\,X\big)=0\,,\qquad \big[\partial P/\partial\lambda\big]\big(R_0(Y\,|\,X);Y\,|\,X\big)>0\,,$$

with $P(\lambda;Y\,|\,X):=\det\big(\lambda\mathbf{I}-\mathbf{L}(Y\,|\,X)\big)$, and

for Y sufficiently close to X,

$$s(Y|X)\approx\frac{\ln(R_0(Y\,|\,X))}{T_{\mathrm{r}}(X\,|\,X)}\,,$$

in particular

$$\frac{\partial s}{\partial Y}(X\,|\,X)=-\frac{\partial s}{\partial X}(X\,|\,X)=\left[\frac{\partial R_0/\partial Y}{T_{\mathrm{r}}}\right](X\,|\,X)$$

and, when $\dfrac{\partial s}{\partial Y}(X\,|\,X)=0$,

$$\frac{\partial^2 s}{\partial Y\partial Y^{\mathrm{T}}}(X\,|\,X)=\left[\frac{\partial^2 R_0/(\partial Y\partial Y^{\mathrm{T}})}{T_{\mathrm{r}}}\right](X\,|\,X)\,,\quad \frac{\partial^2 s}{\partial X\partial X^{\mathrm{T}}}(X\,|\,X)=\left[\frac{\partial^2 R_0/(\partial X\partial X^{\mathrm{T}})}{T_{\mathrm{r}}}\right](X\,|\,X)$$

with $T_{\mathrm{r}}(Y|X)$ the mean age at reproduction of Y-individuals in $E_{\mathrm{attr}}(X)$, $T_{\mathrm{r}}(Y|X)$ $=\left[\int_0^\infty a\;V^{\mathrm{T}}\mathbf{\Lambda}(a)\;U\;\mathrm{d}a\right](Y\,|\,X)$, $\big[\mathbf{\Lambda}(a)\big](Y\,|\,X)$ the matrix of average pro capita birth rates at age a of a Y-individual in $E_{\mathrm{attr}}(X)$ differentiated according to birth states, and U and V the right and left eigenvectors of the next-generation matrix $\mathbf{L}=\int_0^\infty\mathbf{\Lambda}(a)\,\mathrm{d}a$, co-normalised such that $1^{\mathrm{T}}U=1$, $V^{\mathrm{T}}U=1$.

(Durinx *et al.*, 2008). (Note that when X is a column vector, $[\partial s/\partial Y](Y\,|\,X)$ is a row vector and $[\partial^2 s/(\partial Y\partial Y^{\mathrm{T}})](Y\,|\,X)$ and $[\partial^2 s(Y\,|\,X)/(\partial X\partial X^{\mathrm{T}})](Y\,|\,X)$ are square matrices.) Moreover, since

$$s(X\,|\,X)=0\quad\text{and}\quad R_0(X\,|\,X)=1\,,$$

$$\frac{\partial s}{\partial X}(X\,|\,X)=-\frac{\partial s}{\partial Y}(X\,|\,X)\quad\text{and}\quad\frac{\partial R_0}{\partial X}\big(X\,|\,X\big)=-\frac{\partial R_0}{\partial Y}\big(X\,|\,X\big).$$

By differentiating through the equality $P\big(R_0(Y\,|\,X);Y\,|\,X\big)=0$ one gets

$$\frac{\partial P}{\partial\lambda}\big(R_0(Y\,|\,X);Y\,|\,X\big)\frac{\partial R_0}{\partial Y}(Y\,|\,X)+\frac{\partial P}{\partial Y}\big(R_0(Y\,|\,X);Y\,|\,X\big)=0\,.$$

Hence, from now on without explicit arguments,

$$\frac{\partial R_0}{\partial Y}=-\left(\frac{\partial P}{\partial\lambda}\right)^{-1}\frac{\partial P}{\partial Y}\,.$$

Therefore evolutionarily singular points, primarily characterised by $\left[\partial s/\partial Y\right](X \mid X) = 0$, can alternatively be characterised not only by $\left[\partial R_0/\partial Y\right](X \mid X) = 0$, but also by

$$\frac{\partial P}{\partial Y}(1; X \mid X) = 0 .$$

The latter characterisations should of course be appropriately modified when the ESP is partially determined by constraints, see e.g. Intriligator (1971). As otherwise we would have to repeat it many times, please insert the last phrase where needed in all the following deliberations.

Further differentiating through the characteristic equation gives:

$$\frac{\partial^2 R_0}{\partial Y \partial Y^{\mathrm{T}}} = -\left(\frac{\partial P}{\partial \lambda}\right)^{-1}\left[\frac{\partial^2 P}{\partial \lambda \partial Y}\frac{\partial R_0}{\partial Y} + \frac{\partial^2 P}{\partial Y \partial Y^{\mathrm{T}}}\right],$$

and

$$\frac{\partial^2 R_0}{\partial X \partial X^{\mathrm{T}}} = -\left(\frac{\partial P}{\partial \lambda}\right)^{-1}\left[\frac{\partial^2 P}{\partial \lambda \partial X}\frac{\partial R_0}{\partial X} + \frac{\partial^2 P}{\partial X \partial X^{\mathrm{T}}}\right],$$

which at singular points X, since there $\left[\partial R_0/\partial Y\right](X \mid X) = \left[\partial R_0/\partial X\right](X \mid X) = 0$, reduces to

$$\frac{\partial^2 R_0}{\partial Y \partial Y^{\mathrm{T}}}(X \mid X) = -\left[\left(\frac{\partial P}{\partial \lambda}\right)^{-1}\frac{\partial^2 P}{\partial Y \partial Y^{\mathrm{T}}}\right](1; X \mid X),$$

and

$$\frac{\partial^2 R_0}{\partial X \partial X^{\mathrm{T}}}(X \mid X) = -\left[\left(\frac{\partial P}{\partial \lambda}\right)^{-1}\frac{\partial^2 P}{\partial X \partial X^{\mathrm{T}}}\right](1; X \mid X) .$$

Hence, a singular strategy X is uninvadable if the symmetric square matrix

$$-\frac{\partial^2 P}{\partial Y \partial Y^{\mathrm{T}}}(1; X \mid X) \text{ is negative definite,}$$

and only if it is non-positive definite.

Two further properties of interest for evolutionary singular points are strong convergence stability, and mutual invadability of at least some neighbouring strategies (needed for the build-up of a polymorphism).

Strong convergence stability amounts to attractivity of the singular point whatever the mutational covariance matrix for the deterministic evolutionary dynamics that results when the mutational steps are not only rare but also very small and time is rescaled accordingly (Leimar, 2001, 2005, in press). In the case of one-dimensional trait spaces attractivity of the singular point is independent of the mutational variance and the condition for strong convergence stability reduces to the usual condition for Continuous Stability, Eshel, 1983; Taylor, 1989; Geritz et al, 1998. Leimar's (l.c.) result is that in clonally reproducing organisms, haploids and diploids (but not in haplo-diploids, see Section 5) X is strongly convergence stable if the symmetric matrix $\left[\partial^2 s/(\partial X \partial X^{\mathrm{T}}) - \partial^2 s/(\partial Y \partial Y^{\mathrm{T}})\right](X \mid X)$ is positive definite and only if it is non-negative definite. Hence, under the given restrictions on the reproductive system, an evolutionarily singular strategy X is strongly convergence stable if the symmetric matrix

$$-\left[\frac{\partial^2 P}{\partial X \partial X^{\mathrm{T}}}-\frac{\partial^2 P}{\partial Y \partial Y^{\mathrm{T}}}\right](1;X\,|\,X) \text{ is positive definite.}$$

and only if it is non-negative definite.

The criteria for mutual invadability are different in on the one hand the clonal and haploid Mendelian and on the other hand the diploid Mendelian case. In the clonal and haploid case there exist pairs of mutually invadable strategies around a singular strategy X if the matrix $\left[\partial^2 s/(\partial X \partial X^{\mathrm{T}})+\partial^2 s/(\partial Y \partial Y^{\mathrm{T}})\right](X\,|\,X)$ is negative definite and only if it is non-positive definite, or equivalently if the symmetric matrix

$$-\left[\frac{\partial^2 P}{\partial Y \partial Y^{\mathrm{T}}}+\frac{\partial^2 P}{\partial X \partial X^{\mathrm{T}}}\right](1;X\,|\,X) \text{ is negative definite,}$$

and only if it is non-positive definite. In the diploid case this is the case if the matrix $\left[\partial^2 s/(\partial X \partial X^{\mathrm{T}})\right](X\,|\,X)$ is positive definite and only if it is non-negative definite (van Dooren, 2006), or equivalently if the symmetric matrix

$$-\frac{\partial^2 P}{\partial X \partial X^{\mathrm{T}}}(1;X\,|\,X) \text{ is positive definite,}$$

and only if it is non-negative definite.

4½. The fitness proxy Q

The preceding observations can be summarised in the statement that

$$Q(Y\,|\,X) := -P(1;Y\,|\,X)$$

can act as fitness proxy in all local calculations related to evolutionarily singular points. If the trait space is connected, Q can also act as fitness proxy for the checking of global uninvadability.

In the next sections we present three case studies demonstrating the usefulness of Q. In addition, each of these studies has some interest in its own right.

5. Case study I: ESSes in haplo-diploids

Although the opposite possibility is not excluded by rules of logic alone, we shall for definiteness take the hymenopteran situation as reference and assume that females are diploid and males are haploid. In that case only the female reproductive output needs to be discounted with $\frac{1}{2}$. We allow any physiological structure, and only assume that everybody is born equal but for the sex difference, and mating is random. These assumptions lead to the next-generation matrix

$$\mathbf{L}=\begin{pmatrix} \frac{1}{2}f_{\mathrm{f}}\left(Y\middle|X\right) & m\left(Y\middle|X\right) \\ \frac{1}{2}f_{\mathrm{m}}\left(Y\middle|X\right) & 0 \end{pmatrix}$$

with f_{f} : expected lifetime number of female offspring of a female,
f_{m} : expected lifetime number of male offspring of a female,
m : expected lifetime number of (female) offspring of a male.

Of these quantities f_f and f_m depend only on the female traits and m only on the male traits.

As is usual in models with more than one birth state, with some spatial models with a good amount of symmetry as only exception, the expression for R_0

$$R_0 = \tfrac{1}{4} f_\mathrm{f}(Y \mid X) + \tfrac{1}{4}\sqrt{f_\mathrm{f}^2(Y \mid X) + \tfrac{1}{2} m f_\mathrm{m}(Y \mid X)}$$

does not excel in transparency.

Since **L** has the structure of a Leslie matrix,

$$Q(Y \mid X) = \tfrac{1}{2}\left[f_\mathrm{f} + f_\mathrm{m} m\right](Y \mid X) - 1$$

is a full fitness proxy, without any need for restrictions on the nature of the trait space. The quantity

$$T_\mathrm{f} = Q + 1 = \tfrac{1}{2}\left(f_\mathrm{f} + f_\mathrm{m} m\right)$$

allows a nice direct interpretation as the average number of alleles transmitted from female to female, direct or through a male vector. (The reason for our choice of the notation T_f is that similarly constructed quantities were introduced with this notation by Roberts and Heesterbeek (2003) and Heesterbeek and Roberts (2007) under the name of Type reproduction number.)

Evolutionarily singular strategies can be calculated by setting

$$\frac{\partial Q}{\partial Y}(X \mid X) = \tfrac{1}{2}\left[\frac{\partial f_\mathrm{f}}{\partial Y} + m\frac{\partial f_\mathrm{m}}{\partial Y} + f_\mathrm{m}\frac{\partial m}{\partial Y}\right](X \mid X) = 0\,.$$

This equation can be written in a more elegant as well as meaningful form by observing that since at population dynamical equilibrium the resident females should just replace themselves, the population sex ratio equals $f_\mathrm{m}(X \mid X)/f_\mathrm{f}(X \mid X)$, and the females are all offspring of males, that is,

$$f_\mathrm{f}(X \mid X) = 1\,, \qquad f_\mathrm{m}(X \mid X) = r(X)\,, \qquad m(X \mid X) = r^{-1}(X)\,,$$

$r(X)$ the resident sex ratio (*i.e.*, density of males divided by density of females). Expressed in the contributions of the two sexes:

$$\left[\frac{\partial \ln(f_\mathrm{f})}{\partial Y_\mathrm{f}} + \frac{\partial \ln(f_\mathrm{m})}{\partial Y_\mathrm{f}}\right](X_\mathrm{f} \mid X_\mathrm{f}, X_\mathrm{m}) = 0\,, \qquad \left[\frac{\partial \ln(m)}{\partial Y_\mathrm{m}}\right](X_\mathrm{m} \mid X_\mathrm{f}, X_\mathrm{m}) = 0\,,$$

or alternatively

$$\left[p_\mathrm{m}\frac{\partial f_\mathrm{f}}{\partial Y_\mathrm{f}} + p_\mathrm{f}\frac{\partial f_\mathrm{m}}{\partial Y_\mathrm{f}}\right](X_\mathrm{f} \mid X_\mathrm{f}, X_\mathrm{m}) = 0\,, \qquad \left[\frac{\partial m}{\partial Y_\mathrm{m}}\right](X_\mathrm{m} \mid X_\mathrm{f}, X_\mathrm{m}) = 0\,,$$

with $p_\mathrm{m}(X)$ and $p_\mathrm{f}(X)$ the resident fractions males and females, $p_\mathrm{m} = r/(1+r)$, $p_\mathrm{f} = 1/(1+r)$.

Invadability close to a singular strategy X can be determined from

$$\frac{\partial^2 Q}{\partial Y \partial Y^{\mathrm{T}}}(X \mid X) = \tfrac{1}{2}\left[\frac{\partial^2 f_{\mathrm{f}}}{\partial Y \partial Y^{\mathrm{T}}} + m\frac{\partial^2 f_{\mathrm{m}}}{\partial Y \partial Y^{\mathrm{T}}} + f_{\mathrm{m}}\frac{\partial^2 m}{\partial Y \partial Y^{\mathrm{T}}}\right](X \mid X)\ ,$$

or, written out in the male and female components

$$\frac{\partial^2 Q}{\partial Y \partial Y^{\mathrm{T}}}(X \mid X) = \frac{1}{2}\begin{pmatrix} \dfrac{\partial^2 f_{\mathrm{f}}}{\partial Y_{\mathrm{f}} \partial Y_{\mathrm{f}}^{\mathrm{T}}} + r^{-1}\dfrac{\partial^2 f_{\mathrm{m}}}{\partial Y_{\mathrm{f}} \partial Y_{\mathrm{f}}^{\mathrm{T}}} & 0 \\ 0 & r\dfrac{\partial^2 m}{\partial Y_{\mathrm{m}} \partial Y_{\mathrm{m}}^{\mathrm{T}}} \end{pmatrix}(X \mid X)\,.$$

Apparently in the ESS conditions males and females behave as separate species with as only coupling the feedback loop through $E_{\mathrm{attr}}(X)$.

The determination of conditions for strong convergence for haplo-diploids is an open problem. The reason is that the canonical equation of adaptive dynamics (see Dieckmann and Law, 1996; Champagnat, 2003; and in particular Durinx *et al.*, 2008), which was used by Leimar (2001, 2005, in press) to derive his criteria, takes an unusual form for haplo-diploids (Metz and De Kovel, in prep). In diploids, if there are no parental effects, gene expression becomes additive for small enough mutational steps. Invasion fitness is a property of heterozygotes. However, after a substitution the population again consists of homozygotes. The eventual substitution step is therefore twice as large as the phenotypic step used in calculating the invasion fitness. This leads to an additional factor 2 in the canonical equation for diploids as compared to haploids or clonal reproducers. Otherwise the canonical equation for diploids is an exact copy of the canonical equation for clonal reproducers. This factor 2 appears in front of the mutational covariance matrix. So all that happens compared to the clonal case is that the mutational covariance matrix is effectively replaced by a matrix that is twice as large. Therefore, Leimar's (*l.c.*) results apply equally to the clonal and the standard Mendelian case. In haplo-diploids the factor 2 comes in for the diploid sex, but not for the haploid one. Therefore this factor cannot be absorbed in the mutational covariance matrix. Only when the mutational steps of the two sexes are fully uncorrelated the if part, but not the only if part, of the Leimar theorem applies without further ado.

The situation for mutual invadability is similar to that for strong convergence.

In the, at first sight maybe attractive but on second thought rather contrived, case that $X_{\mathrm{m}} = \mathrm{G}(X_{\mathrm{f}})$,

$$Q(Y_{\mathrm{f}}, Y_{\mathrm{m}} \mid X_{\mathrm{f}}) = \tfrac{1}{2}\left[f_{\mathrm{f}}(Y_{\mathrm{f}} \mid X_{\mathrm{f}}) + f_{\mathrm{m}}\left(Y_{\mathrm{f}} \mid X_{\mathrm{f}}\right)m(Y_{\mathrm{m}} \mid X_{\mathrm{f}})\right] - 1\,,$$

with $Y_{\mathrm{m}} = G(Y_{\mathrm{f}}')$, Y_{f}' the trait value of the additional homozygote corresponding to the heterozygote Y_{f} and homozygote X_{f}. (In haplo-diploid species, the developmental systems of the males and females are bound to be even more different than in diploids as they start from different complements of genes.) If there are no parental effects on gene expression, for small mutational steps $X_{\mathrm{f}}' = X_{\mathrm{f}} + 2(Y_{\mathrm{f}} - X_{\mathrm{f}}) + \mathrm{o}\left(\left\|Y_{\mathrm{f}} - X_{\mathrm{f}}\right\|\right)$ and hence

$$Y_{\mathrm{m}} - X_{\mathrm{m}} = 2\frac{\mathrm{d}G}{\mathrm{d}X}(X_{\mathrm{f}})\left(Y_{\mathrm{f}} - X_{\mathrm{f}}\right) + \mathrm{o}\left(\left\|Y_{\mathrm{f}} - X_{\mathrm{f}}\right\|\right).$$

Therefore, the equation for the evolutionarily singular strategies becomes

$$\frac{\partial f_{\mathrm{f}}}{\partial Y_{\mathrm{f}}}\left(X_{\mathrm{f}} \mid X_{\mathrm{f}}\right)+r^{-1}\frac{\partial f_{\mathrm{m}}}{\partial Y_{\mathrm{f}}}\left(X_{\mathrm{f}} \mid X_{\mathrm{f}}\right)+r\frac{\partial m}{\partial Y_{\mathrm{m}}}\left(X_{\mathrm{m}} \mid X_{\mathrm{f}}\right)2\frac{\mathrm{d}G}{\mathrm{d}X_{\mathrm{f}}}\left(X_{\mathrm{f}}\right)=0\,.$$

Their invadability can be determined from the criteria given in Section 4, using the second derivatives of $Q(Y_{\mathrm{f}},Y_{\mathrm{m}} \mid X_{\mathrm{f}})$ for Y_{f} and X_{f} calculated as if $\mathrm{d}Y_{\mathrm{m}}/\mathrm{d}Y_{\mathrm{f}}=2\left[\mathrm{d}G/\mathrm{d}X\right](X)$. In view of the contrivedness of the assumption $X_{\mathrm{m}}=G(X_{\mathrm{f}})$ we refrain from giving the long and ugly explicit formula.

6. Case study II: Invasion of a genetic dimorphism by either a different allele or a modifier under Hardy-Weinberg conditions

In this and the next section we shall consider the evolution of a dimorphism on a locus called A. In agreement with the implicit practice of population genetical modelers, we assume the non-focal loci to be either without phenotypic effects or monomorphic, at least in the resident population. The dimorphism may evolve by either the substitution of alternative alleles on the focal locus or by substitutions on other loci, referred to as modifiers and generically called B. All individuals are assumed to be born equal but for genetic differences, and to be formed by random mating. Otherwise there are no restrictions on the physiological structure. In this section we shall moreover take on board one further standard assumption of population genetics: the numbers of macro- and micro-gametes that end up in zygotes are at all times proportional (*i.e.*, for all genotypes and h-states). This assumption is usually encountered in its equivalent form as the assumption that under random union of gametes newly formed zygotes occur in Hardy-Weinberg proportions. (Actually, as we shall only consider equilibria and their invadability, it suffices to assume proportionality of the lifetime effective micro- and macro-gametic outputs.)

When we consider allelic evolution the individuals (*i.e.*, objects to the type of which we assign fitnesses) to consider are the gene copies. Their h-state consists of the h-state of their carrier together with the type of the other allele with whom they share this carrier, which may be *a* or *A*. In the case of modifier evolution the individuals correspond to the usual biological ones, but now with as additional birth state component the genotype on the A-locus.

Notation:

alleles on the dimorphic locus:	A, a (residents), α (mutant),
resident allele on a modifier locus:	b (generally suppressed in the notation),
mutant allele on a modifier locus:	B;
resident trait vectors:	$X_{aa} \equiv X_{aabb}$, $X_{AA} \equiv X_{AAbb}$ $X_{aA} = X_{Aa} \equiv X_{aAbb} = X_{Aabb}$,
mutant heterozygote trait vectors:	$Y = X_{a\alpha}, X_{A\alpha}, X_{aaB}, X_{aAB}, X_{AAB}$, with $X_{aaB} \coloneqq X_{aabB}, X_{aAB} \coloneqq X_{aAbB}, X_{AAB} \coloneqq X_{AAbB}$;
relative frequency of haplotypes:	p_{a}, p_A (residents; depend on X_{aa}, X_{aA}, X_{AA}), p_α, p_{aB}, p_{AB} (mutants);
lifetime offspring numbers:	$2\,w\left(Y \mid X_{aa}, X_{aA}, X_{AA}\right)$
with specific cases abbreviated as	$w_{a\alpha} \coloneqq w\left(X_{a\alpha} \mid X_{aa}, X_{aA}, X_{AA}\right)$, $w_{aaB} \coloneqq w\left(X_{aaB} \mid X_{aa}, X_{aA}, X_{AA}\right)$, etc.;
recombination probability of AB:	c, with $0 \le c \le \frac{1}{2}$.

It is possible to develop a consistent population dynamical formalism based on the mental construction of (generalised) individuals described in the introduction (Metz in press). However, when genetic differentiation is involved it is usually far easier to use the standard population genetical formalism as this more effectively exploits the symmetry inherent in Mendel's laws. After working out the relevant linearisations one ends up with exactly the same formulas as for the population dynamical formalism (Metz *l.c.*).

The linearised generation dynamics of the gene frequency of a mutant in one of the alleles constituting the polymorphism is

$$p'_\alpha = \mathbf{L}_\alpha p_\alpha = w_{\bullet\alpha} p_\alpha \qquad \text{with} \qquad w_{\bullet\alpha} := p_a w_{a\alpha} + p_A w_{A\alpha}$$

In population genetics $w_{\bullet\alpha}$ is known as the marginal fitness of the α-allele. Hence,

$$R_{0,\alpha}\left(\begin{pmatrix} X_{a\alpha} \\ X_{A\alpha} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \end{pmatrix}, \begin{pmatrix} X_{Aa} \\ X_{AA} \end{pmatrix}\right) = w_{\bullet\alpha},$$

where the form of the formula brings out that the phenotype engendered by an allele consists of two components, expressing the dependence on the two intra-individual environments that it may encounter.

The linearised generation dynamics of the gene frequency of a mutant on a modifier locus is

$$\begin{aligned} p'_{aB} &= w_{aaB} p_a p_{aB} + w_{aAB}(1-c) p_A p_{aB} + w_{aAB} c p_a p_{AB}, \\ p'_{AB} &= w_{AAB} p_A p_{AB} + w_{aAB}(1-c) p_a p_{AB} + w_{aAB} c p_A p_{aB}. \end{aligned}$$

This can be rewritten in vector-matrix form as

$$\begin{pmatrix} p_{aB} \\ p_{AB} \end{pmatrix}' = \mathbf{L}_B \begin{pmatrix} p_{aB} \\ p_{AB} \end{pmatrix} \text{ with } \mathbf{L}_B = \mathbf{L}_{B,\text{sel}} + c\mathbf{L}_{B,\text{rec}} = \begin{pmatrix} w_{\bullet aB} & 0 \\ 0 & w_{\bullet AB} \end{pmatrix} + c \begin{pmatrix} -w_{aAB} \\ w_{aAB} \end{pmatrix} \begin{pmatrix} p_A & -p_a \end{pmatrix}$$

and

$$w_{\bullet aB} = p_a w_{aaB} + p_A w_{aAB}, \qquad w_{\bullet AB} = p_a w_{aAB} + p_A w_{AAB}.$$

(Please note that formulas (33) and (34) in Metz (2008) are wrong and have to be replaced with the ones above.) Hence

$$Q_B\left(c, \begin{pmatrix} X_{aaB} \\ X_{aAB} \\ X_{AAB} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix}\right) = -\left(w_{\bullet aB} - 1\right)\left(w_{\bullet AB} - 1\right) + c w_{aAB}\left(p_a w_{\bullet aB} + p_A w_{\bullet AB} - 1\right)$$

where the form of the formula brings out that a mutant modifier allele is characterised by a phenotype that consists of three components expressing the dependence on the three intra-individual environments that it may encounter as well as the recombination fraction between its and the focal locus.

A Dimorphism is Evolutionarily Steady if it is uninvadable by both alternative alleles and modifiers. The first can be judged from whether $w_{\bullet\alpha} < 1$ for all possible values of $X_{a\alpha}$ and $X_{A\alpha}$, the second from Q_B. First consider the case where $c = 0$. This case is similar to that of invasion attempts by alternative alleles, but possibly for a

difference in the set of accessible phenotypes. Hence if both $w_{\bullet aB} < 1$ and $w_{\bullet AB} < 1$, the dimorphism is uninvadable by modifiers with $c = 0$. A closer look at the formula for Q_B shows that in that case Q_B is also negative whatever the value of c. So $w_{\bullet aB} < 1$ and $w_{\bullet AB} < 1$ for all possible modifiers is a sufficient condition for a dimorphism to be globally uninvadable. Without any constraint on the genetic architecture this condition with the strict inequality signs replaced with their non-strict counterparts is also necessary. More precisely, if the genetic and developmental architecture allow for alleles or modifiers for which $w_{\bullet aB} > 1$ or $w_{\bullet AB} > 1$, and, in the special case that there happen to be no such alleles and there only exist such modifiers for which $p_a w_{\bullet aB} + p_A w_{\bullet AB} < 1$, at least one of these is sufficiently closely linked to the focal locus, then the dimorphism is invadable.

Remark: Modifiers entering genetic dimorphisms present an interesting subtlety with respect to the use of Q that in other classes of problems tends to be non-generic. In the special case where $c = 0$ the next-generation matrix of the resident has more than one eigenvalue equal to 1. In Figure 7 the residents are located at the point $(\text{trace}, \det) = (2,1)$ connecting the stable region with the troublesome region where both zero crossings of the characteristic polynomial are larger than 1. Hence the first alternative of condition (iv) in the theorem in Section 3 does not hold true, and it is possible for the trait vector Y of a pair of pseudo-alleles (aB, AB) to move away from the resident value X directly into the troublesome region. However, if both $w_{\bullet aB} < 1$ and $w_{\bullet AB} < 1$ for all possible modifiers, the second alternative of condition (iv) in the theorem in Section 3 holds true. Moreover, $Q_B(c, Y \mid X) < 0$ for all modifiers. On the other hand, if there are modifiers such that either $w_{\bullet aB} > 1$ or $w_{\bullet AB} > 1$ then $Q_B(c, Y \mid X) > 0$ if $p_a w_{\bullet aB} + p_A w_{\bullet AB} > 1$ or the A and B loci are sufficiently strongly linked. Finally, consider modifiers such that both $w_{\bullet aB} > 1$ and $w_{\bullet AB} > 1$: For very small c these modifiers correspond to values of trace and det in the troublesome region where both zero crossings of the characteristic polynomial are larger than one. In that region Q_B is negative and yet the polymorphism is invadable. The latter result extends to larger c as then $1 < p_a w_{\bullet aB} + p_A w_{\bullet AB} < R_0 < \max\{w_{\bullet aB}, w_{\bullet AB}\}$. To prove these inequalities differentiate through the characteristic equation

$$-\left(w_{\bullet aB} - R_0\right)\left(w_{\bullet AB} - R_0\right) + c w_{aAB}\left(p_a w_{\bullet aB} + p_A w_{\bullet AB} - R_0\right) = 0$$

for c and solve for $\mathrm{d}R_0/\mathrm{d}c$ to arrive at

$$\frac{\mathrm{d}R_0}{\mathrm{d}c} = -\frac{w_{aAB}\left(p_a w_{\bullet aB} + p_A w_{\bullet AB} - R_0\right)}{w_{\bullet aB} + w_{\bullet AB} - c w_{aAB} - 2R_0},$$

which should be combined with $R_0 = \max\{w_{\bullet aB}, w_{\bullet AB}\}$ at $c = 0$. The denominator is negative for c very small, and cannot pass through zero for $0 < c < 1$ since $w_{\bullet aB} + w_{\bullet AB} - c w_{aAB} - 2R_0 = 0$ would imply that the two roots of the characteristic polynomial coincide, which is impossible since for $0 < c < 1$ the matrix $\mathbf{A}_B$ is non-negative and irreducible. Hence the, continuous, right hand side is negative for $p_a w_{\bullet aB} + p_A w_{\bullet AB} < R_0 < \max\{w_{\bullet aB}, w_{\bullet AB}\}$ and zero when $R_0 = p_a w_{\bullet aB} + p_A w_{\bullet AB}$. Therefore R_0 decreases with c and cannot pass below $p_a w_{\bullet aB} + p_A w_{\bullet AB}$. □

The next step is to derive an equation for hunting down prospective ESDs. To this end it helps first to look at the population dynamical and genetical equilibrium equations (Charlesworth, 1994; Diekmann *et al.* 2003):

$$\bar{w}\left(X_{aa}, X_{aA}, X_{AA}\right) = 1 \qquad \text{with} \qquad \bar{w} := p_a^2 w_{aa} + 2 p_a p_A w_{aA} + p_A^2 w_{AA}.$$

respectively

$$p_A w_{AA} + (1 - p_A) w_{aA} = \bar{w}, \quad \text{or equivalently} \qquad p_a w_{aa} + (1 - p_a) w_{aA} = \bar{w}.$$

Hence at the step where the invaders are set equal to the resident one may substitute $w_{\bullet\alpha} = w_{\bullet a} = 1$, $w_{\bullet\alpha} = w_{\bullet A} = 1$, $w_{\bullet aB} = w_{\bullet a} = 1$ and $w_{\bullet AB} = w_{\bullet A} = 1$. (Of course, this result also follows immediately from the fact that R_0 of the resident alleles should be 1.)

First consider the modifier evolution case. Prospective ESDs can be determined from

$$\frac{\partial Q_B}{\partial \begin{pmatrix} X_{aaB} \\ X_{aAB} \\ X_{AAB} \end{pmatrix}} \left(c, \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix} \right) =$$

$$c w_{aA} \left(p_a \frac{\partial w}{\partial Y}\left(X_{aa} \mid X_{aa}, X_{aA}, X_{AA}\right), \frac{\partial w}{\partial Y}\left(X_{aA} \mid X_{aa}, X_{aA}, X_{AA}\right), p_A \frac{\partial w}{\partial Y}\left(X_{AA} \mid X_{aa}, X_{aA}, X_{AA}\right) \right) = 0,$$

or equivalently,

$$\frac{\partial w}{\partial Y}\left(X_{aa} \mid X_{aa}, X_{aA}, X_{AA}\right) = \frac{\partial w}{\partial Y}\left(X_{aA} \mid X_{aa}, X_{aA}, X_{AA}\right) = \frac{\partial w}{\partial Y}\left(X_{AA} \mid X_{aa}, X_{aA}, X_{AA}\right) = 0,$$

their local uninvadability from whether

$$\frac{\partial^2 Q_B}{\partial \begin{pmatrix} X_{aaB} \\ X_{aAB} \\ X_{AAB} \end{pmatrix} \partial \begin{pmatrix} X_{aaB} \\ X_{aAB} \\ X_{AAB} \end{pmatrix}^{\mathrm{T}}} \left(c, \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix} \right) =$$

$$c w_{aA} \begin{pmatrix} p_a \dfrac{\partial^2 w}{\partial \partial Y \partial Y^{\mathrm{T}}}\left(X_{aaB} \mid X_{aa}, X_{aA}, X_{aA}\right) & 0 & 0 \\ 0 & \dfrac{\partial^2 w}{\partial Y \partial Y^{\mathrm{T}}}\left(X_{aAB} \mid X_{aa}, X_{aA}, X_{aA}\right) & 0 \\ 0 & 0 & p_A \dfrac{\partial^2 w}{\partial Y \partial Y^{\mathrm{T}}}\left(X_{AAB} \mid X_{aa}, X_{aA}, X_{aA}\right) \end{pmatrix}$$

or equivalently,

$$\frac{\partial^2 w}{\partial \partial Y \partial Y^{\mathrm{T}}}\left(X_{aaB} \mid X_{aa}, X_{aA}, X_{aA}\right), \frac{\partial^2 w}{\partial Y \partial Y^{\mathrm{T}}}\left(X_{aAB} \mid X_{aa}, X_{aA}, X_{aA}\right) \text{ and } \frac{\partial^2 w}{\partial Y \partial Y^{\mathrm{T}}}\left(X_{AAB} \mid X_{aa}, X_{aA}, X_{aA}\right)$$

are negative definite. Apparently at modifier evolution based ESDs each comprising type has locally the maximal lifetime reproductive output that is possible under the circumstances. Moreover, the conditions satisfied by a modifier evolution based local ESD make that locally also no alternative alleles can invade.

Deriving the latter results by differentiating $R_0 = \frac{\text{trace} + \sqrt{\text{trace}^2 - 4\det}}{2}(\mathbf{A}_B)$ may be possible, but is not immediately trivial.

If for each of the types the maximum of the lifetime reproductive output is global on the trait space minus the two other types, the ESD is also global. In that case necessarily all the maxima are equal, and hence $w_{AA} = w_{aA} = w_{AA} = 1$. Such fitness equalising evolutionarily stable polymorphisms are known in the literature as Ideal Free (*e.g.* Bulmer, 1994). The reason for this name is the following. Let $\mathbb{X}$ denote the space of all possible trait vectors that may somehow be genetically realised. The Ideal Free hypothesis says that from any (X_{aa},X_{aA},X_{AA}) the support of the distribution of a mutant triple $(X_{aaB},X_{aAB},X_{AAB})$ equals $\mathbb{X}^3$. (Hence under the Ideal Free hypothesis the discussion is implicitly confined to global ESDs.)

Proposition: Under the Ideal Free hypothesis any ESD equalises the lifetime offspring numbers of the three phenotypes.

Proof: Suppose that the average effective lifetime offspring numbers were not equalised. In that case a modifier mutant that as a heterozygote has a phenotype equal to that of the resident genotype with the maximal effective lifetime offspring number, can act as a phenotypically monomorphic invader with $R_0 = \max\{w_{aa}, w_{aA}, w_{AA}\} > 1$ (the latter since not all *w*'s are equal and $\bar{w} = 1$). □

The Ideal Free hypothesis can be flouted in two manners. One is by local constraints, *i.e.*, the possible mutants depend on the starting position, *e.g.* since large steps are forbidden. The other is by global genetic constraints, *i.e.*, the set of phenotypes achievable by heterozygotes is larger than that achievable by homozygotes. Sickle cell anemia stands as an example. From a mathematical perspective this and other sorts of global constraints derive from the structure of the genotype to phenotype map:

$\Phi : (X_{\mathcal{A}_1}, X_{\mathcal{A}_2}; \cdots; X_{\mathcal{B}_1}, X_{\mathcal{B}_2}; \cdots) \mapsto X_{\mathcal{A}_1\mathcal{A}_2\cdots\mathcal{B}_1\mathcal{B}_2\cdots}$, written as $X_{\mathcal{A}_1\mathcal{A}_2\mathcal{B}_1\mathcal{B}_2}$ for short,

with $\mathcal{A}_i = a, A$, $\mathcal{B}_i = b, B$, and X_a, X_A, X_b, X_B vectors of allelic traits.

Remarks: Biologically you may think of these allelic traits as corresponding to *e.g.* the gene expression levels under various micro-environmental circumstances and/or at various times in the life cycle and/or in various parts of the body, with alleles corresponding not so much to different variants of the coding as well as of the regulatory regions of the gene. In this view alleles are more extensive stretches of DNA than just the coding regions; mathematically alleles and modifiers differ by the fact that for alleles the probability of a recombination within the allele during a substitution run is neglected, whereas between alleles and modifiers such recombinations are assumed to be relatively frequent.

As an aside we mention that in the general case phenotypes also are not what one may naïvely expect. In keeping with the general ecological view that also formed

the basis for the ecological definition of fitness, phenotypes should in principle be interpreted as reaction norms (another term is conditional strategies), i.e., maps from (micro-)environmental conditions to phenotypes in the naïve sense, i.e., characteristics of individuals. These reaction norms supposedly come as families with the phenotypic traits as identifying parameters. Only in the simplest cases these reaction norms are degenerate, taking only a single value, which we then may use as the phenotypic trait, so that the general abstract and naïve sense phenotypes coincide. □

At this moment there is no systematic theory classifying genotype to phenotype maps in view of their evolutionary consequences. Tantalizing glimpses of what such a theory might do may be seen in the work of Sean Rice (1998, 2000,2002, 2004a, 2004b, 2008) and by various people around Günter Wagner (*e.g.* Wagner and Mezey, 2000; Hansen and Wagner 2003; Bagheri-Chaichian *et al.*, 2003; Bagheri-Chaichian and Wagner, 2004; Hansen *et al.*, 2006). Most research so far considers either quantitative genetics or the dynamics of gene frequencies, with but little connection to ESS theory (for the most notable exception see Van Dooren, 1999, 2000, 2006).

The classification of the interplay between allelic and modifier evolution when there are developmental or genetic constraints requires a sufficiently general framework for dealing with genotype to phenotype maps. For lack of such a framework, we confine ourselves to the special case of calculating ESDs when only alleles evolve without any involvement of modifiers (for example since Φ is such that other loci than A have only negligible influence on the traits under consideration), since this problem is of some interest in its own right, were it only for the number of publications that make this or a very similar assumption (*e.g.* Kisdi and Geritz, 1999;Van Dooren, 1999, 2000; Van Doorn and Dieckmann, 2006; Proulx and Phillips, 2006; Peischl and Bürger, 2008).

ESDs resulting from the co-evolution of alleles in an otherwise fixed or un-influential genetic background can be calculated by setting the derivative of $Q_B\left(c,\begin{pmatrix}\Phi(X_a,X_\alpha)\\ \Phi(X_A,X_\alpha)\end{pmatrix}\middle|\begin{pmatrix}X_{aa}\\ X_{aA}\end{pmatrix},\begin{pmatrix}X_{Aa}\\ X_{AA}\end{pmatrix}\right)$ for X_α equal to 0 at $X_\alpha = X_a$ and $X_\alpha = X_A$ resulting in the equations

$$p_a\frac{\partial w}{\partial Y}\left(X_{aa}\mid X_{aa},X_{aA},X_{AA}\right)\frac{\partial\Phi}{\partial X_\alpha}\left(X_a,X_a\right)+p_A\frac{\partial w}{\partial Y}\left(X_{aA}\mid X_{aa},X_{aA},X_{AA}\right)\frac{\partial\Phi}{\partial X_\alpha}\left(X_A,X_a\right)=0,$$

$$p_a\frac{\partial w}{\partial Y}\left(X_{aA}\mid X_{aa},X_{aA},X_{AA}\right)\frac{\partial\Phi}{\partial X_\alpha}\left(X_a,X_A\right)+p_A\frac{\partial w}{\partial Y}\left(X_{AA}\mid X_{aa},X_{aA},X_{AA}\right)\frac{\partial\Phi}{\partial X_\alpha}\left(X_A,X_A\right)=0,$$

which, as always, should be solved in combination with the population dynamical and genetical equilibrium equations. Let the phenotypes be n-dimensional and the allelic traits m-dimensional. When $2m<3n$, generically the solutions, if they exist, are isolated, and the ESDs fail to maximise the lifetime reproductive output of the three participating phenotypes (are not "full maximisers"); in other words, generically any ESDs are co-determined by genetic constraints. When $2m\geq 3n$ fully maximising ESDs become possible. When $2m=3n$ any ESDs are generically isolated in the space of pairs of allelic trait vectors. When $2m>3n$, generically any ESDs are full maximisers and are underlain by a $2m-3n$ dimensional manifold of phenotypically equivalent pairs of allelic trait vectors.

7. Case study III: Invasion of a genetic dimorphism by a different allele or a modifier when the trait may differentially affect the micro- and macro-gametic contributions to the next generation

One of the things that we became uncomfortably aware of when working on equations for physiologically structured populations with genetic differentiation is that it is hard to justify the implicit assumption of standard population genetics that the expected lifetime macro- and micro-gametic outputs ending up in zygotes are at all time proportional. Take for example an organism that seemingly almost ideally conforms to the assumptions of the classical population genetical models, to wit a hermaphroditic annual plant. Most genetic differences that influence competitive ability will also operate in the seed setting phase when the anthers are already gone. Hence, their influence on the reproductive output through the ova will differ from that through pollen production. Therefore, we believe it to be important to spend more than the now customary education and research time on the study of population genetical tools that do not assume proportional effective macro- and micro-gametic outputs. As a small contribution we reconsider in this section the problem treated in the previous section without making the proportionality assumption.

In general the notation in this section is the same as in the previous one but for the changes indicated below.

Notation:

relative frequency of haplotypes: p (micro-gametes), q (macro-gametes);

average lifetime micro-gametic output that ends up in zygotes: $m_{A\alpha} := m(X_{a\alpha} \mid X_{aa}, X_{aA}, X_{AA})$, etc.;

average lifetime macro-gametic output that ends up in zygotes: $f_{A\alpha} := f(X_{A\alpha} \mid X_{aa}, X_{aA}, X_{AA})$, etc..

The allelic invasion reproduction ratio equals the dominant eigenvalue of the next generation matrix

$$\mathbf{L}_\alpha = \frac{1}{2}\begin{pmatrix} m_{a\alpha}q_a + m_{A\alpha}q_A & m_{a\alpha}p_a + m_{A\alpha}p_A \\ f_{a\alpha}q_a + f_{A\alpha}q_A & f_{a\alpha}p_a + f_{A\alpha}p_A \end{pmatrix}.$$

To see this, observe that the next generation of successful α-micro-gametes is produced by the αa and αA individuals. Over their lifetime these produce $m_{a\alpha}$ respectively $m_{A\alpha}$ successful micro-gametes, half of which are of the α type. The individuals themselves came about through the combination of an α-micro-gamete with either an a- or A-macro-gamete, giving the upper left component of $\mathbf{L}_\alpha$, or through the combination of an α-macro-gamete with an a- or A-micro-gamete, giving the upper right component of $\mathbf{L}_\alpha$. The story for the lower components of $\mathbf{L}_\alpha$ is the same except that we now have to consider successful macro-gametes.

From $\mathbf{L}_\alpha$ we calculate the allelic invasion fitness proxy

$$Q_\alpha\left(\begin{pmatrix} X_{a\alpha} \\ X_{A\alpha} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \end{pmatrix}, \begin{pmatrix} X_{Aa} \\ X_{AA} \end{pmatrix}\right) = -\det\left(\mathbf{I} - \mathbf{L}_\alpha\right) =$$

$$\tfrac{1}{2}\left(p_a f_{a\alpha} + p_A f_{A\alpha} + q_a m_{a\alpha} + q_A m_{A\alpha}\right) - \tfrac{1}{4}\left(p_a q_A - p_A q_a\right)\left(f_{a\alpha} m_{A\alpha} - f_{A\alpha} m_{a\alpha}\right) - 1.$$

(To keep the expression for Q_α symmetric in a and A we have refrained from using that $p_a q_A - p_A q_a = p_a - q_a = q_A - p_A$.)

The modifier invasion reproduction ratio equals the dominant eigenvalue of the next generation matrix

$$\mathbf{L}_B = \mathbf{L}_{B,\mathrm{sel}} + c\mathbf{L}_{B,\mathrm{rec}}$$

with

$$\mathbf{L}_{B,\mathrm{sel}} = \begin{pmatrix} \mathbf{L}_{aB} & 0 \\ 0 & \mathbf{L}_{AB} \end{pmatrix}$$

with $\mathbf{L}_{aB}$ and $\mathbf{L}_{AB}$ the equivalents of $\mathbf{L}_\alpha$ for the pseudo-allele $\alpha = aB$ respectively $\alpha = AB$, and

$$\mathbf{L}_{B,\mathrm{rec}} = \frac{1}{2}\begin{pmatrix} -m_{aAB} \\ -f_{aAB} \\ m_{aAB} \\ f_{aAB} \end{pmatrix}\begin{pmatrix} q_A & p_A & -q_a & -p_a \end{pmatrix}.$$

$\mathbf{L}_{B,\mathrm{sel}}$ is derived by observing that without recombination the aB and AB gametic types reproduce independently (thanks to the severe dilution of the mutant population) in a manner similar to a new allele. Recombination occurs in the zygotes. It only has an effect when B resides in a zygote that is heterozygous on the A-locus. So we only have to see how the offspring of such individuals are affected. Hence only m_{aAB} and f_{aAB} occur in $\mathbf{L}_{B,\mathrm{rec}}$. A recombination event changes some aB gametes to AB gametes and vice versa via an exchange with the complementary Ab respectively AB haplotype. This is where the signs in $\mathbf{L}_{B,\mathrm{rec}}$ come from. For the remainder $\mathbf{L}_{B,\mathrm{rec}}$ is constructed so that the resident frequencies of A and a (i.e., Ab and ab) combine in the right manner with the frequencies of the mutant aB and AB gametes to get the frequencies of the $ab.AB$ and $Ab.aB$ heterozygotes.

The calculation of the required determinant is made easy by the fact that determinants are linear in their columns. Hence the determinant of the sum of two $k\times k$ matrices is equal to the sum of the determinants of the 2^k matrices one gets by choosing for each column the corresponding column of either of the two original matrices. Since $\mathbf{L}_{B,\mathrm{rec}}$ has rank one, from these 2^k determinants only the $k+1$ determinants remain that comprise either zero or one column from $\mathbf{L}_{B,\mathrm{rec}}$. The calculation is further facilitated by the many zeros in $\mathbf{L}_{B,\mathrm{sel}}$, and the fact that the result should be invariant under the swapping of a and A. The result is

$$Q_B\left(c, \begin{pmatrix} X_{aaB} \\ X_{aAB} \\ X_{AAB} \end{pmatrix} \middle| \begin{pmatrix} X_{aa} \\ X_{aA} \\ X_{AA} \end{pmatrix}\right) = -\det(\mathbf{I} - \mathbf{L}_B) = -Q_{aB}Q_{AB} + c\left(Q_{aB}R_{AB} + Q_{AB}R_{aB}\right)$$

with

$$Q_{aB} = -\det(\mathbf{I} - \mathbf{L}_{aB}) \qquad Q_{AB} = -\det(\mathbf{I} - \mathbf{L}_{AB})$$

and

$$R_{aB} = \tfrac{1}{2}\left(p_A f_{aAB} + q_A m_{aAB}\right) + \tfrac{1}{4}\left(p_a - q_a\right)\left(f_{aAB}m_{aaB} - f_{aaB}m_{aAB}\right),$$
$$R_{AB} = \tfrac{1}{2}\left(p_a f_{aAB} + q_a m_{aAB}\right) + \tfrac{1}{4}\left(p_A - q_A\right)\left(f_{aAB}m_{AAB} - f_{AAB}m_{aAB}\right).$$

The above expression is linear in c. Hence Q_B is maximal in c for $c = 0$ or $c = \frac{1}{2}$. Therefore, it suffices to consider Q_B for those values of c only. The case $c = 0$ is already covered by the condition that no alternative allele is able to invade. So all that has to be done is to check whether Q_B is negative for $c = \frac{1}{2}$.

Even trying to calculate R_0 explicitly, which is possible in principle as polynomial equations up to degree four allow explicit solutions, is a task for more than a single happy winter evening. And the result will be so horribly complex that you would never dare give it to a student for some ulterior use.

It is also possible to derive equations that have to be satisfied by any ESDs. However, the calculations are complicated and working through them to get at results would take more space than warranted by the present context. The more so since Carolien de Kovel and the first author are presently writing an extended paper on that topic, the upshot of which is that generically in the ecology and the developmental system alleles and modifiers disagree about the combinations of trait values they want to have present in the population. The exceptional cases where there is agreement can be classified and turn out to comprise precisely the main simplified models encountered in the literature, like the Hardy-Weinberg case treated in Section 6, or the evolution of sex determining genes or genes that are expressed in only one of the sexes.

By the same argument as before under the Ideal Free hypothesis any ESDs equalise the average lifetime offspring numbers of the three phenotypes. However, when there is no proportionality between the micro- and macro-gametic contributions, this only amounts to

$$\tfrac{1}{2}\left(f_{aa} + m_{aa}\right) = \tfrac{1}{2}\left(f_{aA} + m_{aA}\right) = \tfrac{1}{2}\left(f_{AA} + m_{AA}\right) = 1,$$

together with

$$f\left(X \mid X_{aa}, X_{aA}, X_{AA}\right) + m\left(X \mid X_{aa}, X_{aA}, X_{AA}\right) \text{ is maximal at } X = X_{aa},\ X = X_{aA},\ X = X_{AA}.$$

(remember the formula for the fitness of Mendelian diploids) leaving open the option for intra-genomic conflict about the sex ratio.

To arrive at an equality of the separate contributions an Extension of the Ideal Free assumption is needed: it should be possible to split up the trait vector into two components,

$$Y = \begin{pmatrix} Y_{\mathrm{f}} \\ Y_{\mathrm{m}} \end{pmatrix} \quad \text{with } Y_{\mathrm{f}} \in \mathbb{X}_{\mathrm{f}} \text{ and } Y_{\mathrm{m}} \in \mathbb{X}_{\mathrm{m}},$$

such that there exist functions $\tilde{f}$ and $\tilde{m}$ such that

$$f\left(Y \mid X_{aa}, X_{aA}, X_{AA}\right) = \tilde{f}\left(Y_{\mathrm{f}} \mid X_{aa}, X_{aA}, X_{AA}\right),\ m\left(Y \mid X_{aa}, X_{aA}, X_{AA}\right) = \tilde{m}\left(Y_{\mathrm{m}} \mid X_{aa}, X_{aA}, X_{AA}\right),$$

and from any (X_{aa},X_{aA},X_{AA}) the support of the distribution of a mutant triple (X_{aaB},X_{aAB},X_{AAB}) should equal $(\mathbb{X}_{\mathrm{f}} \times \mathbb{X}_{\mathrm{m}})^3$, as may *e.g.* be the case when the sexes are separate with the two components corresponding to similar quantities for the two sexes. When the separate contributions are all equalised the macro- and micro-gametic contributions to the effective expected lifetime offspring numbers become proportional, and the zygotes occur in Hardy Weinberg proportions (Dieckmann and Metz, 2006). Therefore under the Extended Ideal Free assumption alleles and

modifiers agree again about the combinations of trait values they want to have present in the population.

8. Concluding remarks

The use of $Q(Y \mid X) := -\det\left(\mathbf{I} - \mathbf{L}(Y \mid X)\right)$ as local fitness proxy was pioneered by Taylor and Bulmer (1980) and Courteau and Lessard (2000). The main contribution of this paper is the result that when the trait space is connected this proxy allows conclusions about global uninvadability to be reached. Secondary contributions are detailed recipes for dealing with long term evolution in haplo-diploid populations and of genetic dimorphisms both with and without the biologically exceptional but commonly made assumption that the effective lifetime micro- and macro-gametic outputs are at all time proportional. When the proportionality assumption is flouted, quite weird phenomena result. The detailed analysis of these will be the subject of another paper (De Kovel & Metz, in prep).

Acknowledgements: We thank Franjo Weissing for bringing the Courteau-Lessard reference to our attention and for helping us out with Eshel (1991). In addition Hans Metz thanks Jacques van Alphen for enticing him into the world of haplo-diploid organisms and Carolien de Kovel for a long-running collaboration on adaptive dynamics under non-Hardy-Weinberg genetics. Finally, we thank a very thorough and knowledgeable anonymous reviewer of an earlier version of the manuscript for correcting a number of errors and giving detailed advice for adapting it for a larger audience, and two reviewers of the so updated version for their constructive criticism which further improved the readability of the paper. OL thanks the Swedish Research Council for support.

References

Bagheri-Chaichian, H., Hermisson, J., Vaisnys, J. R., Wagner, G. P. (2003) Effects of epistasis on phenotypic robustness in metabolic pathways. *Mathematical Biosciences* **184**: 27–51.

Bagheri-Chaichian, H. and Wagner, G. P. (2004) Evolution of dominance in metabolic pathways. *Genetics* **168**: 1713–1735.

Bulmer, M. (1994) *Theoretical Evolutionary Ecology*. Sinauer Associates, Sunderland MA.

Champagnat, N. (2003) Convergence of adaptive dynamics n-morphic jump processes to the canonical equation and degenerate diffusion approximation. Prépublication de l'Université de Nanterre (Paris X) no. 03/7.

Charlesworth, B. (1994) *Evolution in Age-Structured Populations* (2nd edn.). Cambridge University Press, Cambridge.

Courteau, J. and Lessard, S. (2000) Optimal Sex Ratios in Structured Populations. *Journal of Theoretical Biology* 207:159-175.

De Kovel, C.G.F. and Metz, J.A.J. (in prep) The evolution of a genetic polymorphism when male and female interests conflict.

Dieckmann, U. and Law, R. (1996) The dynamical theory of coevolution: a derivation from stochastic ecological processes. *Journal of Mathematical Biology* **34**: 579-612.

Dieckmann, U. and Metz, J.A.J. (2006) Surprising evolutionary predictions from enhanced ecological realism. *Theoretical Population Biology* **69**: 263-281.

Diekmann O., Gyllenberg, M., Huang, H., Kirkilionis, M., Metz, J.A.J. and Thieme, H.R. (2001) On the Formulation and Analysis of General Deterministic Structured

Population Models. II. Nonlinear Theory. *Journal of Mathematical Biology* **43**: 157-189

Diekmann, O., Gyllenberg, M and Metz, J. A. J. (2003) Steady State Analysis of Structured Population Models. *Theoretical Population Biology* **63**:309-338.

Diekmann, O., Heesterbeek, J.A.P., and Metz, J.A.J. (1990) On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations. *Journal of Mathematical Biology* **28**: 365-382.

Durinx, M., Metz, J. A. J. and Meszéna, G. (2008) Adaptive dynamics for physiologically structured models. *Journal of Mathematical Biology* **56**: 673-742.

Eshel, I. (1983) Evolutionary and continuous stability. *Journal of theoretical Biology* **103**: 99-111.

Eshel, I. (1991) Game theory and population dynamics in complex genetical systems: the role of sex in short term and in long term evolution. In Selten, R. (ed.) *Game Equilibrium Models I . Evolution and Game Dynamics*: 6-26. Springer, Berlin.

Ferrière, R. and Gatto, M. (1995) Lyapunov exponents and the mathematics of invasion in oscillatory or chaotic populations. *Theoretical Population Biology* **48**: 126-171.

Geritz, S. A. H., Kisdi, É., Meszéna G. and Metz, J. A. J. (1998). Evolutionarily singular strategies and the adaptive growth and branching of the evolutionary tree. *Evolutionary Ecology* **12**: 35-57.

Hansen, T. F., Álvarez-Castro, J. M., Carter, A. J. R., Hermisson, J. and Wagner, G. P. (2006) Evolution of genetic architecture under directional selection. *Evolution* **60**: 1523–1536.

Hansen, T. F. and Wagner, G. P. (2003) Modeling genetic architecture: a multilinear theory of gene interaction. *Theoretical Population Biology* **59**: 61-86.

Heesterbeek, J. A. P. and Roberts, M. G. (2007) The type-reproduction number *T* in models for infectious disease control. *Mathematical Biosciences* **206**: 3–10.

Hermisson, J., Hansen, T. F. and Wagner, G. P. (2003) Epistasis in polygenic traits and the evolution of genetic architecture under stabilizing selection. *American Naturalist* **161**: 708–734.

Hofbauer, J. and Sigmund, K. (1998) *Evolutionary Games and Population Dynamics*. Cambridge: Cambridge University Press.

Intriligator, M. D. (1971) *Mathematical Optimization and Economic Theory*. Prentice Hall, Englewood Cliffs NJ.

Kisdi E. and Geritz, S. A. H. (1999) Adaptive dynamics in allele space: Evolution of genetic polymorphism by small mutations in a heterogeneous environment. *Evolution* **53**: 993-1008.

Leimar, O. (2001) Evolutionary change and darwinian demons. *Selection* **2**: 65–72.

Leimar, O. (2005) The evolution of phenotypic polymorphism: randomized strategies versus evolutionary branching. *American Naturalist* **165**: 669–681.

Leimar, O. (in press) Multidimensional convergence stability and the canonical adaptive dynamics. In: Dieckmann, U., Metz, J.A.J. (eds.) *Elements of Adaptive Dynamics. Cambridge Studies in Adaptive Dynamics*. Cambridge: Cambridge University Press.

Metz, J. A. J. 2008. Fitness. In Jørgensen, S.E. and Fath, B.D. (eds *Evolutionary Ecology. Encyclopedia of Ecology* #2: 1599-1612. Oxford: Elsevier.

Metz (in press) Invasion fitness, canonical equations, and global invasibility criteria for Mendelian populations. In: Dieckmann, U., Metz, J.A.J. (eds.) *Elements of Adaptive Dynamics. Cambridge Studies in Adaptive Dynamics*. Cambridge: Cambridge University Press.

Metz, J. A. J. and De Kovel, C. G. F. (in prep) The canonical equation of adaptive dynamics for Mendelian diploids and haplo-diploids.

Metz, J. A. J., Geritz, S. A. H., Meszéna, G., Jacobs, F. J. A. and van Heerwaarden, J. S. (1996). Adaptive dynamics, a geometrical study of the consequences of nearly faithful reproduction. In Van Strien, S. J. and Verduyn Lunel, S. M. (eds.) *Stochastic and Spatial Structures of Dynamical Systems*: 183-231. North-Holland, Amsterdam.

Metz, J. A. J., Nisbet, R. M. and Geritz, S. A. H. (1992) How should we define "fitness" for general ecological scenarios? *Trends in Ecology and Evolution*: **7**: 198-202.

Peischl S. and Bürger, R. (2008) Evolution of dominance under frequency-dependent intraspecific competition. *Journal of theoretical Biology* **251**: 210-226.

Proulx S. R. and Phillips, P. C. (2006) Allelic divergence precedes and promotes gene duplication. *Evolution* **60**: 881-892.

Rice, S. H. (1998) The evolution of canalization and the breaking of von Baer's laws: modeling the evolution of development with epistasis. *Evolution* **52**:647-657.

Rice, S. H. (2000) The evolution of developmental interactions: Epistasis, canalization, and integration. In J. B. Wolf, E. D. Brodie III and M. J. Wade, eds. *Epistasis and the evolutionary process*: 82-98. Oxford University Press, New York.

Rice, S. H. (2002) A general population genetic theory for the evolution of developmental interactions. *Procedings of the National Academy of Science* **99**:15518-15523.

Rice, S. H. (2004) Developmental associations between traits: covariance and beyond. *Genetics 166*: 513-526.

Rice, S. H. (2004) *Evolutionary Theory: Mathematical and Conceptual Foundations.* Sinauer Associates, Sunderland MA.

Rice, S. H. (2008) Theoretical approaches to the evolution of development and genetic architecture. *Annals of the New York Academy of Sciences* **1133**: 67–86.

Roberts, M. G. and Heesterbeek, J. A. P. (2003) A new method for estimating the effort required to control an infectious disease. *Proceedings of the Royal Society London B* **270**: 1359–1364.

Taylor P. D. (1989) Evolutionary stability in one-parameter models under weak selection. *Theoretical Population Biology* **36**: 125-143.

Taylor, P. D. and Bulmer, M. G. (1980). Local mate competition and the sex ratio. *Journal of theoretical Biology* **86**: 409-419.

Thieme, H. R. (2009) Spectral bound and reproduction number for infinite dimensional population structure and time heterogeneity. *SIAM Journal of Applied Mathematics* **70**: 188-211.

Van Dooren T. J. M. (1999) The evolutionary ecology of dominance-recessivity. *Journal of theoretical Biology* **198**: 519-532.

Van Dooren T. J. M. (2000). The evolutionary dynamics of direct phenotypic overdominance: emergence possible, loss probable. *Evolution* **54**: 1899-1914.

Van Dooren T. J. M. (2006) Protected polymorphism and evolutionary stability in pleiotropic models with trait specific dominance *Evolution* **60**: 1991-2003.

Van Doorn S. and Dieckmann, U. (2006) The long-term evolution of multi-locus traits under frequency-dependent disruptive selection. *Evolution* **60**: 2226-2238.

Wagner, G. P. and Mezey, J. (2000) Modeling the evolution of genetic architecture: a continuum of alleles model with pairwise A×A epistasis. *Journal of theoretical Biology* **203**: 163-175.