

# Migration-Selection Models in Population Genetics

Reinhard Bürger

(Lecture notes<sup>1</sup>, University of Vienna, Department of Mathematics)

## Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
<b>2</b>	<b>Selection on a multiallelic locus</b>	<b>5</b>
2.1	The Hardy–Weinberg Law . . . . .	6
2.2	Evolutionary dynamics under selection . . . . .	7
2.3	Two alleles and the role of dominance . . . . .	10
2.4	The continuous-time selection model . . . . .	12
<b>3</b>	<b>The general migration-selection model</b>	<b>14</b>
3.1	The recurrence equations . . . . .	15
3.2	The relation between forward and backward migration rates . . . . .	16
3.3	Important special migration patterns . . . . .	18
<b>4</b>	<b>Two alleles and finitely many demes</b>	<b>21</b>
4.1	Protected polymorphism . . . . .	21
4.2	Two demes . . . . .	23
<b>5</b>	<b>Migration and selection in continuous time</b>	<b>26</b>
<b>6</b>	<b>Derivation of the PDE migration-selection model</b>	<b>28</b>
<b>7</b>	<b>PDE models for two alleles</b>	<b>35</b>
7.1	Fisher’s equation . . . . .	36
7.2	Hybrid zones . . . . .	39

---

<sup>1</sup>January 16, 2017

7.3	Clines under spatially heterogeneous selection . . . . .	42
7.3.1	The step environment in the infinite cline . . . . .	42
7.4	Clines in a finite domain . . . . .	48
7.4.1	The ODE model with no dominance and two demes . . . . .	49
7.4.2	The PDE model with no dominance . . . . .	50
7.4.3	Proof of Proposition 7.2 . . . . .	52
7.4.4	Proof of Theorem 7.5 (i) . . . . .	56
7.4.5	Proof of Theorem 7.5 (ii), (iii) . . . . .	60
7.5	Clines in a finite domain with dominance: Results and open problems . . .	61
7.5.1	Complete dominance . . . . .	61
7.5.2	Partial dominance . . . . .	63
7.6	Further directions . . . . .	65
<b>A</b>	<b>Appendix: Perron–Frobenius theory</b>	<b>67</b>
<b>B</b>	<b>Appendix: Maximum principles</b>	<b>69</b>
<b>C</b>	<b>Appendix: Basics from PDE theory</b>	<b>72</b>
<b>D</b>	<b>Appendix: Spectrum of elliptic operators of second order</b>	<b>73</b>
D.1	Principal eigenvalue . . . . .	73
D.2	Spectral theory for $L$ in divergence form . . . . .	74
<b>R</b>	<b>References</b>	<b>76</b>

# 1 Introduction

Population genetics is concerned with the study of the genetic composition of populations. This composition is shaped by selection, mutation, recombination, mating behavior and reproduction, migration, and other genetic, ecological, and evolutionary factors. Therefore, these mechanisms and their interactions and evolutionary consequences are investigated. Traditionally, population genetics has been applied to animal and plant breeding, to human genetics, and more recently to ecology and conservation biology. One of the main subjects is the investigation of the mechanisms that generate and maintain genetic variability in populations, and the study of how this genetic variation, shaped by environmental influences, leads to evolutionary change, adaptation, and speciation. Therefore, population genetics provides the basis for understanding the evolutionary processes that have led to the diversity of life we encounter and admire.

Mathematical models and methods have a long history in population genetics, tracing back to Gregor Mendel, who used his education in mathematics and physics to draw his conclusions. Francis Galton and the biometricians, notably Karl Pearson, developed new statistical methods to describe the distribution of trait values in populations and to predict their change between generations. Yule (1902), Hardy (1908), and Weinberg (1908, 1909) worked out simple, but important, consequences of the particulate mode of inheritance proposed by Mendel in 1866 that contrasted and challenged the then prevailing blending theory of inheritance. However, it was not before 1918 that the synthesis between genetics and the theory of evolution through natural selection began to take shape through Fisher's (1918) work. By the early 1930s, the foundations of modern population genetics had been laid by the work of Ronald A. Fisher, J.B.S. Haldane, and Sewall Wright. They had demonstrated that the theory of evolution by natural selection, proposed by Charles Darwin in 1859, can be justified on the basis of genetics as governed by Mendel's laws. A detailed account of the history of population genetics is given in Provine (1971).

In the following, we explain some basic facts and mechanisms that are needed for our course. Mendel's prime achievement was the recognition of the particulate nature of the hereditary determinants, now called genes. Its position along the DNA is called the *locus*, and a particular sequence there is called an *allele*. In most higher organisms, genes are present in pairs, one being inherited from the mother, the other from the father. Such organisms are called diploid. The allelic composition is called the *genotype*, and the set of observable properties derived from the genotype is the *phenotype*.

*Meiosis* is the process of formation of reproductive cells, or *gametes* (in animals, sperm

and eggs) from somatic cells. Under *Mendelian segregation*, each gamete contains precisely one of the two alleles of the diploid somatic cell and each gamete is equally likely to contain either one. The separation of the paired alleles from one another and their distribution to the gametes is called *segregation* and occurs during meiosis. At mating, two reproductive cells fuse and form a *zygote* (fertilized egg), which contains the full (diploid) genetic information.

Any heritable change in the genetic material is called a *mutation*. Mutations are the ultimate source of genetic variability and form the raw material upon which selection acts. Although the term mutation includes changes in chromosome structure and number, the vast majority of genetic variation is caused by changes in the DNA sequence. Such mutations occur in many different ways, for instance as base substitutions, in which one nucleotide is replaced by another, as insertions or deletions of DNA, as inversions of sequences of nucleotides, or as transpositions. For the population-genetic models treated in this text the molecular origin of a mutant is of no relevance because they assume that the relevant alleles are initially present.

During meiosis, different chromosomes assort independently and *crossing over* between two homologous chromosomes may occur. Consequently, the newly formed gamete contains maternal alleles at one set of loci and paternal alleles at the complementary set. This process is called *recombination*. Since it leads to random association between alleles at different loci, recombination has the potential to combine favorable alleles of different ancestry in one gamete and to break up combinations of deleterious alleles. These properties are generally considered to confer a substantial evolutionary advantage to sexual species relative to asexuals.

The mating pattern may have a substantial influence on the evolution of gene frequencies. The simplest and most important mode is *random mating*. This means that matings take place without regard to ancestry or the genotype under consideration. It seems to occur frequently in nature. For example, among humans, matings within a population appear to be random with respect to blood groups or allozyme phenotypes, but are nonrandom with respect to other traits, for example, height.

*Selection* occurs when individuals of different genotype leave different numbers of progeny because they differ in their probability to survive to reproductive age (*viability*), in their mating success, or in their average number of produced offspring (*fertility*). Darwin recognized and documented the central importance of selection as the driving force for adaptation and evolution. Since selection affects the entire genome, its consequences for the genetic composition of a population may be complex. Selection is measured in

terms of *fitness* of individuals, i.e., by the number of progeny contributed to the next generation. There are different measures of fitness, and it consists of several components because selection may act on each stage of the life cycle.

Because many natural populations are geographically structured and selection varies spatially due to heterogeneity in the environment, it is important to study the consequences of spatial structure for the evolution of populations. Dispersal of individuals is usually modeled in one of two alternative ways, either by diffusion in space or by migration between discrete niches, or demes. If the population size is sufficiently large, so that random genetic drift can be ignored, then the first kind of model leads to partial differential equations (Fisher 1937, Kolmogoroff et al. 1937). This is a natural choice if genotype frequencies change continuously along an environmental gradient, as it occurs in a cline (Haldane 1948).

This lecture course will focus on models in which populations inhabit a continuous habitat and disperse in a way that is similar to diffusion. However, before we turn to this topic, we will briefly introduce the basic theory about selection in a panmictic, i.e., randomly mating and unstructured, population, and then introduce models describing evolution in subdivided populations that inhabit discrete niches. Such models are most appropriate if the dispersal distance is short compared to the scale at which the environment changes, or if the habitat is fragmented. They also provide us with important intuition about the more complex models of migration in continuous space.

For mathematically oriented introductions to the much broader field of population genetics, we refer to the books of Nagylaki (1992), Bürger (2000), Ewens (2004), and Wakeley (2008). The two latter texts treat stochastic models in detail, an important and topical area ignored in this course. As an introduction to evolutionary genetics, we recommend Charlesworth and Charlesworth (2010).

## 2 Selection on a multiallelic locus

Darwinian evolution is based on selection and inheritance. In this section, we summarize the essential properties of simple selection models. It will prepare the ground for the subsequent study of the joint action of spatially varying selection and migration. Proofs and a detailed treatment may be found in Chapter I of Bürger (2000). Our focus is on the evolution of the genetic composition of the population, but not on its size. Therefore, we always deal with relative frequencies of genes or genotypes within a given population.

Unless stated otherwise, we consider a population with discrete, nonoverlapping gen-

erations, such as annual plants or insects. We assume two sexes that need not be distinguished because gene or genotype frequencies are the same in both sexes (as is always the case in monoecious species). Individuals mate at random with respect to the locus under consideration, i.e., in proportion to their frequency. We also suppose that the population is large enough that gene and genotype frequencies can be treated as deterministic, and relative frequency can be identified with probability. Then the evolution of gene or genotype frequencies can be described by difference or recurrence equations. These assumptions reflect an idealized situation which will model evolution at many loci in many populations or species, but which is by no means universal.

## 2.1 The Hardy–Weinberg Law

With the blending theory of inheritance variation in a population declines rapidly, and this was one of the arguments against Darwin’s theory of evolution. With Mendelian inheritance there is no such dilution of variation, as was shown independently by the famous British mathematician Hardy (1908) and, in much greater generality, by the German physician Weinberg (1908, 1909).

We consider a single locus with  $I$  possible alleles  $\mathcal{A}_i$  and write  $\mathcal{I} = \{1, \dots, I\}$  for the set of all alleles. We denote the frequency of the ordered genotype  $\mathcal{A}_i\mathcal{A}_j$  by  $P_{ij}$ , so that the frequency of the unordered genotype  $\mathcal{A}_i\mathcal{A}_j$  is  $P_{ij} + P_{ji} = 2P_{ij}$ . Subscripts  $i$  and  $j$  always refer to alleles. Then the frequency of allele  $\mathcal{A}_i$  in the population is

$$p_i = \sum_j P_{ij} .^2$$

After one generation of random mating the zygotic proportions satisfy<sup>3</sup>

$$P'_{ij} = p_i p_j \quad \text{for every } i \text{ and } j .$$

A mathematically trivial, but biologically very important, consequence is that (in the absence of other forces) gene frequencies remain constant across generations, i.e.,

$$p'_i = p_i \quad \text{for every } i . \tag{2.1}$$

In other words, in a (sufficiently large) randomly mating population reproduction does not change allele frequencies. A population is said to be in *Hardy–Weinberg equilibrium*

---

<sup>2</sup>Sums or products without ranges run over all admissible values; e.g.  $\sum_j = \sum_{j \in \mathcal{I}}$ .

<sup>3</sup>Unless stated otherwise, a prime,  $'$ , always signifies the next generation. Thus, instead of  $P_{ij}(t)$  and  $P_{ij}(t+1)$ , we write  $P_{ij}$  and  $P'_{ij}$  (and analogously for other quantities).

if

$$P_{ij} = p_i p_j. \quad (2.2)$$

In a (sufficiently large) randomly mating population, this relation is always satisfied among zygotes.

Evolutionary mechanisms such as selection, migration, mutation, or random genetic drift distort Hardy-Weinberg proportions, but Mendelian inheritance restores them if mating is random.

## 2.2 Evolutionary dynamics under selection

Selection occurs when genotypes in a population differ in their fitnesses, i.e., in their viability, mating success, or fertility and, therefore, leave different numbers of progeny. The basic mathematical models of selection were developed and investigated in the 1920s and early 1930s by Fisher (1930), Wright (1931), and Haldane (1932).

We will be concerned with the evolutionary consequences of selection caused by differential viabilities, which leads to simpler models than (general) fertility selection (e.g. Hofbauer and Sigmund 1988, Nagylaki 1992). Suppose that at an autosomal locus the alleles  $\mathcal{A}_1, \dots, \mathcal{A}_I$  occur. We count individuals at the zygote stage and denote the (relative) frequency of the ordered genotype  $\mathcal{A}_i \mathcal{A}_j$  by  $P_{ij} (= P_{ji})$ . Since mating is at random, the genotype frequencies  $P_{ij}$  are in Hardy-Weinberg proportions. We assume that the fitness (viability)  $w_{ij}$  of an  $\mathcal{A}_i \mathcal{A}_j$  individual is nonnegative and constant, i.e., independent of time, population size, or genotype frequencies. In addition, we suppose  $w_{ij} = w_{ji}$ , as is usually the case. Then the frequency of  $\mathcal{A}_i \mathcal{A}_j$  genotypes among adults that have survived selection is

$$P_{ij}^* = \frac{w_{ij} P_{ij}}{\bar{w}} = \frac{w_{ij} p_i p_j}{\bar{w}},$$

where we have used (2.2). Here,

$$\bar{w} = \sum_{i,j} w_{ij} P_{ij} = \sum_{i,j} w_{ij} p_i p_j = \sum_i w_i p_i \quad (2.3)$$

is the *mean fitness* of the population and

$$w_i = \sum_j w_{ij} p_j \quad (2.4)$$

is the *marginal fitness* of allele  $\mathcal{A}_i$ . Both are functions of  $p = (p_1, \dots, p_I)^\top$ .<sup>4</sup>

---

<sup>4</sup>Throughout, the superscript  $\top$  denotes vector or matrix transposition.

Therefore, the frequency of  $\mathcal{A}_i$  after selection is

$$p_i^* = \sum_j P_{ij}^* = p_i \frac{w_i}{\bar{w}}. \quad (2.5)$$

Because of random mating, the allele frequency  $p_i'$  among zygotes of the next generation is also  $p_i^*$  (2.1), so that allele frequencies evolve according to the *selection dynamics*

$$p_i' = p_i \frac{w_i}{\bar{w}}, \quad i \in I. \quad (2.6)$$

This recurrence equation preserves the relation

$$\sum_i p_i = 1$$

and describes the evolution of allele frequencies at a single autosomal locus in a diploid population. We view the selection dynamics (2.6) as a (discrete) dynamical system on the simplex

$$S_I = \left\{ p = (p_1, \dots, p_I)^\top \in \mathbb{R}^I : p_i \geq 0 \text{ for every } i \in I, \sum_i p_i = 1 \right\}. \quad (2.7)$$

Although selection destroys Hardy-Weinberg proportions, random mating re-establishes them. Therefore, (2.6) is sufficient to study the evolutionary dynamics.

The right-hand side of (2.6) remains unchanged if every  $w_{ij}$  is multiplied by the same constant. This is very useful because it allows to rescale the fitness parameters according to convenience (also their number is reduced by one). Therefore, we will usually consider relative fitnesses and not absolute fitnesses.

Fitnesses are said to be *multiplicative* if constants  $v_i$  exist such that

$$w_{ij} = v_i v_j \quad (2.8)$$

for every  $i, j$ . Then  $w_i = v_i \bar{v}$ , where  $\bar{v} = \sum_i v_i p_i$ , and  $\bar{w} = \bar{v}^2$ . Therefore, (2.6) simplifies to

$$p_i' = p_i \frac{v_i}{\bar{v}}, \quad i \in I, \quad (2.9)$$

which can be solved explicitly because it is equivalent to the linear system  $x_i' = v_i x_i$ . It is easy to show that (2.9) also describes the dynamics of a haploid population if the fitness  $v_i$  is assigned to allele  $\mathcal{A}_i$ .

Fitnesses are said to be *additive* if constants  $v_i$  exist such that

$$w_{ij} = v_i + v_j \quad (2.10)$$



for every  $i, j$ . Then  $w_i = v_i + \bar{v}$ , where  $\bar{v} = \sum_i v_i p_i$ , and  $\bar{w} = 2\bar{v}$ . Although this assumption is important (it means absence of dominance; see Sect. 2.3), it does not yield an explicit solution of the selection dynamics.

**Example 2.1.** Selection is very efficient. We assume (2.8). Then the solution of (2.9) is

$$p_i(t) = \frac{p_i(0)v_i^t}{\sum_j p_j(0)v_j^t}. \quad (2.11)$$

Suppose that there are only two alleles,  $\mathcal{A}_1$  and  $\mathcal{A}_2$ . If  $\mathcal{A}_1$  is the wild type and  $\mathcal{A}_2$  is a new beneficial mutant, we may set (without loss of generality!)  $v_1 = 1$  and  $v_2 = 1 + s$ . Then we obtain from (2.11):

$$\frac{p_2(t)}{p_1(t)} = \frac{p_2(0)}{p_1(0)} \left(\frac{v_2}{v_1}\right)^t = \frac{p_2(0)}{p_1(0)} (1 + s)^t. \quad (2.12)$$

Thus,  $\mathcal{A}_2$  increases exponentially relative to  $\mathcal{A}_1$ .

For instance, if  $s = 0.5$ , then after 10 generations the frequency of  $\mathcal{A}_2$  has increased by a factor of  $(1 + s)^t = 1.5^{10} \approx 57.7$  relative to  $\mathcal{A}_1$ . If  $s = 0.05$  and  $t = 100$ , this factor is  $(1 + s)^t = 1.05^{100} \approx 131.5$ . Therefore, slight fitness differences may have a big long-term effect, in particular, since 100 generations are short on an evolutionary time scale.

An important property of (2.6) is that *mean fitness is nondecreasing along trajectories (solutions)*, i.e.,

$$\bar{w}' = \bar{w}(p') \geq \bar{w}(p) = \bar{w}, \quad (2.13)$$

and equality holds if and only if  $p$  is an equilibrium.<sup>5</sup>

A particularly elegant proof of (2.13) was provided by Kingman (1961).

The statement (2.13) is closely related to *Fisher's Fundamental Theorem of Natural Selection*, which Fisher (1930) formulated as follows:

“The rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time.”

For recent discussion, see Ewens (2011) and Bürger (2011). In mathematical terms, (2.13) shows that  $\bar{w}$  is a Lyapunov function. This has a number of important consequences. For instance, complex dynamical behavior such as limit cycles or chaos can be excluded.

---

<sup>5</sup> $p$  is called an equilibrium, or fixed point, of the recurrence equation  $p' = f(p)$  if  $f(p) = p$ . We use the term equilibrium point to emphasize that we consider an equilibrium that is a single point. The term equilibrium may also refer to a (connected) manifold of equilibrium points.

From (2.6) it is obvious that the equilibria are precisely the solutions of

$$p_i(w_i - \bar{w}) = 0 \quad \text{for every } i \in I. \quad (2.14)$$

We call an equilibrium internal, or fully polymorphic, if  $p_i > 0$  for every  $i$  (all alleles are present). The  $I$  equilibria defined by  $p_i = 1$  are called monomorphic because only one allele is present.

The following result summarizes a number of important properties of the selection dynamics. Proofs and references to the original literature may be found in Bürger (2000, Chap. I.9); see also Lyubich (1992, Chap. 9).

**Theorem 2.2.** *1. If an isolated internal equilibrium exists, then it is uniquely determined.*

*2.  $\hat{p}$  is an equilibrium if and only if  $\hat{p}$  is a critical point of the restriction of mean fitness  $\bar{w}(p)$  to the minimal subsimplex of  $S_I$  that contains the positive components of  $\hat{p}$ .*

*3. If the number of equilibria is finite, then it is bounded above by  $2^I - 1$ .*

*4. An internal equilibrium is asymptotically stable if and only if it is an isolated local maximum of  $\bar{w}$ . Moreover, it is isolated if and only if it is hyperbolic (i.e., the Jacobian has no eigenvalues of modulus 1).*

*5. An equilibrium point is stable if and only if it is a local, not necessarily isolated, maximum of  $\bar{w}$ .*

*6. If an asymptotically stable internal equilibrium exists, then every orbit starting in the interior of  $S_I$  converges to that equilibrium.*

*7. If an internal equilibrium exists, it is stable if and only if, counting multiplicities, the fitness matrix  $W = (w_{ij})$  has exactly one positive eigenvalue.*

*8. If the matrix  $W$  has  $i$  positive eigenvalues, at least  $(i - 1)$  alleles will be absent at a stable equilibrium.*

*9. Every orbit converges to one of the equilibrium points (even if they are not isolated).*

### 2.3 Two alleles and the role of dominance

For the purpose of illustration, we work out the special case of two alleles. We write  $p$  and  $1 - p$  instead of  $p_1$  and  $p_2$ . Further, we use relative fitnesses and assume

$$w_{11} = 1, \quad w_{12} = 1 - hs, \quad w_{22} = 1 - s, \quad (2.15)$$

where  $s$  is called the *selection coefficient* and  $h$  describes the degree of dominance. We assume  $s > 0$ .

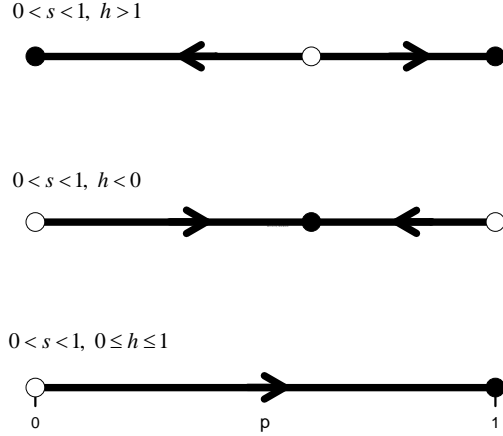


Figure 2.1: Convergence patterns for selection with two alleles.

The allele  $\mathcal{A}_1$  is called *dominant* if  $h = 0$ , partially dominant if  $0 < h < \frac{1}{2}$ , *recessive* if  $h = 1$ , and partially recessive if  $\frac{1}{2} < h < 1$ . *No dominance* refers to  $h = \frac{1}{2}$ . Absence of dominance is equivalent to additive fitnesses (2.10). If  $h < 0$ , there is *overdominance* or *heterozygote advantage*. If  $h > 1$ , there is *underdominance* or *heterozygote inferiority*.

From (2.4), the marginal fitnesses of the two alleles are

$$w_1 = 1 - hs + hsp \quad \text{and} \quad w_2 = 1 - s + s(1 - h)p$$

and, from (2.3), the mean fitness is

$$\bar{w} = 1 - s + 2s(1 - h)p - s(1 - 2h)p^2.$$

It is easily verified that the allele-frequency change from one generation to the next can be written as

$$\Delta p = p' - p = \frac{p(1 - p)}{2\bar{w}} \frac{d\bar{w}}{dp} \tag{2.16a}$$

$$= \frac{p(1 - p)s}{\bar{w}} [1 - h - (1 - 2h)p]. \tag{2.16b}$$

There exists an internal equilibrium if and only if  $h < 0$  (overdominance) or  $h > 1$  (underdominance). It is given by

$$\hat{p} = \frac{1 - h}{1 - 2h}. \tag{2.17}$$

If dominance is intermediate, i.e., if  $0 \leq h \leq 1$ , then (2.16) shows that  $\Delta p > 0$  if  $0 < p < 1$ , hence  $p = 1$  is globally asymptotically stable.

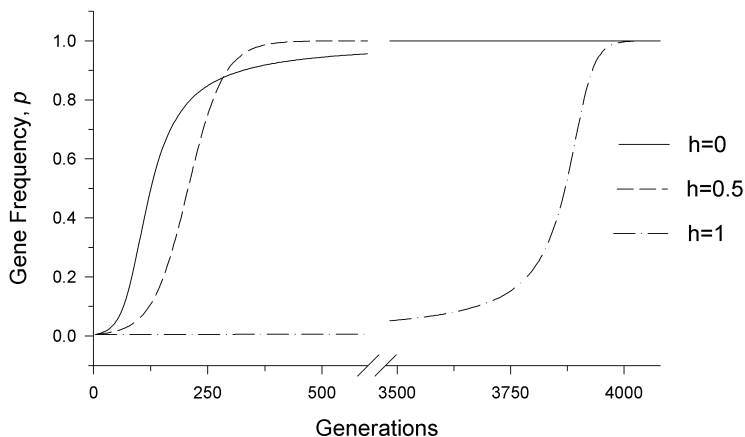


Figure 2.2: Selection of a dominant ( $h = 0$ , solid line), intermediate ( $h = 1/2$ , dashed), and recessive ( $h = 1$ , dash-dotted) allele. The initial frequency is  $p_0 = 0.005$  and the selective advantage is  $s = 0.05$ . If the advantageous allele is recessive, its initial rate of increase is vanishingly small because the frequency  $p^2$  of homozygotes is extremely low when  $p$  is small. However, only homozygotes are ‘visible’ to selection.

If  $h < 0$  or  $h > 1$ , we write (2.16) in the form

$$\Delta p = \frac{sp(1-p)}{\bar{w}}(1-2h)(\hat{p}-p). \quad (2.18)$$

In the case of overdominance ( $h < 0$ ), we have  $0 < sp(1-p)(1-2h)/\bar{w} < 1$  if  $0 < p < 1$ , hence  $\hat{p}$  is globally asymptotically stable and convergence is monotonic. If  $h > 1$ , then the monomorphic equilibria  $p = 0$  and  $p = 1$  each are asymptotically stable and  $\hat{p}$  is unstable.

The three possible convergence patterns are shown in Figure 2.1. Figure 2.2 demonstrates that the degree of (intermediate) dominance strongly affects the rate of spread of an advantageous allele.

## 2.4 The continuous-time selection model

Most higher animal species have overlapping generations because birth and death occur continuously in time. This, however, may lead to substantial complications if one wishes to derive a continuous-time model from biological principles. By contrast, discrete-time models can frequently be derived straightforwardly from simple biological assumptions. If evolutionary forces are weak, a continuous-time version can usually be obtained as an approximation to the discrete-time model.

A rigorous derivation of the differential equations that describe gene-frequency change

under selection in a diploid population with overlapping generations is a formidable task and requires a complex model involving age structure (see Nagylaki 1992, Chap. 4.10). Here, we simply state the system of differential equations and justify it in an alternative way.

In a continuous-time model, the (*Malthusian*) fitness  $m_{ij}$  of a genotype  $\mathcal{A}_i\mathcal{A}_j$  is defined as its birth rate minus its death rate. Then the marginal fitness of allele  $\mathcal{A}_i$  is

$$m_i = \sum_j m_{ij}p_j ,$$

the mean fitness of the population is

$$\bar{m} = \sum_i m_i p_i = \sum_{i,j} m_{ij} p_i p_j ,$$

and the dynamics of allele frequencies becomes

$$\dot{p}_i = \frac{dp_i}{dt} = p_i(m_i - \bar{m}), \quad i \in I. \quad (2.19)$$

This is the analogue of the discrete-time selection dynamics (2.6). Its state space is again the simplex  $S_I$ . The equilibria are obtained from the condition  $\dot{p}_i = 0$  for every  $i$ . The dynamics (2.19) remains unchanged if the same constant is added to every  $m_{ij}$ . We note that (2.19) is a so-called *replicator equation* (Hofbauer and Sigmund 1998).

If we set

$$w_{ij} = 1 + sm_{ij} \quad \text{for every } i, j \in I, \quad (2.20)$$

where  $s > 0$  is (sufficiently) small, the difference equation (2.6) and the differential equation (2.19) have the same equilibria. This is obvious upon noting that (2.20) implies  $w_i = 1 + sm_i$  and  $\bar{w} = 1 + s\bar{m}$ . Importantly, if the same constant is added to every  $m_{ij}$ , equation (2.19) remains unchanged. This allows for convenient scaling of the fitnesses.

Following Nagylaki (1992, p. 99), we approximate the discrete model (2.6) by the continuous model (2.19) under the assumption of weak selection, i.e., small  $s$  in (2.20). We rescale time according to  $t = \lfloor \tau/s \rfloor$ , where  $\lfloor \cdot \rfloor$  denotes the closest smaller integer. Then  $s$  may be interpreted as generation length and, for  $p_i(t)$  satisfying the difference equation (2.6), we write  $\pi_i(\tau) = p_i(t)$ . Then we obtain formally

$$\frac{d\pi_i}{d\tau} = \lim_{s \downarrow 0} \frac{1}{s} [\pi_i(\tau + s) - \pi_i(\tau)] = \lim_{s \downarrow 0} \frac{1}{s} [p_i(t + 1) - p_i(t)] .$$

---

<sup>6</sup>Throughout, a dot,  $\dot{\cdot}$ , indicates a derivative with respect to time.

From (2.6) and (2.20), we obtain  $p_i(t+1) - p_i(t) = sp_i(t)(m_i - \bar{m})/(1 + s\bar{m})$ . Therefore,  $\dot{\pi}_i = \pi_i(m_i - \bar{m})$  and  $\Delta p_i \approx s\dot{\pi}_i = sp_i(m_i - \bar{m})$ . We note that (2.6) is essentially the Euler scheme for (2.19).

The exact continuous-time model reduces to (2.19) only if the mathematically inconsistent assumption is imposed that Hardy-Weinberg proportions apply for every  $t$  which is generally not true. Under weak selection, however, deviations from Hardy-Weinberg decay to order  $O(s)$  after a short period of time Nagylaki (1992).

**Example 2.3.** For two alleles, (2.19) simplifies considerably because it is sufficient to track the allele frequency  $p = p_1$ . In addition, we write  $q = 1 - p$ .

Scaling the Malthusian parameters in the following way

$$\begin{array}{ccc} \mathcal{A}_1\mathcal{A}_1 & \mathcal{A}_1\mathcal{A}_2 & \mathcal{A}_2\mathcal{A}_2 \\ 0 & -hs & -s \end{array},$$

we obtain the simple representations

$$\dot{p} = \frac{1}{2}spq \quad \text{if } h = \frac{1}{2} \text{ (no dominance)} \quad (2.21)$$

and

$$\dot{p} = spq^2 \quad \text{if } h = 0 \text{ (}\mathcal{A}_1 \text{ is dominant)}. \quad (2.22)$$

Equation (2.21) is also obtained for a haploid population in which  $\mathcal{A}_2$  has a selective disadvantage of  $\frac{1}{2}s$  relative to  $\mathcal{A}_1$ .

One of the advantages of models in continuous time is that they lead to differential equations, and usually these are easier to analyze because the formalism of calculus is available. An example for this is that, in continuous time, (2.13) simplifies to

$$\dot{\bar{m}} \geq 0, \quad (2.23)$$

which is *much* easier to prove than (2.13):

$$\dot{\bar{m}} = 2 \sum_{i,j} m_{ij} p_j \dot{p}_i = 2 \sum_i m_i \dot{p}_i = 2 \sum_i (m_i^2 - \bar{m}^2) p_i = 2 \sum_i (m_i - \bar{m})^2 p_i.$$

### 3 The general migration-selection model

We assume a population of diploid organisms with discrete, nonoverlapping generations. This population is subdivided into  $\Gamma$  demes (niches). Viability selection acts within each deme and is followed by adult migration (dispersal). After migration random mating

occurs within each deme. We assume that the genotype frequencies are the same in both sexes (e.g., because the population is monoecious). We also assume that, in every deme, the population is so large that gene and genotype frequencies may be treated as deterministic, i.e., we ignore random genetic drift.

### 3.1 The recurrence equations

As before, we consider a single locus with  $I$  alleles  $\mathcal{A}_i$  ( $i \in I$ ). Throughout, we use letters  $i, j$  to denote alleles, and greek letters  $\alpha, \beta$  to denote demes. We write  $\mathbf{G} = \{1, \dots, \Gamma\}$  for the set of all demes. The presentation below is based on Chapter 6.2 of Nagylaki (1992).

We denote the frequency of allele  $\mathcal{A}_i$  in deme  $\alpha$  by  $p_{i,\alpha}$ . Therefore, we have

$$\sum_i p_{i,\alpha} = 1 \quad (3.1)$$

for every  $\alpha \in \mathbf{G}$ . Because selection may vary among demes, the fitness (viability)  $w_{ij,\alpha}$  of an  $\mathcal{A}_i\mathcal{A}_j$  individual in deme  $\alpha$  may depend on  $\alpha$ . The marginal fitness of allele  $\mathcal{A}_i$  in deme  $\alpha$  and the mean fitness of the population in deme  $\alpha$  are

$$w_{i,\alpha} = \sum_j w_{ij,\alpha} p_{j,\alpha} \quad \text{and} \quad \bar{w}_\alpha = \sum_{i,j} w_{ij,\alpha} p_{i,\alpha} p_{j,\alpha}, \quad (3.2)$$

respectively.

Next, we describe migration. Let  $\tilde{m}_{\alpha\beta}$  denote the probability that an individual in deme  $\alpha$  migrates to deme  $\beta$ , and let  $m_{\alpha\beta}$  denote the probability that an (adult) individual in deme  $\alpha$  immigrated from deme  $\beta$ . The  $\Gamma \times \Gamma$  matrices

$$\tilde{M} = (\tilde{m}_{\alpha\beta}) \quad \text{and} \quad M = (m_{\alpha\beta}) \quad (3.3)$$

are called the *forward* and *backward migration matrices*, respectively. Both matrices are *stochastic*, i.e., they are nonnegative and satisfy

$$\sum_\beta \tilde{m}_{\alpha\beta} = 1 \quad \text{and} \quad \sum_\beta m_{\alpha\beta} = 1 \quad \text{for every } \alpha. \quad (3.4)$$

Given the backward migration matrix and the fact that random mating within each demes does not change the allele frequencies, the allele frequencies in the next generation are

$$p'_{i,\alpha} = \sum_\beta m_{\alpha\beta} p_{i,\beta}^*, \quad (3.5a)$$

where

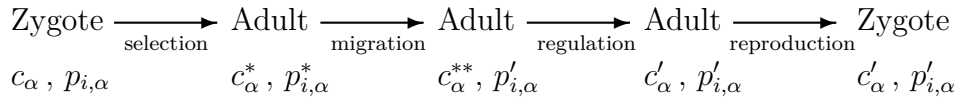
$$p_{i,\alpha}^* = p_{i,\alpha} \frac{w_{i,\alpha}}{\bar{w}_\alpha} \quad (3.5b)$$

describes the change due to selection alone; cf. (2.6). These recurrence equations define a dynamical system on the  $\Gamma$ -fold Cartesian product  $S_I^\Gamma$  of the simplex  $S_I$ .

The difference equations (3.5) require that the backward migration rates are known. In the following, we derive their relation to the forward migration rates and discuss conditions when selection or migration do not change the deme proportions.

### 3.2 The relation between forward and backward migration rates

To derive this relation, we describe the life cycle explicitly. It starts with zygotes on which selection acts (possibly including population regulation). After selection adults migrate and usually there is population regulation after migration (for instance because the number of nesting places is limited). By assumption, population regulation does not change genotype frequencies. Finally, there is random mating and reproduction, which neither changes gene frequencies (Section 2.1) nor deme proportions. The respective proportions of zygotes, pre-migration adults, post-migration adults, and post-regulation adults in deme  $\alpha$  are  $c_\alpha$ ,  $c_\alpha^*$ ,  $c_\alpha^{**}$ , and  $c'_\alpha$ :



Because no individuals are lost during migration, the following must hold:

$$c_\beta^{**} = \sum_\alpha c_\alpha^* \tilde{m}_{\alpha\beta}, \quad (3.6a)$$

$$c_\alpha^* = \sum_\beta c_\beta^{**} m_{\beta\alpha}. \quad (3.6b)$$

The (joint) probability that an adult is in deme  $\alpha$  and migrates to deme  $\beta$  can be expressed in terms of the forward and backward migration rates as follows:

$$c_\alpha^* \tilde{m}_{\alpha\beta} = c_\beta^{**} m_{\beta\alpha}. \quad (3.7)$$

Inserting (3.6a) into (3.7), we obtain the desired connection between the forward and the backward migration rates:

$$m_{\beta\alpha} = \frac{c_\alpha^* \tilde{m}_{\alpha\beta}}{\sum_\gamma c_\gamma^* \tilde{m}_{\gamma\beta}}. \quad (3.8)$$

Therefore, if  $\tilde{M}$  is given, an *ansatz* for the vector  $c^* = (c_1^*, \dots, c_\Gamma^*)^\top$  in terms of  $c = (c_1, \dots, c_\Gamma)^\top$  is needed to compute  $M$  (as well as a hypothesis for the variation, if any, of  $c$ ).



Two frequently used assumptions are the following (Christiansen 1975).

1) *Soft selection*. This assumes that the fraction of adults in every deme is fixed, i.e.,

$$c_\alpha^* = c_\alpha \quad \text{for every } \alpha \in \mathbf{G}. \quad (3.9)$$

This may be a good approximation if the population is regulated within each deme, e.g., because individuals compete for resources locally (Dempster 1955).

2) *Hard selection*. Following Dempster (1955), the fraction of adults will be proportional to mean fitness in the deme if the total population size is regulated. This has been called hard selection and is defined by

$$c_\alpha^* = c_\alpha \bar{w}_\alpha / \bar{w}, \quad (3.10)$$

where

$$\bar{w} = \sum_{\alpha} c_\alpha \bar{w}_\alpha \quad (3.11)$$

is the mean fitness of the total population.

Essentially, these two assumptions are at the extremes of a broad spectrum of possibilities. Soft selection will apply to plants; for animals many schemes are possible.

Under soft selection, (3.8) becomes

$$m_{\beta\alpha} = \frac{c_\alpha \tilde{m}_{\alpha\beta}}{\sum_{\gamma} c_\gamma \tilde{m}_{\gamma\beta}}. \quad (3.12)$$

As a consequence, if  $c$  is constant ( $c' = c$ ),  $M$  is constant if and only if  $\tilde{M}$  is constant. If there is no population regulation after migration, then  $c$  will generally depend on time because (3.6a) yields  $c' = c^{**} = \tilde{M}^\top c$ . Therefore, the assumption of constant deme proportions,  $c' = c$ , will usually require that population control occurs after migration.

A migration pattern that does not change deme proportions ( $c_\alpha^{**} = c_\alpha^*$ ) is called *conservative*. Under this assumption, (3.7) yields

$$c_\alpha^* \tilde{m}_{\alpha\beta} = c_\beta^* m_{\beta\alpha} \quad (3.13)$$

and, by stochasticity of  $M$  and  $\tilde{M}$ , we obtain

$$c_\beta^* = \sum_{\alpha} c_\alpha^* \tilde{m}_{\alpha\beta} \quad \text{and} \quad c_\alpha^* = \sum_{\beta} c_\beta^* m_{\beta\alpha}. \quad (3.14)$$

If there is soft selection and the deme sizes are equal ( $c_\alpha^* = c_\alpha \equiv \text{constant}$ ), then  $m_{\alpha\beta} = \tilde{m}_{\beta\alpha}$ .

**Remark 3.1.** Conservative migration has two interesting special cases.

1) Dispersal is called *reciprocal* if the *number* of individuals that migrate from deme  $\alpha$  to deme  $\beta$  equals the number that migrate from  $\beta$  to  $\alpha$ :

$$c_\alpha^* \tilde{m}_{\alpha\beta} = c_\beta^* \tilde{m}_{\beta\alpha}. \quad (3.15)$$

If this holds for all pairs of demes, then (3.6a) and (3.4) immediately yield  $c_\beta^{**} = c_\beta^*$ . From (3.7), we infer  $m_{\alpha\beta} = \tilde{m}_{\alpha\beta}$ , i.e., the forward and backward migration matrices are identical.

2) A migration scheme is called *doubly stochastic* if

$$\sum_\alpha \tilde{m}_{\alpha\beta} = 1 \quad \text{for every } \beta. \quad (3.16)$$

If demes are of equal size, then (3.6a) shows that  $c_\alpha^{**} = c_\alpha^*$ . Hence, with equal deme sizes a doubly stochastic migration pattern is conservative. Under soft selection, deme sizes remain constant without further population regulation. Hence,  $m_{\alpha\beta} = \tilde{m}_{\beta\alpha}$  and  $M$  is also doubly stochastic.

Doubly stochastic migration patterns arise naturally if there is a periodicity, e.g., because the demes are arranged in a circular way. If we posit equal deme sizes and homogeneous migration, i.e.,  $\tilde{m}_{\alpha\beta} = \tilde{m}_{\beta-\alpha}$  so that migration rates depend only on distance, then the backward migration pattern is also homogeneous because  $m_{\alpha\beta} = \tilde{m}_{\beta\alpha} = \tilde{m}_{\alpha-\beta}$  and, hence, depends only on  $\beta - \alpha$ . If migration is symmetric,  $\tilde{m}_{\alpha\beta} = \tilde{m}_{\beta\alpha}$ , and the deme sizes are equal, then dispersion is both reciprocal and doubly stochastic.

### 3.3 Important special migration patterns

We introduce three migration patterns that play an important role in the population genetics and ecological literature.

**Example 3.2.** *Random outbreeding and site homing*, or the *Deakin (1966) model*. This model assumes that a proportion  $\mu \in [0, 1]$  of individuals in each deme leaves their deme and is dispersed randomly across all demes. Thus, they perform outbreeding whereas a proportion  $1 - \mu$  remains at their home site. If  $c_\alpha^{**}$  is the proportion (of the total population) of post-migration adults in deme  $\alpha$ , then the forward migration rates are defined by  $\tilde{m}_{\alpha\beta} = \mu c_\beta^{**}$  if  $\alpha \neq \beta$ , and  $\tilde{m}_{\alpha\alpha} = 1 - \mu + \mu c_\alpha^{**}$ . If  $\mu = 0$ , migration is absent; if  $\mu = 1$ , the *Levene* model is obtained (see below). Because this migration pattern is reciprocal,  $M = \tilde{M}$  holds.

To prove that migration in the Deakin model satisfies (3.15), we employ (3.7) and find

$$m_{\beta\alpha} = \frac{c_\alpha^*}{c_\beta^{**}} \tilde{m}_{\alpha\beta} = \begin{cases} \mu c_\alpha^* & \text{if } \alpha \neq \beta \\ \frac{c_\beta^*}{c_\beta^{**}}(1 - \mu) + \mu c_\beta^* & \text{if } \alpha = \beta. \end{cases} \quad (3.17)$$

From this we deduce

$$1 = \sum_\alpha m_{\beta\alpha} = \sum_{\alpha \neq \beta} \mu c_\alpha^* + \frac{c_\beta^*}{c_\beta^{**}}(1 - \mu) + \mu c_\beta^* = \mu \cdot 1 + (1 - \mu) \frac{c_\beta^*}{c_\beta^{**}}, \quad (3.18)$$

which immediately yields  $c_\beta^{**} = c_\beta^*$  for every  $\beta$  provided  $\mu < 1$ . Therefore, we obtain  $\tilde{m}_{\beta\alpha} = \mu c_\alpha^*$  if  $\alpha \neq \beta$  and  $c_\beta^* \tilde{m}_{\beta\alpha} = c_\beta^* \mu c_\alpha^* = c_\alpha^* \tilde{m}_{\alpha\beta}$ , i.e., reciprocity.

We will always assume soft selection in the Deakin model, i.e.,  $c_\alpha^* = c_\alpha$ . Thus, for a given (probability) vector  $c = (c_1, \dots, c_\Gamma)^\top$ , the single parameter  $\mu$  is sufficient to describe the migration pattern:

$$m_{\beta\alpha} = \tilde{m}_{\beta\alpha} = \begin{cases} \mu c_\alpha & \text{if } \alpha \neq \beta \\ 1 - \mu + \mu c_\beta & \text{if } \alpha = \beta. \end{cases} \quad (3.19)$$

If all demes have the same size, the so-called *island model* is obtained. Then migration is usually scaled such that individuals stay in their home deme with probability  $1 - m$  and migrate to each of the other demes with probability  $m/(\Gamma - 1)$ .

**Example 3.3.** *The Levene model* (Levene 1953) assumes soft selection and

$$m_{\alpha\beta} = c_\beta. \quad (3.20)$$

Thus, dispersing individuals are distributed randomly across all demes in proportion to the deme sizes. In particular, migration is independent of the deme of origin and  $M = \tilde{M}$ .

Alternatively, the Levene model could be defined by  $\tilde{m}_{\alpha\beta} = \mu_\beta$ , where  $\mu_\beta > 0$  are constants satisfying  $\sum_\beta \mu_\beta = 1$ . Then (3.8) yields  $m_{\alpha\beta} = c_\beta^*$  for every  $\alpha, \beta \in \mathbf{G}$ . With soft selection, we get  $m_{\alpha\beta} = c_\beta$ . This is all we need if demes are regulated to constant proportions. But the proportions remain constant even without regulation, for (3.6a) gives  $c'_\alpha = c_\alpha^{**} = \mu_\alpha$ . This yields the usual interpretation  $\mu_\alpha = c_\alpha$  (Nagylaki 1992, Sect. 6.3).

**Example 3.4.** In the *linear stepping-stone model* the demes are arranged in a linear order and individuals can reach only one of the neighboring demes. It is an extreme case

among migration patterns exhibiting *isolation by distance*, i.e., patterns in which migration diminishes with the distance from the parental deme. In the classical homogeneous version, the forward migration matrix is

$$\tilde{M} = \begin{pmatrix} 1 - m & m & 0 & \dots & 0 \\ m & 1 - 2m & m & & 0 \\ \vdots & & \ddots & & \vdots \\ 0 & & m & 1 - 2m & m \\ 0 & \dots & 0 & m & 1 - m \end{pmatrix}. \quad (3.21)$$

We leave it to the reader to derive the backward migration matrix using (3.8). It is a special case of the following general tridiagonal form:

$$M = \begin{pmatrix} n_1 & r_1 & 0 & \dots & 0 \\ q_2 & n_2 & r_2 & & 0 \\ \vdots & & \ddots & & \vdots \\ 0 & & q_{\Gamma-1} & n_{\Gamma-1} & r_{\Gamma-1} \\ 0 & \dots & 0 & q_{\Gamma} & n_{\Gamma} \end{pmatrix}, \quad (3.22)$$

where  $n_{\alpha} \geq 0$  and  $q_{\alpha} + n_{\alpha} + r_{\alpha} = 1$  for every  $\alpha$ ,  $q_{\alpha} > 0$  for  $\alpha \geq 2$ ,  $r_{\alpha} > 0$  for  $\alpha \leq \Gamma - 1$ , and  $q_1 = r_{\Gamma} = 0$ . This matrix admits variable migration rates between neighboring demes.

If all deme sizes are equal, the homogeneous matrix (3.21) satisfies  $M = \tilde{M}$ , and each deme exchanges a fraction  $m$  of the population with each of its neighboring demes. The stepping-stone model has been used as a starting point to derive the partial differential equations for selection and dispersal in continuous space (Nagylaki 1989). Also circular and infinite variants have been investigated.

*Juvenile migration* is of importance for many marine organisms and plants, where seeds disperse. It can be treated in a similar way as adult migration. Also models with both juvenile and adult migration have been studied. Some authors investigated migration and selection in dioecious populations, as well as selection on X-linked loci (e.g. Nagylaki 1992, pp. 143, 144).

Unless stated otherwise, we assume that the backward migration matrix  $M$  is constant, as is the case for soft selection if deme proportions and the forward migration matrix are constant. Then the recurrence equations (3.5) provide a self-contained description of the migration-selection dynamics. Hence, they are sufficient to study evolution for an arbitrary number of generations.

## 4 Two alleles and finitely many demes

Of central interest is the identification of conditions that guarantee the maintenance of genetic diversity. Often it is impossible to determine the equilibrium structure in detail because establishing existence and, even more so, stability or location of polymorphic equilibria is unfeasible. Below we introduce an important concept that is particularly useful to establish maintenance of genetic variation at diallelic loci. Throughout this section we consider a single locus with two alleles. The number of demes,  $\Gamma$ , can be arbitrary.

### 4.1 Protected polymorphism

There is a *protected polymorphism* (Prout 1968) if, independently of the initial conditions are, a polymorphic population cannot become monomorphic. Essentially, this requires that if an allele becomes very rare, its frequency must increase. In general, a protected polymorphism is neither necessary nor sufficient for the existence of a stable polymorphic equilibrium. For instance, on the one hand, if there is an internal limit cycle that attracts all solutions, then there is a protected polymorphism. On the other hand, if there are two internal equilibria, one asymptotically stable, the other unstable, then selection may remove one of the alleles if sufficiently rare. A generalization of this concept to multiple alleles would correspond to the concept of permanence often used in ecological models (e.g. Hofbauer and Sigmund 1998).

Because we consider only two alleles, we can simplify the notation. We write  $p_\alpha = p_{1,\alpha}$  for the frequency of allele  $\mathcal{A}_1$  in deme  $\alpha$  (and  $1 - p_\alpha$  for that of  $\mathcal{A}_2$  in deme  $\alpha$ ). Let  $p = (p_1, \dots, p_\Gamma)^\top$  denote the vector of allele frequencies. Instead of using the fitness assignments  $w_{11,\alpha}$ ,  $w_{12,\alpha}$ , and  $w_{22,\alpha}$ , it will be convenient to scale the fitness of the three genotypes in deme  $\alpha$  as follows

$$\begin{array}{ccc} \mathcal{A}_1\mathcal{A}_1 & \mathcal{A}_1\mathcal{A}_2 & \mathcal{A}_2\mathcal{A}_2 \\ x_\alpha & 1 & y_\alpha \end{array} \quad (4.1)$$

( $x_\alpha, y_\alpha \geq 0$ ). This can be achieved by setting  $x_\alpha = w_{11,\alpha}/w_{12,\alpha}$  and  $y_\alpha = w_{22,\alpha}/w_{12,\alpha}$ , provided  $w_{12,\alpha} > 0$ .

With these fitness assignments, one obtains

$$w_{1,\alpha} = 1 - p_\alpha + x_\alpha p_\alpha \quad \text{and} \quad \bar{w}_\alpha = x_\alpha p_\alpha^2 + 2p_\alpha(1 - p_\alpha) + y_\alpha(1 - p_\alpha)^2, \quad (4.2)$$

and the migration-selection dynamics (3.5) becomes

$$p_\alpha^* = p_\alpha w_{1,\alpha} / \bar{w}_\alpha \quad (4.3a)$$

$$p'_\alpha = \sum_\beta m_{\alpha\beta} p_\beta^*. \quad (4.3b)$$

We consider this as a (discrete) dynamical system on  $[0, 1]^\Gamma$ .

We call allele  $\mathcal{A}_1$  protected if it cannot be lost. Thus, it has to increase in frequency if rare. In mathematical terms this means that the monomorphic equilibrium  $p = 0$  must be unstable. To derive a sufficient condition for instability of  $p = 0$ , we linearize (4.3) at  $p = 0$ . If  $y_\alpha > 0$  for every  $\alpha$  (which means that  $\mathcal{A}_2\mathcal{A}_2$  is nowhere lethal), a simple calculation shows that the Jacobian of (4.3a),

$$D = \left( \frac{\partial p_\alpha^*}{\partial p_\beta} \right) \Big|_{p=0}, \quad (4.4)$$

is a diagonal matrix with (nonzero) entries  $d_{\alpha\alpha} = y_\alpha^{-1}$ . Because (4.3b) is linear, the linearization of (4.3) is

$$p' = Qp, \quad \text{where } Q = MD, \quad (4.5)$$

i.e.,  $q_{\alpha\beta} = m_{\alpha\beta}/y_\beta$ .

To obtain a simple criterion for protection, we assume that the descendants of individuals in every deme be able eventually to reach every other deme. Mathematically, the appropriate assumption is that  $M$  is irreducible. Then  $Q$  is also irreducible and it is nonnegative. Therefore, the Theorem of Perron and Frobenius (e.g. Seneta 1981) implies the existence of a uniquely determined eigenvalue  $\lambda_0 > 0$  of  $Q$  such that  $|\lambda| \leq \lambda_0$  holds for all eigenvalues of  $Q$ . In addition, there exists a strictly positive eigenvector pertaining to  $\lambda_0$  which, up to multiplicity, is uniquely determined. As a consequence,

$$\mathcal{A}_1 \text{ is protected if } \lambda_0 > 1 \text{ and } \mathcal{A}_1 \text{ is not protected if } \lambda_0 < 1 \quad (4.6)$$

(if  $\lambda_0 = 1$ , then stability cannot be decided upon linearization). This maximal eigenvalue satisfies

$$\min_\alpha \sum_\beta q_{\alpha\beta} \leq \lambda_0 \leq \max_\alpha \sum_\beta q_{\alpha\beta}, \quad (4.7)$$

with equality if and only if all the row sums are the same.

**Example 4.1.** Suppose that  $\mathcal{A}_2\mathcal{A}_2$  is at least as fit as  $\mathcal{A}_1\mathcal{A}_2$  in every deme and more fit in at least one deme, i.e.,  $y_\alpha \geq 1$  for every  $\alpha$  and  $y_\beta > 1$  for some  $\beta$ . Then  $q_{\alpha\beta} = m_{\alpha\beta}/y_\beta \leq$

$m_{\alpha\beta}$  for every  $\beta$ . Because  $M$  is irreducible, there is no  $\beta$  such that  $m_{\alpha\beta} = 0$  for every  $\alpha$ . Therefore, the row sums  $\sum_{\beta} q_{\alpha\beta} = \sum_{\beta} m_{\alpha\beta}/y_{\beta}$  in (4.7) are not all equal to one, and we obtain

$$\lambda_0 < \max_{\alpha} \sum_{\beta} q_{\alpha\beta} \leq \max_{\alpha} \sum_{\beta} m_{\alpha\beta} = 1. \quad (4.8)$$

Thus,  $\mathcal{A}_1$  is not protected, and this holds independently of the choice of the  $x_{\alpha}$ , or  $w_{11,\alpha}$ .

It can be shown similarly that  $\mathcal{A}_1$  is protected if  $\mathcal{A}_1\mathcal{A}_2$  is favored over  $\mathcal{A}_2\mathcal{A}_2$  in at least one deme and is nowhere less fit than  $\mathcal{A}_2\mathcal{A}_2$ .

One obtains the condition for protection of  $\mathcal{A}_2$  if, in (4.6),  $\mathcal{A}_1$  is replaced by  $\mathcal{A}_2$  and  $\lambda_0$  is the maximal eigenvalue of the matrix with entries  $m_{\alpha\beta}/x_{\beta}$ . Clearly, there is a protected polymorphism if both alleles are protected.

In the case of complete dominance the eigenvalue condition (4.6) cannot be satisfied. Consider, for instance, protection of  $\mathcal{A}_1$  if  $\mathcal{A}_2$  is dominant, i.e.,  $y_{\alpha} = 1$  for every  $\alpha$ . Then  $q_{\alpha\beta} = m_{\alpha\beta}$ ,  $\sum_{\beta} q_{\alpha\beta} = \sum_{\beta} m_{\alpha\beta} = 1$ , and  $\lambda_0 = 1$ . This case is treated in Section 6.2 of Nagylaki (1992).

## 4.2 Two demes

It will be convenient to set

$$x_{\alpha} = 1 - r_{\alpha} \quad \text{and} \quad y_{\alpha} = 1 - s_{\alpha}, \quad (4.9)$$

where we assume  $r_{\alpha} < 1$  and  $s_{\alpha} < 1$  for every  $\alpha \in \{1, 2\}$ . We write the backward migration matrix as

$$M = \begin{pmatrix} 1 - m_1 & m_1 \\ m_2 & 1 - m_2 \end{pmatrix}, \quad (4.10)$$

where  $0 < m_{\alpha} < 1$  for every  $\alpha \in \{1, 2\}$ .

Now we derive the condition for protection of  $\mathcal{A}_1$ . The characteristic polynomial of  $Q$  is proportional to

$$\varphi(x) = (1 - s_1)(1 - s_2)x^2 - (2 - m_1 - m_2 - s_1 - s_2 + s_1m_2 + s_2m_1)x + 1 - m_1 - m_2. \quad (4.11)$$

It is convex and satisfies

$$\varphi(1) = s_1s_2(1 - \kappa), \quad (4.12a)$$

$$\varphi'(1) = (1 - s_1)(m_2 - s_2) + (1 - s_2)(m_1 - s_1), \quad (4.12b)$$

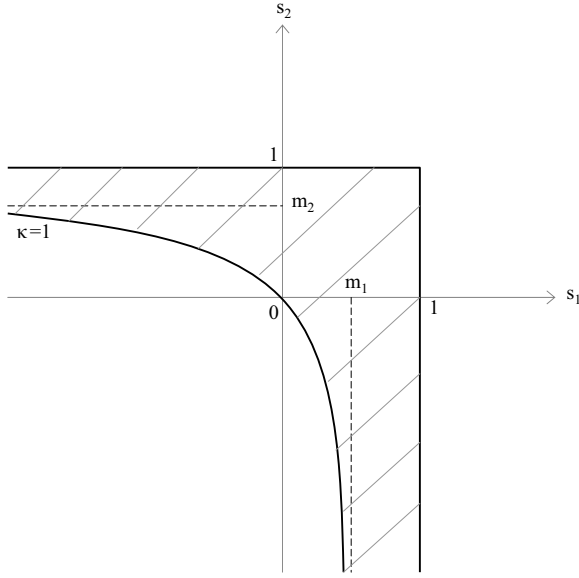


Figure 4.1: The region of protection of  $\mathcal{A}_1$  (hatched) (from Nagylaki and Lou 2008).

where

$$\kappa = \frac{m_1}{s_1} + \frac{m_2}{s_2}. \quad (4.13)$$

By Example 4.1,  $\mathcal{A}_1$  is not protected if  $\mathcal{A}_1\mathcal{A}_2$  is less fit than  $\mathcal{A}_2\mathcal{A}_2$  in both demes (more generally, if  $s_1 \leq 0$ ,  $s_2 \leq 0$ , and  $s_1 + s_2 < 0$ ). Of course,  $\mathcal{A}_1$  will be protected if  $\mathcal{A}_1\mathcal{A}_2$  is fitter than  $\mathcal{A}_2\mathcal{A}_2$  in both demes (more generally, if  $s_1 \geq 0$ ,  $s_2 \geq 0$ , and  $s_1 + s_2 > 0$ ). Hence, we restrict attention to the most interesting case when  $\mathcal{A}_1\mathcal{A}_2$  is fitter than  $\mathcal{A}_2\mathcal{A}_2$  in one deme and less fit in the other, i.e.,  $s_1 s_2 < 0$ .

The Perron-Frobenius Theorem informs us that  $\varphi(x)$  has two real roots. We have to determine when the larger ( $\lambda_0$ ) satisfies  $\lambda_0 > 1$ . Because  $\varphi''(x) > 0$ , this is the case if and only if  $\varphi(1) < 0$  or  $\varphi(1) \geq 0$  and  $\varphi'(1) < 0$ . By noting that  $m_1 \geq s_1$  if  $\kappa \geq 1$  and  $s_2 < 0$ , it is straightforward to show that  $\varphi(1) \geq 0$  and  $\varphi'(1) < 0$  is never satisfied if  $s_1 > 0$  and  $s_2 < 0$ . By symmetry, we conclude that allele  $\mathcal{A}_1$  is protected if  $\varphi(1) < 0$ , i.e., if

$$\kappa < 1; \quad (4.14)$$

cf. Bulmer (1972). It is not protected if  $\kappa > 1$ . Figure 4.1 displays the region of protection of  $\mathcal{A}_1$  for given  $m_1$  and  $m_2$ .

If there is no dominance ( $r_\alpha = -s_\alpha$  and  $0 < |s_\alpha| < 1$  for  $\alpha = 1, 2$ ), then further simplification can be achieved. From the preceding paragraph the results depicted in



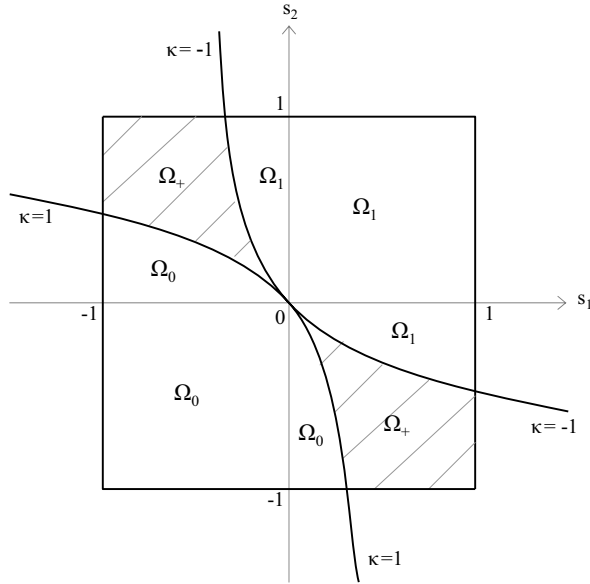


Figure 4.2: The regions of protection of  $\mathcal{A}_2$  only ( $\Omega_0$ ),  $\mathcal{A}_1$  only ( $\Omega_1$ ), and both  $\mathcal{A}_1$  and  $\mathcal{A}_2$  ( $\Omega_+$ ) in the absence of dominance (from Nagylaki and Lou 2008).

Figure 4.2 are obtained. The region of a protected polymorphism is

$$\Omega_+ = \{(s_1, s_2) : s_1 s_2 < 0 \text{ and } |\kappa| < 1\} . \quad (4.15)$$

In this case, there is a unique internal equilibrium and it is globally asymptotically stable (Campbell 1983).

In a panmictic population, a stable polymorphism can not occur in the absence of overdominance. Protection of both alleles in a subdivided population requires that selection in the two demes is in opposite direction and sufficiently strong relative to migration. Therefore, the study of the maintenance of polymorphism is of most interest if selection acts in opposite direction and dominance is intermediate, i.e.,

$$r_\alpha s_\alpha < 0 \text{ for } \alpha = 1, 2 \text{ and } s_1 s_2 < 0. \quad (4.16)$$

**Example 4.2.** In the *Deakin model*, the condition (4.14) for protection of allele  $\mathcal{A}_1$  becomes

$$\kappa = \mu \left( \frac{c_2}{s_1} + \frac{c_1}{s_2} \right) < 1, \quad (4.17)$$

where  $s_1 s_2 < 0$ . Therefore, for given  $s_1$ ,  $s_2$ , and  $c_1$ , there is a critical value  $\mu_0$  such that allele  $\mathcal{A}_1$  is protected if and only if  $\mu < \mu_0$ . This implies that for two diallelic demes a protected polymorphism is favored by a smaller migration rate.

**Example 4.3.** In the *Levene model*, the condition for a protected polymorphism is

$$\frac{c_2}{s_1} + \frac{c_1}{s_2} < 1 \quad \text{and} \quad \frac{c_2}{r_1} + \frac{c_1}{r_2} < 1. \quad (4.18)$$

We close this subsection with an example showing that already with two alleles and two demes the equilibrium structure can be quite complicated.

**Example 4.4.** In the absence of migration, the recurrence equations for the allele frequencies  $p_1, p_2$  in the two demes are two decoupled one-locus selection dynamics of the form (2.16). Therefore, if there is underdominance in each deme, the top convergence pattern in Figure 2.1 applies to each deme. As a consequence, in the absence of migration, the complete two-deme system has nine equilibria, four of which are asymptotically stable and the others are unstable. Under sufficiently weak migration all nine equilibria are admissible and the four stable ones remain stable, whereas the other five are unstable. Two of the stable equilibria are internal. For increasing migration rate, several of these equilibria are extinguished in a sequence of bifurcations (Karlin and McGregor 1972a).

## 5 Migration and selection in continuous time

Following Nagylaki and Lou (2007), we assume that both selection and migration are weak and approximate the discrete migration-selection dynamics (3.5) by a differential equation which is easier accessible. Accordingly, let

$$w_{ij,\alpha} = 1 + \epsilon r_{ij,\alpha} \quad \text{and} \quad \tilde{m}_{\alpha\beta} = \delta_{\alpha\beta} + \epsilon \tilde{\mu}_{\alpha\beta}, \quad (5.1)$$

where  $r_{ij,\alpha}$  and  $\tilde{\mu}_{\alpha\beta}$  are fixed for every  $i, j \in I$  and every  $\alpha, \beta \in G$ , and  $\epsilon > 0$  is sufficiently small. From (3.2) we deduce

$$w_{i,\alpha} = 1 + \epsilon r_{i,\alpha} \quad \text{and} \quad \bar{w}_\alpha = 1 + \epsilon \bar{r}_\alpha, \quad (5.2a)$$

where

$$r_{i,\alpha} = \sum_j r_{ij,\alpha} p_{j,\alpha} \quad \text{and} \quad \bar{r}_\alpha = \sum_{i,j} r_{ij,\alpha} p_{i,\alpha} p_{j,\alpha}. \quad (5.2b)$$

To approximate the backward migration matrix  $M$ , note that (3.10) and (5.2a) imply that, for both soft and hard selection,

$$c_\alpha^* = c_\alpha + O(\epsilon) \quad (5.3)$$

as  $\epsilon \rightarrow 0$ . Substituting (5.1) and (5.3) into (3.8) leads to

$$m_{\alpha\beta} = \delta_{\alpha\beta} + \epsilon\mu_{\alpha\beta} + O(\epsilon^2) \quad (5.4)$$

as  $\epsilon \rightarrow 0$ , where

$$\mu_{\alpha\beta} = \frac{1}{c_\alpha} \left( c_\beta \tilde{\mu}_{\beta\alpha} - \delta_{\alpha\beta} \sum_\gamma c_\gamma \tilde{\mu}_{\gamma\alpha} \right). \quad (5.5)$$

Because  $\tilde{M}$  is stochastic, we obtain for every  $\alpha \in \Gamma$ ,

$$\tilde{\mu}_{\alpha\beta} \geq 0 \text{ for every } \beta \neq \alpha \quad \text{and} \quad \sum_\beta \tilde{\mu}_{\alpha\beta} = 0. \quad (5.6)$$

As a simple consequence,  $\mu_{\alpha\beta}$  shares the same properties.

The final step in our derivation is to rescale time as in Sect. 2.4 by setting  $t = \lfloor \tau/\epsilon \rfloor$  and  $\pi_{i,\alpha}(\tau) = p_{i,\alpha}(t)$ . Inserting all this into the difference equations (3.5) and expanding yields

$$\pi_{i,\alpha}(\tau + \epsilon) = \pi_{i,\alpha} \{1 + \epsilon[r_{i,\alpha}(\pi_{\cdot,\alpha}) - \bar{r}_\alpha(\pi_{\cdot,\alpha})]\} + \epsilon \sum_\beta \mu_{\alpha\beta} \pi_{i,\beta} + O(\epsilon^2) \quad (5.7)$$

as  $\epsilon \rightarrow 0$ , where  $\pi_{\cdot,\alpha} = (\pi_{1,\alpha}, \dots, \pi_{I,\alpha})^\top \in \mathbf{S}_I$ . Rearranging and letting  $\epsilon \rightarrow 0$ , we arrive at

$$\frac{d\pi_{i,\alpha}}{d\tau} = \sum_\beta \mu_{\alpha\beta} \pi_{i,\beta} + \pi_{i,\alpha} [r_{i,\alpha}(\pi_{\cdot,\alpha}) - \bar{r}_\alpha(\pi_{\cdot,\alpha})]. \quad (5.8)$$

Absorbing  $\epsilon$  into the migration rates and selection coefficients and returning to  $p(t)$ , we obtain the slow-evolution approximation of (3.5),

$$\dot{p}_{i,\alpha} = \sum_\beta \mu_{\alpha\beta} p_{i,\beta} + p_{i,\alpha} [r_{i,\alpha}(p_{\cdot,\alpha}) - \bar{r}_\alpha(p_{\cdot,\alpha})]. \quad (5.9)$$

In contrast to the discrete-time dynamics (3.5), here the migration and selection terms are decoupled. This is a general feature of many other slow-evolution limits (such as mutation and selection, or selection, recombination and migration). Because of the decoupling of the selection and migration terms, the analysis of explicit models is often facilitated.

With multiple alleles, there are few general results on the dynamics of (5.9). For two alleles, we set  $p_\alpha = p_{1,\alpha}$  and write (5.9) in the form

$$\dot{p}_\alpha = \sum_\beta \mu_{\alpha\beta} p_\beta + \varphi_\alpha(p_\alpha). \quad (5.10)$$

Since  $\mu_{\alpha\beta} \geq 0$  whenever  $\alpha \neq \beta$ , the system (5.10) is quasimonotone or cooperative, i.e.,  $\partial \dot{p}_\alpha / \partial p_\beta \geq 0$  if  $\alpha \neq \beta$ . As a consequence, (5.10) cannot have an exponentially stable limit

cycle. However, Akin (personal communication) has proved for three diallelic demes that a Hopf bifurcation can produce unstable limit cycles. This precludes global convergence, though not generic convergence. If  $\Gamma = 2$ , then every trajectory converges (Hirsch 1982; Hadeler and Glas 1983; see also Hofbauer and Sigmund 1998, p. 28).

**Example 5.1.** Eyland (1971) provided a global analysis of (5.9) for the special case of two diallelic demes without dominance. As in Sect. 4.2, we assume that the fitnesses of  $\mathcal{A}_1\mathcal{A}_1$ ,  $\mathcal{A}_1\mathcal{A}_2$ , and  $\mathcal{A}_2\mathcal{A}_2$  in deme  $\alpha$  are  $1 + s_\alpha$ , 1, and  $1 - s_\alpha$ , respectively, where  $s_\alpha \neq 0$  ( $\alpha = 1, 2$ ). Moreover, we set  $\mu_1 = \mu_{12} > 0$ ,  $\mu_2 = \mu_{21} > 0$ , and write  $p_\alpha$  for the frequency of  $\mathcal{A}_1$  in deme  $\alpha$ . Then (5.9) becomes

$$\dot{p}_1 = \mu_1(p_2 - p_1) + s_1 p_1(1 - p_1), \quad (5.11a)$$

$$\dot{p}_2 = \mu_2(p_1 - p_2) + s_2 p_2(1 - p_2). \quad (5.11b)$$

The equilibria can be calculated explicitly. At equilibrium,  $p_1 = 0$  if and only if  $p_2 = 0$ , and  $p_1 = 1$  if and only if  $p_2 = 1$ . In addition, there may be an internal equilibrium point. We set

$$\sigma_\alpha = \frac{\mu_\alpha}{s_\alpha}, \quad \kappa = \sigma_1 + \sigma_2, \quad (5.12)$$

and

$$B = (1 - 4\sigma_1\sigma_2)^{1/2}. \quad (5.13)$$

The internal equilibrium exists if and only if  $s_1 s_2 < 0$  and  $|\kappa| < 1$ ; cf. (4.15). If  $s_2 < 0 < s_1$ , it is given by

$$\hat{p}_1 = \frac{1}{2}(1 + B) - \sigma_1 \quad \text{and} \quad \hat{p}_2 = \frac{1}{2}(1 - B) - \sigma_2. \quad (5.14)$$

It is straightforward to determine the local stability properties of the three possible equilibria. Global asymptotic stability follows from the results cited above about quasi-monotone systems. Let  $p = (p_1, p_2)^\top$ . Then allele  $\mathcal{A}_1$  is eliminated in the region  $\Omega_0$  in Figure 4.2, i.e.,  $p(t) \rightarrow (0, 0)$  as  $t \rightarrow \infty$ , whereas  $\mathcal{A}_1$  is ultimately fixed in the region  $\Omega_1$ . In  $\Omega_+$ ,  $p(t)$  converges globally to the internal equilibrium point  $\hat{p}$  given by (5.14).

## 6 Derivation of the PDE migration-selection model

Our aim is the motivation and derivation of a model that describes dispersal of individuals or alleles in continuous space. The most common approach is to model dispersal by diffusion in space (Fisher 1937, Kolmogorov et al. 1937, Haldane 1948; see Nagylaki and Lou 2008 for a recent review). This is appropriate if the dispersal distance is typically

small relative to changes in the environment. In this section we demonstrate how the well known partial differential equation can be obtained as an approximation to the discrete-time discrete-demes model. The derivation outlined below is inspired by the more general ones given by Nagylaki (1989, 1996).

The starting point is the model derived in Section 3. Here, it will be convenient to use the number  $N_\alpha$  of individuals in deme  $\alpha$  instead of the deme proportions  $c_\alpha$ . Then (3.8) becomes

$$m_{\beta\alpha} = \frac{N_\alpha^* \tilde{m}_{\alpha\beta}}{\sum_\gamma N_\gamma^* \tilde{m}_{\gamma\beta}}. \quad (6.1)$$

Using (6.1), we can rewrite (3.5a) as

$$\left( \sum_\gamma N_\gamma^* \tilde{m}_{\gamma\alpha} \right) p'_{i,\alpha} = \sum_\beta N_\beta^* \tilde{m}_{\beta\alpha} p_{i,\beta}^*, \quad (6.2a)$$

where

$$p_{i,\beta}^* = p_{i,\beta} \frac{w_{i,\beta}}{\bar{w}_\beta}. \quad (6.2b)$$

We measure time,  $t$ , in generations and suppose that  $w_{ij,\alpha}(p_\alpha, t)$ ,  $\tilde{m}_{\alpha\beta}(t)$ , and  $N_\alpha(t)$  are given for every  $i, j, \alpha, \beta, t$ , and that  $N_\alpha^* = N_\alpha^*(N_\alpha, p_\alpha, t)$ , where  $p_\alpha = (p_{1,\alpha}, \dots, p_{I,\alpha})^\top$ . Then (6.2) describes the model completely.

We treat only the one-dimensional case and assume that demes are arranged in a linear array. Examples include organisms confined to a river, riverbank, seashore, or mountain range. The model applies to populations in two-dimensional habitats if only one coordinate, such as latitude, altitude on a mountain range, or distance from a river or seashore matter.

We scale space and time as follows:

$$x = \epsilon\alpha, \quad y = \epsilon\beta, \quad t = \lfloor \tau/\lambda \rfloor. \quad (6.3)$$

In the new units,  $\epsilon$  is a measure of distance between adjacent colonies and  $\lambda$  corresponds to the length of one generation. We let

$$\epsilon \rightarrow 0 \text{ and } \lambda \rightarrow 0 \text{ such that } \frac{\epsilon^2}{\lambda} \text{ remains fixed.} \quad (6.4)$$

We suppose that there are numbers  $r_{ij,\alpha}(p_\alpha, t) \in [-1, 1]$  such that

$$w_{ij,\alpha}(p_\alpha, t) = 1 + \lambda r_{ij,\alpha}(p_\alpha, t) \quad (6.5)$$

holds for every  $i, j, \alpha$ , and  $t$ . Therefore, we obtain from (6.2b)

$$p_{i,\alpha}^* = p_{i,\alpha} + \lambda s_{i,\alpha}(p_\alpha, t) + o(\lambda) \quad (6.6)$$

because  $w_{i,\alpha}/\bar{w}_\alpha = 1 + \lambda(r_{i,\alpha} - \bar{r}_\alpha) + o(\lambda)$  and  $s_{i,\alpha} = p_{i,\alpha}(r_{i,\alpha} - \bar{r}_\alpha)$ .

In terms of the scaled variables  $x, y$  and  $\tau$ , we write

$$N_\alpha(t) = \hat{\rho}(x, \tau), \quad p_{i,\alpha}(t) = \hat{\pi}_i(x, \tau), \quad s_{i,\alpha}(p_\alpha, t) = \hat{S}_i(\hat{\pi}, x, \tau). \quad (6.7)$$

Here and below, we assume that all quantities marked with a caret ( $\hat{\cdot}$ ) have uniform and continuous limits in  $x$  as  $\lambda \rightarrow 0$ . We omit the carets in this limit. Thus, our aim is to derive the system of PDEs that the  $\pi_i(x, \tau)$  have to satisfy if they are the  $\lambda \rightarrow 0$  limit of the solution  $p_\alpha(t)$  of (6.2).

Our assumptions imply that (6.6) holds uniformly in  $x$  for every  $\tau$ , i.e.,

$$\limsup_{\lambda \rightarrow 0} \sup_x \left| \frac{\hat{\pi}_i^*(x, \tau) - \hat{\pi}_i(x, \tau)}{\lambda} - \hat{S}_i(\hat{\pi}, x, \tau) \right| = 0 \quad (6.8)$$

or, simply,

$$\hat{\pi}_i^*(x, \tau) = \hat{\pi}_i(x, \tau) + \lambda \hat{S}_i(\hat{\pi}, x, \tau) + o(\lambda) \quad (6.9)$$

uniformly in  $x$  as  $\lambda \rightarrow 0$ , where the superscript  $*$  again denotes frequencies after selection.

Because we want to model migration by diffusion we require the following diffusion hypothesis:

$$\lim_{\lambda \rightarrow 0} \frac{\epsilon}{\lambda} \sum_{\beta: |\alpha - \beta| < \theta/\epsilon} (\beta - \alpha) \tilde{m}_{\alpha\beta}(t) = M(x, \tau), \quad (6.10a)$$

$$\lim_{\lambda \rightarrow 0} \frac{\epsilon^2}{\lambda} \sum_{\beta: |\alpha - \beta| < \theta/\epsilon} (\beta - \alpha)^2 \tilde{m}_{\alpha\beta}(t) = V(x, \tau), \quad (6.10b)$$

$$\lim_{\lambda \rightarrow 0} \frac{1}{\lambda} \sum_{\beta: |\alpha - \beta| \geq \theta/\epsilon} \tilde{m}_{\alpha\beta} = 0, \quad (6.10c)$$

uniformly in  $x$  and for every  $\theta > 0$ . Here,  $M$  and  $V$  represent the mean and variance of displacement by dispersal per new time unit in new length units. The corresponding quantities in generations are  $\lambda M$  and  $\lambda V$ , respectively. We note that in the limit  $\lambda \rightarrow 0$  the variance of migrational displacement equals its mean square. We assume that the partial derivatives that appear below are the uniform limits as  $\lambda \rightarrow 0$  of the corresponding discrete quantities and are continuous.

In view of (6.5) we assume that

$$N_\alpha^* = N_\alpha(1 + O(\lambda)), \quad (6.11)$$

which includes both soft and hard selection; cf. (5.3).

For a bounded function  $f_\alpha(t) = F(x, \tau)$ , such that  $F_{xx}$ <sup>7</sup> is twice continuously differentiable, the diffusion hypothesis (6.10) together with Taylor's theorem imply

$$\sum_{\alpha} \tilde{m}_{\beta\alpha} f_{\alpha}(t) = F(y, \tau) + \lambda M(y, \tau) F_y(y, \tau) + \frac{1}{2} \lambda V(y, \tau) F_{yy}(y, \tau) + o(\lambda) \quad (6.12)$$

uniformly as  $\lambda \rightarrow 0$ .

[Proof: We decompose

$$\sum_{\alpha} \tilde{m}_{\beta\alpha} f_{\alpha} = \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} f_{\alpha} + \sum_{\alpha: |\beta-\alpha| \geq \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} f_{\alpha},$$

where  $\sum_{\alpha: |\beta-\alpha| \geq \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} f_{\alpha} = o(\lambda)$  by (6.10c) because  $F$  is bounded. To approximate the first term, we use first Taylor expansion of  $f_{\alpha} = F(x)$ , then (6.10):

$$\begin{aligned} \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} f_{\alpha} &= \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} \left( F(y) + (y-x) F_y(y) + \frac{1}{2} (y-x)^2 F_{yy}(y) + o((y-x)^2) \right) \\ &= \left( \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} \right) F(y) + \left( \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} \epsilon (\beta-\alpha) \right) F_y(y) \\ &\quad + \frac{1}{2} \left( \sum_{\alpha: |\beta-\alpha| < \frac{\theta}{\epsilon}} \tilde{m}_{\beta\alpha} \epsilon^2 (\beta-\alpha)^2 \right) F_{yy}(y) + o((y-x)^2) \\ &= F(y) (1 + o(\lambda)) + \lambda (M(y) + o(1)) F_y(y) + \frac{\lambda}{2} (V(y) + o(1)) F_{yy}(y) + o(\epsilon^2), \end{aligned}$$

which yields (6.12). ]

Now we choose test functions  $\phi_\alpha(t) = \Phi(x, \tau)$  such that  $\Phi$ ,  $\Phi_x$ , and  $\Phi_{xx}$  are continuous and vanish outside of the interval  $(x_1, x_2)$ , where  $x_1 < x_2$  are arbitrary but fixed. We multiply the discrete recursion (6.2) by  $\phi_\alpha$  and sum over all  $\alpha$ :

$$\sum_{\alpha, \beta} N_{\beta}^* \tilde{m}_{\beta\alpha} p'_{i,\alpha} \phi_{\alpha} = \sum_{\alpha, \beta} N_{\beta}^* \tilde{m}_{\beta\alpha} p_{i,\beta}^* \phi_{\alpha}. \quad (6.13)$$

Using first (6.6) and (6.12), then (6.7), we obtain for the right hand side of (6.13)

$$\begin{aligned} &\sum_{\beta} N_{\beta}^* p_{i,\beta}^* \sum_{\alpha} \tilde{m}_{\beta\alpha} \phi_{\alpha} \\ &= \sum_{\beta} N_{\beta}^* (p_{i,\beta} + \lambda s_{i,\beta} + o(\lambda)) \left( \Phi(y) + \lambda M(y, \tau) \Phi_y(y) + \frac{1}{2} \lambda V(y, \tau) \Phi_{yy}(y) + o(\lambda) \right) \\ &= \sum_{\beta} N_{\beta}^* \left[ \hat{\pi}_i(y, \tau) \Phi(y) + \lambda \hat{S}_i(\hat{\pi}, y, \tau) \Phi(y) \right. \\ &\quad \left. + \lambda M(y, \tau) \Phi_y(y) \hat{\pi}_i(y, \tau) + \frac{1}{2} \lambda V(y, \tau) \Phi_{yy}(y) \hat{\pi}_i(y, \tau) + o(\lambda) \right]. \quad (6.14) \end{aligned}$$

---

<sup>7</sup>We denote first and second partial derivatives with respect to  $x$  by  $F_x$  and  $F_{xx}$  respectively.

Using  $p'_{i,\alpha} = \hat{\pi}_i(x, \tau) + \lambda \hat{\pi}_{i,\tau}(x, \tau) + o(\lambda)$  and (6.12), we obtain for the left hand side of (6.13) in essentially the same way as above:

$$\begin{aligned} & \sum_{\alpha,\beta} N_\beta^* \tilde{m}_{\beta\alpha} p'_{i,\alpha} \phi_\alpha \\ &= \sum_{\beta} N_\beta^* \left[ \hat{\pi}_i(y, \tau) \Phi(y) + \lambda \hat{\pi}_{i,\tau}(y, \tau) \Phi(y) + \lambda M(y, \tau) [\hat{\pi}_i(y, \tau) \Phi(y)]_y \right. \\ & \quad \left. + \frac{1}{2} \lambda V(y, \tau) [\hat{\pi}_i(y, \tau) \Phi(y)]_{yy} + o(\lambda) \right]. \end{aligned} \quad (6.15)$$

Equating (6.14) and (6.15), we get

$$\begin{aligned} & \sum_{\beta} N_\beta^* \left[ \lambda \Phi(y) \left( \hat{\pi}_{i,\tau}(y, \tau) - \hat{S}_i(\hat{\pi}, y, \tau) + M(y, \tau) \hat{\pi}_{i,y}(y) + \frac{1}{2} V(y, \tau) \hat{\pi}_{i,yy}(y, \tau) \right) \right. \\ & \quad \left. + \lambda V(y, \tau) \hat{\pi}_{i,y}(y, \tau) \Phi_y(y) + o(\lambda) \right] = 0. \end{aligned}$$

If we take the limit  $\lambda \rightarrow 0$ , the left side converges to the integral

$$\begin{aligned} & \int_{x_1}^{x_2} \left[ \rho(y, \tau) \left( \pi_{i,\tau}(y, \tau) - S_i(\pi, y, \tau) + M(y, \tau) \pi_{i,y}(y, \tau) + \frac{1}{2} V(y, \tau) \pi_{i,yy}(y, \tau) \right) - \right. \\ & \quad \left. - \left( \rho(y, \tau) V(y, \tau) \pi_{i,y}(y, \tau) \right)_y \right] \Phi(y) dy = 0, \end{aligned} \quad (6.16)$$

where we have used that  $N_\beta^* = N_\beta(1 + O(\lambda)) \rightarrow \rho(y, \tau)$  as  $\lambda \rightarrow 0$  (6.7), and  $V(y) \pi_{i,y} \Phi_y$  was integrated by parts. Since  $\Phi$  is arbitrary, the term in brackets must vanish for all  $y \in (x_1, x_2)$  if we assume  $\rho(y, \tau) > 0$  for all  $y$  and  $\tau$ .

Therefore, after performing the differentiation  $(\rho V \pi_{i,y})_y = (\rho V)_y \pi_{i,y} + \rho V \pi_{i,yy}$ , we obtain the PDE

$$\pi_{i,\tau} = \frac{1}{2} V(y, \tau) \pi_{i,yy} - M(y, \tau) \pi_{i,y} + \frac{1}{\rho(y, \tau)} \left( (\rho(y, \tau) V(y, \tau))_y \pi_{i,y} \right) + S_i(\pi, y, \tau),$$

which we rewrite as

$$p_{i,t} = \frac{1}{2} V p_{i,xx} + \left[ \rho^{-1} (\rho V)_x - M \right] p_{i,x} + S_i, \quad (6.17)$$

where we suppressed the dependence of  $M$ ,  $V$ , and  $\rho$  on  $x$  and  $t$ , and that of  $S_i$  on  $p$ ,  $x$ , and  $t$ . We assume (6.17) holds on a (spatial) domain  $\Omega$  that is a bounded or unbounded open interval. For extensions to more than one space dimension, we refer to Nagylaki and Lou (2008). In general, (6.17) is a complicated PDE, not simply a reaction-diffusion equation.



In the important special case in which  $\rho = \text{const.}$  and migration is homogeneous and isotropic, so that  $M = 0$  and  $V = \sigma^2$  (a positive constant), (6.17) simplifies to

$$p_{i,t} = \frac{1}{2}\sigma^2 p_{i,xx} + S_i. \quad (6.18a)$$

This is the form most frequently studied in the literature. Usually, we assume that

$$S_i = S_i(p, x) = p_i(x, t)[r_i(x) - \bar{r}(x)], \quad (6.18b)$$

where  $r_i(x) = \sum_j r_{ij}(x)p_j(x, t)$  and  $\bar{r}(x) = \sum_{ij} r_{ij}(x)p_i(x, t)p_j(x, t)$ ; cf. (6.5) – (6.7) and Chapter 2. In addition, we always assume

$$p_i(x, 0) \geq 0, \quad p_i(x, 0) \not\equiv 0, \quad \sum_j p_j(x, 0) \equiv 1 \quad \text{for every } x \in \Omega, \quad (6.18c)$$

as well as the boundary condition

$$p_{i,x}(b, t) = 0 \quad \text{for every } i \text{ and } t > 0, \quad (6.18d)$$

which is assumed to hold at every endpoint  $b$  of the spatial domain  $\Omega$ . Thus, equations (6.18a), (6.18b), (6.18c), and (6.18d) constitute our basic model.

It remains to derive the boundary condition (6.18d). It follows from the condition that at the boundary, there is no flux of individuals or of alleles. Let us assume, for instance, that the habitat is  $[0, \infty)$ , with no migration left of the origin. We start with a discrete model, and consider colonies  $0, 1, 2, \dots$ . We assume  $m_{0\alpha} = 0$  if  $\alpha > \Gamma$ . Inserting (6.5) into the recursion, we obtain

$$p'_{i,0} = \sum_{\alpha=0}^{\Gamma} m_{0\alpha} p_{i,\alpha} + O(\lambda)$$

as  $\lambda \rightarrow 0$ . A simple calculation yields

$$\frac{\lambda p'_{i,0} - p_{i,0}}{\lambda} = \sum_{\alpha=0}^{\Gamma} m_{0\alpha} \frac{p_{i,\alpha} - p_{i,0}}{\epsilon} + O(\epsilon). \quad (6.19)$$

Letting  $\lambda \rightarrow 0$ , we obtain  $(p'_{i,0} - p_{i,0})/\lambda = (\hat{\pi}_i(0, \tau + \lambda) - \hat{\pi}_i(0, \tau))/\lambda \rightarrow \pi_{i,\tau}(0, \tau)$ , whence the left-hand side of (6.19) converges to zero. Similarly, letting  $\lambda \rightarrow 0$ , we obtain  $(p_{i,\alpha} - p_{i,0})/\epsilon = (\pi_i(\epsilon\alpha, \tau) - \pi_i(\epsilon 0, \tau))/\epsilon \rightarrow \alpha\pi_{i,x}(0, \tau)$ . Therefore, the right-hand side of (6.19) converges to  $\pi_{i,x}(0, \tau) \sum_{\alpha=0}^{\Gamma} \alpha m_{0\alpha}$ , from which we conclude that the boundary condition is  $p_{i,x}(0, t) = 0$  for every  $i$  and  $t$ .

We conclude with results concerning existence and uniqueness of solutions.

**Remark 6.1.** *Hölder continuity.* A function  $f : \mathbb{R} \rightarrow \mathbb{R}$  is Hölder continuous if there exist constants  $c$  and  $\alpha \in (0, 1]$ , such that

$$|f(x) - f(y)| \leq c|x - y|^\alpha$$

for every  $x, y$  in the domain of  $f$ . A Hölder continuous function is uniformly continuous; if  $\alpha = 1$ , then it is Lipschitz continuous.

Denote by  $C(\Omega)$  the continuous real-valued functions on  $\Omega$ , by

$$C^k(\Omega) = \{u : D^m u \in C(\Omega), 0 \leq m \leq k\},$$

and by  $C^k(\bar{\Omega})$  those functions in  $C^k(\Omega)$  with the property that  $D^m u$  has a continuous extension to  $\bar{\Omega}$ , for each  $m$  with  $0 \leq m \leq k$ . Finally, denote by  $C^{k,\alpha}(\bar{\Omega})$  those  $u \in C^k(\bar{\Omega})$  that have the property that  $D^k u$  is Hölder continuous with exponent  $\alpha$ .

Then  $C^k(\bar{\Omega})$  and  $C^{k,\alpha}(\bar{\Omega})$  are separable Banach spaces with the norms

$$\|u\|_{C^k} = \max_{0 \leq m \leq k} \sup_{x \in \Omega} |D^m u(x)|$$

and

$$\|u\|_{C^{k,\alpha}} = \|u\|_{C^k} + \sup_{x,y \in \bar{\Omega}, x \neq y} \frac{|D^k u(x) - D^k u(y)|}{|x - y|^\alpha},$$

respectively (Friedman 1969).

We assume that  $\rho(x)$ ,  $M(x)$ ,  $V(x)$ , and  $r_{ij}(x)$  are all Hölder continuous and  $p_i(x, 0)$  is continuous on  $\bar{\Omega}$ . Then the standard existence theory of evolution equations (e.g., Sell and You 2002) shows that the problem (6.18), or the more general version in which (6.18a) is replaced by (6.17), has a unique classical solution  $p(x, t)$  that exists for all time,  $p_i \in C(\bar{\Omega} \times [0, \infty)) \cap C^{2,1}(\bar{\Omega} \times (0, \infty))$  and  $p_i(x, t) \geq 0$  for every  $i$ , every  $x \in \bar{\Omega}$ , and every  $t > 0$ . Therefore, without loss of generality, we posit that  $0 < p_i(x, 0) < 1$  for every  $i$  and every  $x \in \bar{\Omega}$ .

Finally, we show that  $0 < p_i(x, t) < 1$  holds for all  $i$ ,  $x$ , and  $t > 0$ , and  $\sum_i p_i(x, t) \equiv 1$  for every  $x \in \Omega$  and  $t > 0$ . By summation, we obtain from (6.18a)

$$\frac{\partial}{\partial t} \left( \sum_i p_i \right) = \frac{\sigma^2}{2} \frac{\partial^2}{\partial x^2} \left( \sum_i p_i \right) + \lambda \bar{r} \left[ 1 - \left( \sum_i p_i \right) \right], \quad (6.20)$$

from (6.18c)

$$\sum_i p_i(x, 0) \equiv 1, \quad (6.21)$$

and from (6.18d)

$$\frac{\partial}{\partial x} \left( \sum_i p_i \right) (b, t) = 0. \quad (6.22)$$

By the uniqueness of the solutions of linear parabolic equations (e.g., Friedman 1969), we obtain  $\sum_i p_i(x, t) \equiv 1$  for every  $x \in \Omega$  and every  $t > 0$ . By the maximum principle for parabolic equations (Appendix B or Protter and Weinberger 1984), if  $p_i(x, 0) \neq 0$ , then  $p_i(x, t) > 0$  for every  $x \in \bar{\Omega}$  and  $t > 0$ . Hence, without loss of generality, we assume that  $p_i(x, t) > 0$  for every  $i$ ,  $x \in \bar{\Omega}$ , and  $t \geq 0$ .

## 7 PDE models for two alleles

The majority of available theory about the PDE migration-selection model assumes two alleles per locus. In this section, we shall treat three classical scenarios: Fisher waves, hybrid zones, and clines. Because we assume only two alleles, the notation can be simplified. Instead of using the vector  $(p_1, p_2)^\top$ , it is sufficient to use  $p(x, t) = p_1(x, t)$ . In addition, we set  $S(x, p) = S_1((p_1, p_2)^\top, x)$ . Throughout, we assume the initial condition

$$0 \leq p(x, 0) \leq 1, \quad p(x, 0) \neq 0, \quad p(x, 0) \neq 1 \quad \text{on } \Omega. \quad (7.1)$$

We will factor out the selection intensity  $s$ , i.e., we assume that the fitness of  $\mathcal{A}_i \mathcal{A}_j$  is  $sr_{ij}(x)$ , and  $r_{ij}$  is independent of  $p$  and  $t$ . Then we obtain

$$\begin{aligned} S(x, p) &= sp(r_1(x, p) - \bar{r}(x, p)) \\ &= sp(1 - p) \left( r_{12}(x) - r_{22}(x) + [r_{11}(x) - 2r_{12}(x) + r_{22}(x)]p \right). \end{aligned} \quad (7.2)$$

In general,  $S(x, p)$  cannot be factored into the form

$$S(x, p) = sg(x)f(p). \quad (7.3)$$

However, in the following important special cases this is possible.

a) No dominance:  $r_{ij}(x) = v_i(x) + v_j(x)$  on  $\bar{\Omega}$ . Then

$$S(x, p) = s[v_1(x) - v_2(x)]p(1 - p). \quad (7.4)$$

b)  $\mathcal{A}_1$  is dominant:  $r_{11}(x) = r_{12}(x)$  on  $\bar{\Omega}$ . Then

$$S(x, p) = s[r_{11}(x) - r_{22}(x)]p(1 - p)^2. \quad (7.5)$$

c)  $\mathcal{A}_1$  is recessive:  $r_{22}(x) = r_{12}(x)$  on  $\bar{\Omega}$ . Then

$$S(x, p) = s[r_{11}(x) - r_{22}(x)]p^2(1 - p). \quad (7.6)$$

d) All selection coefficients have the same spatial dependence  $g(x)$ . Then we can choose

$$r_{11}(x) = g(x), \quad r_{12}(x) = hg(x), \quad r_{22}(x) = -g(x), \quad (7.7)$$

where  $h$  signifies the degree of dominance, and obtain

$$S(x, p) = sg(x)p(1 - p)(1 + h - 2hp); \quad (7.8)$$

cf. (2.16). Note that  $h = 0, 1, -1$  yields the cases a), b), c), respectively.

## 7.1 Fisher's equation

This model was introduced independently by Fisher (1937) and Kolmogorov et al. (1937). It assumes that fitnesses are independent of the spatial position and exhibit no dominance. Fisher envisaged to model the spread of a mutant that has a constant fitness advantage over the wild type. These assumptions together with (7.4) show that (6.18a) becomes

$$p_t = \frac{\sigma^2}{2} p_{xx} + sp(1 - p), \quad (7.9)$$

where  $x \in \Omega = (-\infty, \infty)$ . By rescaling time and space according to  $\tau = st$  and  $y = x\sqrt{2s/\sigma^2}$ , (7.9) simplifies to

$$p_t = p_{xx} + p(1 - p). \quad (7.10)$$

Fisher wanted to find out how fast a new favorable mutant spreads through a spatially distributed population.

It turns out that the (biologically relevant) solutions are “wave like”. In general, PDEs can have quite different kinds of wave-like solutions. We shall be mainly concerned with *wave fronts*. They have the following properties:

$$0 \leq u \leq 1, \quad u(-\infty) = 1, \quad \text{and} \quad u(\infty) = 0. \quad (7.11)$$

(One can also assume  $u(-\infty) = 0$  and  $u(\infty) = 1$ . Then the wave front will travel in the opposite direction.) A *solitary wave* (*soliton*, *pulse*) satisfies

$$u \geq 0, \quad u \neq 0, \quad u(-\infty) = u(\infty) = 0. \quad (7.12)$$

To find wave-front solutions of (7.10), we set

$$p(x, t) = u(x - ct). \quad (7.13)$$

Then (7.10) becomes  $-cu'(x - ct) = u''(x - ct) + u(x - ct)[1 - u(x - ct)]$ , i.e.,

$$u'' + cu' + u(1 - u) = 0. \quad (7.14)$$

Here,  $u'$  indicates differentiation with respect to the (single) variable on which  $u$  depends. If we introduce  $v = u'$ , then (7.14) can be written as the following system of linear ODEs:

$$\begin{aligned} u' &= v, \\ v' &= -cv - u(1 - u). \end{aligned} \quad (7.15)$$

We study the system (7.15). The equilibria are  $(0, 0)$  and  $(1, 0)$ . A wave front corresponds to a heteroclinic orbit joining these two equilibria and satisfying  $0 \leq u \leq 1$ . The Jacobian of (7.15) is

$$J = \begin{pmatrix} 0 & 1 \\ -1 + 2u & -c \end{pmatrix}. \quad (7.16)$$

Therefore, the Jacobians at the two equilibria are

$$J_{(0,0)} = \begin{pmatrix} 0 & 1 \\ -1 & -c \end{pmatrix} \quad \text{and} \quad J_{(1,0)} = \begin{pmatrix} 0 & 1 \\ 1 & -c \end{pmatrix}. \quad (7.17)$$

We find that the eigenvalues at  $(0, 0)$  are  $-\frac{1}{2}c \pm \frac{1}{2}\sqrt{c^2 - 4}$ . Therefore,  $(0, 0)$  is asymptotically stable if and only if  $c > 0$ , and it is a nodal sink if and only if  $c \geq 2$ . The eigenvalues at  $(1, 0)$  are  $-\frac{1}{2}c \pm \frac{1}{2}\sqrt{c^2 + 4}$ . Therefore,  $(1, 0)$  is always a saddle. The case  $c < 0$  is without interest because then both equilibria are unstable and a connecting, i.e., heteroclinic, orbit is repelling. Therefore, we focus on the case  $c > 0$ . If  $0 < c < 2$ , the heteroclinic orbit spirals. Therefore, it is not positive everywhere. Because the eigenvectors corresponding to the two eigenvalues are  $(c + \sqrt{c^2 + 4}, 2)$  and  $(c - \sqrt{c^2 + 4}, 2)$ , we can draw the phase portrait (see Figure 7.1). (Also note that  $v' < 0$  if  $v = 0$  and  $0 \leq u \leq 1$ , and  $v' > 0$  if  $v < -u(1 - u)/c$ .)

A wave front exists if and only if  $c \geq 2$ . For every  $c > 2$ , there exists a unique wave front (Kolmogorov et al. 1937; Aronson and Weinberger 1975, 1978). The reason is that then one of the branches of the unstable manifold of  $(1, 0)$  must connect to  $(0, 0)$ . Because the heteroclinic orbit satisfies  $v < 0$  if  $0 < u < 1$ , we have  $u' = v < 0$ . Hence, the wave front is strictly monotone decreasing. The point of inflection is given by  $u'' = v' = 0$ , i.e., it satisfies  $v = -u(1 - u)/c$ . In advance of this point,  $u'' > 0$ .

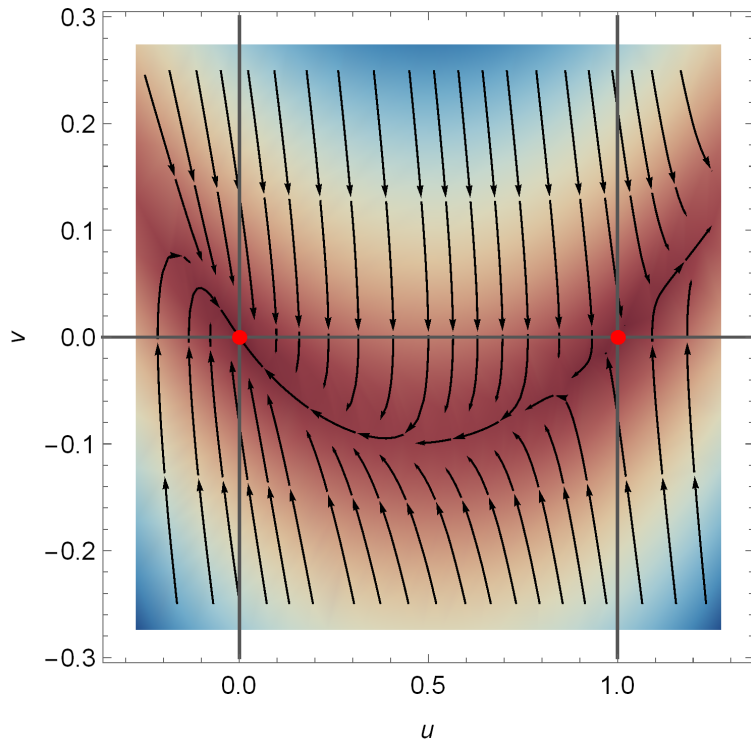


Figure 7.1: Phase portrait of (7.15) for  $c = 2.5$ .

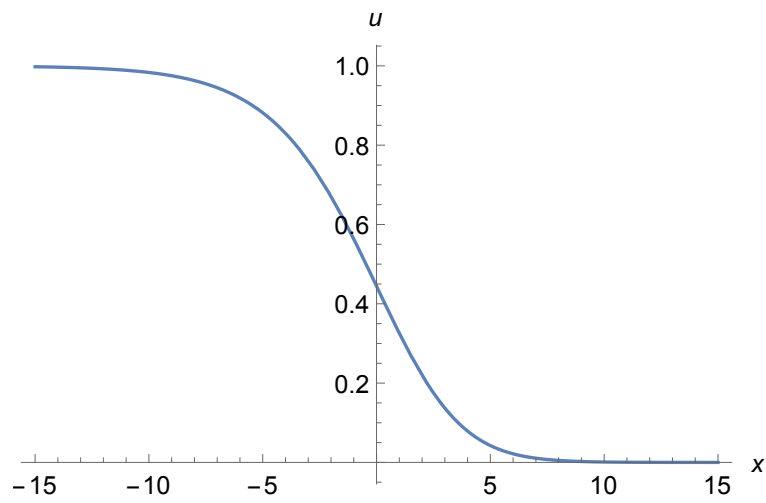


Figure 7.2: The explicit wave-front solution (7.18) with  $r = -\frac{1}{2}$  and  $c = 5/\sqrt{6}$ .

An explicit wave-front solution of (7.10) is known for  $c = \pm 5/\sqrt{6} \approx \pm 2.0412$  (Ablowitz and Zeppetella, 1979):

$$u(z) = \left(1 - re^{z/\sqrt{6}}\right)^{-2}, \quad (7.18)$$

where  $r < 0$  is arbitrary (Figure 7.2). Of course, if  $z \rightarrow u(z)$  is a solution, then also  $z \rightarrow u(z + a)$  for every  $a$ .

Kolmogorov et al. (1937) proved that the initial datum  $p(x, 0) = 1$  if  $x < 0$ , and  $p(x, 0) = 0$  if  $x > 0$  converges to a wave with speed  $c=2$ . McKean (1975) extended this result to initial data that converge sufficiently rapidly to 1 or 0 as  $x \rightarrow -\infty$  and  $x \rightarrow \infty$ , respectively. In addition, he proved that if for given  $c > 2$ , the initial function converges to 1 at an appropriate (exponential) rate as  $x \rightarrow -\infty$ , the corresponding solution converges to a wave front with speed  $c$ . Thus, wave fronts are stable. For the original equation (7.9), the condition  $c > 2$  transforms into  $c > \sqrt{2\sigma^2 s}$ .

Of course, it is unnatural that the speed is indeterminate. The reason is that diffusion (with a constant) rate can be expected to approximate biological reality only if sufficiently many individuals of both types are present. Clearly, this is not the case at the extreme front or back of the wave. Therefore, in sufficiently large populations the wave speed should be close to the minimum possible value of  $c = 2$ . Finally, initial data satisfying  $p(x, 0) \rightarrow 0$  as  $x \rightarrow \pm\infty$  may converge to double waves, similar to those in Figure 7.4.

There exist other types of simple solutions of (7.9). For instance,

$$p(x, t) = \frac{ae^{st}}{1 - a + ae^{st}} \quad (7.19)$$

is a family of solutions that is constant in  $x$  and  $p(x, 0) \equiv a$ .

## 7.2 Hybrid zones

A hybrid zone exists where two subspecies or differentiated populations meet and cross-fertilize. However, if the populations have been separated for a long time, hybrids usually have reduced fitness. To model this situation, we follow Bazykin (1967) and Barton (1979). We assume that the fitnesses of the three genotypes  $\mathcal{A}_1\mathcal{A}_1$ ,  $\mathcal{A}_1\mathcal{A}_2$ , and  $\mathcal{A}_2\mathcal{A}_2$  are spatially independent and given by  $1 + 2s$ ,  $1 + s - h$ , and 1, respectively, where  $0 \leq s, h \ll 1$ . Essentially, allele  $\mathcal{A}_1$  ( $\mathcal{A}_2$ ) is assumed to be characteristic of population 1 (2). If migration is homogeneous and isotropic, we obtain from (6.18a) and (7.2) the PDE

$$p_t = \frac{1}{2}\sigma^2 p_{xx} + sp(1-p) + hp(1-p)(2p-1) \quad (7.20)$$

on  $\Omega = (-\infty, \infty)$ . Obviously,  $p \equiv 0$  and  $p \equiv 1$  are always solutions.

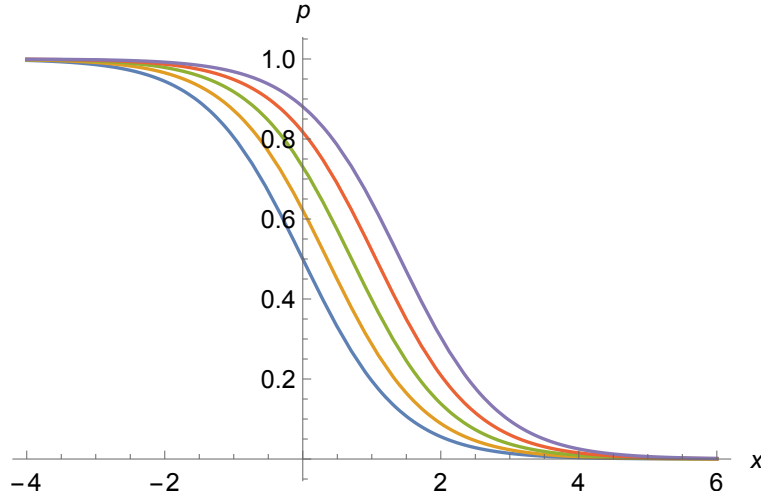


Figure 7.3: Graph of  $p_-(x, t)$  (7.21) for  $x_0 = 0$ ,  $\sigma^2 = 0.2$ ,  $s = 0.05$ ,  $h = 0.2$ . The blue, yellow, green, red, and violet curves are for  $t = 0, 10, 20, 30, 40$ , respectively.

It is straightforward to check that the following family of non-trivial solutions exists:

$$p_{\pm}(x, x_0, t) = \frac{1}{2} \left[ 1 \pm \tanh \left( \sqrt{\frac{h}{2\sigma^2}} (x - x_0) \pm \frac{st}{2} \right) \right]. \quad (7.21)$$

(Recall that  $\tanh(x) = (e^x - e^{-x})/(e^x + e^{-x})$ .) If  $s > 0$ , these solutions are wave fronts;  $p_-$  satisfies (7.11) and travels to the right (Figure 7.3). If  $h \neq 0$ , in contrast to Fisher's equation (where  $h = 0$ ), the speed and shape are uniquely determined. If  $h = 0$ , the solution (7.21) is constant in space. Note that  $s$  does not affect shape; it determines only the speed at which the wave front advances.

If  $s = 0$ ,  $p(x, x_0, t)$  is time independent, and represents a family ( $x_0 \in \mathbb{R}$ ) of stationary solutions. The inverse of the maximum gradient,

$$w = \frac{1}{|p'(x_0, x_0)|} = 2 \sqrt{\frac{2\sigma^2}{h}}, \quad (7.22)$$

may be called their width. Then  $p(x_0 - w/2) = 1/(1 + e^2) \approx 0.119$  and  $p(x_0 + w/2) = e^2/(1 + e^2) \approx 0.881$ . As expected, the solutions become steeper around their center  $x_0$  as selection against hybrids increases or dispersal decreases.

If  $h > s$ , the solutions  $p_-(x, x_0, t)$  are globally stable modulo appropriate initial conditions (Fife and McLeod 1977; Sattinger, 1976, 1977). In fact, much more complicated asymptotic states can exist. For instance, the existence of infinitely many periodic and other non-monotone unstable asymptotic states has been proved (Fife 1978, 1979).



We now formulate a more general and precise result.

Consider the initial-value problem

$$u_t = u_{xx} + f(u), \quad x \in \Omega = (-\infty, \infty), \quad t > 0, \quad (7.23a)$$

where

$$u(x, 0) = \varphi(x), \quad x \in \Omega. \quad (7.23b)$$

Assume that  $f \in C^1[0, 1]$  satisfies for some  $\alpha \in (0, 1)$

$$f(0) = f(1) = 0, \quad f'(0) < 0, \quad f'(1) < 0, \quad f \text{ changes sign once at } \alpha. \quad (7.24)$$

(Note that the last assumption implies that the ODE  $\dot{u} = f(u)$  has the asymptotically stable equilibria 0 and 1, and the unstable equilibrium  $\alpha$ ; hence,  $\dot{u} = f(u)$  exhibits bistability.)

**Theorem 7.1** (Fife and McLeod, 1977).

1. *There exists a unique (except for translation) monotone traveling front  $U(x - ct)$  (Kanel' 1960).*
2. *Suppose that  $0 \leq \varphi(x) \leq 1$  for all  $x \in \Omega$ , and*

$$\liminf_{x \rightarrow -\infty} \varphi(x) > \alpha \text{ and } \limsup_{x \rightarrow \infty} \varphi(x) < \alpha. \quad (7.25)$$

*Then for some  $x_0$  the solution of the initial-value problem approaches  $U(x - ct - x_0)$  uniformly in  $x$  as  $t \rightarrow \infty$ . Further,  $c \geq 0$  ( $c \leq 0$ ) according as  $\int_0^1 f(u)du \geq 0$  ( $\leq 0$ ), and the rate at which the limit is approached is exponential.*

3. *Suppose that  $\varphi$  is of bounded support or, more generally, that  $\limsup_{x \rightarrow \pm\infty} \varphi(x) < \alpha$  and that  $\varphi(x) > \alpha + \eta$  for some  $\eta > 0$  and  $|x| < L$ . If  $L$  is large enough, depending on  $\eta$ , and  $\int_0^1 f(u)du > 0$ , then the solution develops (uniformly in  $x$ ) into a pair of diverging traveling fronts*

$$U(x - ct - x_0) + U(-x - ct - x_1) - 1. \quad (7.26)$$

Fife and McLeod (1977) prove more general results by admitting that  $f$  has more than one zero. They consider fronts traveling to the left.

Figure 7.4 documents the double waves of the third statement. With  $f(u) = u(1 - u)(s - h + 2hu)$ , as in (7.20), we have  $\alpha = \frac{h-s}{2h}$  and  $\int_0^1 f(u)du = s/6 > 0$  (if  $s > 0$ ). Therefore, statements 2 and 3 of the above theorem apply if  $h > s$ . It can be shown that if  $s > 2h$ , then asymmetric wave fronts at speed  $c > \sqrt{2\sigma^2(s - h)}$  become stable.

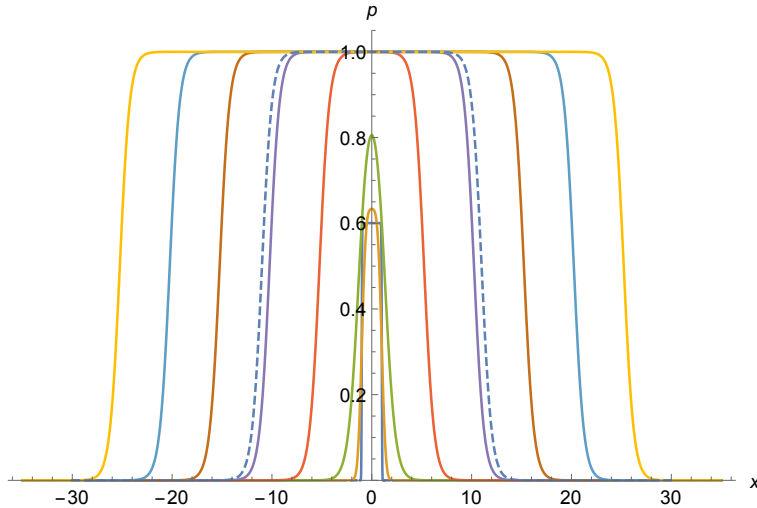


Figure 7.4: Numerical solution of (7.20) with the initial condition  $p(x, 0) = 0.6$  if  $|x| \leq 1$ , and  $p(x, 0) = 0$  otherwise. The blue, orange, green, red, violet, brown, light blue, and yellow curves show the solution for  $t = 0, 1, 20, 100, 200, 300, 400$ , and  $500$ , respectively. The blue dashed line shows the solution (7.26) with  $U$  given by  $p_-(x, 200)$  from (7.21). The parameters are  $\sigma^2 = 0.1$ ,  $s = 0.1$ ,  $h = 0.2$ .

### 7.3 Clines under spatially heterogeneous selection

If genotypic fitnesses vary in space, then equilibrium allele frequencies can be expected to vary, too. One says a *cline* (in allele frequencies) occurs if the allele frequencies depend monotonically on the spatial variable. Such patterns are frequently observed in spatially distributed populations if there is an environmental gradient, for a instance in temperature. The first model of a cline is due to Haldane (1948), who motivated his study by the problem of measuring selection in the deer mouse. Further important early theoretical work includes Fisher (1950), Slatkin (1973), Fleming (1975), and Nagylaki (1975).

First, we investigate explicit examples; then we will turn to the general theory.

#### 7.3.1 The step environment in the infinite cline

We assume  $\Omega = (-\infty, \infty)$ ,

$$p_t = \frac{\sigma^2}{2} p_{xx} + sg(x)f(p), \quad (7.27)$$

where  $f(p) = p(1-p)(1+h-2hp)$ ,

$$g(x) = \begin{cases} 1 & \text{if } x \geq 0, \\ -a & \text{if } x < 0, \end{cases} \quad (7.28)$$

and  $a > 0$ ; cf. (7.8). Of course, we are only interested in solutions satisfying  $0 \leq p(x, t) \leq 1$  for all  $x$  and  $t$ .

If a stationary solution (a cline) exists, it must satisfy

$$p'' + \lambda f(p) = 0 \quad \text{if } x \geq 0, \quad (7.29a)$$

$$p'' - a\lambda f(p) = 0 \quad \text{if } x < 0, \quad (7.29b)$$

where  $\lambda = 2s/\sigma^2$ . Slatkin (1973) called  $\sqrt{2/\lambda} = \sigma/\sqrt{s}$  the critical length of the cline. We require the conditions

$$p'(\infty) = p'(-\infty) = 0, \quad (7.30a)$$

$$p \text{ and } p' \text{ are continuous at } x = 0. \quad (7.30b)$$

Obviously,  $p \equiv 0$  and  $p \equiv 1$  are always solutions.

Now suppose that there is *no dominance*, i.e.,  $h = 0$ . Then  $f(p) = p(1 - p)$  and the following solution of (7.29a) exists and is unique with respect to the above conditions (cf. Haldane 1948, Slatkin 1973, Nagylaki 1976):

$$p(x) = -\frac{1}{2} + \frac{3}{2} \tanh^2 \left[ \frac{\sqrt{\lambda}}{2} x + \tanh^{-1} \sqrt{\frac{1+2b}{3}} \right] \quad \text{if } x \geq 0, \quad (7.31a)$$

$$p(x) = \frac{3}{2} - \frac{3}{2} \tanh^2 \left[ \frac{\sqrt{a\lambda}}{2} x - \tanh^{-1} \sqrt{1 - \frac{2b}{3}} \right] \quad \text{if } x < 0, \quad (7.31b)$$

where  $b = p(0)$  is the unique solution in  $(0, 1)$  of

$$(1 + a)(3b^2 - 2b^3) = 1. \quad (7.32)$$

The solution (7.31) satisfies (7.30a), (7.30b),  $\lim_{x \rightarrow \infty} p(x) = 1$ ,  $\lim_{x \rightarrow -\infty} p(x) = 0$ , and

$$p'(0) = b \sqrt{3 - 2b} \sqrt{\frac{a\lambda}{3}} = \sqrt{\frac{a\lambda}{3(1+a)}}, \quad (7.33)$$

where the last equality follows from (7.32). The second derivative at  $x = 0$  is not continuous because  $p''(0+) = -b(1 - b)\lambda$ , whereas  $p''(0-) = ab(1 - b)\lambda$ .

*Proof.* We set  $\varphi(x, p) = p'(x)$ . Then  $p'' = \frac{\partial \varphi}{\partial x} = \frac{\partial \varphi}{\partial p} \frac{\partial p}{\partial x} = \frac{\partial \varphi}{\partial p} \varphi$ . Therefore, (7.29a) can be written as  $\frac{\partial \varphi}{\partial p} \varphi = -\lambda p(1 - p)$ . Separating variables and integrating, we obtain  $\varphi^2 = C - 2\lambda(p^2/2 - p^3/3)$ . Because  $\varphi(x, p) \rightarrow 0$  as  $x \rightarrow \infty$  (and  $p(x) \rightarrow 1$  as  $x \rightarrow \infty$ ), we obtain  $C = \lambda/3$ . Therefore, we have to solve

$$\left( \frac{dp}{dx} \right)^2 = \frac{\lambda}{3} (1 - p)^2 (1 + 2p). \quad (7.34)$$

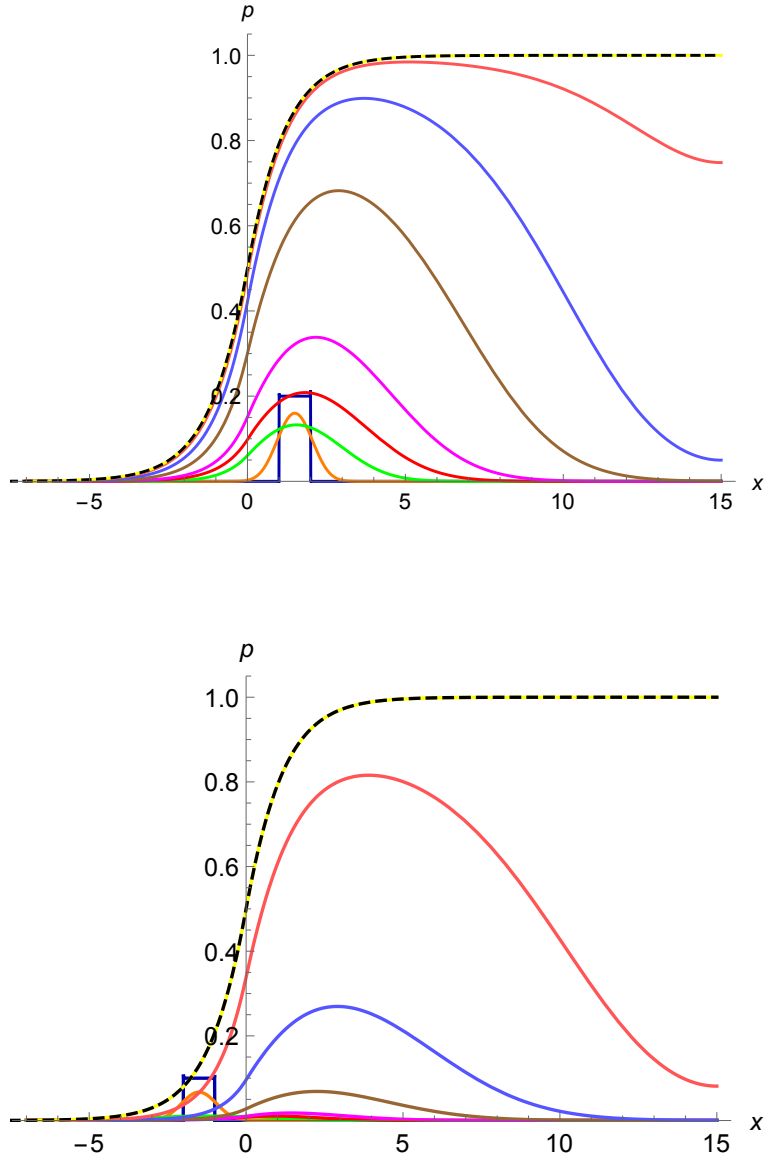


Figure 7.5: Numerical solution of (7.27) with no dominance ( $h = 0$ ),  $\sigma^2 = 2$ ,  $s = 1$ , the step environment (7.28), and (in the upper panel) the initial condition  $p(x, 0) = 0.2$  if  $1 < x < 2$  and  $p(x, 0) = 0$  otherwise, and (in the lower panel)  $p(x, 0) = 0.2$  if  $-2 < x < -1$  and  $p(x, 0) = 0$  otherwise. The blue, orange, green, red, magenta, brown, light blue, light red, and yellow curves show the solution for  $t = 0, 0.1, 1, 2, 3, 5, 7, 10, 20$ , respectively. The black dashed line shows the solution (7.31) with  $\lambda = 1$ .

Separation of variables and integration yields (7.31a) if  $p(0) = b$ . Analogously, (7.29b) can be written as  $\frac{\partial \varphi}{\partial p} \varphi = a\lambda p(1-p)$ , from which we obtain

$$\left(\frac{dp}{dx}\right)^2 = \frac{a\lambda}{3}p^2(3-2p). \quad (7.35)$$

In this case, separation of variables and integration yields (7.31b) if  $p(0) = b$ .

Because we require continuity of  $p'(x)$  at  $x = 0$ , the right-hand sides of (7.34) and (7.35) must coincide at  $x = 0$ . This yields (7.32).  $\square$

Stationary, or equilibrium, solutions of biological significance need to be stable (in an appropriate sense). We will study stability in a subsequent section. Stability of the cline is suggested by the convergence of time-dependent solutions in Figure 7.5.

Now we assume arbitrary dominance. Then  $f(p) = p(1-p)(1+h-2hp)$  (7.7) and, analogously to the above proof, we find

$$\varphi^2 = C_1 - \frac{\lambda p^2}{3}\phi(p) \quad \text{if } x \geq 0 \quad (7.36)$$

and

$$\varphi^2 = C_2 + \frac{a\lambda p^2}{3}\phi(p) \quad \text{if } x < 0, \quad (7.37)$$

where  $\phi(p) = 3 + 3h(1-p)^2 - 2p$ . Because  $\varphi(x) \rightarrow 0$  and  $p(x) \rightarrow 1$  as  $x \rightarrow \infty$  and  $\varphi(x) \rightarrow 0$  and  $p(x) \rightarrow 0$  as  $x \rightarrow -\infty$ , we get  $C_1 = \lambda/3$  and  $C_2 = 0$ . Therefore, instead of (7.34) and (7.35),

$$\left(\frac{dp}{dx}\right)^2 = \frac{\lambda}{3} - \frac{\lambda p^2}{3}\phi(p) \quad \text{if } x \geq 0 \quad (7.38)$$

and

$$\left(\frac{dp}{dx}\right)^2 = \frac{\lambda a p^2}{3}\phi(p) \quad \text{if } x < 0 \quad (7.39)$$

respectively, are obtained. From the conditions (7.30b), we infer

$$\frac{\lambda}{3} - \frac{\lambda b^2}{3}\phi(b) = \frac{\lambda a b^2}{3}\phi(b), \quad (7.40)$$

where  $b = p(0+) = p(0-)$ . This yields

$$\phi(b) = \frac{1}{b^2(a+1)}. \quad (7.41)$$

Substituting this expression into (7.39), evaluated for  $x \rightarrow 0-$ , we find

$$p'(0) = p'(0+) = p'(0-) = \sqrt{\frac{\lambda a}{3(a+1)}}; \quad (7.42)$$

cf. (7.33).

In analogy to (7.22), we call

$$w = \frac{1}{|p'(0)|} = \sqrt{\frac{3}{\lambda}} \sqrt{\frac{a+1}{a}} \quad (7.43)$$

the width of the cline. Therefore, the dependence of the width of the cline on  $\lambda$ , or on  $s$  and  $\sigma^2$ , is in accordance with intuition: The cline gets wider as selection decreases or dispersal increases. Interestingly, the width of the cline is independent of the degree of dominance,  $h$ , and of  $b = p(0)$  (this is true only if  $|h| \leq 1$ ; see below). Also in accordance with intuition, its width increases and tends to  $\infty$  as  $a \rightarrow 0$ ; the cline “disappears” at  $p = 1$  in this limit. Finally, for given  $a > 0$ ,  $b = p(0)$  is the unique solution in  $(0, 1)$  of (7.41). Because the steepness or width is often relatively easy to measure, the strength of selection (dispersal) can be inferred from estimates of the strength of dispersal (selection).

Figure 7.6 displays the clines for five different dominance parameters and  $a = 1$ . It confirms that the clines have the same slope at  $x = 0$  although they are asymmetric unless there is no dominance.

It appears that, in general,  $p(x)$  cannot be obtained explicitly in terms of well known functions by integrating (7.38) and (7.39) (though the latter ODE can be solved explicitly). However, an explicit solution can be derived for the important case of a completely recessive favorable allele (Haldane 1948). Then  $h = -1$ ,  $f(p) = 2p^2(1 - p)$ , and (7.38) and (7.39) become

$$\left(\frac{dp}{dx}\right)^2 = \frac{\lambda}{3}(1 - p)^2(1 + 2p + 3p^2) \quad (7.44)$$

and

$$\left(\frac{dp}{dx}\right)^2 = \frac{a\lambda}{3}p^3(4 - 3p), \quad (7.45)$$

respectively. The first differential equation is solved by noting that

$$\frac{d}{dx} \sinh^{-1} \left[ \frac{\sqrt{2}(1 + 2p)}{1 - p} \right] = \frac{\sqrt{6}}{(1 - p) \sqrt{1 + 2p + 3p^2}}. \quad (7.46)$$

It follows that the cline can be written as

$$p(x) = 1 - \frac{3\sqrt{2}}{2\sqrt{2} + \sinh \left[ \sqrt{2\lambda}x + \sinh^{-1} \left( \frac{\sqrt{2}(1+2b)}{1-b} \right) \right]} \quad \text{if } x \geq 0, \quad (7.47a)$$

$$p(x) = \frac{3b}{3 - x \sqrt{3ab(4 - 3b)\lambda + x^2 ab\lambda}} \quad \text{if } x < 0, \quad (7.47b)$$

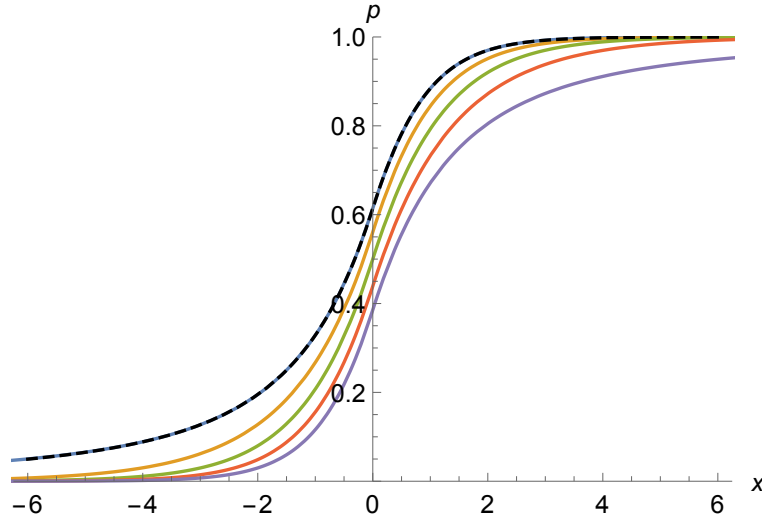


Figure 7.6: Numerical solution of (7.27) with dominance,  $\lambda = 1$ , and the step environment (7.28) with  $a = 1$  and (7.7). The blue, orange, green, red, and magenta curves show the solution for  $h = -1, -0.5, 0, 0.5, \text{ and } 1$ , respectively. The black dashed line shows the solution (7.47) with  $h = 1$ .

where  $b$  is the unique solution in  $(0, 1)$  of

$$1 - (1 + a)b^3(4 - 3b) = 0. \quad (7.48)$$

If  $a = 1$ , then  $b \approx 0.6143$ . This solution has the properties  $p(0) = b$ ,  $\lim_{x \rightarrow \infty} p(x) = 1$ , and  $\lim_{x \rightarrow -\infty} p(x) = 0$ .

The above analyses for  $h = 0$  and  $h = -1$  show that a cline exists always, i.e., independently of  $s > 0$ ,  $a > 0$ , and  $\sigma^2 > 0$ . This is different from the two-deme models treated in Sections 4.2 and 5, in which a protected polymorphism vanishes under sufficiently strong migration, except under extreme symmetry. For instance, in the Deakin model the protected polymorphism does not vanish if  $\frac{c_2}{s_1} + \frac{c_1}{s_2} = 0$  (4.17), or in Example 5.1 it does not vanish if  $\frac{1}{s_1} + \frac{1}{s_2} = 0$  and  $\mu_1 = \mu_2 = \mu$ . At first, this discrepancy may seem surprising because in the PDE model with  $g(x)$  given by (7.28) there are two different environments, just as in the two-deme models. However, the main difference is that in the present PDE model the habitat is unbounded, i.e., the region is infinitely large in which each of the alleles is advantageous. If the habitat is bounded or if it is semi-infinite, e.g.,  $\Omega = (0, \infty)$ , then generically clines vanish if the dispersal variance becomes very large. We shall treat such cases below.

Conley (1975) proved that a cline always exists for  $h = 0$  and  $g(x)$  subject only to the

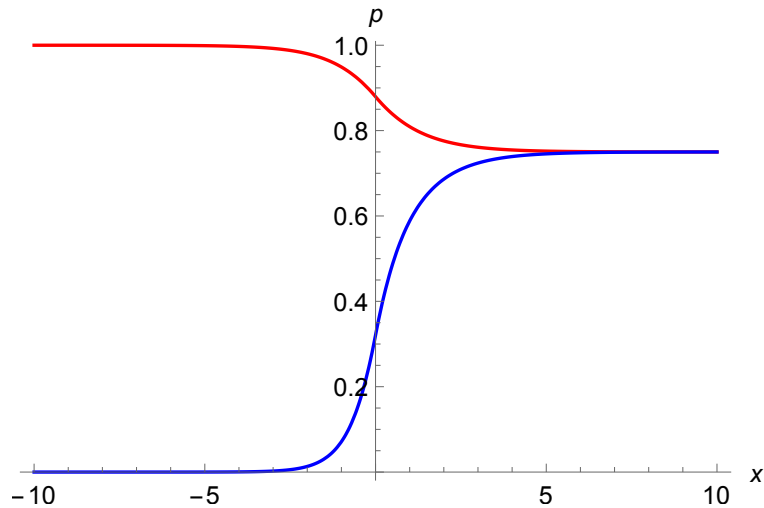


Figure 7.7: Numerical solution of (7.27) with  $h = 2$ ,  $\lambda = 1$ , and the step environment (7.28) with  $a = 1$ . In the limit  $x \rightarrow \infty$ , both clines converge to the pure selection equilibrium  $\hat{p} = (1 + h)/2h = 3/4$ . Which cline evolves depends on the initial data.

conditions  $\text{sgn } g(x) = \text{sgn } x$  for sufficiently large  $|x|$ , and that  $g(x)$  be not integrable as  $x \rightarrow \pm\infty$ . His proof applies for arbitrary  $h$  (Nagylaki 1975).

If there is overdominance or underdominance  $|h| > 1$ , there exist two clines. If  $h > 1$ , then in the absence of migration there is the stable equilibrium  $\hat{p} = (1 + h)/2h$ ; if  $h < -1$ , this equilibrium is unstable (Section 2.3). With the step environment (7.28) and  $h > 1$ , there is overdominance if  $x \geq 0$  and underdominance if  $x < 0$ . Therefore, in the presence of migration, there will be two clines (Figure 7.7). In this case, the steepness of the clines at  $x = 0$  is no longer given by (7.42). An analogous formula can be derived by taking into account the limiting behavior as  $x \rightarrow \pm\infty$ .

Some other environments than the step environment (7.28) were investigated by Slatkin (1973) and Nagylaki (1975). The latter study is devoted to semi-infinite clines, i.e.,  $\Omega = [0, \infty)$ . They include, for instance, the case of an environmental pocket.

## 7.4 Clines in a finite domain

We shall first concentrate on the simplest case, which is that of no dominance. For this case we shall outline the proof of the main result, Theorem 7.5. Then we shall review the available theory for intermediate and for complete dominance.



### 7.4.1 The ODE model with no dominance and two demes

To motivate the approach below for analyzing the PDE model, we recall Example 5.1 in which we investigated the ODE model for two alleles without dominance and two demes. We define

$$M = \begin{pmatrix} -1 & 1 \\ 1 & -1 \end{pmatrix} \text{ and } f(p) = \begin{pmatrix} p_1(1-p_1) \\ p_2(1-p_2) \end{pmatrix},$$

and assume  $s_1 s_2 < 0$  and  $\mu_1 = \mu_2 = \mu$ . After rescaling time and setting  $\lambda = 1/\mu$ , we can rewrite the differential equation (5.11) as

$$\dot{p} = Mp + \lambda \begin{pmatrix} s_1 & 0 \\ 0 & s_2 \end{pmatrix} f(p).$$

To derive the asymptotic stability of equilibria, we calculate the Jacobian and obtain

$$J(p) = M + \lambda \begin{pmatrix} s_1(1-2p_1) & 0 \\ 0 & s_2(1-2p_2) \end{pmatrix}.$$

Obviously, the equilibrium  $p = (0, 0)^\top$  is asymptotically stable if the leading eigenvalue of  $J(0, 0)$  is negative. This eigenvalue has a strictly positive eigenvector. An analogous result holds for  $p = (1, 1)^\top$ .

Therefore, it is natural to study the eigenvalue problem

$$-My - \lambda \begin{pmatrix} s_1 & 0 \\ 0 & s_2 \end{pmatrix} y = \sigma y, \tag{7.49}$$

where  $\lambda$  is considered as a parameter. Then  $p = (0, 0)^\top$  is asymptotically stable if the leading eigenvalue  $\sigma_1 > 0$ . Let  $\lambda_1$  denote an eigenvalue satisfying

$$-My = \lambda_1 \begin{pmatrix} s_1 & 0 \\ 0 & s_2 \end{pmatrix} y \tag{7.50}$$

for a strictly positive  $y$ , i.e.,  $y_1 > 0$  and  $y_2 > 0$  (provided it exists). Then we have  $\sigma_1 = 0$  if and only if  $\lambda = \lambda_1$ ; one can show that  $\sigma_1 > 0$  if and only if  $0 < \lambda < \lambda_1$  (we are only interested in  $\lambda > 0$ ); and  $\sigma_1 < 0$  if and only if  $\lambda > \lambda_1$ .

From (7.50), we obtain easily that  $\lambda_1$  is unique and given by  $\lambda_1 = \frac{1}{s_1} + \frac{1}{s_2}$  (the corresponding eigenvector is  $(-s_2, s_1)$  if  $s_1 > 0 > s_2$ ). There is a second eigenvalue, which is zero. Therefore,  $\sigma_1 > 0$  if and only if  $\frac{1}{\mu} = \lambda < \lambda_1$ , which is precisely the condition for stability of  $p = (0, 0)^\top$ , or non-protection of  $\mathcal{A}_1$ , i.e.,  $\kappa = \frac{\mu}{s_1} + \frac{\mu}{s_2} > 1$ ; cf. (4.14). Finally, we note that  $\lambda_1 = 0$  if and only if  $s_1 + s_2 = 0$ , and  $\lambda_1 > 0$  if and only if  $s_1 + s_2 < 0$ .

### 7.4.2 The PDE model with no dominance

Our presentation essentially follows Lou et al. (2013). We assume that  $\Omega$  is a bounded open (connected) domain in  $\mathbb{R}^n$  with a  $C^2$  boundary  $\partial\Omega$ . We write

$$\Delta f = \sum_{i=1}^n \frac{\partial^2 f}{\partial x_i^2} \quad \text{and} \quad \nabla f = \left( \frac{\partial f}{\partial x_1}, \dots, \frac{\partial f}{\partial x_n} \right) \quad (7.51)$$

for the Laplace and the gradient (nabla) operator, respectively. Note that  $\Delta f = \nabla \cdot \nabla f$ .

Our goal is to study the dynamics of

$$\frac{\partial p}{\partial t} = \Delta p + \lambda g(x)p(1-p) \quad \text{in } \Omega \times (0, \infty), \quad (7.52a)$$

subject to the boundary condition

$$\frac{\partial p}{\partial \nu} = 0 \quad \text{on } \partial\Omega \times (0, \infty), \quad (7.52b)$$

where  $\frac{\partial p}{\partial \nu} = \nu \cdot \nabla p$  denotes the derivative in direction of  $\nu$ , the outward unit normal vector on  $\partial\Omega$ , and

$$0 \leq p(x, 0) \leq 1, \quad p(x, 0) \not\equiv 0, \quad p(x, 0) \not\equiv 1 \text{ in } \Omega. \quad (7.52c)$$

If  $n = 1$  then  $\Omega = (b_1, b_2)$ , where  $-\infty < b_1 < b_2 < \infty$ . In this much simpler one-dimensional case, the equilibrium solution of (7.52) can be determined from the ordinary differential equation

$$p'' + \lambda g(x)p(1-p) = 0, \quad (7.53)$$

and the boundary condition (7.52b) simplifies to

$$p'(b_1, t) = p'(b_2, t) = 0 \quad \text{for } t \in (0, \infty). \quad (7.52b')$$

The following eigenvalue problem will play a crucial role in our investigation of the dynamics (7.52):

$$-\Delta \varphi = \lambda g(x)\varphi \quad \text{in } \Omega, \quad (7.54a)$$

$$\frac{\partial \varphi}{\partial \nu} = 0 \quad \text{on } \partial\Omega \times (0, \infty) \quad \text{and } \varphi > 0 \quad \text{in } \Omega. \quad (7.54b)$$

We say that  $\lambda$  is a principal eigenvalue of (7.54) if (7.54) has a solution. Clearly, zero is always a principal eigenvalue of (7.54) with positive constants as eigenfunctions. However, only positive principal eigenvalues of (7.54) are relevant in analyzing the dynamics of (7.52). In the one-dimensional (ODE) case, (7.54) is a special case of the Sturm-Liouville eigenvalue problem. Our first result is the following:

**Proposition 7.2.** *Suppose that  $g$  is not identically zero. Then (7.54) has a positive eigenvalue if and only if  $g$  changes sign in  $\Omega$  and*

$$\int_{\Omega} g(x) dx < 0. \quad (7.55)$$

For the one-dimensional case, this problem was solved by Picone (1910) and Bocher (1914) using Sturm's theory. The  $n$ -dimensional case was settled by Brown and Lin (1980), the general elliptic case by Senn and Hess (1982). We will prove this result in Section 7.4.3.

**Remark 7.3.** We note the analogy to the two-deme model outlined in Section 7.4.1, in which  $M$  plays the role of  $\Delta$  and  $\begin{pmatrix} s_1 & 0 \\ 0 & s_2 \end{pmatrix}$  that of  $g$ .

**Remark 7.4.** It is well known that if the principle eigenvalue  $\lambda_1(g)$  of (7.54) exists, it is simple and its corresponding eigenfunction can be chosen positive in  $\bar{\Omega}$ . Moreover, if  $\lambda$  is a positive eigenvalue of (7.54), then  $\lambda \geq \lambda_1(g)$ . Hence, we call  $\lambda_1(g)$  the smallest positive eigenvalue of (7.54). No other eigenvalue than  $\lambda_1(g)$  has an eigenfunction that does not change sign. We will prove these statements in Section 7.4.3.

We call an equilibrium globally asymptotically stable if it is asymptotically stable and every solution  $p(x, t)$  of (7.52a) satisfying the initial condition (7.52c) converges to it uniformly, i.e., in  $L^\infty(\Omega)$ .

The following is the main result of this section.

**Theorem 7.5.** *(i) Suppose that  $\int_{\Omega} g(x) dx < 0$  and  $g$  changes sign in  $\Omega$ . If  $\lambda \leq \lambda_1(g)$ , the equilibrium  $p \equiv 0$  of (7.52) is globally asymptotically stable. If  $\lambda > \lambda_1(g)$ , then (7.52) has a unique equilibrium  $\hat{p}$  satisfying  $0 < \hat{p} < 1$  in  $\bar{\Omega}$ , which is globally asymptotically stable.*

*(ii) Suppose that  $\int_{\Omega} g(x) dx = 0$  and  $g$  changes sign in  $\Omega$ . Then for every  $\lambda > 0$ , (7.52) has a unique nontrivial equilibrium, which is globally asymptotically stable.*

*(iii) Suppose that  $\int_{\Omega} g(x) dx > 0$  and  $g$  changes sign in  $\Omega$ . There exists a  $\lambda^* > 0$  such that if  $0 < \lambda \leq \lambda^*$ , then  $p \equiv 1$  is globally asymptotically stable. If  $\lambda > \lambda^*$ , then (7.52) has a unique equilibrium  $p^*$  satisfying  $0 < p^* < 1$  in  $\bar{\Omega}$ , which is globally asymptotically stable.*

A non-trivial equilibrium of (7.52) is not constant because this would imply  $g \equiv 0$ . It represents a cline. The proof of Theorem 7.5 consists of several steps and is deferred to Section 7.4.4. It will be sufficient to prove (i) and (ii).

**Remark 7.6.** Fleming (1975) derived the conditions for the stability of the trivial solutions  $p \equiv 0$  and  $p \equiv 1$  and proved existence of a stable nontrivial solution if both trivial solutions are unstable. Henry (1981) proved the above result for the Laplace operator on an open bounded domain in  $\mathbb{R}^n$ . Lou and Nagylaki (2002, Theorem 2.1) generalized this to arbitrary elliptic operators on an open bounded domain in  $\mathbb{R}^n$ , in particular to multivariate versions of the differential operator occurring in (6.17). Thus, their result applies to much more general migration patterns, which need not to be isotropic or homogeneous. Also varying population density is covered by their model.

**Remark 7.7.** 1. We point out the analogy to the results about protection of alleles and existence of a stable equilibrium in Sections 4.2 and 5. The condition  $\int_{\Omega} g(x) dx < 0$  corresponds to  $s_1 + s_2 < 0$ . Therefore,  $\mathcal{A}_1$  is not protected ( $p = 0$  asymptotically stable) if  $\kappa = \mu/s_1 + \mu/s_2 > 1$  and protected if  $\kappa < 1$ . In the latter case, we indeed have a protected polymorphism because  $\kappa > 0$  if  $s_1 + s_2 < 0$ . As already noted at the end of Section 7.4.1, we have  $\kappa = \mu\lambda_1 = \lambda_1/\lambda$ . Therefore, the condition  $\lambda > \lambda_1(g)$  in Theorem 7.5 (i) corresponds to  $\kappa < 1$ .

2. If  $s_1 + s_2 = 0$ , then  $\kappa = 0$  for every  $\mu > 0$  and a stable interior equilibrium exists always, just as if  $\int_{\Omega} g(x) dx = 0$ .

3. We recall from Section 7.3.1 that for the step environment in  $\Omega = (-\infty, \infty)$ , a cline exists for every  $\lambda > 0$  even if the selection is asymmetric.

The following result shows that (in the sense specified) the cline gets steeper as selection gets stronger or dispersal weaker.

**Proposition 7.8.** *For  $\lambda > \lambda_1(g)$ , i.e., when the cline  $\hat{p}$  exists,  $\|\nabla \hat{p}\|_{L^2(\Omega)}$  is a strictly monotone increasing function of  $\lambda$ .*

For the proof, see Lou et al. (2013).

### 7.4.3 Proof of Proposition 7.2

We first establish necessity. If (7.54) has a positive eigenvalue with eigenfunction  $\varphi > 0$  in  $\Omega$ , then by the strong maximum principle for elliptic equations (Appendix B), we have  $\varphi > 0$  in  $\bar{\Omega}$ . (In the one-dimensional case, this follows from the elementary Theorem B.1.) Therefore, dividing (7.54a) by  $\varphi$  and integrating over  $\Omega$ , we obtain by using Green's first identity<sup>8</sup> (partial integration in the 1-d case) and observing the boundary condition on  $\varphi$

---

<sup>8</sup>  $\int_{\Omega} (\psi \Delta \varphi + \nabla \psi \cdot \nabla \varphi) dx = \int_{\partial \Omega} \psi \frac{\partial \varphi}{\partial \nu} dS$

(7.54b)

$$\begin{aligned}
\int_{\Omega} g(x) dx &= \frac{1}{\lambda} \int_{\Omega} -\varphi^{-1} \Delta \varphi dx \\
&= \frac{1}{\lambda} \left( \int_{\partial\Omega} -\varphi^{-1} \frac{\partial \varphi}{\partial \nu} dS + \int_{\Omega} \nabla(\varphi^{-1}) \cdot \nabla \varphi dx \right) \\
&= -\frac{1}{\lambda} \int_{\Omega} \frac{|\nabla \varphi|^2}{\varphi^2} dx < 0,
\end{aligned} \tag{7.56}$$

where the last inequality is strict because  $\varphi$  is not constant. (If  $\varphi$  were constant, then  $g \equiv 0$  would follow from (7.54a), a contradiction to our assumption.) Furthermore, integrating (7.54a) in  $\Omega$ , we find by a similar calculation  $\int_{\Omega} g(x)\varphi(x) dx = 0$ , which together with positivity of  $\varphi$  implies that  $g$  must change sign.

The proof of sufficiency is deeper. In a series of lemmas, we will show that

$$\lambda_1(g) = \inf_{\psi \in \mathcal{S}} K(g, \psi) \tag{7.57}$$

is the desired eigenvalue. Here,

$$K(g, \psi) = \frac{-\int_{\Omega} \psi \Delta \psi dx}{\int_{\Omega} g \psi^2 dx} = \frac{\int_{\Omega} |\nabla \psi|^2 dx}{\int_{\Omega} g \psi^2 dx} \tag{7.58}$$

is a ‘Rayleigh quotient’ and

$$\mathcal{S} = \{\psi \in H^1(\Omega) : \int_{\Omega} g \psi^2 > 0 \text{ and } \partial \psi / \partial \nu = 0 \text{ on } \partial \Omega\}, \tag{7.59}$$

where  $H^1(\Omega)$  is the Sobolov space in  $L^2(\Omega)$  with weak derivatives of first order in  $L^2(\Omega)$  (C.2) (Appendix C). Essentially, the proof follows Brown and Lin (1980). Indeed, we will also prove most of the statements of Remark 7.4.

We define

$$Q_{\lambda}(\psi) = \langle -\Delta \psi, \psi \rangle - \lambda \int_{\Omega} g \psi^2 dx = \int_{\Omega} |\nabla \psi|^2 dx - \lambda \int_{\Omega} g \psi^2 dx, \tag{7.60}$$

where  $\langle u, v \rangle = \int_{\Omega} uv dx$ . Then  $Q_{\lambda}(\psi) \geq 0$  if and only if  $\lambda \leq K(g, \psi)$ , and

$$Q_{\lambda}(\psi_{\lambda}) = 0 \tag{7.61}$$

if  $\lambda$  is an eigenvalue of (7.54) with eigenfunction  $\psi_{\lambda}$ .

**Lemma 7.9.** *If there is a nonnegative eigenfunction of (7.54), then  $Q_{\lambda}(\psi) \geq 0$  for every  $\psi \in \mathcal{S}$ . Therefore, any eigenvalue  $\lambda$  of (7.54) with a nonnegative eigenfunction satisfies  $\lambda \leq \lambda_1(g)$ .*

*Proof.* On

$$D(L_1) = \{u \in H^2(\Omega) : \partial u / \partial \nu = 0 \text{ on } \partial \Omega\}, \quad (7.62)$$

we define the operators  $L_1 u = -\Delta u$  and

$$(Tu)(x) = -\Delta u(x) - \lambda g(x)u(x) \quad \text{for } x \in \Omega, \quad (7.63)$$

Then  $T$  is self-adjoint and its spectrum consists of the eigenvalues  $\mu_1 < \mu_2 \leq \dots$ . The eigenvalue  $\mu_1$  is simple and the corresponding eigenfunction  $\psi_1$  can be chosen such that  $\psi_1 > 0$  in  $\bar{\Omega}$  (Appendix D). Now suppose that  $\varphi$  is a nonnegative eigenfunction of (7.54). Therefore,  $\mu_1 = 0$  must be an eigenvalue of  $T$ . Because only the smallest eigenvalue has a nonnegative eigenfunction, and its eigenspace is one-dimensional,  $\varphi$  must pertain to  $\mu_1 = 0$ . From the spectral decomposition (Remark D.7), we obtain  $\langle Tu, u \rangle \geq \mu_1 \langle u, u \rangle = 0$ , i.e.,  $Q_\lambda(u) \geq 0$ , for every  $u \in D(L_1)$ .  $\square$

**Lemma 7.10.** *If  $\int_\Omega g \, dx < 0$ , then  $\lambda_1(g) > 0$ .*

This result is quite intuitive because  $\psi = \text{const} \notin \mathbf{S}$  if  $\int_\Omega g \, dx < 0$ . The proof is a little bit technical.

*Proof.* First, we show that there exist  $\epsilon > 0$  and  $\eta > 0$  such that

$$\int_\Omega |\nabla \psi|^2 \, dx \geq \epsilon \int_\Omega \psi^2 \, dx \quad (7.64)$$

for every  $\psi \in D(L_1)$  that satisfies  $\int_\Omega g \psi^2 \, dx > -\eta \int_\Omega \psi^2 \, dx$ . The proof is by contradiction. Suppose that  $\{\psi_n\} \subset D(L_1)$  such that  $\int_\Omega \psi_n^2 \, dx = 1$ ,  $\int_\Omega |\nabla \psi_n|^2 \, dx \leq 1/n$ , and  $\int_\Omega g \psi_n^2 \, dx \geq -1/n$  for every  $n$ . Then  $\{\psi_n\}$  is bounded in  $H^1(\Omega)$  and therefore has a subsequence,  $\{\psi_k\}$ , that converges to some  $\psi \in L^2(\Omega)$ . Since  $\int_\Omega |\nabla \psi_k|^2 \, dx \leq 1/k$  for all  $k$ ,  $\{\psi_k\}$  is a Cauchy sequence in  $H^1(\Omega)$ , thus converges to  $\psi \in H^1(\Omega)$ , which satisfies

$$\int_\Omega \psi^2 \, dx = 1, \quad \int_\Omega |\nabla \psi|^2 \, dx = 0, \quad \text{and} \quad \int_\Omega g \psi^2 \, dx \geq 0. \quad (7.65)$$

The first two properties imply that  $\psi \equiv c \neq 0$ , hence  $\int_\Omega g \psi^2 \, dx = c \int_\Omega g \, dx < 0$ , a contradiction.

For  $\psi \in \mathbf{S}$ , we have  $\int_\Omega g \psi^2 \, dx > 0$  and

$$K(g, \psi) = \frac{\int_\Omega |\nabla \psi|^2 \, dx}{\int_\Omega g \psi^2 \, dx} \geq \frac{\int_\Omega |\nabla \psi|^2 \, dx}{\max_{x \in \Omega} |g(x)| \int_\Omega \psi^2 \, dx} \geq \epsilon / \max_{x \in \Omega} |g(x)|.$$

Therefore,  $\lambda_1(g) \geq \epsilon / \max_{x \in \Omega} |g(x)| > 0$ , which finishes the proof.  $\square$

**Lemma 7.11.** *Let  $\int_{\Omega} g dx < 0$ . If  $\lambda > \lambda_1(g)$ , then  $\lambda$  is not an eigenvalue with a nonnegative eigenfunction. If  $0 < \lambda < \lambda_1(g)$ , then  $\lambda$  is not an eigenvalue.*

*Proof.* The first statement is already contained in Lemma 7.9. To prove the second statement, by (7.61) it is sufficient to show that (for given  $\lambda$ ) there exists  $a > 0$  such that  $Q_{\lambda}(\psi) \geq a\|\psi\|^2$  for every  $\psi \in D(L_1)$ .

Let  $\lambda = (1 - \tau)\lambda_1(g)$ , where  $0 < \tau < 1$  and  $\psi \in D(L_1)$ . Then

$$\begin{aligned} Q_{\lambda}(\psi) &= \int_{\Omega} |\nabla\psi|^2 dx - \lambda \int_{\Omega} g\psi^2 dx \\ &= \frac{\lambda}{\lambda_1} Q_{\lambda_1}(\psi) + \left(1 - \frac{\lambda}{\lambda_1}\right) \int_{\Omega} |\nabla\psi|^2 dx \geq \tau \int_{\Omega} |\nabla\psi|^2 dx. \end{aligned}$$

Let  $\epsilon$  and  $\eta$  be the constants in the proof of Lemma 7.10. If  $\int_{\Omega} g\psi^2 dx > -\eta \int_{\Omega} \psi^2 dx$ , we obtain from (7.64)

$$Q_{\lambda}(\psi) \geq \tau \int_{\Omega} |\nabla\psi|^2 dx \geq \tau\epsilon\|\psi\|^2. \quad (7.66)$$

If  $\int_{\Omega} g\psi^2 dx \leq -\eta \int_{\Omega} \psi^2 dx$ , we have

$$Q_{\lambda}(\psi) = \int_{\Omega} |\nabla\psi|^2 dx - \lambda \int_{\Omega} g\psi^2 dx \geq \lambda\eta\|\psi\|^2. \quad (7.67)$$

□

**Lemma 7.12.** *If  $\int_{\Omega} g dx < 0$ , then  $\lambda_1(g)$  is a simple eigenvalue with an eigenfunction that can be chosen positive on  $\bar{\Omega}$ .*

*Proof.* We consider the linear eigenvalue problem

$$-\Delta\varphi - \lambda_1(g)g(x)\varphi = \sigma\varphi \quad \text{in } \Omega, \quad (7.68a)$$

$$\frac{\partial\varphi}{\partial\nu} = 0 \quad \text{on } \partial\Omega \quad (7.68b)$$

and define the operator  $T_1 : D(L_1) \rightarrow L^2(\Omega)$  by

$$(T_1u)(x) = -\Delta u(x) - \lambda_1(g)g(x)u(x). \quad (7.69)$$

Then  $\lambda_1(g)$  is an eigenvalue of (7.54) with corresponding eigenfunction  $\varphi$  if and only if 0 is an eigenvalue of  $T_1$ , hence of (7.68), with corresponding eigenfunction  $\varphi$ . The least eigenvalue  $\sigma_1$  of  $T_1$  is given by

$$\sigma_1 = \inf\{Q_{\lambda_1}(\psi) : \psi \in D(L_1)\} \quad (7.70)$$

(Theorem D.9). Since  $Q_{\lambda_1}(\psi) \geq 0$  for all  $\psi \in D(L_1)$ , we have  $\sigma_1 \geq 0$ . From the definition of  $\lambda_1(g)$  it follows that there is a sequence  $\{\psi_n\} \subset D(L_1)$  such that  $\int_{\Omega} g\psi_n^2 dx = 1$  and  $\lim_{n \rightarrow \infty} \int_{\Omega} |\nabla\psi_n|^2 dx = \lambda_1(g)$ . Therefore,  $\lim_{n \rightarrow \infty} Q_{\lambda_1}(\psi_n) = 0$ , whence  $\sigma_1 = 0$ . Therefore,  $\sigma_1 = 0$  is the smallest eigenvalue of (7.68), hence simple and the corresponding eigenfunction can be chosen positive on  $\Omega$ . By the strong maximum principle, it is positive on  $\bar{\Omega}$ .  $\square$

Obviously, Lemma 7.12 completes the proof of sufficiency in Proposition 7.2. The other lemmas show that  $\lambda_1(g) > 0$  and that  $\lambda_1(g)$  is the only positive eigenvalue with the desired properties.

**Remark 7.13.** The variational characterization (7.57) of  $\lambda_1(g)$  is related to Courant's Minimum-Maximum Principle (and to the min-max principle for Hermitian matrices). For Hermitian matrices, the Rayleigh quotient is simply  $(Ax, x)/(x, x)$  (cf. Appendix D).

#### 7.4.4 Proof of Theorem 7.5 (i)

Throughout, we assume  $\int_{\Omega} g(x) dx < 0$  and  $g$  changes sign in  $\Omega$ .

(a) First, we investigate the local stability of the equilibria  $p \equiv 1$  and  $p \equiv 0$ .

**Lemma 7.14.** *The equilibrium  $p \equiv 1$  is unstable for every  $\lambda > 0$ .*

*Proof.* The linearization of the right-hand side of (7.52a) evaluated at  $p \equiv 1$  is  $\Delta - \lambda g(x)$ . Therefore,  $p \equiv 1$  is asymptotically stable (in the Lyapunov sense) if the smallest eigenvalue  $\sigma_1$  of

$$-\Delta\psi + \lambda g(x)\psi = \sigma\psi \quad \text{in } \Omega, \quad (7.71a)$$

$$\frac{\partial\psi}{\partial\nu} = 0 \quad \text{on } \partial\Omega, \quad \psi > 0 \quad \text{in } \partial\Omega \quad (7.71b)$$

is positive. It is unstable if  $\sigma_1 < 0$ . This smallest eigenvalue exists, is simple, and has an eigenfunction  $\psi_1 > 0$  on  $\bar{\Omega}$  (Appendix D). We infer from (7.71)

$$-\frac{\Delta\psi_1}{\psi_1} + \lambda g(x) = \sigma_1 \quad (7.72)$$

and, by integration,

$$-\int_{\Omega} \frac{|\nabla\psi_1|^2}{\psi_1^2} dx + \lambda \int_{\Omega} g dx = |\Omega| \sigma_1. \quad (7.73)$$

Our assumptions imply that  $\sigma_1 < 0$  if  $\lambda > 0$ .  $\square$



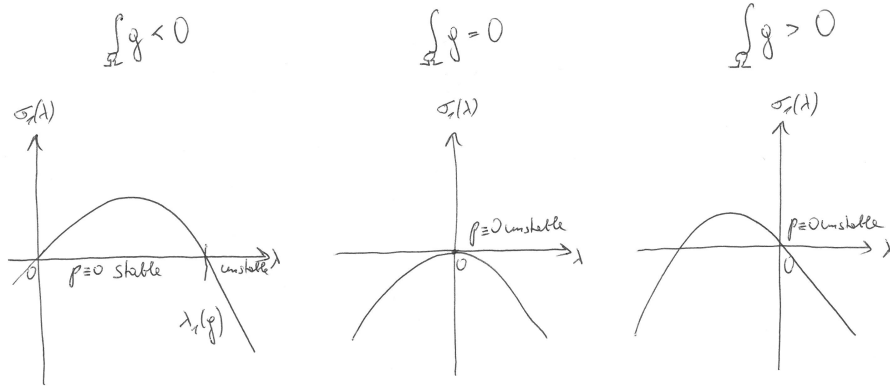


Figure 7.8: The eigenvalue  $\sigma_1(\lambda)$ .

Now we turn to the more interesting and important stability of the equilibrium  $p \equiv 0$ . We recall that  $\lambda_1(g)$  is the principal, i.e., smallest positive, eigenvalue of (7.54). It exists by Proposition 7.2.

**Lemma 7.15.** *The equilibrium  $p \equiv 0$  is asymptotically stable if  $0 < \lambda < \lambda_1(g)$  and unstable if  $\lambda > \lambda_1(g)$ .*

*Proof.* The linearization of the right-hand side of (7.52a) evaluated at  $p \equiv 0$  is  $\Delta + \lambda g(x)$ . Therefore,  $p \equiv 0$  is asymptotically stable if the smallest eigenvalue  $\sigma_1$  of

$$-\Delta\varphi - \lambda g(x)\varphi = \sigma\varphi \quad \text{in } \Omega, \quad (7.74a)$$

$$\frac{\partial\varphi}{\partial\nu} = 0 \quad \text{on } \partial\Omega \quad (7.74b)$$

is positive. This smallest eigenvalue exists, is simple, and has an eigenfunction  $\varphi_1 > 0$  on  $\bar{\Omega}$  (Appendix D).

We claim that

$$\sigma_1 \begin{cases} > 0 & \text{if } 0 < \lambda < \lambda_1(g), \\ = 0 & \text{if } \lambda = \lambda_1(g), \\ < 0 & \text{if } \lambda > \lambda_1(g). \end{cases} \quad (7.75)$$

Obviously, this claim establishes the lemma.

Let us consider  $\sigma_1$  as a function of  $\lambda$ . Because  $\sigma_1(0) = \sigma_1(\lambda_1(g)) = 0$ , (7.75) is an immediate consequence of Lemma 7.16 below.  $\square$

**Lemma 7.16.** *If  $g$  is a nonconstant function, then  $\sigma_1(\lambda)$  is strictly concave downward.*

*Proof.* By the variational characterization of  $\sigma_1(\lambda)$  (Appendix D, Theorem D.9), we obtain for any pair  $\lambda \neq \bar{\lambda}$

$$\begin{aligned}
& \sigma_1\left(\frac{1}{2}(\lambda + \bar{\lambda})\right) \\
&= \inf_{\{\psi \in H^1, \int_{\Omega} \psi^2 = 1\}} \int_{\Omega} \left[ |\nabla \psi(x)|^2 - \frac{1}{2}(\lambda + \bar{\lambda})g(x)\psi(x)^2 \right] dx \\
&= \inf_{\{\psi \in H^1, \int_{\Omega} \psi^2 = 1\}} \left[ \frac{1}{2} \int_{\Omega} (|\nabla \psi|^2 - \lambda g \psi^2) dx + \frac{1}{2} \int_{\Omega} (|\nabla \psi|^2 - \bar{\lambda} g \psi^2) dx \right] \\
&> \frac{1}{2} \inf_{\{\psi \in H^1, \int_{\Omega} \psi^2 = 1\}} \int_{\Omega} (|\nabla \psi|^2 - \lambda g \psi^2) dx + \frac{1}{2} \inf_{\{\psi \in H^1, \int_{\Omega} \psi^2 = 1\}} \int_{\Omega} (|\nabla \psi|^2 - \bar{\lambda} g \psi^2) dx \\
&= \frac{1}{2}[\sigma_1(\lambda) + \sigma_1(\bar{\lambda})],
\end{aligned}$$

where the inequality is strict because the eigenfunctions of  $\sigma_1(\lambda)$  and  $\sigma_1(\bar{\lambda})$  are linearly independent (since  $g$  is not constant).  $\square$

(b) Now we establish existence of a nontrivial equilibrium (the cline). We apply the supersolution-subsolution method to show that if  $\lambda > \lambda_1(g)$ , then (7.52) has at least one nontrivial equilibrium  $\hat{p}$ , i.e.,  $\hat{p}$  satisfies  $0 < \hat{p} < 1$  in  $\bar{\Omega}$ .

To establish a subsolution for given  $\lambda > \lambda_1(g)$ , let  $\varphi_1$  denote the eigenfunction of the smallest eigenvalue  $\sigma_1$  of (7.74) that is uniquely determined by  $\max_{\bar{\Omega}} \varphi_1 = 1$ . Set  $\underline{p} = \epsilon \varphi_1$ , where  $\epsilon > 0$  is to be determined. Hence,

$$\begin{aligned}
\Delta \underline{p} + \lambda g \underline{p}(1 - \underline{p}) &= \Delta(\epsilon \varphi_1) + \lambda g \epsilon \varphi_1 - \lambda g \epsilon^2 \varphi_1^2 \\
&= -\sigma_1 \epsilon \varphi_1 - \lambda g \epsilon^2 \varphi_1^2 \\
&= (-\sigma_1 - \epsilon \lambda g \varphi_1) \epsilon \varphi_1 > 0,
\end{aligned} \tag{7.76}$$

where the inequality holds if  $0 < \epsilon < -\sigma_1(\lambda)/(\lambda \|g\|_{\infty})$  because  $\sigma_1(\lambda) < 0$  if  $\lambda > \lambda_1(g)$ .

To establish a supersolution, let  $\psi_1$  denote the eigenfunction of the smallest eigenvalue  $\sigma_1$  of (7.71) such that  $\max_{\bar{\Omega}} \psi_1 = 1$ . Set  $\bar{p} = 1 - \epsilon \psi_1$ . As above, one shows easily that

$$\Delta \bar{p} + \lambda g \bar{p}(1 - \bar{p}) = \epsilon \psi_1 (\sigma_1 - \epsilon \lambda g \psi_1) < 0, \tag{7.77}$$

where the inequality holds if  $0 < \epsilon < -\sigma_1/(\lambda \|g\|_{\infty})$  because  $\sigma_1 < 0$  for every  $\lambda > 0$ .

By the supersolution and subsolution method (e.g., Cantrell and Cosner 2003), for any  $\lambda > \lambda_1(g)$ , the problem (7.52) has at least one equilibrium  $\hat{p}$  satisfying  $\underline{p} < \hat{p} < \bar{p}$  in  $\Omega$ .

(c) Next, we show uniqueness of the nontrivial equilibrium and asymptotic stability. A main ingredient is

**Lemma 7.17.** *Any equilibrium  $p^*$  of (7.52) satisfying  $0 < p^* < 1$  is asymptotically stable; in particular, it is nondegenerate and isolated.*

*Proof.* The linearized stability of  $p^*$  is determined by the smallest eigenvalue (denoted as  $\sigma_1$ ) of

$$-\Delta\psi - \lambda g(1 - 2p^*)\psi = \sigma\psi \quad \text{in } \Omega, \quad \frac{\partial\psi}{\partial\nu} = 0 \quad \text{on } \partial\Omega. \quad (7.78)$$

Let  $\psi_1 > 0$  denote an eigenfunction of  $\sigma_1$ , i.e.,

$$\Delta\psi_1 + \lambda g(1 - 2p^*)\psi_1 = -\sigma_1\psi_1. \quad (7.79)$$

Multiplying (7.79) by  $f(p^*) = p^*(1 - p^*)$  and integrating (using Green's identity and  $\frac{\partial\psi_1}{\partial\nu} = 0$ ), we find

$$\begin{aligned} -\sigma_1 \int_{\Omega} p^*(1 - p^*)\psi_1 dx &= \int_{\Omega} p^*(1 - p^*)\Delta\psi_1 dx + \lambda \int_{\Omega} p^*(1 - p^*)g(1 - 2p^*)\psi_1 dx \\ &= - \int_{\Omega} \nabla(p^*(1 - p^*)) \cdot \nabla\psi_1 dx + \lambda \int_{\Omega} gp^*(1 - p^*)(1 - 2p^*)\psi_1 dx \\ &= - \int_{\Omega} (1 - 2p^*)\nabla(p^*) \cdot \nabla\psi_1 dx + \lambda \int_{\Omega} gp^*(1 - p^*)(1 - 2p^*)\psi_1 dx. \end{aligned} \quad (7.80)$$

Recalling (7.52a), i.e.,  $\Delta p^* + \lambda g(x)p^*(1 - p^*) = 0$ , multiplying the equation by  $(1 - 2p^*)\psi_1$  and integrating, we obtain after a similar calculation

$$2 \int_{\Omega} \psi_1 |\nabla p^*|^2 dx - \int_{\Omega} (1 - 2p^*)\nabla(p^*) \cdot \nabla\psi_1 dx + \lambda \int_{\Omega} gp^*(1 - p^*)(1 - 2p^*)\psi_1 dx = 0. \quad (7.81)$$

From (7.80) and (7.81) we infer

$$\sigma_1 \int_{\Omega} p^*(1 - p^*)\psi_1 dx = 2 \int_{\Omega} \psi_1 |\nabla p^*|^2 dx > 0, \quad (7.82)$$

where the inequality is strict because  $\psi_1 > 0$  in  $\Omega$  and  $p^*$  is not constant. Hence,  $\sigma_1 > 0$  and the lemma is proved.  $\square$

This lemma settles not only asymptotic stability of any equilibrium  $p^*$  satisfying  $0 < p^* < 1$ , but also uniqueness as we show now. Because both trivial equilibria  $p \equiv 0$  and  $p \equiv 1$  are isolated, the construction of the supersolution  $\bar{p}$  and subsolution  $\underline{p}$  implies for sufficiently small  $\epsilon$  that all nontrivial equilibria must lie between  $\underline{p}$  and  $\bar{p}$ . It is well known that the total (Leray-Schauder) degree (e.g., O'Regan et al., 2006) of nontrivial equilibria between a supersolution and a subsolution is equal to one. Hence, the total degree of all nontrivial equilibria is equal to one. By Lemma 7.17, each nontrivial equilibrium is linearly stable, so it must be isolated and have Leray-Schauder degree one. Therefore, (7.52) has at most one nontrivial equilibrium.

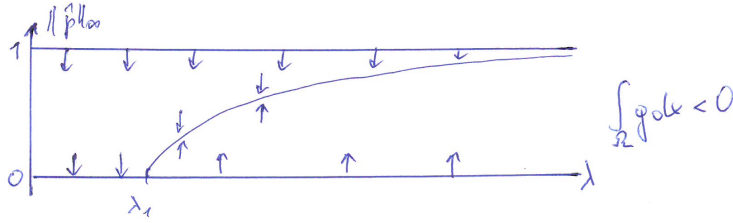


Figure 7.9: Bifurcation diagram for the model (7.85) with no dominance.

(d) For the proof of global convergence, we refer to Henry (1981) or Lou and Nagylaki (2002). For the Laplace operator global convergence follows from the fact that (7.52) is a gradient system with ‘potential’

$$V(u) = \int_{\Omega} \left[ \nabla u \cdot \nabla u - \lambda g \left( u^2 - \frac{2}{3} u^3 \right) \right] dx. \quad (7.83)$$

Indeed,

$$\begin{aligned} \frac{dV}{dt}(u) &= \int_{\Omega} \left[ 2 \nabla u \cdot \nabla u_t - \lambda g (2uu_t - 2u^2u_t) \right] dx \\ &= 2 \int_{\Omega} [-\Delta u - \lambda g u(1 - u)] u_t dx \\ &= 2 \int_{\Omega} -u_t^2 dx \leq 0, \end{aligned}$$

where the second equality uses Green’s identity and the last follows from (7.52a). From the theory of gradient systems together with compactness arguments, one can conclude that the  $\omega$ -limit set of any solution contains only equilibria. Because there exists only one asymptotically stable equilibrium, global convergence follows.

The bifurcation diagram in Figure 7.9 illustrates the equilibrium and stability properties formulated in statement (i) of Theorem 7.5.

#### 7.4.5 Proof of Theorem 7.5 (ii), (iii)

The proofs of statements (ii) and (iii) are very similar to the proof of (i). Statements (i) and (iii) are symmetric upon interchanging the roles of the equilibria  $p \equiv 0$  and  $p \equiv 1$ . The key observation in the proof of (ii) is that if  $\int_{\Omega} g dx = 0$ , then  $\sigma(\lambda) \leq 0$  for every  $\lambda$  and equality holds only if  $\lambda = 0$ ; see Fig. 7.8. The shapes of  $\sigma_1(\lambda)$  displayed in Fig. 7.8 follow from Lemma 7.16 and the following calculation.

Let  $\varphi' = \frac{\partial \varphi}{\partial \lambda}(x, \lambda)$ . Then differentiation of (7.74) with respect to  $\lambda$  yields

$$\begin{aligned} -\Delta \varphi' - \lambda g(x) \varphi' - g(x) \varphi &= \sigma_1'(\lambda) \varphi + \sigma_1(\lambda) \varphi' \quad \text{in } \Omega, \\ \frac{\partial \varphi'}{\partial \nu} &= 0 \quad \text{on } \partial \Omega. \end{aligned}$$

Evaluation at  $\lambda = 0$  produces

$$\begin{aligned} -\Delta \varphi' \Big|_{\lambda=0} - g(x) &= \sigma_1'(0) \quad \text{in } \Omega, \\ \frac{\partial \varphi'}{\partial \nu} &= 0 \quad \text{on } \partial \Omega \end{aligned}$$

because  $\sigma_1(0) = 0$  and the corresponding eigenfunction can be chosen  $\varphi \equiv 1$ . Finally, integration yields

$$\sigma_1'(0) = -\frac{1}{|\Omega|} \int_{\Omega} g(x) dx. \quad (7.84)$$

## 7.5 Clines in a finite domain with dominance: Results and open problems

In this section, we review the most important results about the existence of clines in the presence of dominance. We will also mention some open problems. Our exposition is largely based on the review of Lou et al. (2013). We focus on the following PDE:

$$\frac{\partial p}{\partial t} = \Delta p + \lambda g(x) f(p) \quad \text{in } \Omega \times (0, \infty), \quad (7.85a)$$

$$\frac{\partial p}{\partial \nu} = 0 \quad \text{on } \partial \Omega \times (0, \infty), \quad (7.85b)$$

$$0 \leq p(x, 0) \leq 1, \quad p(x, 0) \not\equiv 0, \quad p(x, 0) \not\equiv 1 \text{ in } \Omega, \quad (7.85c)$$

where  $f \in C^1([0, 1])$ ,  $f(0) = f(1) = 0$  and  $f > 0$  in  $(0, 1)$ . The most important example is

$$f(p) = p(1-p)(1+h-2hp), \quad (7.86)$$

where  $-1 \leq h \leq 1$ , i.e., dominance is intermediate; cf. eqs. (7.4) – (7.8). Throughout we suppose that  $g$  changes sign.

First, we contrast the case of no dominance with that of complete dominance.

### 7.5.1 Complete dominance

We assume complete dominance of  $\mathcal{A}_2$ , or recessivity of  $\mathcal{A}_1$ , i.e.,

$$f(p) = 2p^2(1-p); \quad (7.87)$$

cf. (7.6). This case turns out to be quite different from that of no dominance. In fact, this is already obvious from the model with two demes.

One reason why the model with complete dominance is more complicated than with no dominance is that the equilibrium  $p \equiv 0$  is degenerate. Indeed, the linearization of the right-hand side of (7.85a) is  $\Delta + 2\lambda gp(2 - 3p)$  which simplifies to  $\Delta$  at  $p \equiv 0$ . Hence, 0 is an eigenvalue. Nevertheless, the following result can be proved:

**Theorem 7.18** (Lou et al. 2010).

- (i) If  $\int_{\Omega} g dx \geq 0$ , then  $p \equiv 0$  is unstable for every  $\lambda > 0$ .
- (ii) If  $\int_{\Omega} g dx < 0$ , then  $p \equiv 0$  is stable for every  $\lambda > 0$ .

Obviously, statement (ii) differs markedly from Lemma 7.15 for no dominance.

The equilibrium  $p \equiv 1$  is not degenerate because  $f'(1) = -2$ . Therefore, its stability properties follow from Sections 7.4.4 and 7.4.5. It is unstable for every  $\lambda > 0$  if  $\int_{\Omega} g dx \leq 0$ . If  $\int_{\Omega} g dx > 0$ , there exists  $\lambda^* > 0$  such that  $p \equiv 1$  is stable if  $0 < \lambda < \lambda^*$  and unstable if  $\lambda > \lambda^*$  (cf. Theorem 7.5).

In addition, the following results have been proved:

**Theorem 7.19** (Lou et al. 2010, Nakashima et al. 2010).

- (i) If  $\int_{\Omega} g dx \neq 0$ , then for sufficiently small  $\lambda > 0$ , (7.85) has no nontrivial equilibrium.
- (ii) If  $\int_{\Omega} g dx < 0$ , then for sufficiently large  $\lambda$ , (7.85) has at least two nontrivial equilibria, one stable and one unstable.
- (iii) If  $\int_{\Omega} g dx > 0$ , then for sufficiently large  $\lambda$ , (7.85) has a stable nontrivial equilibrium.

**Theorem 7.20** (Nakashima et al. 2010). Suppose that  $\int_{\Omega} g dx = 0$ .

- (i) For every  $\lambda > 0$ , (7.85) has at least one stable nontrivial equilibrium  $p^*$ .
- (ii) As  $\lambda \rightarrow 0+$ , any sequence of nontrivial equilibria of (7.85) has a subsequence converging to the constant function  $2/3$  in  $C^2(\bar{\Omega})$ .
- (iii) As  $\lambda \rightarrow \infty$ ,  $p^* \rightarrow 1$  uniformly on any compact subset of  $\overline{\Omega_+} \setminus \overline{\partial\Omega_+ \cap \Omega}$ , and  $p^* \rightarrow 0$  uniformly on any compact subset of  $\overline{\Omega_-} \setminus \overline{\partial\Omega_- \cap \Omega}$ , where  $\Omega_+ = \{x \in \Omega : g(x) > 0\}$  and  $\Omega_- = \{x \in \Omega : g(x) < 0\}$ .

The main results are illustrated in Figure 7.10. They should be compared with the bifurcation diagram for the case of no dominance (Figure 7.9).

Analogous of the above results, in fact considerably stronger results, were derived by Nagylaki (2009) for the continuous-time two-deme model. He proved that the number of

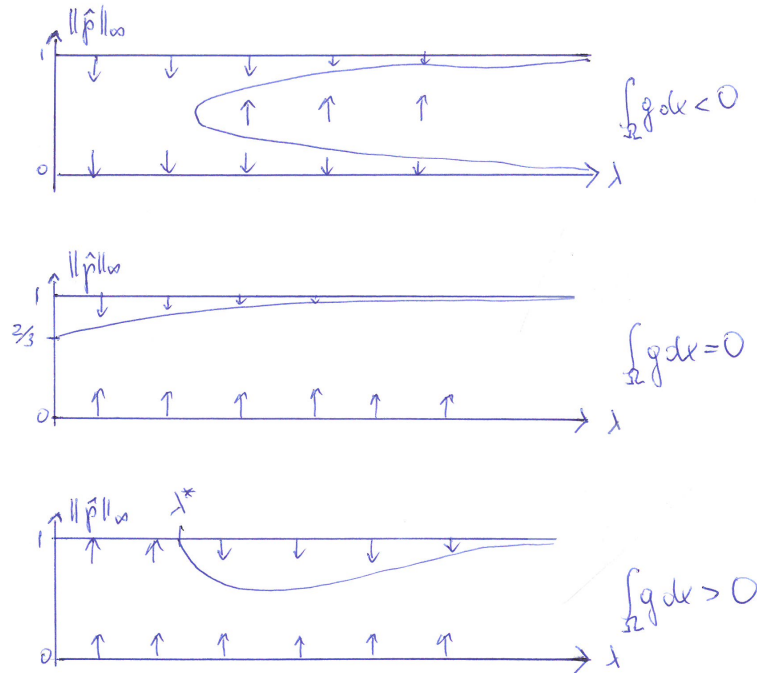


Figure 7.10: Bifurcation diagrams for the model (7.85) with complete dominance.

equilibria is precisely one or two in the above theorems instead of at least one or two. If there is only a single stable equilibrium, it is globally asymptotically stable. Therefore, Figure 7.10 illustrates his results precisely. Whether this is also true for the PDE model (i.e., if the number of equilibria is as in this figure) is an open problem. As briefly discussed in Lou et al. (2013), the structure of the nontrivial equilibria in the PDE model (7.85) with complete dominance may be more complicated than in the ODE case with two demes.

### 7.5.2 Partial dominance

Henry (1981) showed for  $f''(p) \leq 0$  that (7.85) has at most one nontrivial equilibrium, which, if it exists, is globally asymptotically stable among initial data that are nonnegative and not identically zero. This holds independently of the sign of  $\int_{\Omega} g dx$ . If  $f(p)$  is given by (7.86), then  $f''(p) \leq 0$  if and only if  $-\frac{1}{3} \leq h \leq \frac{1}{3}$ . Therefore, Theorem 7.5 (with an appropriate  $\tilde{\lambda}_1 > 0$  instead of  $\lambda_1(g)$ ) holds not only if  $h = 0$  but also if  $h$  is in this interval.

It has been conjectured (Lou and Nagylaki 2002, Nagylaki and Lou 2008) that for the case  $\int_{\Omega} g dx < 0$ , the condition  $f''(p) \leq 0$  can be generalized to the condition that  $f(p)/p$

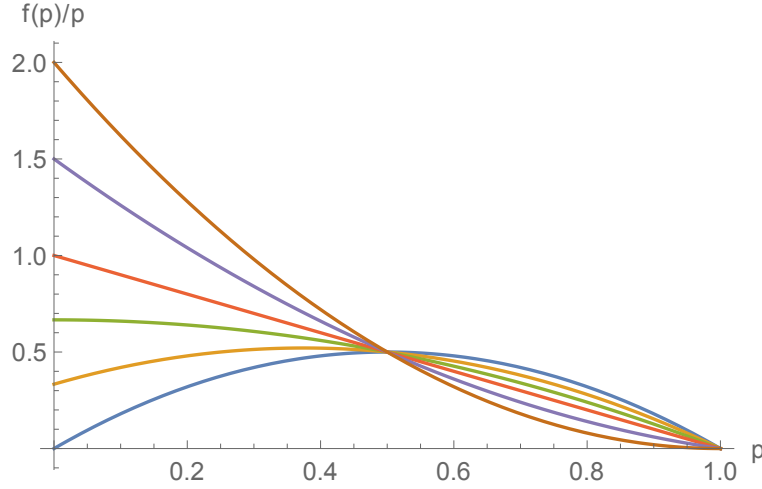


Figure 7.11: Graphs of  $f(p)/p$  for the following values of  $h$ :  $-1$ ,  $-\frac{2}{3}$ ,  $-\frac{1}{3}$ ,  $0$ ,  $\frac{1}{2}$ ,  $1$  (from bottom to top at  $p = 0$ ).

is monotone decreasing in  $(0, 1)$ . If  $f(p)$  is as in (7.86), this would generalize statement (a) of Theorem 7.5 to  $-\frac{1}{3} \leq h \leq 1$ . By symmetry, the statement (c) can then be generalized to  $-1 \leq h \leq \frac{1}{3}$ . Concerning part (b), i.e., the case  $\int_{\Omega} g dx = 0$ , it has been conjectured that a unique nontrivial equilibrium, which is globally asymptotically stable, exists for every  $f$  such that  $f(0) = f(1) = 0$ ,  $f > 0$  in  $(0, 1)$ , and  $f$  has unique critical point (hence a maximum) in  $(0, 1)$ .

We motivate the above conjecture that the equilibrium structure is determined by monotonicity of  $f(p)/p$  by a brief analysis of the continuous-time continent-island model (consult Nagylaki 1975 for details). In this model it is assumed that there is one-way migration from one deme (the continent) to another deme (the island) at backward rate  $m$ . In addition, it is assumed that on the continent allele  $\mathcal{A}_2$  is fixed, and on the island allele  $\mathcal{A}_1$  is advantageous. We assume that on the island the fitnesses of the genotypes  $\mathcal{A}_1\mathcal{A}_1$ ,  $\mathcal{A}_1\mathcal{A}_2$ , and  $\mathcal{A}_2\mathcal{A}_2$  are  $s$ ,  $hs$ , and  $-s$ , respectively; cf. Sections 4 and 5. If the frequency of  $\mathcal{A}_1$  on the island is denoted by  $p$ , its evolution is described by the ODE

$$\dot{p} = -mp + sf(p), \quad (7.88)$$

where  $f(p)$  is given by (7.86). The equilibria are given by the solutions of

$$\frac{m}{s} = \frac{f(p)}{p} = (1-p)(1+h-2hp). \quad (7.89)$$

Obviously, there exists no solution in  $(0, 1)$  if  $m/s > \mu_1 = \max_{0 \leq p \leq 1} \frac{f(p)}{p}$ . In this case,  $p = 0$  is globally asymptotically stable. If  $m/s < \mu_1$ , there exist one or two solutions. If



$f(p)/p$  is strictly monotone decreasing on  $[0, 1]$ , which is the case if and only if  $-\frac{1}{3} \leq h \leq 1$ , then there exists a unique solution for every  $m/s < \mu_1$ . If  $f(p)/p$  is not strictly monotone decreasing, there exist two equilibria if  $\mu_2 < m/s < \mu_1$ , where  $\mu_2 = \lim_{p \rightarrow 0} \frac{f(p)}{p} = 1 + h$ , and one equilibrium if  $0 \leq m/s \leq \mu_2$  (cf. Figure 7.11). If two nontrivial equilibria exist, the one with the lower equilibrium frequency of  $p$  is unstable, the other is asymptotically stable, as is  $p = 0$ . If only one nontrivial equilibrium exists, it is globally asymptotically stable.

This model has been generalized by assuming discrete time (Nagylaki 1992) and by admitting evolution on the continent (Nagylaki 2009). The analysis of these discrete-time models is much more complicated. Also the results differ slightly because the critical value for  $h$  below which a pair of nontrivial equilibria may exist depends on  $m$  and is between  $-1$  and  $-\frac{1}{3}$ .

## 7.6 Further directions

Several generalizations and variants of the cline models treated above have been investigated. Here, we give a very brief guide to the most relevant literature.

For a bounded domain  $\Omega \subset \mathbb{R}^n$ , a considerably body of theory has been developed for models with arbitrary migration, i.e., elliptic operators, and for multiple alleles (Lou and Nagylaki 2002, 2004, 2006; Nagylaki and Lou 2008). Most of this work is devoted to either necessary or sufficient conditions for the loss of one or several alleles, or for the maintenance of a polymorphism. However, already for three alleles and in the absence of dominance the dynamics may become rather complex (Lou and Nagylaki 2006).

Interesting and important problems occur if migration varies within the spatial domain, for instance because of a barrier, if migration is asymmetric, or if population density varies. Such models have been studied by Slatkin (1973), Nagylaki (1976, 1978, 1996), ten Eikelder (1979), Fife and Peletier (1981), Pauwelussen and Peletier (1981), Piálek and Barton (1997).

In the classical treatments of clines, the domain is assumed to be  $(-\infty, \infty)$ . It is in this case that explicit solutions can be derived (Section 7.3). The mathematical theory, however, has been further developed under the assumption of a bounded domain (Section 7.4). Despite additional technical complications, also for an unbounded domain important results have been proved (e.g., ten Eikelder 1979, Fife and Peletier 1981, Pauwelussen and Peletier 1981). An important special case is that of an environmental pocket, in which one allele is favored in a bounded interval whereas the alternative allele is favored in the

unbounded complement. This situation can be efficiently modeled on the domain  $[0, \infty)$  (or its higher dimensional generalizations) and leads to semi-infinite clines (Nagylaki 1975, Tertikas 1988, Brown and Tertikas 1991). For environments such as a step environment, these models admit solutions that are almost as explicit as for the step environment on  $(-\infty, \infty)$ . They share interesting properties with models of continent-island type.

In a recent series of papers, Nagylaki and collaborators extended the diffusion model, which approximates short-distance migration, to models that include short- and long-distance migration. The latter is approximated by assuming that a fraction of the population reproduces panmictically. It gives rise to an integral term so that the resulting model becomes an integro-PDE model. Numerous aspects of the classical theory have been extended to this setting, and qualitatively new results and properties have been found. However, many challenging open problems remain (Nagylaki 2012a,b; Lou et al. 2013; Nagylaki and Zeng 2014; Nagylaki et al. 2014; Su and Nagylaki 2015; and references therein).

## Acknowledgments

I am grateful to all students, who participated in this course and continuously helped to improve this manuscript. Many thanks to Prof. Thomas Nagylaki, Dr. Linlin Su, and Sarah Henze for comments and for pointing out errors. Special thanks go to Dr. Linlin Su for providing Appendix D.

## A Appendix: Perron–Frobenius theory

In this appendix we summarize some important results from the spectral theory of nonnegative matrices. These were discovered by Perron and Frobenius around 1910 and are useful tools in proving existence, uniqueness, positivity, and stability of equilibrium solutions in many discrete-time or continuous-time models. For a more complete account of the spectral theory of nonnegative matrices, including proofs, the reader is referred to Gantmacher (1959), Schaefer (1974, Chapter I), or Seneta (1981). The latter reference contains, in particular, a detailed treatment of countably infinite matrices.

A  $k \times k$  matrix  $\mathbf{A} = (a_{ij})$  is called *nonnegative*,  $\mathbf{A} \geq 0$ , if  $a_{ij} \geq 0$  for every  $i, j$ . It is called *positive*,  $\mathbf{A} > 0$ , if  $a_{ij} > 0$  for every  $i, j$ . Similarly, a vector  $\mathbf{x} = (x_1, \dots, x_k)^\top$  is said to be nonnegative (positive) if  $x_i \geq 0$  ( $x_i > 0$ ) for every  $i$ .

The *spectral radius*  $r = r(\mathbf{A})$  of an arbitrary matrix  $\mathbf{A}$  is the radius of the smallest circle in the complex plane that contains all eigenvalues of  $\mathbf{A}$ , i.e.,  $|\lambda| \leq r$  for all eigenvalues  $\lambda$  of  $\mathbf{A}$ . It can be shown that  $r = \lim_n \|\mathbf{A}^n\|^{1/n}$ , where  $\|\mathbf{A}\|$  is an arbitrary norm of the matrix  $\mathbf{A}$ , e.g.,  $\|\mathbf{A}\| = \max_i \sum_{j=1}^k |a_{ij}|$ . (Throughout this appendix,  $\lim_n$  denotes the limit for  $n \rightarrow \infty$ .) Since the sequence  $\|\mathbf{A}^n\|^{1/n}$  is monotone decreasing,  $r \leq \|\mathbf{A}^n\|^{1/n}$  holds for every  $n \geq 1$ . Nonnegative matrices have the following important property:

**Theorem A.1.** *Let  $\mathbf{A} \geq 0$ . Then the spectral radius  $r$  of  $\mathbf{A}$  is an eigenvalue and there is at least one nonnegative eigenvector  $\mathbf{x} \geq 0$  ( $\mathbf{x} \neq 0$ ), i.e.,  $\mathbf{A}\mathbf{x} = r\mathbf{x}$ . In addition, if  $\mathbf{A}$  has an eigenvalue  $\lambda$  with an associated positive eigenvector, then  $\lambda = r$ .*

We use the notation  $\mathbf{A}^n = (a_{ij}^{(n)})$  for  $n$ th powers. A nonnegative matrix  $\mathbf{A}$  is called *irreducible* if for every pair of indices  $(i, j)$  an integer  $n = n(i, j) \geq 1$  exists such that  $a_{ij}^{(n)} > 0$ . Now we state the *Theorem of Perron–Frobenius*.

**Theorem A.2.** *If  $\mathbf{A}$  is irreducible, then the following hold:*

1. *The spectral radius  $r$  is positive and a simple root of the characteristic equation.*
2. *To  $r$  there corresponds a positive right eigenvector  $\mathbf{x} > 0$  such that  $\mathbf{A}\mathbf{x} = r\mathbf{x}$ , and  $\mathbf{x}$  is unique except for multiplication by a positive constant.*
3. *No other eigenvalue of  $\mathbf{A}$  is associated with a nonnegative eigenvector.*

This theorem is often sufficient to prove our existence, uniqueness, and stability results in continuous time. For models in discrete time, usually a stronger condition than irreducibility is needed.

A nonnegative matrix  $\mathbf{A}$  is called *primitive* if an integer  $n \geq 1$  exists such that  $\mathbf{A}^n > 0$ . Obviously, every positive matrix is primitive, and every primitive matrix is irreducible.

**Theorem A.3.** *For an irreducible matrix  $\mathbf{A}$  with spectral radius  $r$ , the following assertions are equivalent:*

1.  $\mathbf{A}$  is primitive.
2.  $|\lambda| < r$  for all eigenvalues  $\lambda \neq r$  of  $\mathbf{A}$ .
3.  $\lim_n (r^{-1}\mathbf{A})^n$  exists.

Concerning property 3, it is readily shown that for an arbitrary matrix  $\mathbf{A}$ ,  $\lim_n \mathbf{A}^n = 0$  is equivalent to  $r(\mathbf{A}) < 1$ , and that  $r(\mathbf{A}) > 1$  always implies that  $\lim_n \mathbf{A}^n$  does not exist. If  $r(\mathbf{A}) = 1$ , then  $\lim_n \mathbf{A}^n$  exists if and only if  $r(\mathbf{A}) = 1$  is a simple root of the minimal polynomial and all other eigenvalues satisfy  $|\lambda| < 1$ .

A stronger result than statement 3 of Theorem A.3 is the following:

**Theorem A.4.** *Let  $\mathbf{A}$  be primitive with spectral radius  $r$  and corresponding eigenvector  $\mathbf{x} > 0$ . Then there exists a decomposition  $\mathbf{A} = r\mathbf{P} + \mathbf{B}$ , where  $\mathbf{P}$  is a projection on the eigenspace spanned by  $\mathbf{x}$  (i.e., for every  $\mathbf{y} \in \mathbb{R}^k$  there is a constant  $c$  such that  $\mathbf{P}\mathbf{y} = c\mathbf{x}$ , and  $\mathbf{P}\mathbf{x} = \mathbf{x}$ ),  $\mathbf{P}\mathbf{B} = \mathbf{B}\mathbf{P} = 0$ , and  $r(\mathbf{B}) < 1$ . Consequently,*

$$\lim_n (r^{-1}\mathbf{A})^n \mathbf{y} = c\mathbf{x} + \lim_n (r^{-1}\mathbf{B})^n \mathbf{y} = c\mathbf{x} \quad (\text{A.1})$$

holds for all  $\mathbf{y} \in \mathbb{R}^k$ .

Finally, the exponential

$$e^{\mathbf{A}} = \sum_{n=0}^{\infty} \frac{1}{n!} \mathbf{A}^n \quad (\text{A.2})$$

of an irreducible matrix  $\mathbf{A}$  is always positive and, hence, primitive. It follows that

$$\lim_{t \rightarrow \infty} e^{-rt} e^{\mathbf{A}t} \mathbf{y} = c\mathbf{x} \quad (\text{A.3})$$

for some constant  $c$  depending on  $\mathbf{y}$ .

## B Appendix: Maximum principles

Maximum principles are very important tools in the analysis of PDEs. For motivation, we start with the simplest case of a maximum principle. Our exposition follows Protter and Weinberger (1984), the standard work on the topic. For a concise summary, see Sweers (2000).

A function  $u(x)$  that is continuous on the closed interval  $[a, b]$  takes on its maximum at a point in this interval. If  $u(x)$  has a continuous second derivative, and if  $u$  has a relative maximum at some point  $c$  between  $a$  and  $b$ , then

$$u'(c) = 0 \quad \text{and} \quad u''(c) \leq 0. \quad (\text{B.1})$$

Suppose that in an open interval  $(a, b)$ ,  $u$  satisfies a differential inequality of the form

$$L(u) \equiv u'' + g(x)u' > 0, \quad (\text{B.2})$$

where  $g(x)$  is any bounded function. Then it is obvious that (B.1) cannot be satisfied at any  $c \in (a, b)$ . Hence, if (B.2) holds, the maximum of  $u$  cannot be assumed in  $(a, b)$ ; it can be assumed only at the boundary, i.e., at  $a$  or  $b$ .

Now suppose that  $u$  satisfies

$$L(u) \equiv u'' + g(x)u' \geq 0 \quad (\text{B.3})$$

on  $(a, b)$ . Obviously, this admits the solution  $u \equiv \text{const.}$  For such a solution, the maximum is attained at every point. One can prove that this exception is the only possible:

**Theorem B.1** (One dimensional maximum principle; Protter and Weinberger 1984, Chap. 1.1, Theorems 1 and 2). *Suppose  $u = u(x)$  satisfies (B.3) for every  $x \in (a, b)$ , with  $g(x)$  a bounded function. If  $u(x) \leq M$  in  $(a, b)$  and if the maximum  $M$  of  $u$  is attained at an interior point  $c$  of  $(a, b)$ , then  $u \equiv M$ .*

*In addition, if the maximum is attained at  $a$  and  $g$  is bounded below at  $x = a$ , then  $u'(a) < 0$ ; if the maximum is attained at  $b$  and  $g$  is bounded above at  $x = b$ , then  $u'(b) > 0$ .*

The second statement is easy to show if  $L(u) = 0$  holds. Assume  $u(a) = M$ . Then  $u'(a) \leq 0$  must hold because  $u(x) \leq M$ . If  $u'(a) = 0$ , the uniqueness of solutions implies  $u(x) \equiv M$ , a contradiction to  $u(x) < M$  if  $a < x < b$ .

Next we treat elliptic equations. Let  $\Omega$  denote an open bounded domain (connected) in  $\mathbb{R}^n$ . The second-order differential operator  $L$  defined by

$$L(u) \equiv \sum_{i,j=1}^n a_{ij}(x) \frac{\partial^2 u}{\partial x_i \partial x_j} + \sum_{i=1}^n b_i(x) \frac{\partial u}{\partial x_i}, \quad (\text{B.4})$$

where  $a_{ij} \in L^\infty_{\text{loc}}(\Omega)$  and  $b_i \in L^\infty(\Omega)$ , is called uniformly elliptic on  $\Omega$  if for every  $x \in \Omega$  there are numbers  $A > a > 0$  such that

$$a |\xi|^2 \leq \sum_{i,j=1}^n a_{ij}(x) \xi_i \xi_j \leq A |\xi|^2 \quad \text{for all } \xi \in \mathbb{R}^n \text{ and } x \in \Omega. \quad (\text{B.5})$$

The operator  $L$  is strictly elliptic if the first inequality holds. If the  $a_{ij}$  are bounded on  $\bar{\Omega}$ , then strictly elliptic implies uniformly elliptic.

The following is called the weak maximum principle for elliptic operators.

**Theorem B.2.** *Suppose  $L$  is strictly elliptic and  $h \leq 0$  is in  $L^\infty(\Omega)$ . If  $u \in C^2(\Omega) \cap C(\bar{\Omega})$  satisfies*

$$(L + h)(u) \geq 0 \quad \text{in } \Omega, \quad (\text{B.6})$$

*then  $u$  attains a nonnegative maximum at the boundary  $\bar{\Omega}$ .*

Note that in the above theorem it is not excluded that, in addition to the boundary, the maximum is attained in the interior of  $\Omega$ .

The following is called the strong maximum principle for elliptic operators.

**Theorem B.3.** *Suppose  $L$  is strictly elliptic and  $h \leq 0$  is in  $L^\infty(\Omega)$ . If  $u \in C^2(\Omega) \cap C(\bar{\Omega})$  satisfies*

$$(L + h)(u) \geq 0 \quad \text{in } \Omega, \quad (\text{B.7})$$

*then either  $u \equiv \sup_{\Omega} u$  or  $u$  does not attain a nonnegative maximum in  $\Omega$ .*

Concerning a maximum on the boundary, the following result (due to E. Hopf) holds:

**Theorem B.4.** *Suppose that for  $x_0 \in \partial\Omega$  there is a ball  $B \subset \Omega$  with  $x_0 \in \partial B$ . If the assumptions of Theorem B.3 are satisfied,  $\max_{\bar{\Omega}}(u) = u(x_0)$ , and  $u \in C^1(\Omega \cup x_0)$ , then either  $u \equiv u(x_0)$  or  $\frac{\partial u}{\partial \nu}(x_0) = \nu \cdot \nabla u(x_0) < 0$ .*

The so-called interior-sphere assumption in this theorem is satisfied if the boundary of  $\Omega$  is  $C^2$  (as in Section 7.4.2).

Without a sign assumption on  $h$ , the following simple corollary holds, which requires a stronger assumption on  $u$ .

**Theorem B.5.** *Suppose  $L$  is strictly elliptic and  $h \in L^\infty(\Omega)$  (no sign assumption). If  $u \in C^2(\Omega) \cap C(\bar{\Omega})$  satisfies*

$$(L + h)(u) \geq 0 \quad \text{in } \Omega \text{ and } u \leq 0 \text{ in } \bar{\Omega}, \quad (\text{B.8})$$

then either  $u < 0$  in  $\Omega$  or  $u \equiv 0$ .

Moreover, if the additional conditions of Theorem B.4 are satisfied with  $u < u(x_0) = 0$  in  $\Omega$ , then  $\frac{\partial u}{\partial \nu}(x_0) < 0$  for every direction  $\nu$  pointing into an interior sphere.

The first statement is a simple consequence of Theorem B.3. Write  $h(x) = h^+(x) - h^-(x)$ , where  $h^+$  and  $h^-$  are the positive and negative part, respectively, of  $h$ . Then  $-h^+ \leq 0$  and from  $u \leq 0$  it follows that  $(L - h^+)u \geq -h^+u \geq 0$ . The conclusion for the derivative follows from Theorem B.4.

Finally, we turn to a simple version of the maximum principle for one-dimensional parabolic PDEs (Chap. 3 in Protter and Weinberger 1984). We consider the uniformly parabolic operator

$$L(u) \equiv \alpha(x, t)u_{xx} + \beta(x, t)u_x - u_t \quad (\text{B.9})$$

on the domain  $D = (a, b) \times (0, \infty)$ , where uniformly parabolic means  $\alpha(x, t) \geq \alpha_0 > 0$  and  $\beta(x, t) \geq \beta_0 > 0$  on  $D$ .

**Theorem B.6.** *Suppose  $u = u(x)$  satisfies*

$$(L + h)(u) \geq 0, \quad (\text{B.10})$$

where  $h$  is a given function of  $(x, t)$  that satisfies  $h \leq 0$  in a rectangular region  $E = \{a < x < b, 0 < t \leq T\} \subset D$  for some  $T > 0$ . If  $u \leq M$  in  $E$ ,  $M \geq 0$ , and if  $u$  attains the maximum  $M$  at an interior point  $(x_1, t_1)$  of  $E$ , then  $u \equiv M$  for every  $(x, t) \in E$  such that  $t \leq t_1$ . If a nonnegative maximum occurs at a boundary point ( $a$  or  $b$ ), then  $\partial u / \partial x > 0$  at this point.

This is a special case of Theorem 4 in Chapter 3.2 of Protter and Weinberger (1984), in which much more general regions  $E$  are treated (then the conclusion needs to be modified).

For solutions of  $(L+h)(u) \leq 0$  there is an associated minimum principle if the minimum is nonpositive. The result follows by applying the above theorem to  $-u$ .

## C Appendix: Basics from PDE theory

Sobolev spaces are defined as follows. Let  $k$  be a positive integer,  $1 \leq p \leq \infty$ , and  $\alpha = (\alpha_1, \dots, \alpha_n)$  a multiindex. For a locally integrable function  $f$  on  $\Omega \subset \mathbb{R}^n$ , let

$$D^{(\alpha)} f = \frac{\partial^{|\alpha|} f}{\partial x_1^{\alpha_1} \dots \partial x_n^{\alpha_n}} \quad (\text{C.1})$$

denote the partial derivative of order  $\alpha$  (in the distribution sense). Then the Sobolev space  $W^{k,p}$  is defined as

$$W^{k,p}(\Omega) = \{u \in L^p(\Omega) : D^{(\alpha)} u \in L^p(\Omega) \text{ for every } \alpha \text{ with } |\alpha| \leq k\}. \quad (\text{C.2})$$

For  $p < \infty$ , the norm can be defined as

$$\|u\|_{W^{k,p}(\Omega)} = \left( \sum_{|\alpha| \leq k} \|D^{(\alpha)} u\|_{L^p(\Omega)}^p \right)^{1/p}. \quad (\text{C.3})$$

If  $p = 2$ , these are Hilbert spaces and  $W^{k,2}$  is often denoted by  $H^k$ . We note that functions in  $W^{k,p}$  can be approximated by smooth functions.

A subscript 0, such as  $H_0^1$ , indicates that the functions in this space vanish at the boundary of  $\Omega$ .

The differential operator  $L_1$  defined by  $L_1 u = -\Delta u$  for  $u \in D(L_1) = \{u \in H^2(\Omega) : \partial u / \partial \nu = 0 \text{ on } \partial \Omega\}$  is a densely defined self-adjoint operator on  $L^2(\Omega)$  whose spectrum consists only of the eigenvalues  $0 = \alpha_1 < \alpha_2 < \dots$  (see Appendix D for more general results).



# D Appendix: Spectrum of elliptic operators of second order

(Compiled by Dr. Linlin Su, South University of Science and Technology of China)

## D.1 Principal eigenvalue

We consider eigenvalue problem of the type

$$L\varphi + \lambda\varphi = 0 \quad \text{in } \Omega, \quad (\text{D.1a})$$

$$B\varphi = 0 \quad \text{on } \partial\Omega, \quad (\text{D.1b})$$

where  $\Omega$  is a smoothly bounded domain (open, connected) in  $\mathbb{R}^n$ .

Here

$$Lu = \sum_{i,j=1}^n a_{ij}(x) \frac{\partial^2 u}{\partial x_i \partial x_j} + \sum_{i=1}^n b_i(x) \frac{\partial u}{\partial x_i} + c(x)u, \quad (\text{D.2})$$

where  $a_{ij}$ ,  $b_i$ , and  $c$  are sufficiently smooth, and there exist constants  $\mu_1, \mu_2 > 0$  such that

$$a_{ij}(x) = a_{ji}(x), \quad \sum_{i,j=1}^n a_{ij}(x) \xi_i \xi_j \geq \mu_1 \sum_{i=1}^n \xi_i^2 \quad \forall x \in \bar{\Omega}, \quad \xi = (\xi_i) \in \mathbb{R}^n, \quad (\text{D.3a})$$

$$c(x) \leq \mu_2 \quad \forall x \in \bar{\Omega}. \quad (\text{D.3b})$$

We consider  $B$  for two alternative forms

$$Bu = u \quad (\text{Dirichlet b.c.}) \quad (\text{D.4a})$$

and

$$Bu = \frac{\partial u}{\partial \nu} + b(x)u \quad (\text{Robin b.c., or Neumann if } b = 0), \quad (\text{D.4b})$$

where  $\nu$  is the unit outer normal to  $\partial\Omega$  and  $b$  is sufficiently smooth and  $b(x) \geq 0$  on  $\partial\Omega$ .

**Theorem D.1.** *The eigenvalue problem (D.1) – (D.4) has a unique (up to a constant multiple) positive eigenfunction  $\varphi_1$  and the corresponding eigenvalue  $\lambda_1$  is real and simple. All other eigenvalues  $\lambda$  have real part strictly greater than  $\lambda_1$ . Furthermore, in case of (D.4b),  $\varphi_1 > 0$  holds on  $\partial\Omega$ .*

**Remark D.2.** We call  $(\lambda_1, \varphi_1)$  the principal eigenvalue and eigenfunction.

**Remark D.3.** Theorem 1.1 follows from the strong maximum principle [79] and the Krein-Rutman Theorem [46]. Some details of the proof can be found in, e.g., [81, pp. 20-23].

**Remark D.4.** Theorem D.1 still holds if the boundary operator  $B$  has the following more general form than (D.4b)

$$Bu = (V\nabla u) \cdot \nu + b(x)u, \quad (\text{D.5})$$

where  $V = (V_{ij}(x))$  is a  $n$  by  $n$  symmetric positive definite matrix for every  $x \in \partial\Omega$  and  $b(x)$  is as above. Note that under (D.5) the strong maximum principle holds, which is essential for the conclusions in Theorem D.1.

## D.2 Spectral theory for $L$ in divergence form

In this section we study  $L$  in divergence form, which is a special case of (D.2).

$$Lu := \sum_{i,j=1}^n \frac{\partial}{\partial x_i} \left[ a_{ij}(x) \frac{\partial u}{\partial x_j} \right] + c(x)u, \quad (\text{D.6})$$

$$Bu = u \quad (\text{Dirichlet b.c.}), \text{ or} \quad (\text{D.7a})$$

$$Bu = (A\nabla u) \cdot \nu + b(x)u \quad (\text{Neumann co-normal type if } b = 0 \text{ or mixed b.c.}), \quad (\text{D.7b})$$

where  $A = (a_{ij}(x))$  and  $a_{ij}$ ,  $b_i$ ,  $b$ , and  $c$  are as before. Then the operators  $(L, B)$  induce a self-adjoint operator on  $H_0^1(\Omega)$  in case (D.7a) and on  $H^1(\Omega)$  in case (D.7b). Hence, it follows from Hilbert space theory for self-adjoint operators that

**Theorem D.5.** *There is an orthogonal basis for  $L^2(\Omega)$  consisting of eigenfunctions for  $(L, B)$  as in (D.6) – (D.7) which are  $C^\infty$  on  $\bar{\Omega}$ . The eigenvalues are all real and bounded below and accumulate only at  $+\infty$ :*

$$\lambda_1 < \lambda_2 \leq \lambda_3 \leq \dots, \quad \lambda_k \nearrow +\infty. \quad (\text{D.8})$$

**Remark D.6.** In (D.8) multiple eigenvalues are repeated according to their multiplicity. We know in particular that  $\lambda_1$  is simple from Theorem D.1.

**Remark D.7.** By Theorem D.5 the eigenfunctions  $\varphi_i$  pertaining to the eigenvalues  $\lambda_i$  can be chosen to form an orthonormal basis of  $H^1(\Omega)$  ( $\subset L^2(\Omega)$ ). Therefore, if  $u \in H^1(\Omega)$  and  $u = \sum_i \alpha_i \varphi_i$ , we obtain

$$\langle -Lu, u \rangle = \sum_i \lambda_i \alpha_i^2 \geq \lambda_1 \sum_i \alpha_i^2 = \lambda_1 \langle u, u \rangle, \quad (\text{D.9})$$

where  $\langle u, v \rangle = \int_{\Omega} u(x)v(x) dx$  denotes the inner product on  $L^2(\Omega)$ . In fact, we have the following variational characterization of the eigenvalues.

In case (D.7a), we define a bi-linear form on  $H_0^1(\Omega)$

$$D_1(u, v) = \int_{\Omega} \left[ \sum_{i,j=1}^n a_{ij}(x) \frac{\partial u}{\partial x_i} \frac{\partial v}{\partial x_j} - c(x)uv \right] dx. \quad (\text{D.10})$$

**Theorem D.8.** *Assume  $L$  and  $B$  are as in (D.6) and (D.7a), respectively. Then the variational characterizations of eigenvalues hold*

$$\lambda_1 = \min \left\{ D_1(u, u) : u \in H_0^1(\Omega), \int_{\Omega} u^2 dx = 1 \right\}; \quad (\text{D.11a})$$

$$\lambda_k = \min \left\{ D_1(u, u) : u \in W_k, \int_{\Omega} u^2 dx = 1 \right\}, \quad (\text{D.11b})$$

where  $W_k = \{u \in H_0^1(\Omega) : \int_{\Omega} u \varphi_i dx = 0 \text{ for } i = 1, \dots, k-1\}$ .

In case (D.7b), we define a bi-linear form on  $H^1(\Omega)$

$$D_2(u, v) = \int_{\Omega} \left[ \sum_{i,j=1}^n a_{ij}(x) \frac{\partial u}{\partial x_i} \frac{\partial v}{\partial x_j} - c(x)uv \right] dx + \int_{\partial\Omega} b(x)uv dS(x). \quad (\text{D.12})$$

**Theorem D.9.** *Assume  $L$  and  $B$  are as in (D.6) and (D.7b), respectively. Then the variational characterizations of eigenvalues hold*

$$\lambda_1 = \min \left\{ D_2(u, u) : u \in H^1(\Omega), \int_{\Omega} u^2 dx = 1 \right\}; \quad (\text{D.13a})$$

$$\lambda_k = \min \left\{ D_2(u, u) : u \in \tilde{W}_k, \int_{\Omega} u^2 dx = 1 \right\}, \quad (\text{D.13b})$$

where  $\tilde{W}_k = \{u \in H^1(\Omega) : \int_{\Omega} u \varphi_i dx = 0 \text{ for } i = 1, \dots, k-1\}$ .

**Remark D.10.** Theorems D.5 – D.9 can be extracted from Section 7.E in [32], where the theory is stated in somewhat more general and abstract settings and some special examples such as for the Laplacian with zero Dirichlet and Neumann boundary conditions are discussed.

**Remark D.11.** The Laplacian with zero Dirichlet b.c. is treated in, e.g., [32, Corollary 7.24] and [88, pp. 283-297]. We infer from (D.10) that  $D_1(u, u) = \int_{\Omega} |\nabla u|^2 dx$ , and hence (D.11a) implies  $\lambda_1 > 0$ .

**Remark D.12.** The Laplacian with zero Neumann b.c. is treated in, e.g., [32, Theorem 7.28] and [88, pp. 293-297]. We infer from (D.12) that  $D_2(u, u) = \int_{\Omega} |\nabla u|^2 dx$ , and hence (D.13a) implies  $\lambda_1 = 0$  with  $\varphi_1 \equiv 1$  in  $\Omega$ .

## R References

- [1] Ablowitz, M.J., Zeppetella, A. 1979. Explicit solutions of Fisher's equation for a special wave speed. *Bull. Math. Biol.* 41, 835-840.
- [2] Aronson, D.G., Weinberger, H.F. 1975. Nonlinear diffusion in population genetics, combustion, and nerve propagation. In: *Partial Differential Equations and Related Topics*. Lect. Notes Math. 446. Berlin: Springer.
- [3] Aronson, D.G., Weinberger, H.F. 1978. Multidimensional nonlinear diffusion arising in population genetics. *Adv. Math.* 30, 33-76.
- [4] Barton, N.H. 1999. Clines in polygenic traits. *Genetical Research* 74, 223-236.
- [5] Bôcher, M. 1914. The smallest characteristic numbers in a certain exceptional case. *Bull. Amer. Math. Soc.* 21, 6-9.
- [6] Brown, K.J., Lin, S.S., 1980. On the existence of positive eigenfunctions for an eigenvalue problem with indefinite weight function. *J. Math. Anal. Appl.* 75, 112-120.
- [7] Brown, K.J., Tertikas, A. 1991. On the bifurcation of radially symmetric steady-state solutions arising in population genetics. *SIAM J. Math. Anal.* 22, 400-413.
- [8] Bulmer, M.G. 1972. Multiple niche polymorphism. *Amer. Natur.* 106, 254-257.
- [9] Bürger, R. 2000. *The Mathematical Theory of Selection, Recombination, and Mutation*. Chichester: Wiley.
- [10] Bürger, R. 2011. Some mathematical models in evolutionary genetics. In: *The Mathematics of Darwin's Legacy* (eds. F.A.C.C. Chalub and J.F. Rodrigues), pp. 67-89. Basel: Birkhäuser
- [11] Bürger, R. 2014. A survey of migration-selection models in population genetics. *Discrete Cont. Dyn. Syst. B* 19, 883 - 959.
- [12] Campbell, R.B. 1983. Uniqueness of polymorphic equilibria under soft selection. *Theor. Popul. Biol.* 24, 295 - 301.
- [13] Cantrell, R.S., Cosner, C. 2003. *Spatial Ecology via Reaction-Diffusion Equations*. Chichester: Wiley.
- [14] Charlesworth B., Charlesworth, D. 2010. *Elements of Evolutionary Genetics*. Greenwood Village: Roberts & Co.
- [15] Christiansen, F.B. 1974. Sufficient conditions for protected polymorphism in a subdivided population. *Amer. Naturalist* 108, 157-166.
- [16] Christiansen, F.B. 1975. Hard and soft selection in a subdivided population. *Amer. Natur.* 109, 11-16.
- [17] Conley, C.C. 1975. An application of Wazewski's method to a non-linear boundary value problem which arises in population genetics. *J. Math. Biol.* 2, 241-249.
- [18] Deakin, M.A.B. 1966. Sufficient conditions for genetic polymorphism. *Amer. Natur.* 100, 690-692.

- [19] Dempster, E.R. 1955. Maintenance of genetic heterogeneity. Cold Spring Harbor Symp. Quant. Biol. 20, 25-32.
- [20] ten Eikelder, H.M.M. 1979. A nonlinear diffusion problem arising in population genetics. Report NA-25. Delft Univ. of Technology.
- [21] Ewens, W. J. 1969. Mean fitness increases when fitnesses are additive. Nature 221, 1076.
- [22] Ewens, W.J. 2004. Mathematical Population Genetics. 2nd edition. Springer, New York.
- [23] Ewens, W.J. 2011. What changes has mathematics made to the Darwinian theory? In: *The Mathematics of Darwin's Legacy* (eds. F. A. C. C. Chalub and J. F. Rodrigues), pp. 7–26. Basel: Birkhäuser
- [24] Feller, W., 1968. An Introduction to Probability Theory and Its Applications, vol. I, third edn. Wiley, New York.
- [25] Fife, P.C. 1978. Asymptotic states for equations of reaction and diffusion. Bull. Amer. Math. Soc. 84, 693-726.
- [26] Fife, P.C. 1979. Mathematical aspects of reacting and diffusing systems. Lect. Notes in Biomathematics 28. Berlin-New York: Springer.
- [27] Fife, P.C., McLeod, J.B. 1977. The approach of solutions of nonlinear diffusion equations to travelling front solutions. Arch. Rational. Mechanics and Analysis 65, 335-361.
- [28] Fife, P.C., Peletier, L.A. 1981. Clines induced by variable selection and migration. Proc. R. Soc. Lond. B 214, 99-123.
- [29] Fisher, R.A. 1937. The wave of advance of advantageous genes. Ann. Eugenics 7, 355-369.
- [30] Fisher, R.A. 1950. Gene frequencies in a cline determined by selection and diffusion. Biometrics 6, 353-361.
- [31] Fleming, W.H., 1975. A selection-migration model in population genetics. J. Math. Biol. 2, 219-233.
- [32] Folland, G.B. 1995. Introduction to Partial Differential Equations, second ed., Princeton University Press, Princeton.
- [33] Friedman, A. 1969. Partial Differential Equations. New York: Holt, Rinehart, and Winston.
- [34] Haldane, J.B.S. 1930. A mathematical theory of natural and artificial selection. Part VI. Isolation. Proc. Camb. Phil. Soc. 28, 224-248.
- [35] Haldane, J.B.S. 1948. The theory of a cline. J. Genetics 48, 277-284.
- [36] Hardy, G.H. 1908. Mendelian proportions in a mixed population. Science 28, 49-50.
- [37] Heuser, H. 1989. Gewöhnliche Differentialgleichungen. Stuttgart: B.G. Teubner.
- [38] Hofbauer, J., Sigmund, K. 1998. Evolutionary Games and Population Dynamics. Cambridge: University Press.
- [39] Kanel', Ya.I. 1960. On the stabilization of solutions of the Cauchy problem for equations arising in the theory of combustion. Soviet Math. Dokl. 1, 533-536.

- [40] Karlin, S. 1982. Classification of selection-migration structures and conditions for a protected polymorphism. *Evol. Biol.* 14, 61-204.
- [41] Karlin, S., Campbell, R.B. 1980. Selection-migration regimes characterized by a globally stable equilibrium. *Genetics* 94, 1065-1084.
- [42] Karlin, S., McGregor, J. 1972a. Application of method of small parameters to multi-niche population genetics models. *Theor. Popul. Biol.* 3, 186-208.
- [43] Karlin, S., McGregor, J. 1972b. Polymorphism for genetic and ecological systems with weak coupling. *Theor. Popul. Biol.* 3, 210-238.
- [44] Kingman, J.F.C. 1961. An inequality in partial averages. *Quart. J. Math.* 12, 78-80.
- [45] Kolmogorov, A., Petrowsky, I., Piscounoff, N. 1937. Étude de l'équation de la diffusion avec croissance de la quantité de matière et son application à un problème biologique. (French) *Bull. Univ. Etat Moscou, Ser. Int., Sect. A, Math. et Mecan.* 1, Fasc. 6, 1-25.
- [46] Krein, M.G., Rutman, M. A. 1950. Linear operators leaving invariant a cone in a Banach space, *Amer. Math. Soc. Transl.* 26, 1-128.
- [47] LaSalle, J.P. 1977. Stability theory for difference equations. In: J.K. Hale (Ed.), *Studies in Ordinary Differential Equations. Studies in Mathematics*, vol. 14. Mathematical Association of America, Washington, DC, pp. 1-31.
- [48] Levene, H. 1953. Genetic equilibrium when more than one ecological niche is available. *Amer. Natur.* 87, 331-333.
- [49] Li, C.C. 1955. The stability of an equilibrium and the average fitness of a population. *Amer. Natur.* 89, 281-295.
- [50] Li, C.C. 1967. Fundamental theorem of natural selection. *Nature* 214, 505-506.
- [51] Lou, Y., Nagylaki, T., 2002. A semilinear parabolic system for migration and selection in population genetics. *J. Differential Equations* 181, 388-418.
- [52] Lou, Y., Nagylaki, T., 2004. Evolution of a semilinear parabolic system for migration and selection in population genetics. *J. Differential Equations* 204, 292-322.
- [53] Lou, Y., Nagylaki, T., 2006. Evolution of a semilinear parabolic system for migration and selection without dominance.. *J. Differential Equations* 225, 624-665.
- [54] Lou, Y., Nagylaki, T., Ni, W.-M. 2013. An introduction to migration-selection PDE models. *Disc. Cont. Dyn. Syst. A* 33, 4349-4373.
- [55] Lou, Y., Nagylaki, T., Su, L. 2013. An integro-PDE model from population genetics. *J. Differential Equations* 254, 2367-2392.
- [56] Lou, Y., Ni, W.-M., Su, S. 2010. An indefinite nonlinear diffusion problem in population genetics, II: Stability and multiplicity. *Disc. Cont. Dyn. Syst. A* 27, 643-655.
- [57] Lyubich Yu.I. 1971. Basic concepts and theorems of evolutionary genetics of free populations. *Russ. Math. Surv.* 26, 51-123.

- [58] Lyubich Yu.I. 1992. *Mathematical Structures in Population Genetics*. Berlin Heidelberg New York: Springer.
- [59] McKean, H.P. 1975. Application of Brownian motion to the equation of Kolmogorov-Petrovskii-Piskunov. *Comm. Pure Appl. Math.* 28, 323-331.
- [60] Nagylaki, T., 1975. Conditions for the existence of clines. *Genetics* 80, 595-615.
- [61] Nagylaki, T., 1976. Clines with variable migration. *Genetics* 83, 867-886.
- [62] Nagylaki, T., 1978. Clines with asymmetric migration. *Genetics* 88, 813-827.
- [63] Nagylaki, T. 1989. The diffusion model for migration and selection. Pp. 55-75 in: Hastings, A. (Ed.), *Some Mathematical Questions in Biology*. *Lecture Notes on Mathematics in the Life Sciences*, vol. 20. American Mathematical Society, Providence, RI.
- [64] Nagylaki, T. 1992. *Introduction to Theoretical Population Genetics*. Berlin: Springer.
- [65] Nagylaki, T. 1996. The diffusion model for migration and selection in a dioecious population. *J. Math. Biol.* 34, 334-360.
- [66] Nagylaki, T. 2009. Polymorphism in multiallelic migration-selection models with dominance. *Theor. Popul. Biol.* 75,239-259.
- [67] Nagylaki, T. 2012a. Clines with partial panmixia. *Theor. Popul. Biol.* 81, 45-68.
- [68] Nagylaki, T. 2012b. Clines with partial panmixia in an unbounded unidimensional habitat. *Theor. Popul. Biol.* 82, 22-28.
- [69] Nagylaki, T., Lou, Y. 2007. Evolution under multiallelic migration-selection models. *Theor. Popul. Biol.* 72, 21-40.
- [70] Nagylaki, T., Lou, Y. 2008. The dynamics of migration-selection models. In: Friedman, A. (ed) *Tutorials in Mathematical Biosciences IV*. *Lect. Notes Math.* 1922, pp. 119 - 172. Berlin Heidelberg New York: Springer.
- [71] Nagylaki, T., Su, L., Alevy, I., Dupont, T.F. 2014. Clines with partial panmixia in an environmental pocket. *Theor. Popul. Biol.* 95, 24-32.
- [72] Nagylaki, T., Zeng, K. 2014. Clines with complete dominance and partial panmixia in an unbounded unidimensional habitat. *Theor. Popul. Biol.* 93, 63-74.
- [73] Nakashima, K., Ni, W.-M., Su, S. 2010. An indefinite nonlinear diffusion problem in population genetics, I: Existence and limiting profiles. *Disc. Cont. Dyn. Syst. A* 27, 617-641.
- [74] O'Regan, D., Cho, Y.J., Chen, Y.-Q. 2006. *Topological Degree Theory and Applications*. Boca Raton, FL: Chapman & Hall/CRC.
- [75] Pauwelussen, J.W., Peletier, L.A. 1981. Clines in the presence of asymmetric migration. *J. Math. Biol.* 11, 207-233.
- [76] Piálek, J., Barton, N.H. 1997. The spread of an advantageous allele across a barrier: the effect of random drift and selection against heterozygotes. *Genetics* 145, 493-504.
- [77] Picone, M. 1910. Sui valori eccezionali di un parametro. *Ann. Scuola Norm. Sup. Pisa* 11, 1-143.

- [78] Prout, T. 1968. Sufficient conditions for multiple niche polymorphism. *Amer. Natur.* 102, 493-496.
- [79] Protter, M.H., Weinberger, H.F. 1984. *Maximum Principles in Differential Equations*. New York: Springer.
- [80] Provine, W.B. 1971. *The Origins of Theoretical Population Genetics*. Chicago: Univ. of Chicago Press.
- [81] Sattinger, D.H. 1973. Topics in stability and bifurcation theory, *Lecture Notes in Mathematics*, Vol. 309, Springer-Verlag, Berlin-New York.
- [82] Sattinger, D.H. 1976. On the stability of waves of nonlinear parabolic systems. *Advances in Math.* 22, 312-355.
- [83] Sattinger, D.H. 1977. Weighted norms for the stability of traveling waves. *J. Differential Equations* 25, 130-144.
- [84] Sell, G.R., You, Y. 2002. *Dynamics of Evolutionary Equations*. New York: Springer.
- [85] Seneta, E. 1981. *Non-negative Matrices*, 2nd ed. London: Allen and Unwin.
- [86] Senn, S., Hess, P., 1982. On positive solutions of a linear elliptic boundary value problem with Neumann boundary conditions. *Math. Ann.* 258, 459-470.
- [87] Slatkin, M. 1973. Gene flow and selection in a cline. *Genetics* 75, 773-756.
- [88] Strauss, W.A. 1992. *Partial Differential Equations: An Introduction*, 1st ed. John Wiley & Sons, Inc., New York.
- [89] Su, L., Nagylaki, T. 2015. Clines with directional selection and partial panmixia in an unbounded unidimensional habitat. *Disc. Cont. Dynam. Sys Series A* 35, 1697-1741.
- [90] Sweers, G. 2000. *Maximum principles, a start*. Lecture Notes, Delft Univ. of Technology.
- [91] Tertikas, A. 1988. Existence and uniqueness of solutions for a nonlinear diffusion problem arising in population genetics. *Arch. Rational Mech. Anal.* 103, 289-317.
- [92] Teschl, G. 2012. *Ordinary Differential Equations and Dynamical Systems*. Providence: Amer. Math. Soc.
- [93] Wakeley, J. 2008. *Coalescent Theory: An Introduction*. Roberts & Company Publishers, Greenwood Village, Colorado.
- [94] Weinberg, W. 1908. Über den Nachweis der Vererbung beim Menschen. *Jahreshefte des Vereins für vaterländische Naturkunde in Württemberg* 64, 368-382.
- [95] Weinberg, W. 1909. Über Vererbungsgesetze beim Menschen. *Zeitschrift für induktive Abstammungs- und Vererbungslehre* 1, 377-392, 440-460; 2, 276-330.
- [96] Wright, S. 1931. Evolution in Mendelian populations. *Genetics* 16, 97-159.