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GRADIENTS VERSUS CYCLING IN
GENETIC SELECTION MODELS

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PREFACE

In this paper, J. Hofbauer classifies many models of population genetics in terms of the complexity of the associated dynamics. The simplest models are gradients with respect to an appropriate Riemann metric. For more complex models cycling may occur, thus precluding gradient-type dynamics.

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GRADIENTS VERSUS CYCLING IN GENETIC SELECTION MODELS

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We review the hierarchy of (continuous time) selection models starting with the classical Fisher's viability selection model, and its generalizations when allowing mutations, recombination, sex-dependent viabilities, fertility selection and different mortality rates. We analyse the question in which way Fisher's "Fundamental Theorem of Natural Selection" and Kimura's Maximum Principle can be extended to these more general situations. It turns out that in many cases this is principally impossible since the dynamics becomes cycling or even chaotic.

1. VIABILITY SELECTION

1.1. The basic selection model in population genetics was introduced by Fisher (1930). He considered one gene locus with n possible alleles A_1, \dots, A_n . Let x_1, \dots, x_n be the frequencies of these alleles within the gene pool of the adult population. Assuming random mating, the frequency of the genotype $A_i A_j$ among the zygotes will be - according to the Hardy-Weinberg law - $2x_i x_j$ (if $i \neq j$) resp. x_i^2 (if $i = j$). Now assume that the individuals are not equally adapted to the environment and that a genotype $A_i A_j$ will survive until adult age only with probability w_{ij} . Then $w_{ij} \geq 0$, $w_{ij} = w_{ji}$ and w_{ij} is also called the fitness of $A_i A_j$. The number of adults $A_i A_j$ in the next generation is therefore proportional to $w_{ij} x_i x_j$ and the frequency of the gene A_i is then given by the recurrence relation

$$x_i' = x_i \frac{\sum_{j=1}^n w_{ij} x_j}{\bar{w}} \quad (1)$$

where

$$\bar{w} = \sum_{r,s=1}^n w_{rs} x_r x_s \quad (2)$$

the mean fitness of the whole population is needed as a normalization factor to guarantee $\sum x_i = \sum x_i' = 1$. Instead of assuming separate generations one may also consider overlapping generations, which leads to the differential

equation

$$\dot{x}_i = x_i \left(\sum_{j=1}^n w_{ij} x_j - \bar{w} \right) \quad (3)$$

which could also be obtained by a limiting argument from (1), since $x_i' - x_i = \dot{x}_i / \bar{w}$. The state space of both (1) and (3) is the probability simplex

$$S_n = \{x = (x_1, \dots, x_n) : \sum x_i = 1, x_i \geq 0\}.$$

The selection equations (1) and (3) are rather well understood and their dynamics is characterized by two essential features:

1) FISHER's Fundamental Theorem of Natural Selection: The mean fitness \bar{w} increases steadily along the orbits of both (1) and (3).

Mathematically speaking this means that mean fitness is a Lyapunov function:

$$\dot{\bar{w}}/2 = \sum w_{ij} \dot{x}_i x_j = \sum x_i w_i (w_i - \bar{w}) = \sum x_i (w_i^2 - \bar{w}^2) = \sum x_i (w_i - \bar{w})^2 \geq 0.$$

i.e. the change in mean fitness is twice the variance of fitness of the population. For (1) the proof is more technical (see e.g. EWENS (1979)). As a consequence all orbits of (1) and (3) will converge to the fixed points.

This picture of a population steadily climbing uphill in a fitness landscape is very attractive and satisfying and still very common among population genetists (despite the contrary results we will discuss below). Historically it was a justification of Darwinism on the basis of Mendelism, two (r)evolutionary theories which had been considered to be incompatible before.

2) KIMURA's Maximum Principle (1958) states that the change of the state of the population proceeds in such a way that the increase of mean fitness is the maximal possible. Mathematically this would mean that (3) is a gradient system: The orbits follow the steepest ascent on the fitness landscape \bar{w} , they are orthogonal to its contour lines. But this assertion is obviously wrong since e.g. the boundary of the state space S_n would not be an invariant set.

But as often, when great men make "obviously wrong" statements, there is some truth behind it. It was Shahshahani (1979) who noticed that one needs only to redefine "orthogonality", i.e. to introduce a new Riemannian metric at every point of the simplex. This Shahshahani metric at $p \in S_n$ is simply given by

$$\langle x, y \rangle_p = \sum \frac{x_i y_i}{p_i} \quad \text{for } x, y \in T_p S_n. \quad (4)$$

More generally it can be shown (see e.g. Sigmund(1984)), that

$$\dot{x}_i = x_i (f_i(x) - \bar{f}), \quad \bar{f} = \sum x_i f_i \quad (5)$$

is a Shahshahani gradient on S_n , if $\dot{x}_i = f_i(x)$ is a usual gradient, i.e.

$f_i(x) = \partial V / \partial x_i$. For the selection equation (3) $f_i(x) = \sum w_{ij} x_j = \frac{1}{2} \frac{\partial \bar{w}}{\partial x_i}$ holds, since the fitness matrix (w_{ij}) is symmetric.

Another (equivalent) possibility to "save" Kimura's principle would be to make a change of coordinates: with $y_i = x_i^{1/2}$, (3) becomes a gradient system (with respect to the usual Euclidean metric) on the sphere $\sum y_i^2 = 1$. (see Akin (1979)).

1.2. As a first generalization of this basic selection model we consider a model allowing mutations. Following Crow - Kimura (1970) or Hadeler (1981) mutations occur within the pool of newly produced genes, with probability ϵ_{ij} from A_j to A_i , after selection has changed the gene frequencies as before from x_i to $x_i w_i / \bar{w}$. So the action of selection and mutation is described by the recurrence equation

$$\bar{w} x_i' = \sum_j \epsilon_{ij} x_j \sum_k w_{jk} x_k \quad (6)$$

which is usually replaced by the analogous differential equation

$$\dot{x}_i = \sum_{j,k} \epsilon_{ij} x_j w_{jk} x_k - x_i \bar{w}. \quad (7)$$

Akin (1979) considers a different model, with simultaneous action of selection and mutation:

$$\dot{x}_i = x_i \left(\sum_j w_{ij} x_j - \bar{w} \right) + \sum_j \left(\epsilon_{ij} x_j - \epsilon_{ji} x_i \right) \quad (8)$$

Mathematically, Akin's uncoupled version can be obtained as limit case $\delta \rightarrow 0$ from (7), after the scaling

$$\epsilon_{ij} \rightarrow \delta \epsilon_{ij} \quad (i \neq j), \quad w_{ij} \rightarrow 1 + \delta w_{ij}, \quad t \rightarrow t/\delta. \quad (9)$$

The special case of equal mutation rates, say

$$\epsilon_{ij} = \epsilon_i \quad (i \neq j), \quad \epsilon_{ii} = 1 - (n-1)\epsilon_i \quad (10)$$

deserves separate analysis. Hadeler (1981) studied in detail the case $\epsilon_i = \epsilon/n$, and after proving local stability, he posed the problem to find a Lyapunov function for (7) to globalize his results. This is now easily done: With his assumptions, (7) simplifies to (for the more general case (10) see Hofbauer (1984)):

$$\begin{aligned} \dot{x}_i &= x_i (w_i - \bar{w}) + \epsilon (\bar{w}/n - x_i w_i) \\ &= x_i (f_i(x) - \bar{f}) \bar{w} \end{aligned} \quad (11)$$

with

$$f_i(x) = (1-\epsilon) \frac{w_i}{w} + \frac{\epsilon}{n x_i}, \quad \bar{f} = \sum x_i f_i = 1.$$

Since the $f_i(x)$ fulfill the integrability conditions, Sigmund's result on (5) applies and (11) is a Shahshahani gradient with the potential function

$$V(x) = \frac{1-\varepsilon}{2} \log \bar{w} + \frac{\varepsilon}{n} \sum_{i=1}^n \log x_i. \quad (12)$$

In particular one can take $\bar{w} \cdot (x_1 x_2 \dots x_n)^\alpha$, $\alpha = 2\varepsilon/n(1-\varepsilon)$ as the Lyapunov function for the selection - mutation equation (7) under Haldane's conditions which generalizes the mean fitness function \bar{w} in Fisher's selection model. So in this special case all the results on gradient - like behaviour carry over. For Akin's equations (8) essentially the same result holds, but with a different potential:

$$V(x) = \frac{1}{2} \bar{w} + \frac{\varepsilon}{n} \sum_{i=1}^n \log x_i. \quad (13)$$

Now suppose that the mutation rates are not equal. Thanks to Akin's geometric analysis we know now that then the situation is much more delicate: The mutation field $\dot{x}_i = \sum \varepsilon_{ij} x_j - x_i$ is then no longer a gradient with respect to the Shahshahani metric. And Akin (1979) proved that - given any mutation matrix (ε_{ij}) not of the form (10) - one can always find selection matrices (w_{ij}) , such that the combined field (8) undergoes a Hopf bifurcation and periodic orbits occur. By the above approximation argument (9) this result carries over to Haldane's equations (7). This shows that the picture of an adaptive topography (see e.g. Wright (1931)) is no longer reasonable for arbitrary interactions of selection and mutation. The dynamics is no longer gradient-like. The frequency distribution need no longer converge to a stationary equilibrium state, but may oscillate forever. And it is very likely that even chaotic motions should be possible for these differential equations.

1.3. One simplistic assumption in Fisher's selection model is to allow selective differences of alleles at one gene locus only. But even the most primitive species have thousands of different loci on their chromosomes. So let us consider at least the case of two loci A and B with possible alleles A_i ($1 \leq i \leq n$), B_j ($1 \leq j \leq m$). Then there are nm different types of gametes $A_i B_j$, the frequency of which we denote by x_{ij} . Assuming random mating the proportion of $A_i B_j / A_k B_l$ individuals will change from $x_{ij} x_{kl}$ to $w_{ij,kl} x_{ij} x_{kl}$ from zygote to adult age by natural selection. When haploid gametes are produced during meiosis, besides the parental combinations $A_i B_j$ and $A_k B_l$ also "recombinants" $A_i B_l$ and $A_k B_j$ will appear due to cross-overs which happen with a certain probability r depending on the distance between the two loci. This recombination fraction r takes its maximum possible value $1/2$ if the two loci are on different chromosomes. This leads to the following modification of the recurrence equations (1) for the gamete frequencies x_{ij} (see e.g. Karlin (1978), Pollak (1979)):

$$\begin{aligned} \bar{w} x_{ij}' &= (1-r)x_{ij} \sum_{k,l} w_{ij,kl} x_{kl} + r \sum_{k,l} w_{il,kj} x_{il} x_{kj} \\ &= x_{ij} \sum_{k,l} w_{ij,kl} x_{kl} - r D_{ij} \end{aligned} \quad (14)$$

with

$$D_{ij} = \sum_{k,l} (w_{ij,kl} x_{ij} x_{kl} - w_{il,kj} x_{il} x_{kj}) \quad (15)$$

The D_{ij} are called linkage disequilibria. Since usually $w_{ij,kl} = w_{il,kj}$ holds (= no "position effects"), $D_{ij} = 0$ holds if the gamete frequencies x_{ij} can be written as product of the gene frequencies $p_i = \sum_{j=1}^m x_{ij}$ of A_i and $q_j = \sum_{i=1}^n x_{ij}$ of B_j , i.e. if linkage equilibrium holds. It is easy to see that for recombination without selection all D_{ij} tend to 0 and $x_{ij} = p_i q_j$ holds in the limit. On the other hand, if $r = 0$ (= very tight linkage), (14) may be viewed as a selection equation for nm "alleles" $A_i B_j$ and so the selection part is again a gradient with respect to Shahshahani's metric on S_{nm} . But the recombination field is not and Akin (1979) could again prove that

the interaction of both fields may lead to cycling. For the simplest case of two alleles at each of the two loci (TLTA) he computed also the higher order terms which govern the stability of the cycles and showed that both stable and unstable limit cycles are possible (see Akin (1982,1983)). In this case the differential equation version of (14) simplifies to

$$\dot{x}_i = x_i \left(\sum_{j=1}^4 w_{ij} x_j - \bar{w} \right) + \xi_i r b D, \quad i = 1,2,3,4 \quad (16)$$

where x_1, x_2, x_3, x_4 are now the frequencies of the gametes $A_1 B_1, A_1 B_2, A_2 B_1, A_2 B_2$ resp., $D = x_1 x_4 - x_2 x_3$ is the linkage disequilibrium (15), $\xi_1 = -\xi_2 = -\xi_3 = \xi_4 = -1$, and b is the birth rate of the double heterozygote.

1.4. One basic assumption in all our previous models is that there are no sex-differences, i.e. the population may be treated essentially to be monocious. We will now briefly discuss the simplest possible way of allowing sex-differences in the basic viability model. Let there again be n alleles A_1, \dots, A_n at one gene locus, let x_i, y_i be their frequencies in the adult female and male population and let f_{ij} (m_{ij}) be the fitness of an $A_i A_j$ female (male) individual. Now a gene A_i in the female gene pool comes from females $A_i A_j$ which have frequency $x_i y_j + x_j y_i$ at time of conception (random mating) of which only a proportion of f_{ij} will survive. Hence the equations read as (see e.g. Ewens (1979), Karlin (1972,1984), Roux (1977))

$$\begin{aligned} x_i' &= \frac{1}{2} \left[x_i \sum_j f_{ij} y_j + y_i \sum_j f_{ij} x_j \right] / \sum_{r,s} f_{rs} x_r y_s \\ y_i' &= \frac{1}{2} \left[y_i \sum_j m_{ij} x_j + x_i \sum_j m_{ij} y_j \right] / \sum_{r,s} m_{rs} x_r y_s \end{aligned} \quad (17)$$

The differential equations are obtained in the usual way. If $m_{ij} = f_{ij}$ the subspace $x_i = y_i$ of the state space $S_n \times S_n$ is invariant and globally attracting and so (17) reduces to (1). Interesting special cases of (17) are $f_{ij} = 1$, where selection acts only on one sex, or $m_{ij} = \alpha f_{ij} + b$, where selection acts in the same way in both sexes but at a different scale. Here $x_i = y_i$ holds at equilibria and all eigenvalues are real. So it is likely that these equations are gradients. For other cases, e.g. $m_{ij} + f_{ij} = 1$, which is used for sex-ratio models by Karlin (1984), nonsymmetric equilibria are also possible. In any case, no global results seem to be known for the two-sex equation (17), if $n \geq 3$. For two alleles see the next section.

2. FERTILITY SELECTION

2.1. In all selection models described in § 1 the two main assumptions were random mating to have the zygote population in Hardy-Weinberg proportions, and selection acting only by viability differences on the different genotypes. These assumptions are essential in order to deal with gene frequencies x_i of alleles A_i only. In a more general selection model one has to consider genotype frequencies x_{ii} of $A_i A_i$ - zygotes and $2x_{ij}$ of $A_i A_j$ - zygotes ($i \neq j$), so that $\sum_{i,j=1}^n x_{ij} = 1$. Now let $m_{ij}(f_{ij})$ be the viabilities for (fe) male genotypes $A_i A_j$ and let $h(ij,rs)$ be the probability for a mating of an $A_i A_j$ - male with an $A_r A_s$ - female times the fecundity of this type of mating. An $A_i A_j$ - zygote is issued either from an $A_i A_r \times A_j A_s$ or an $A_j A_s \times A_i A_r$ mating (with any r,s). This gives the frequencies of the next zygote generation (see e.g. Roux (1977)):

$$\Phi x'_{ij} = \sum_{r,s} \frac{1}{2} [h(ir,js) m_{ir} f_{js} + h(js,ir) m_{js} f_{ir}] x_{ir} x_{js}. \quad (18)$$

With

$$F(ij,rs) = h(ij,rs) m_{ij} f_{rs} \quad (19)$$

and

$$f(ij,rs) = (F(ij,rs) + F(rs,ij))/2 \quad (20)$$

we observe that mathematically a viability + fertility selection model is reduced to a pure fertility selection model (since we count zygotes here instead of adults):

$$\Phi x'_{ij} = \sum_{r,s} f(ir,js) x_{ir} x_{js} \quad (21)$$

with

$$\Phi = \sum f(ij,kl) x_{ij} x_{kl} \text{ the mean fertility of the population.}$$

The corresponding differential equation reads

$$\dot{x}_{ij} = \sum_{r,s} f(ir,js) x_{ir} x_{js} - x_{ij} \Phi \quad (22)$$

These equations define a dynamics on the $\frac{n(n+1)}{2}$ - simplex which is now forward invariant. Up to the special cases of additive and multiplicative fertilities which will be treated in 2.3, almost nothing is known for the fertility equation (22) if $n \geq 3$. Only the case of $n = 2$ alleles is well-studied and essentially completely analysed (Hadeler and Liberman (1975), Hadeler and Glas (1983), Koth (1984)). In this case the equations reduce to (with $x_{11} = x$, $x_{12} = y$, $x_{22} = z$, and numbering the genotypes A_1A_1, A_1A_2, A_2A_2 by 1,2,3 resp.):

$$\begin{aligned} \dot{x} &= f_{11}x^2 + 2f_{12}xy + f_{22}y^2 - x\phi \\ \dot{y} &= f_{22}y^2 + f_{12}xy + f_{23}yz + f_{13}xz - y\phi \\ \dot{z} &= f_{33}z^2 + 2f_{23}yz + f_{22}y^2 - z\phi \end{aligned} \quad (23)$$

To get rid of the condition $x + 2y + z = 1$, (23) is best studied in the new variables $X = x/y$, $Y = z/y$, leading to

$$\begin{aligned} \dot{X} &= f_{22} + (2f_{12} - f_{22})X + (f_{11} - f_{12})X^2 - f_{23}XY - f_{13}X^2Y \\ \dot{Y} &= f_{22} + (2f_{23} - f_{22})Y + (f_{33} - f_{23})Y^2 - f_{12}XY - f_{13}XY^2 \end{aligned} \quad (24)$$

The main problem when studying a two-dimensional system like (24) is whether it admits periodic orbits. This question was recently solved by Hadeler and Glas (1983), who observed that (24) is "quasimonotone", i.e. all off-diagonal terms of the Jacobian are negative on the whole state space. They have excluded the existence of exponentially stable limit cycles for such systems (in any dimension!) and the existence of periodic orbits in two dimensions. Similar results were obtained by Hirsch (1982) who called such systems "competitive". Now our equations are of a more special form

$$\begin{aligned} \dot{X} &= a(X) - Y b(X) \\ \dot{Y} &= c(Y) - X d(Y) \end{aligned} \quad (25)$$

with $b(X), d(Y) > 0$ implying the "competitive" character. This leads to a more refined result: (24) is a gradient if we again choose a suitable Riemannian metric, or make a change of coordinates. The potential is given by

$$V(X,Y) = \int \frac{a(X)}{b(X)} dx - XY + \int \frac{c(Y)}{d(Y)} dY. \quad (26)$$

Then

$$\dot{V} = \left(\frac{a(X)}{b(X)} - Y \right) \dot{X} + \left(\frac{c(Y)}{d(Y)} - X \right) \dot{Y} \equiv b(X)^{-1} \dot{X}^2 + d(Y)^{-1} \dot{Y}^2 \geq 0$$

and so V is a Lyapunov function. The concrete form of V however is rather messy and it seems to be impossible to generalize this result to $n \geq 3$ alleles. In fact nothing concerning existence of Lyapunov functions or cycling is known for the general n -allelic fertility equation.

2.2. Now reconsidering the derivation of the fertility equation (22) - or any of the above differential equations - we see that it was obtained by a limit process or rather by analogy from the discrete time model (21), a point which has often been criticized, especially for the selection equation (3), see e.g. Ewens (1979). A true model for overlapping generations leading to a differential equation was first worked out by Nagylaki and Crow (1974), see also Ewens (1979), which can be roughly described as follows: the frequencies $x_{ij}(t)$ of $A_i A_j$ will increase in a small time interval Δt due to births by $f(ir,js)x_{ir}x_{js} \Delta t$, with $f(ir,js)$ measuring again the fertility of a $A_i A_r \times A_j A_s$ mating, and decrease due to deaths by $d_{ij} x_{ij} \Delta t$, with d_{ij} being the death rate of $A_i A_j$. This leads to

$$\dot{x}_{ij} = \sum_{r,s} f(ir,js) x_{ir} x_{js} - d_{ij} x_{ij} - x_{ij} \Phi \quad (27)$$

with

$$\Phi = \sum_{ij,kl} f(ij,kl) x_{ij} x_{kl} - \sum_{ij} d_{ij} x_{ij}$$

denoting the mean fecundity minus the mean mortality, whose appearance in (27) ensures again that the relation $\sum_{i,j} x_{ij} = 1$ is kept invariant. So within a continuous time model, not only different fertility rates but also different mortality rates arise in a natural way. The continuous fertility-mortality equation is therefore more general than (22). Only in the case of equal mortality rates $d_{ij} \equiv d$, (27) is equivalent to (22).

With different mortality rates, (27) cannot be a gradient, even for $n = 2$, as was recently discovered by Koth (1984): Introducing the same coordinates X, Y which simplify (23) to (24), (27) transforms for $n = 2$ into the following generalization of (24):

$$\begin{aligned} \dot{X} &= f_{22} + (2f_{12} - f_{22} + 2(d_2 - d_1)) X + (f_{11} - f_{12} + d_2 - d_1) X^2 + \\ &\quad + (-f_{23} + d_2 - d_1) XY - f_{13} X^2 Y \\ \dot{Y} &= f_{22} + (2f_{32} - f_{22} + 2(d_2 - d_3)) Y + (f_{33} - f_{32} + d_2 - d_3) Y^2 + \\ &\quad + (-f_{12} + d_2 - d_3) XY - f_{13} XY^2 \end{aligned} \quad (28)$$

But now the coefficients of XY need no longer be negative and the system is not competitive in general. So the above argument does not work. And in fact Koth (1984) constructed examples where (28) has a fixed point with complex eigenvalues (so it cannot be a gradient), which - when varying some parameter - cross the imaginary axis. Hence Hopf bifurcations occur and periodic orbits are possible for (28). A more refined analysis of the higher order terms, using Marsden - Mc Cracken's (1976) formula, shows that both stable and unstable periodic orbits may occur. But it seems that these orbits are limited in size, they generally disappear very soon by a blue-sky (= homoclinic) bifurcation.

2.3. We conclude with some remarks concerning the interrelationship of the fertility equation with other selection models, in order to obtain more insight into the logical hierarchy of selection models, as indicated in the diagram in 3.2.

The first observation is rather unexpected and surprising: the two-allelic fertility-mortality equation occurs as a subsystem of the TLTA-system (16). Akin (1983) proposed to study (16) equipped with some additional symmetry, e.g. that A_1B_2 and A_2B_1 should behave equally, i.e. $w_{2i} = w_{3i}$ for all i . Then the plane $x_2 = x_3$ is invariant and with $X = x_1/x_2$ and $Y = x_4/x_2$ the flow is there given by

$$\begin{aligned}\dot{X} &= X \{2(w_{12}-w_{22}) + (w_{11}-w_{12})X + (w_{14}-w_{24})Y\} + rb(1+X)(1-XY) \\ \dot{Y} &= Y \{2(w_{42}-w_{22}) + (w_{44}-w_{42})Y + (w_{14}-w_{21})X\} + rb(1+Y)(1-XY)\end{aligned}\quad (29)$$

Obviously these equations are identical with (28). So the limit cycles found for (28) carry over to (29) and one has at the same time given another (simpler) proof of Akin's result on cycling in TLTA.

Let us now consider the special case of (22) when the parents contribute additively to the fertility rates: $f(ij,kl) = m_{ij} + f_{kl}$. Then (22) reduces to

$$\dot{x}_{ij} = x_i F(j) + x_j F(i) - x_{ij} \Phi \quad (30)$$

with

$$F(i) = \frac{1}{2} \sum_{k=1}^n (m_{ik} + f_{ik}) x_{ik} \quad \text{and} \quad \Phi = 2 \sum_{i=1}^n F(i).$$

For the gene frequency $x_i = \sum_{k=1}^n x_{ik}$ of A_i we obtain

$$\dot{x}_i = F(i) - x_i \Phi/2 \quad (31)$$

Then $(x_{ij} - x_i x_j)' = - (x_{ij} - x_i x_j) \Phi$ implies that in the limit $t \rightarrow +\infty$, $x_{ij} = x_i x_j$ holds, and the population is in Hardy - Weinberg equilibrium. But then (31) simplifies to Fisher's selection equation (3) with $w_{ij} = (m_{ij} + f_{ij})/2$. So the case of additive fertilities is essentially equivalent to the basic viability model.

Finally we consider the case of multiplicative contributions to the fertility rates: $f(ij,kl) = m_{ij} f_{kl}$. Then (21) reads as

$$x_{ij}' = \frac{M(i)F(j) + M(j)F(i)}{2\Phi} \quad (32)$$

with $M(i) = \sum_{k=1}^n m_{ik} x_k$, $F(i) = \sum_{k=1}^n f_{ik} x_k$, $M = \sum_{i=1}^n M(i)$, $F = \sum_{i=1}^n F(i)$, $\Phi = MF$.

Then for the new variables $X_i = F(i)/F$ and $Y_i = M(i)/M$, (32) reduces exactly to the two-sex equation (17), as is also clear from the derivation of (18). A similar connection holds for the differential equations. In particular, if the male and female contributions are equal, $m_{ij} = f_{ij}$, (22) leads to

$$\dot{x}_{ij} = M(i)M(j) - x_{ij}M^2 \quad (33)$$

and

$$\dot{X}_i = X_i (\sum_{ij} X_j - \bar{m}) M \quad (34)$$

Hence the multiplicative fertility case with sex-independent contributions is also equivalent to Fisher's selection equation (1) resp. (3) and is therefore a gradient. The Hardy-Weinberg law however holds only for the discrete time model, but not for (33).

3. CONCLUDING REMARKS

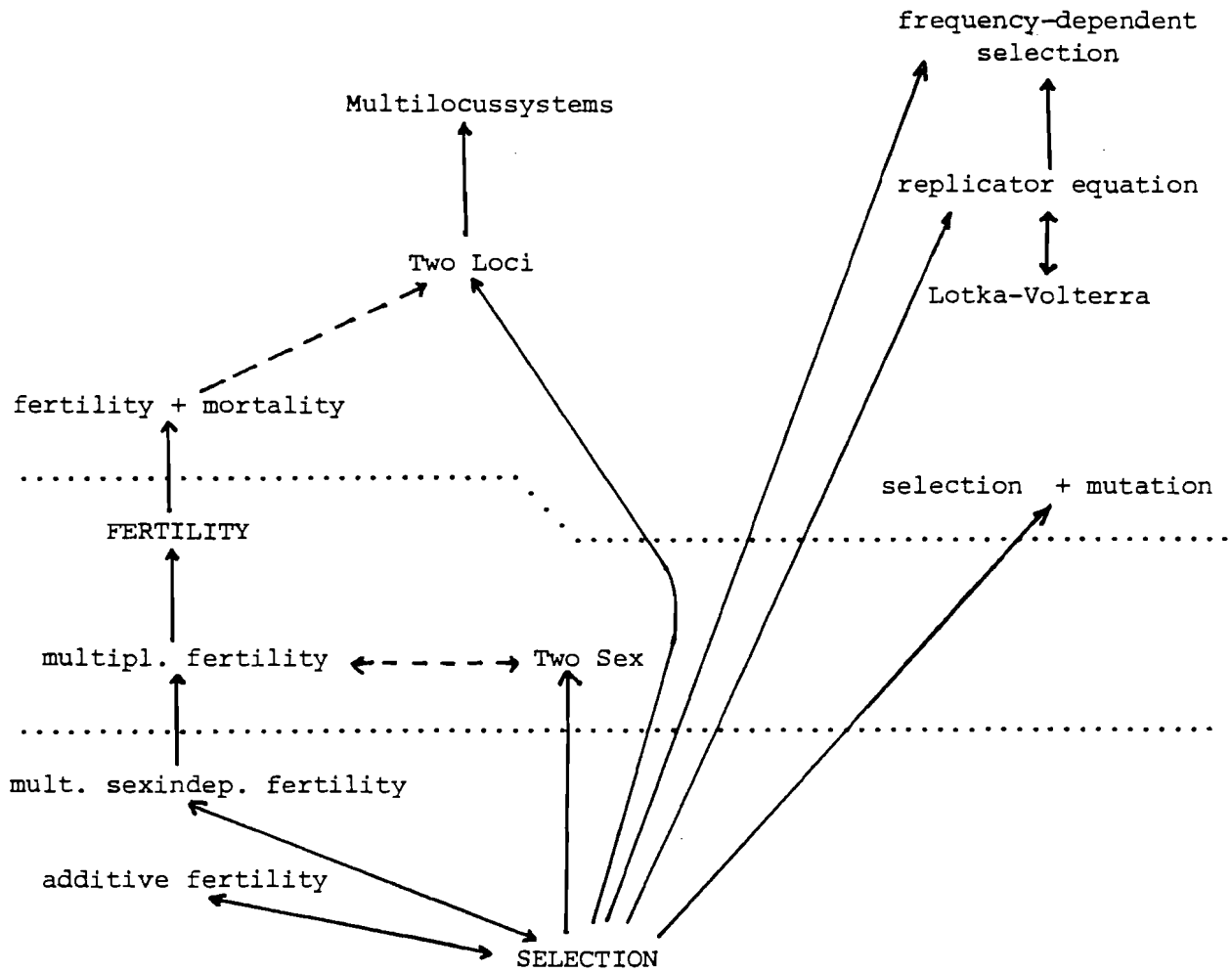
3.1. In this paper I wanted to give some survey on the different selection models used in population genetics. The basic model is Fisher's viability selection model (1), (3) which behaves very nicely, since it is a gradient with mean fitness as a potential. This led to the wide-spread view among population geneticists that the evolution of gene (or genotype) frequencies within a population can be described by an "adaptive topography" and mean fitness or some suitable generalization of it will be optimized by evolution. However, research in the last years, mainly due to Akin, shows that this optimistic view cannot be maintained. Most of the generalizations of the basic model, allowing e.g. mutations, recombination, different fertility, and mortality rates etc. do not show gradient-like behaviour. The dynamics becomes much richer and more complicated: Oscillations (and probably also chaotic motions) occur.

Such periodic oscillations are well-known in other parts of biomathematics, the classical example being predator-prey interactions in population ecology. But population geneticists generally believed their equations to be free of such behaviour - maybe with the exception of frequency dependent selection. For a recent example of cycling in a frequency dependent TLTA system modelling the "battle of sexes" see Maynard Smith and Hofbauer (1984).

I confined myself to the dynamical behaviour of the differential equations. Now it is well-known that difference equations can play much worse things than corresponding differential equations. So it is not surprising that the results on cycling carry over to the discrete time models whenever they are found in the continuous time models. Mathematically this follows from a theorem in Hofbauer and Iooss (1984). For the basic selection model, which in continuous time is a gradient, the difference equation behaves equally well. Hopefully this can be extended to the selection-mutation equation with equal mutation rates. For the discrete version of the two-allelic fertility equation however, the function V from (26) cannot be a Lyapunov function, since stable periodic points of period 2 may arise by overshooting effects (see Haderler and Liberman (1975)).

3.2. The hierarchy of genetic selection models

The diagram below lists all selection models treated in this paper and shows the interrelations between them. The two dotted lines separate the models which lead to gradients from those which may produce cycles. For the intermediate region the problem is not yet solved.



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