\[
\left[ \frac{\partial}{\partial x} \right] \mathcal{H} - \frac{i}{\hbar} \left[ \frac{\partial}{\partial \pi} \right] \mathcal{H} \frac{\partial}{\partial \pi} = \{ x, \mathcal{H} \}
\]

where

\[
\{ x, \mathcal{H} \} \equiv \left( \frac{\partial}{\partial x} \mathcal{H} \right) \left( \frac{\partial}{\partial \pi} \mathcal{H} \right) - \left( \frac{\partial}{\partial \pi} \mathcal{H} \right) \left( \frac{\partial}{\partial x} \mathcal{H} \right)
\]

is the Poisson bracket of \( x \) and \( \mathcal{H} \).

The function \( \{ x, \mathcal{H} \} \) defines the evolution of \( x \) under the Hamiltonian flow generated by \( \mathcal{H} \).

The evolution equation of the evolution function is given by

\[
\frac{\partial}{\partial t} \mathcal{H}(x, t) = \{ x, \mathcal{H}(x, t) \}
\]

This equation is known as the Poisson bracket evolution equation.

The Poisson bracket \( \{ x, \mathcal{H} \} \) is a central concept in Hamiltonian mechanics, as it describes the rate of change of \( x \) under the Hamiltonian flow.

1. **Introduction**

During the past century, the development of the quantum mechanical theory of quantum mechanics has been driven by the need to understand the fundamental principles governing the behavior of quantum systems.

The **quantum mechanics** framework provides a formalism for describing the evolution of quantum states, which are represented by **wave functions**.

The **Schrödinger equation** is a central equation in quantum mechanics, describing the time evolution of a quantum state.

The **Heisenberg picture** formulation of quantum mechanics is based on the idea of evolving the system's operators rather than the state vectors.

The **Poincaré-Birkhoff-Witt theorem** is a fundamental result in the theory of Lie algebras, which provides a basis for understanding the structure of quantum operators.

The **Pauli exclusion principle** states that no two fermions in a quantum system can occupy the same quantum state simultaneously.

The **Heisenberg uncertainty principle** is a fundamental concept in quantum mechanics, which places limits on the accuracy with which certain pairs of physical properties of a particle can be known.

The **quantum field theory** extends the principles of quantum mechanics to include the behavior of fields, such as electromagnetic fields.

The **quantum gravity** and **quantum cosmology** are areas of research that seek to unify quantum mechanics with general relativity, aiming to describe the universe at the smallest scales.

The **quantum Hall effect** is a quantum mechanical phenomenon observed in two-dimensional electron systems subjected to a strong magnetic field, which leads to the formation of quantized Hall conductances.

The **quantum information theory** is a branch of quantum mechanics that deals with the processing of quantum information, including quantum computing and cryptography.

The **quantum entanglement** phenomenon, where particles become connected in such a way that the state of one particle can instantaneously affect the state of another, regardless of the distance between them, is a fascinating aspect of quantum mechanics.

The **quantum teleportation** is a process that transfers quantum information from one place to another, utilizing quantum entanglement.

The **quantum error correction** is a set of techniques used to protect quantum information from errors due to decoherence and other quantum phenomena.

The **quantum cryptography** leverages quantum mechanics to securely transmit information, making it impossible for unauthorized parties to intercept the data.

The **quantum computing** field aims to develop computers based on quantum-mechanical phenomena, which can potentially perform certain types of calculations much faster than classical computers.

The **quantum field theory** and **quantum mechanics** provide the theoretical framework for understanding the behavior of elementary particles and their interactions, which are the building blocks of the universe.

The **quantum mechanics** and **quantum field theory** have been successful in describing a wide range of phenomena, from the behavior of subatomic particles to the structure of the universe itself.

The **quantum mechanics** and **quantum field theory** are essential tools for physicists, engineers, and technologists who work on problems ranging from materials science to computer science, from medicine to finance.
\[
\frac{\partial}{\partial t} = \frac{1}{2\hbar} \left[ \frac{\langle F(x) \rangle^2}{A} + \frac{\partial F(x)}{\partial x} \right].
\]

Equation (4) is known as the real Schrödinger equation. If \( t \) is replaced by \( \hbar \beta \), where \( \hbar^2 \beta = \frac{1}{\hbar^2} \), equation (4), with some change of symbols, becomes the Bloch equation for the one-particle canonical density matrix of the Bloch canonical density matrix of a constant (effective) mass in the thermodynamic equilibrium at the temperature \( T \) [3]. Thus, when comparing equations (1) and (4), we can always juxtapose the Brownian dynamics and the quantum theory. (This juxtaposition can also be based on Feynman's path-integral theory [4, 5].) The transition from the formalism of the Brownian theory to the formalism of the quantum theory is easy since if we define the driving force \( \langle F(x) \rangle = -\partial V_{\text{eff}}(x)/\partial x \), we can directly calculate the function \( V(x) \) according to equation (5). (\textit{Vice versa}, if one tries to find \( F(x) \) corresponding to a given function \( V(x) \), one has to solve equation (5) which is nonlinear.)

Equation (5) is known as the Riccati equation. As any handbook on nonlinear differential equations will tell you, the Riccati equation itself has been widely corroborated [7 - 11]. Nonetheless, except for the rare possibility to derive analytical solutions \( F(x) \) of this equation in some cases when \( V(x) \) is chosen in a very simple and very special form, equation (5) cannot be solved otherwise than numerically. Thus, the problem of finding a Brownian model to a given quantum-mechanical model is relatively difficult.

In evolutionary theories of various populations, we may use \( x(t) = \ln n(t) - \ln n(t) \), taking \( n(t) \) as the number of individuals of a certain kind at the time instant \( t \) and defining \( \ln n(t) \) as an average value of \( \ln n(t) \). Since \( n(t) \) may represent very large numbers, \( n(t) \) may be treated as a continuous function so that the values of \( x(t) \) may span the whole set of real numbers. Since changes are random events, a formal stochastic theory of the population genetics can certainly be based on the use of the Langevin equation and, correspondingly, of the Fokker-Planck equation (1). If it is advantageous, we may also use the equivalent Schrödinger-type equation (4).

Notwithstanding, recently Waxman has shown that there is another mathematical relation between the population genetics and the quantum mechanics [12]. Waxman’s theory concerns a simplified, but well-founded, model that we call the Waxman-Peck model. (Cf. [13, 14] and references quoted therein.) Waxman’s Schrödinger-type equation involves, in the x-representation, the ‘potential energy’ function

\[
V(x) = -\mu \exp \left( -\frac{\sigma_{\text{in}} x^2}{2} \right)
\]

with two mutation parameters, \( \mu > 0 \) and \( \sigma_{\text{in}} > 0 \). The ‘kinetic-energy’ operator \( T \) in Waxman’s equation was chosen in the usual form, \( T = -\partial^2 / \partial x^2 \).

In the present paper, we will generalize Waxman’s theory. In the momentum representation, Waxman’s kinetic energy is quadratic, \( \langle \hat{p}^2 \rangle = p^2 \), as it is in the quantum mechanics. On the other hand, we assume that \( \langle \hat{p}^2 \rangle \) being a positive function, need not be quadratic; we only require its analyticity along the real \( p \)-axis. This variability offers further possibilities to model the genetic evolution by adequate fitness functions (cf. Section II).

Obviously, if \( \langle \hat{p}^2 \rangle > 0 \) is non-quadratic, the mathematical relation between the evolution equation of the population genetics and the quantum theory becomes somewhat more sophisticated than in Waxman’s case. Namely, when paying heed to the \( x \)-representation, we have generally to consider a more complicated equation than the real Schrödinger equation: in general, our equation, with the Hamilton operator \( \hat{H} = \hat{p}^2 + V(x) \), where \( \hat{H} = -\hbar^2 \partial^2 / \partial x^2 + \hat{V}(x) \), is a functional differential equation. (Note that \( \mu = -i \hbar \partial / \partial x \).) The McLaurin development of \( \hat{V}(x) \) may involve an infinite number of terms.) For solid state theorists, such an equation is familiar as the transformed effective mass equation (cf. e.g. the monograph [15] or our paper [16]).

This equation was invented for envelope wave functions of electrons in crystalline solids. (Synchronously, we may also speak of the real Schrödinger-Wannier equation. It is identical with the ‘one-particle Bloch equation’ for the canonical density-matrix with the Hamiltonian \( \hat{H}(p) = \hat{V}(x) \).)

From the viewpoint of the effectiveness of calculations in the present paper, we deem the momentum representation better than the \( x \)-representation. Under the assumption of the smallness of the parameter \( \mu \), we can apply the ‘plane-wave perturbation theory’ (Section II) of the density-matrix theory. For a broad class of fitness functions, the distribution function of the theory of the population genetics can be expressed as a linear expression of the mutation parameter \( \mu \).

II. THE WAXMAN-PECK MODEL OF THE POPULATION GENETICS

Let us assume that a large enough habitat (such as a given volume of soil) hosts bacteria of a certain kind. The habitat yields space, food, moisture, temperature, inhibitory substances and other needs for the survival of the bacteria in the sense that the total number of the bacteria will never decrease to zero and will never increase to infinity. Most of bacteria are free-living microorganisms multiplying by simple fission. This means that their reproduction is asexual. In other words, each bacterial individual has only one parent. The typical number of bacteria may be huge indeed: one gram of soil may contain several hundreds million bacteria. Although the bacteria are small organisms — usually 0.3 - 2 micrometres in diameter — their morphology is well distinguishable microscopically.

There are two most frequent shapes of soil bacteria: short rods and (slightly deformed) spheres. In both these cases, we may characterize each bacterium by its size
s. For instance, if the bacterium resembles a rod, we define s as the length of the rod. Denoting the average of ln s as ln s, we define the phenotypic parameter as \( p = \ln s - \ln s \). Recalling to biology, we consider the phenotypic parameter as an inheritable value. If there were no mutations in the reproduction of the bacteria, all the bacterial individuals in each generation would be equally long, i.e. \( p \) would be a constant equal to \( p_n = 0 \). But then, the mutations — however infrequent they may be — account for a dispersal of the value \( p \) among the individuals, despite the fact that all individuals under consideration do still belong to the same biological type.

Generally, the theory has to respect both mutations caused by environmental effects and spontaneous mutations. For the sake of simplicity, we will consider no other than the spontaneous mutations. The spontaneous mutations are mainly due to transcription mistakes in the replication of the DNA, i.e. in the transmission of the genetic information just at the reproduction events. Let \( \mu > 0 \) be the probability of the occurrence of such a mutation. In the case of soil bacteria, biologists have estimated the values of \( \mu \) between \( 10^{-8} \) and \( 10^{-5} \). If a mother bacterium is the carrier of the phenotypic value \( p \), the daughter bacterium will carry the same value \( p \) with the probability equal to \( 1 - \mu \). (We assume that a new-born daughter bacterium grows quickly enough to the adult size before becoming mature so that we need not distinguish between the size of young and adult bacteria.) If the birth of the daughter bacterium is accompanied with a mutation of the DNA, then there is a non-zero probability \( M(q - p) dq \) for the possibility that the phenotypic value \( q \) of the daughter bacterium may lie in the interval \((q, q + dq)\), provided that the phenotypic value of the mother bacterium was equal to \( p \). Following Waxman, we take the function \( M(p) \) as a Gaussian,

\[
M(p) = M(p; \sigma_m) = \left( \frac{1}{2\pi\sigma_m^2} \right)^{1/2} \exp\left( -\frac{p^2}{2\sigma_m^2} \right). \tag{7}
\]

Here \( \sigma_m^2 \) is the dispersion of values of \( p \).

Now, to formulate the evolution equation of the population genetics, we have to introduce the average generation time \( \tau \). Simplifying the problem, we may consider a discrete time variable as follows. Let the births of the bacteria happen at the time instants \( t_n = (n - 1)\tau \), \( n = 1, 2, \ldots \). Then we may say that the bacteria of the \( n \)th generation live between \( t_{n-1} \) and \( t_n \). Thus, \( n \) is the generation index. The time discretization is an auxiliary, rather formal, mathematical trick which loses its significance if the time \( t \) is continuous. For each \( n \), we define the distribution function \( \Phi_n(p) \) so that \( \Phi_n(p) dp \) may be interpreted as the probability of the occurrence of the phenotypic value \( p \) in the interval \((p, p + dp)\) in the \( n \)th generation. The basic problem is to relate the distribution function of the generation number \( n + 1 \) (‘generation of daughters’) with the distribution function of the generation number \( n \) (‘generation of mothers’).

Before writing the recurrent formula between the functions \( \Phi_{n+1}(p) \) and \( \Phi_n(p) \), which is our primary goal in this section, we have still to mention one important point. Even if we have neglected the environmental influence upon the mutations, we do have to consider environmental effects in a Darwinian sense. Namely, we have to respect that not all bacteria, after their birth, are equally fit to survive over the whole generation time \( \tau \). Only those bacteria whose age is equal to \( \tau \) give birth to offspring. Some of the bacteria die before becoming mature. These bacteria do not take part in producing the individuals of the next generation. (However, we assume that even the fittest mother bacterium dies soon after giving birth to the daughter bacterium. Therefore, we do not include the mother bacteria in the number of the bacteria living in the time interval \((t_n, t_{n+1})\). The mother bacteria have been included in the number of the bacteria living in the time interval \((t_{n-1}, t_n)\).) The fitness of the bacteria to live in their environment until their maturity can be modeled by a non-negative function \( w(p) \). Requiring that

\[
0 < w(p) < 1, \tag{8}
\]

we may give the function \( w(p) \) a probabilistic meaning. We assume that a new-born carrier of the phenotypic value \( p \) has the chance to live until the maturity with the probability \( w(p) \). The number of mature carriers of the phenotypic value \( p \) from the interval \((p, p + dp)\) in the \( n \)th generation is proportional to \( w(p) \Phi_n(p) \). To determine the shape of the function \( w(p) \) should be a matter of thorough biological investigations from case to case. We suppose, as Waxman and Peck did, that \( w(p) \) behaves analytically around the value \( p_0 = 0 \) and that this value corresponds to the maximum value of \( w(p) \). (Apparently, the fittest bacterial individuals are those whose phenotypic parameter \( p \) is equal to the average value \( \bar{p} \). However, \( \bar{p} = 0 \).)

Waxman and Peck have chosen the function \( w(p) \) in the special form

\[
w(p) = w(0) \exp(-\gamma p^2), \quad 0 < w(0) < 1, \tag{8a}
\]

assuming that \( 0 < \gamma \ll 1 \). (In fact, expression (8a) defines the Waxman-Peck model. The value of \( w(0) \) is insignificant since the distribution functions \( \Phi_n(p) \) are independent of \( w(0) \).)

There are, of course, many other possibilities to model \( w(p) \) by slowly varying functions with the maximum at \( p_0 = 0 \). These functions need not tend to zero if \( |p| \to \infty \). (The fitness function has been defined as a probability, not as a probability density!) In order to illustrate how the theory may depend on the choice of the function \( w(p) \), we will treat, in addition to the Waxman-Peck model, also an alternative model. Our model (considered as an example) is defined by the fitness function

\[
w(p) = w(0) \left[ 1 - \gamma[1 - \exp(-ap^2)] \right]. \tag{8b}
\]

Here we suppose that \( 0 < \gamma \ll 1 \), admitting that \( a > 0 \) need not be a small number. Expression (8b) tends to \( w(0)(1 - \gamma) > 0 \) if \( |p| \to \infty \).
The distribution function $\Phi_{n+1}(p)$ of the generation of daughters is determined by two contributions from the generation of mothers. The first stems from the births without mutations. The phenotypic value $p$ is unchanged at such births and the probability of the occurrence of such births is equal to $1 - \mu$. The first contribution to $\Phi_{n+1}(p)$ is proportional to $(1 - \mu) w(p) \Phi_{n}(p)$. The second contribution to $\Phi_{n+1}(p)$ is proportional to $\mu \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_{M}) w(q) \Phi_{n}(q)$. The interpretation of this expression is clear: if the birth of the carrier of the phenotypic value $p$ is accompanied with a mutation, we have to consider mature individuals, allowing all possible phenotypic values $q$ of potential mothers.

To exhaust all such possibilities, we have to integrate $M(p - q; \sigma_{M}) w(q) \Phi_{n}(q)$ with respect to $q$. Since both $\Phi_{n}(p)$ and $\Phi_{n+1}(p)$ are probability densities, we have to require that

$$\int_{-\infty}^{\infty} dp \, \Phi_{n}(p) = \int_{-\infty}^{\infty} dp \, \Phi_{n+1}(p) = 1. \tag{9}$$

Therefore, we write the equality

$$\Phi_{n+1}(p) = \frac{(1 - \mu) w(p) \Phi_{n}(p) + \mu \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_{M}) w(q) \Phi_{n}(q)}{\int_{-\infty}^{\infty} dq \, w(q) \Phi_{n}(q)}. \tag{10}$$

With realistic values of $p$ around $p_0 = 0$, the values of $\gamma p^2$ are small. Thus, in the case of the Waxman-Peck model, the values of $c(p)$ are also small and

$$c(p) = \gamma p^2 + \mathcal{O}(\gamma^2). \tag{11'}$$

On the other hand, in the case of the model defined by function $(8b)$, we have to keep expression $(11b)$ intact since $a$ need not be a small parameter.

The denominator in the r.h. side of equation $(10)$ warrants the fulfillment of condition $(9)$. Since $\gamma$ is small, it is convenient to introduce the complementary function $c(p)$ to $w(p)/w(0)$:

$$c(p) = 1 - \frac{w(p)}{w(0)}. \tag{11}$$

In the case of the Waxman-Peck model,

$$c(p) \equiv 1 - \exp(-\gamma p^2), \tag{11a}$$

whilst in the case of the model defined by function $(8b)$,

$$c(p) = \gamma \left[ 1 - \exp(-\gamma p^2) \right]. \tag{11b}$$

From the viewpoint of biology, the smallness of $\gamma$ implies that the comparison of the survival fitness of the majority of the bacteria with the survival fitness of the fittest bacteria should not reveal too conspicuous differences.

When using the function $c(p)$, we can rewrite formula $(10)$ in the form

$$\Phi_{n+1}(p) = \frac{(1 - \mu) [1 - c(p)] \Phi_{n}(p) + \mu \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_{M}) [1 - c(q)] \Phi_{n}(q)}{1 - \int_{-\infty}^{\infty} dq \, c(q) \Phi_{n}(q)}. \tag{10'}$$

We may take advantage of the possibility to neglect all terms of the order of magnitude of $\gamma^2$, as well as of $\gamma \mu$. So we write

$$\frac{1}{1 - \int_{-\infty}^{\infty} dq \, c(q) \Phi_{n}(q)} = 1 + \int_{-\infty}^{\infty} dq \, c(q) \Phi_{n}(q) + \ldots$$

and

$$\Phi_{n+1}(p) = \Phi_{n}(p) - \left[ c(p) - \int_{-\infty}^{\infty} dq \, c(q) \Phi_{n}(q) \right] \Phi_{n}(p) - \mu \left[ \Phi_{n}(p) - \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_{M}) \Phi_{n}(q) \right] + \ldots \tag{10''}$$

Now, in the approximation neglecting the terms symbolized by the dots, we are ready to go over into the formalism employing the continual time variable $t$, realizing that the value of the generation index $n$ may be high. Typically, the generation time $\tau$ of soil bacteria is about 20 minutes. This means that after elapsing hum-
dred days, the genetic information passes over more than seven thousand generations of the bacteria. If \( n \gg 1 \), we may identify \( \Phi_n(p) \) with \( \Phi(p, t) \) and approximate the difference \( \Phi_{n+1}(p) - \Phi_n(p) \) as the time derivative:

\[
\Phi_{n+1}(p) - \Phi_n(p) = \tau \frac{\partial \Phi(p, t)}{\partial t} + \ldots
\]

Thus, we can rewrite equation (10') in the approximate integro-differential form

\[
\frac{\partial \Phi(p, t)}{\partial t} = -1 \left[ c(p) - \int_{-\infty}^{\infty} dq \, c(q) \Phi(q, t) \right] \Phi(p, t) - \frac{\mu}{\tau} \left[ \Phi(p, t) - \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_m) \Phi(q, t) \right].
\]

It remains still to discuss the initial condition. Whichever initial function

\[
\Phi(p, 0) = \Phi_0(p)
\]

is chosen, the solution \( \Phi(p, t) \) for \( t > 0 \) of equation (13) is unique. Since equation (15) is linear, we may multiply \( \varphi(p, t) \) by an arbitrary constant \( \lambda \). If \( \varphi(p, t) \) gives the function \( \Phi(p, t) \) then \( \lambda \varphi(p, t) \) does also give the same function \( \Phi(p, t) \). Therefore, we may choose the integral \( \int_{-\infty}^{\infty} dq \varphi(q, 0) \) (which is a constant) equal to unity. Then formula (14) and equality (19) give us the initial condition

\[
\varphi(p, 0) = \Phi_0(p)
\]

for the function \( \varphi(p, t) \).

If \( \Phi_0(p) \) is an even function, equation (15) implies that the function \( \varphi(p, t) \) is also even in the variable \( p \) and \( \Phi(-p, t) = \Phi(p, t) \) at all times \( t > 0 \). In this case, the mean value of \( p \) is an invariant in time (i.e. a constant):

\[
\bar{p} = \int_{-\infty}^{\infty} dp \varphi(p, t) = 0.
\]

Equation (15) is formally the same as the Schrödinger-Wannier equation in the momentum representation. It can easily be Fourier-transformed. We define the function

\[
\psi(x, t) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} dp \exp(\text{i}px) \varphi(p, t).
\]

This function is the solution of the functional differential equation

\[
\frac{\partial \psi(x, t)}{\partial t} = -\frac{1}{\tau} \left[ -\text{i} \frac{\partial}{\partial x} \right] \psi(x, t)
\]

\[
+ \frac{\mu}{\tau} \exp \left( -\frac{\sigma_m x^2}{2} \right) \psi(x, t).
\]

In Wannier’s approximation, equation (23) reads:

\[
\frac{\partial \psi(x, t)}{\partial t} = \frac{\gamma}{\tau} \frac{\partial^2 \psi(x, t)}{\partial x^2}.
\]

When equalizing the r.h. sides of equations (15) and (17) and when respecting identity (16), we obtain equation (13) for the function \( \Phi(p, t) \). Thus, instead of directly solving equation (13), we may solve Wannier’s equation (15) at first. This task, as we will show in Section III, is not difficult. If the function \( \Phi(p, t) \) obeys linear boundary conditions, the function \( \varphi(p, t) \) has to obey the same boundary conditions. We will simply assume that

\[
\Phi(p, t) \rightarrow 0 \quad \text{and} \quad \varphi(p, t) \rightarrow 0 \quad \text{if} \quad |p| \rightarrow \infty.
\]
\[ + \frac{\mu}{\tau} \exp \left( - \frac{\sigma_{m}^{2} x^{2}}{2} \right) \psi(x, t) . \] (23a)

If \( c(p) \) is taken in the form of expression (11b), the functional differential equation for \( \psi(x, t) \) reads
\[
\frac{\partial \psi(x, t)}{\partial t} = \frac{\gamma}{\tau} \left[ \exp \left( a \frac{\partial^{2}}{\partial x^{2}} \right) - 1 \right] \psi(x, t)
\]
\[ + \frac{\mu}{\tau} \exp \left( - \frac{\sigma_{m}^{2} x^{2}}{2} \right) \psi(x, t) . \] (23b)

III. THE PLANE-WAVE PERTURBATION THEORY

Instead of solving equation (23a) or equation (23b) and carrying out the integration
\[
\varphi(p, t) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} dx \exp(-ipx) \psi(x, t),
\] (24)
we prefer to calculate the function \( \varphi(p, t) \) directly. Defining the ‘potential-energy operator’ \( \hat{V}(p) \)
\[
\hat{V}(p) \varphi(p, t) = \frac{1}{\tau} \int_{-\infty}^{\infty} dq \, M(p - q; \sigma_{m}) \varphi(q, t),
\] (25)
let us write equation (15) in the form
\[
\frac{\partial \varphi(p, t)}{\partial t} = - \frac{c(p)}{\tau} \varphi(p, t) + \mu \hat{V}(p) \varphi(p, t)
\] (26)
and define the Green function \( G(p, t; p_{0}) \) of this equation. Employing the Green function, we write \( \varphi(p, t) \) (for \( t > 0 \)) as the integral
\[
\varphi(p, t) = \int_{-\infty}^{\infty} dp_{0} \, G(p, t; p_{0}) \varphi(p_{0}, 0). \] (27)

The initial function \( \varphi(p, 0) \) has been defined by equality (20). The Green function itself obeys the equation
\[
\frac{\partial G(p, t; p_{0})}{\partial t} = - \frac{c(p)}{\tau} G(p, t; p_{0}) + \mu \hat{V}(p) G(p, t; p_{0}), \] (28)
According to equality (27), \( G(p, t; p_{0}) \) satisfies the initial condition
\[
G(p, 0; p_{0}) = \delta(p - p_{0}). \] (29)

In the special case when \( c(p) \) is approximated by the quadratic function, equation (28) is formally identical with the Bloch equation for the one-particle canonical density matrix \( C_{j}(p, p_{0}) \) in the thermodynamic equilibrium. In the case of a general function \( c(p) \) we have to speak of quasiparticles with a non-parabolic dispersion law. The function \( C_{j}(p, p_{0}) \) is equal to \( \delta(p - p_{0}) \) for quantum-mechanical reasons. When transforming equation (28) into the \( x \)-representation form, one observes that the ‘potential energy’ corresponds to a well; it is an inverted Gaussian (cf. expression (6)).

We can derive \( G(p, t; p_{0}) \) as the series
\[
G(p, t; p_{0}) = \sum_{j=0}^{\infty} \mu^{j} K_{j}(p, t; p_{0}) .
\] (30)
The zero-order term is the solution of the equation
\[
\frac{\partial G_{0}(p, t; p_{0})}{\partial t} = - \frac{c(p)}{\tau} G_{0}(p, t; p_{0})
\] (31)
with respect to the condition
\[
G_{0}(p, 0; p_{0}) = \delta(p - p_{0}) .
\] (32)

When solving equation (31), we obtain, for \( t > 0 \), the function
\[
G_{0}(p, t; p_{0}) = \delta(p - p_{0}) \exp \left( - \frac{c(p)t}{\tau} \right). \] (33)

With this function, we can write down the integral form of equation (28):
\[
G(p, t; p_{0}) = G_{0}(p, t; p_{0})
\]
\[ + \mu \int_{-\infty}^{t} dt_{1} \int_{-\infty}^{\infty} dp_{1} \, G(p, t - t_{1}; p_{1}) G_{0}(p_{1}, t_{1}; p_{0}) \] (34)
This is a Dyson-type series (cf. e.g. [17].) The first-order term in this series (linear in \( \mu \)) reads:
\[
\mu G_{1}(p, t; p_{0}) =
\]
\[ \mu \int_{-\infty}^{t} dt_{1} \int_{-\infty}^{\infty} dp_{1} \, G_{0}(p, t - t_{1}; p_{1}) G_{0}(p_{1}, t_{1}; p_{0}) \]
\[ = \frac{\mu}{\tau} \int_{0}^{t} dt_{1} \int_{-\infty}^{\infty} dp_{1} \, G_{0}(p, t - t_{1}; p_{1}) \]
\[ \times \int_{-\infty}^{\infty} dq \, M(p_{1} - q, \sigma_{m}) \varphi(q, t_{1}; p_{0}) . \] (35)

After inserting expressions (7) and (33) here, we obtain the function
\[
\mu G_{1}(p, t; p_{0}) = \frac{\mu}{\tau} \left( \frac{1}{2\pi\sigma_{m}^{2}} \right)^{1/2} \exp \left( - \frac{(p - p_{0})^{2}}{2\sigma_{m}^{2}} \right)
\]
\[ \times \int_{0}^{t} dt_{1} \exp \left( - \frac{c(p)(t - t_{1}) + c(p_{1})t_{1}}{\tau} \right). \] After performing the integration with respect \( t_{1} \), we arrive, respecting formula (7), at the final result.
\[ \mu G_1(p; t; p_0) = \]
\[ \mu M(p - p_0; \sigma_m) \exp[-c(p) t / \tau] - \exp[-c(p) t / \tau] \]
\[ \exp[-c(p) t / \tau] \]
\[ \exp[-c(p) t / \tau] \]
\[ \frac{\exp[-c(p) t / \tau]}{c(p) - c(p_0)} \]
\[ \mu M(p; \sigma_m) \exp[-c(p) t / \tau] \]

At all times \( t > 0 \). Hence, in the linear approximation with respect to \( \mu \), we have got the function
\[ \varphi(p, t) = \delta(p) + \mu M(p; \sigma_m) 1 - \exp[-c(p) t / \tau] \]
\[ \exp[-c(p) t / \tau] \]
\[ \exp[-c(p) t / \tau] \]
\[ \frac{1}{c(p) - c(p_0)} \]
\[ \mu M(p; \sigma_m) \exp[-c(p) t / \tau] \]
\[ \exp[-c(p) t / \tau] \]

\[ \int_{-\infty}^{\infty} dp \varphi(p, t) = 1 + \mu \left( \frac{1}{2 \pi \sigma_m^2} \right)^{1/2} \]
\[ \int_{-\infty}^{\infty} dp \exp \left( - \frac{p^2}{2 \sigma_m^2} \right) \frac{1 - \exp[-c(p) t / \tau]}{\gamma p^2} \]
\[ \frac{1 - \exp[-c(p) t / \tau]}{\gamma p^2} \]
\[ \frac{1 - \exp[-c(p) t / \tau]}{\gamma p^2} \]

Recall that, according to (14),
\[ \Phi(p, t) = N(t) \varphi(p, t) \]

Where
\[ N(t) = \left[ \int_{-\infty}^{\infty} dp \varphi(p, t) \right]^{-1} \]

We will calculate the function \( N(t) \) approximately assuming that \( 0 < \sigma_m < 1 \). (In fact, it is probable that \( \sigma_m \ll 1 \).) The most relevant values of \( p \) contributing to the value of the integral in the r.h. side of formula (42) lie in the interval \( (-\sigma_m, \sigma_m) \).

A. Distribution function \( \Phi(p, t; 0) \) in the model where \( c(p) = 1 - \exp(-\gamma p^2) \) (the Waxman–Peck model)

Since \( 0 < \gamma \sigma_m^2 \ll 1 \), we may use, when calculating integral (42), the approximation expressed by formula (11’a). Thus,

\[ \int_{-\infty}^{\infty} dp \varphi(p, t) \approx 1 + \frac{\mu}{\tau} \left( \frac{1}{2 \pi \sigma_m^2} \right)^{1/2} \int_{0}^{\infty} dt_1 \int_{-\infty}^{\infty} dp \left[ - \exp \left( \frac{1}{2 \sigma_m^2} + \frac{\gamma t_1}{\tau} \right) p^2 \right] \]

After carrying out the integration with respect to \( p \), we obtain the simple result
\[ \int_{-\infty}^{\infty} dp \varphi(p, t) \approx 1 + \frac{\mu}{\tau} \int_{0}^{\infty} dt_1 \frac{dt_1}{\left( 1 + 2 \sigma_m t_1 / \tau \right)^{1/2}} \]

Hence, according to formula (14), we obtain the distribution function
\[ \Phi(p, t; 0) = N(t) \left[ \delta(p) + \frac{\mu}{\gamma} M(p; \sigma_m) \frac{1 - \exp(-\gamma p^2 t/\tau)}{p^3} \right] \]  

with the normalizing coefficient

\[ N(t) = \left\{ 1 + \frac{\mu}{\gamma \sigma_m^2} \left[ \left( 1 + \frac{2\gamma \sigma_m^2 t}{\tau} \right)^{1/2} - 1 \right] \right\}^{-1}. \]  

(43a)

From the probabilistic viewpoint, the function \( N(t) \) is well understandable. When counting all bacteria living at the time instant \( t \), we have to distinguish whether they are carriers of the original phenotypic value \( p_0 = 0 \) or whether they carry other values, \( p \neq 0 \). Since \( \int_0^t \Phi(p, t; 0) = N(t) \) (if \( t \to +0 \), we may say that a randomly chosen bacterium may be the carrier of the value \( p_0 = 0 \) with the probability equal to \( N(t) \). If \( t \to \infty \), the probability \( N(t) \) decreases towards zero. However, this decreasing = the process influenced both by the mutations and by the fitness of the bacteria to live in their environment = is slow. Indeed, let us take \( \gamma = 0.02 \), \( \sigma_m = 0.05 \) and \( \mu = 10^{-5} \). Then \( \mu/\gamma \sigma_m^2 = 0.2 \) and \( 2\gamma \sigma_m^2 t/\tau = 1 \) for the generation number \( t/\tau = 10^4 \). If these values of \( \gamma \) and \( \sigma_m \), together with the value 20 minutes for the generation time \( \tau \), may be taken as realistic for some soil bacteria, the total time \( t \) comprising the lifetime of ten thousand generations of these bacteria equals about five months. If the time \( t \) is roughly ten times (or more than ten times) shorter, formula (44a) can be simplified:

\[ N(t) \approx \left( 1 + \frac{\mu t}{\gamma \sigma_m^2} \right)^{-1} \quad \text{if} \quad \frac{2\gamma \sigma_m^2 t}{\tau} \ll 1. \]  

(45)

As a rule, the mutation probability \( \mu \) is smaller than \( 2\gamma \sigma_m^2 \). Thus, we may write

\[ N(t) \approx 1 - \frac{\mu t}{\gamma \sigma_m^2} \quad \text{if} \quad \frac{2\gamma \sigma_m^2 t}{\tau} \ll 1. \]  

(45')

B. Distribution function \( \Phi(p, t; 0) \) in the model where \( c(p) = \gamma [1 - \exp(-ap^2)] \)

Now we consider a small parameter \( \gamma (0 < \gamma \ll 1) \) and another parameter, \( a > 0 \), which need not be small. Only if \( a \ll 1/\sigma_m^2 \), we may accept the approximation \( c(p) \approx \gamma ap^2 \) and there is no essential difference from the Waxman-Peck model, only \( \gamma \) is replaced by \( \gamma a \).

Otherwise, if \( a \sigma_m^2 \) is comparable with unity, the integration of the function \( \varphi(p, t) \) with respect to \( p \) is much more complicated but can be accomplished explicitly. (It is presented in Appendix.)

Here we confine ourselves to discussing what comes about if \( a \sigma_m^2 \gg 1 \). Essentially, under this condition, we may approximate \( 1 - \exp(-ap^2) \) by unity. Then we obtain the simple result

\[ \int_{-\infty}^{\infty} dp \varphi(p, t) \approx 1 + \frac{\mu}{\gamma} \left[ 1 - \exp \left( -\frac{2 \gamma^2}{\tau} \right) \right]. \]

Correspondingly, if \( a \sigma_m^2 \gg 1 \), then

\[ \Phi(p, t; 0) \approx N(t) \left\{ \delta(z) + \frac{\mu}{\gamma} M(p; \sigma_m) \left[ 1 - \exp \left( -\frac{2 \gamma^2}{\tau} \right) \right] \right\}, \]  

(43b)

where

\[ N(t) = \left\{ 1 + \frac{\mu}{\gamma} \left[ 1 - \exp \left( -\frac{2 \gamma^2}{\tau} \right) \right] \right\}^{-1}. \]  

(44b)

In the short-time approximation, formulae (45) and (45') are equal valid as in the case A. Note that expression (43b) for the distribution function \( \Phi(p, t) \) would be correct if \( c(p) = 1 - w(p)/w(0) \) might be approximated by a small constant \( \gamma > 0 \). In this case, \( N(t) \) may again be approximated as \( 1 - \mu t/\gamma \) at short enough times. However, if \( t \to \infty \), then \( N(t) \) does not tend to zero (in contrast to the case analyzed in the preceding subsection):

\[ \lim_{t \to \infty} N(t) = \frac{\gamma}{\gamma + \mu}. \]

V. CONCLUDING REMARKS

In the present paper, we have focused attention on the importance of the fitness function \( w(p) \) in the theory of the population genetics. Assuming that \( 0 < c(p) = 1 - w(p)/w(0) \ll 1 \), we have essentially followed Waxman and Peck who derived the distribution function \( \Phi(p, t) \) of the population genetics as a functional of a function \( \varphi(p, t) \) (cf. expression (14)) satisfying a linear integro-differential equation (cf. equation (15)). However, in contrast with paper [12] where \( c(p) \) was approximated as \( \gamma p^2 \) with some small parameter \( \gamma > 0 \), we emphasize that \( c(p) \) may be chosen from a wider class of functions. In particular, we have dealt with the model defined by the function \( c(p) = \gamma [1 - \exp(-ap^2)] \).

We have calculated the distribution function as a series with respect to the mutation probability \( \mu \). Our iteration scheme for calculating the Green function \( G(p, t; p_0) \) of the equation for \( \varphi(p, t) \) has been used in the same manner as in the density-matrix theory.

The replacement of \( c(p) \) by \( E(p) \), \( t \) by \( \beta \) (with \( \beta = 1 \)) and \( G(p, t; p_0) \) by the unperturbed canonical density matrix \( G^{(0)} \) yields the equation

\[ - \frac{\partial G^{(0)}(p, p_0)}{\partial \beta} = E(p) G^{(0)}(p, p_0). \]  

(46)
With adequately chosen function $E(p)$, this equation may concern conduction electrons in a homogeneous non-degenerate semiconductor. (Since $E(p)$ is not equal to the kinetic energy of an electron in vacuum, we may interpret the conduction electrons as quasiparticles defined by the dispersion law $E = E(p)$.)

Our second remark concerns the analogy with the diffusion theory. The Fourier transform of the function $G(p, x; t)$ (multiplied by a constant) can be interpreted as the concentration $C(x, t; x_0)$ of diffusants which all were initially, at the time $t_0 = 0$, localized in the point $x_0$. In the approximation of the present paper, we may generally write the equation

$$\frac{\partial C_0(x, t; x_0)}{\partial t} = \frac{1}{\tau} c \left( -i \frac{\partial}{\partial x} \right) C_0(x, t; x_0) + \frac{\mu}{\tau} \exp \left( -\frac{c^2 m^2 \gamma^2}{2} \right) C(x, t; x_0). \quad (47)$$

If $c(p) = \gamma p^2$, the concentration $C(x, t; x_0)$ obeys the usual diffusion equation with the diffusion coefficient $D = \gamma / \tau$. If $c(p) \neq \gamma p^2$, the diffusion is anomalous. In any case, the positivity of the ‘potential-energy term’ means that equation (47) involves a creation of diffusants.

If $\mu = 0$, we observe that $N_0 = \int_{-\infty}^{\infty} dx C_0(x, t; x_0)$ is a quantity not varying in time. Therefore, we may define the probability density $P_0(x, t; x_0) = C_0(x, t; x_0) / N_0$ and put the theory on an equal footing with the theory of the Brownian motion.

If $c(p) = \gamma p^2$ and $\mu = 0$, we may write down the Langevin equation $\dot{x}(u) = (2\gamma/\tau)^{1/2} \tilde{f}(u)$ for the stochastic paths $x(u) (0 \leq u \leq t)$ which all start from the common point $x(0) = x_0$ at the time instant $u_0 = 0$. The value of the end-point $x(t) = x$ at a given time instant $t > 0$ may be arbitrary and $P_0(x, t; x_0) = \langle \delta(x - x(t)) \rangle$. In the terminology of the theory of stochastic processes, $x(u)$ is the Wiener process.

But then a natural question arises: which stochastic process does correspond to the case when the fitness function $w(p)$ is modeled by function (8b) with which we have exemplified our problem? About ten years ago, we dealt with the equation

$$\frac{\partial P_0(x, t; x_0)}{\partial t} = \frac{\gamma}{\tau} \left[ \exp \left( \frac{a \partial^2}{\partial x^2} \right) - 1 \right] P_0(x, t; x_0) + D_0 \frac{\partial^2 P_0(x, t; x_0)}{\partial x^2}. \quad (48)$$

(Cf. equation (45) in [18]; see also [19].) Equation (48) corresponds to a stochastic process with paths $x(u)$ defined by the stochastic equation $\dot{x}(u) = [2D_0(x) + a \sum_{j} \delta(u - u_j)] \tilde{f}(u)$, where $\tilde{f}(u)$ is the standard zero-centered Gaussian white-noise function and where the sum represents a point process in which $u_j$ are random time instants distributed in the Poissonian way.

The Poissonian process consists of equal delta-pulses: all the pulses are taken with the same amplitude $a$. The average frequency of these pulses is equal to $\gamma / \tau$. Clearly, we consider a multiplicative stochastic process $x(u) (0 \leq u \leq t)$. If $D_0 = 0$, then the probability density $P_0(x, t; x_0) = \langle \delta(x - x(t)) \rangle$ is the fundamental solution of equation (48). Alternatively (as we have shown in [18]), equation (48) can be written in the equivalent integro-differential form:

$$\frac{\partial P_0(x, t; x_0)}{\partial t} = \frac{\gamma}{\tau} \int_{-\infty}^{\infty} dx' \left[ \frac{1}{(2\pi a)^{1/2}} \exp \left( -\frac{(x - x')^2}{2a} \right) \right] \delta(x - x') \left[ P_0(x, t; x_0) + D_0 \frac{\partial^2 P_0(x, t; x_0)}{\partial x^2} \right]. \quad (49)$$

In the case when $D_0 = 0$, equation (49) was employed by Laskin [20] in a theory of the channeling of high-energy particles in crystals. (The channeling occurs when a ray of equi-energy particles bombarding a crystal is collimated very precisely in a favorable direction.)

In the framework of the diffusion theory, we may conclude that the parameter $\gamma$ of the theory of the population genetics corresponds to an environmental noise. If $\gamma = 0$, the noise is absent.

Section IV of the present paper has been devoted to the problem of the evolution of a population in which all individuals are initially equal, being the carriers of the phenotypic value $p_0 = 0$. The distribution function $\Phi(p, t; 0)$ of the population is a sum of a sharp delta-function component, $N(t) \delta(p)$, and a blurred component. Similarly as in the thermodynamics, we may distinguish two phases in the population at any time $t > 0$. Let us denote them as phase $S$ and phase $B$. The phase $S$ consists of the carriers of the initial phenotypic value $p_0 = 0$. The phase $B$ consists of the individuals carrying the phenotypic values $p \neq p_0$. In the Waxman-Peck model (cf. expressions (43a) and (44a)), the probability $N(t)$ tends to zero if $t \rightarrow \infty$. Therefore, we may say that the phase $S$ dissolves gradually in the phase $B$. In the model with the fitness function $w(p)$ defined by expression (8b) (or by another similar expression), the probability $N(t)$ does not tend asymptotically to zero: this model predicts that both the phases $S$ and $B$ may coexist if $t \rightarrow \infty$.

Acknowledgments

This work has been supported by the Grant Agency VEGA of the Slovak Academy of Sciences and of the Ministry of Education of the Slovak Republic under contract No. 1/7565/20. I thank D. Waxman for sending me some reprints of his papers. I thank R. Hlubina and A. Plecenik for their critical reading of my manuscript. I thank also two referees for valuable notes to the first version of the present paper.

*
**APPENDIX A**

In the model where \( c(p) = \gamma [1 - \exp(-ap^2)] \), we have to manage the function

\[
\frac{1 - \exp[-c(p)t/\tau]}{c(p)} = \frac{1 - \exp\left\{ - \frac{\gamma [1 - \exp(-ap^2)] t}{\tau} \right\}}{\gamma [1 - \exp(-ap^2)]} = \frac{1}{\tau} \int_0^t dt_1 \exp \left\{ - \frac{\gamma t_1}{\tau} \right\} \exp\left(-\frac{\gamma t_1}{\tau} \right) \left\{ \frac{\gamma t_1}{\tau} \exp\left(-\frac{\gamma t_1}{\tau} \right) \right\}.
\]

We have to calculate the integral

\[
\int_{-\infty}^{\infty} dp \varphi(p, t) = 1 + \frac{\mu}{\gamma} \int_0^t dt_1 \exp \left\{ - \frac{\gamma t_1}{\tau} \right\} I(t_1),
\]

where

\[
I(t_1) = \left( \frac{1}{2\pi \sigma_m^2} \right)^{1/2} \int_{-\infty}^{\infty} dp \exp \left\{ - \frac{p^2}{2\sigma_m^2} \right\} \exp \left\{ \frac{\gamma t_1}{\tau} \right\} \exp\left(-\frac{\gamma t_1}{\tau} \right).
\]

When developing the second exponential in the MacLaurin series, we obtain the following sum of the Laplace integrals:

\[
I(t_1) = \left( \frac{1}{2\pi \sigma_m^2} \right)^{1/2} \sum_{j=0}^{\infty} \frac{t_1^j}{j! \tau^j} \int_{-\infty}^{\infty} dp \exp \left\{ - \left( \frac{1}{2\sigma_m^2} + ja \right) p^2 \right\}.
\]

Hence,

\[
I(t_1) = \sum_{j=0}^{\infty} \frac{1}{j! \tau^j \left( 1 + 2ja\sigma_m^2 \right)^{1/2}} t_1^j.
\]

In this way we have obtained the result

\[
\int_{-\infty}^{\infty} dp \varphi(p, t) = 1 + \frac{\mu}{\gamma} \sum_{j=0}^{\infty} \frac{t_1^j}{j! \tau^j \left( 1 + 2ja\sigma_m^2 \right)^{1/2}} \int_0^t dt_1 \exp \left\{ - \frac{\gamma t_1}{\tau} \right\} t_1^j.
\]

The integral in the r.h. side of this equality is easily calculable:

\[
\int_0^t dt_1 \exp \left\{ - \frac{\gamma t_1}{\tau} \right\} t_1^j = \frac{\gamma^{j+1}}{\gamma^{j+1}} \left[ 1 - \exp \left\{ - \frac{\gamma t}{\tau} \right\} \sum_{k=0}^j \frac{\gamma^k t^k}{k! \tau^k} \right].
\]

Thus we have obtained the distribution function

\[
\Phi(p, t; 0) = N(t) \left( \delta(p) + \frac{\mu}{\gamma} M(p; \sigma_m) \frac{1 - \exp \left\{ - \frac{\gamma [1 - \exp(-ap^2)] t}{\tau} \right\}}{1 - \exp(-ap^2 t/\tau)} \right),
\]

where

\[
N(t) = \left\{ 1 + \frac{\mu}{\gamma} \sum_{j=0}^{\infty} \frac{1}{j! \left( 1 + 2ja\sigma_m^2 \right)^{1/2}} \left[ 1 - \exp \left\{ - \frac{\gamma t}{\tau} \right\} \sum_{k=0}^j \frac{\gamma^k t^k}{k! \tau^k} \right] \right\}^{-1}.
\]

**REFERENCES**


