Cumulant dynamics of a population under multiplicative selection, mutation and drift

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Abstract

We revisit the classical population genetics model of a population evolving under multiplicative selection, mutation and drift. The number of beneficial alleles in a multi-locus system can be considered a trait under exponential selection. Equations of motion are derived for the cumulants of the trait distribution in the diffusion limit and under the assumption of linkage equilibrium. Because of the additive nature of cumulants, this reduces to the problem of determining equations of motion for the expected allele distribution cumulants at each locus. The cumulant equations form an infinite dimensional linear system and in an authored appendix Adam Prügel-Bennett provides a closed form expression for these equations. We derive approximate solutions which are shown to describe the dynamics well for a broad range of parameters. In particular, we introduce two approximate analytical solutions: (1) Perturbation theory is used to solve the dynamics for weak selection and arbitrary mutation rate. The resulting expansion for the system’s eigenvalues reduces to the known diffusion theory results for the limiting cases with either mutation or selection absent. (2) For low mutation rates we observe a separation of time-scales between the slowest mode and the rest which allows us to develop an approximate analytical solution for the dominant slow mode. The solution is consistent with the perturbation theory result and provides a good approximation for much stronger selection intensities.
I. INTRODUCTION

When modelling the dynamics of a finite population it is necessary to consider the effects of fluctuations introduced by genetic drift. The most influential theoretical approach to this problem has been to formulate a model of the allele frequency dynamics which incorporates drift and selection at the genic level (for models of molecular evolution we might be considering individual nucleotides but we will adopt gene nomenclature and talk of the alternative alleles at each locus). The resulting model can be analysed using the theory of Markov chains or more usually by invoking a diffusion approximation (see, for example, Crow and Kimura, 1970; Ewens, 1979). Alternatively, a number of theoretical models of selection have been developed which describe evolution at the phenotype level. These models typically describe the population by a small number of descriptive statistics, such as moments or cumulants of a trait distribution. Such models are useful when describing selection on quantitative traits (Bulmer, 1981; Bürger, 1991; Dawson, 1999; Turelli and Barton, 1994) and have also been used to develop theories of asexual evolution in finite populations (Higgs and Woodcock, 1995; Prügel-Bennett, 1997). Bürger (1991) provided one of the first analyses of polygenic dynamics using cumulants and in a recent book he provides a detailed account of the cumulant dynamics associated with various evolutionary models (Bürger, 2000). Cumulants have also been used for modelling the population dynamics of genetic algorithms, where an accurate characterisation of finite population effects is crucial (see, for example, Prügel-Bennett and Shapiro, 1994; Rattray and Shapiro, 1996). Cumulants have a number of features which make them attractive for modelling polygenic dynamics. Cumulants of increasing order will often have decreasing impact, a feature not shared by the distribution moments. Another important feature is that cumulants are additive, in the sense that the cumulants of a sum of random variables is equal to the sum of the cumulants of each random variable. Standard cumulants are most appropriate when describing deviations from a Gaussian trait distribution (Stuart and Ord, 1987) while factorial cumulants can be useful for distributions close to Poisson (Dawson, 1999).

In this work we explore the relationship between the allele frequency dynamics and trait distribution dynamics using a diffusion approximation. Dynamical equations for the trait distribution cumulants are derived for a finite population undergoing multiplicative selection and reversible mutation, assuming recombination maintains linkage equilibrium. Because of the additive nature of cumulants, this reduces to the problem of determining equations of motion for the expected allele distribution cumulants at each locus. This is a classical model in population genetics for
which the non-equilibrium diffusion theory is not solved for the general case, although solutions exist for the restricted cases when either mutation or selection is absent (Crow and Kimura, 1970). Analysis of the cumulant dynamics allows a new perspective as well as some new results. The cumulants form an infinite dimensional linear dynamical system and two approximate analytical solutions are found which accurately describe the dynamics for a broad range of parameter values. In the first case we use perturbation theory to solve the dynamics for weak selection and arbitrary mutation rate. The perturbation expansion is consistent with Kimura’s eigenvalue expansion for the zero mutation case (Kimura, 1955). Secondly, we show how a separation of time-scales between the leading mode and the rest can be used to develop an approximation to the dynamics which holds for low mutation rates and a greater range of selection intensities. This separation of time-scales allows a remarkably simple and novel approximation to the transient dynamics under selection and weak mutation. The theory is compared to simulation results of finite populations undergoing free recombination, showing good agreement.

II. EQUATIONS OF MOTION

A. The model

We consider a haploid population which is assumed to be at linkage equilibrium. The population has two alleles \( x_i \in \{1, 0\} \) at each of \( L \) loci distributed according to the following factorised distribution,

\[
\phi(x) = \prod_{i=1}^{L} \left( p_i \delta_{x_i,1} + (1-p_i) \delta_{x_i,0} \right),
\]

(1)

where \( \phi(x) \) represents the probability mass function and \( \delta_{x,y} \) is the Kronecker delta. Each population member is labelled \( n = 1, 2, \ldots, N \) where \( N \) is the population size and we consider multiplicative selection with the fitness defined,

\[
w_n = \prod_{i=1}^{L} (1-s)^{1-x_i^n}.
\]

(2)

We also include symmetric mutation with rate \( u \) at each generation.

B. Allele frequency dynamics

If we take \( s \sim O(N^{-1}) \) and \( u \sim O(N^{-1}) \) then for large \( N \) the allele frequency at each locus is subject to an independent diffusion process. We identify \( \alpha \equiv sN \) and \( \beta \equiv uN \) to be the relevant
dimensionless quantities of order unity. The dynamics is completely determined by the mean and variance of the allele frequency change each generation and under the standard multinomial selection model we find (see, for example, [Ewens, 1979]),

$$E(\Delta p_i | p_i) = a(p_i) \delta t \quad \text{where} \quad a(p_i) = \alpha p_i (1 - p_i) + \beta (1 - 2p_i),$$

$$\text{Var}(\Delta p_i | p_i) = b(p_i) \delta t \quad \text{where} \quad b(p_i) = p_i (1 - p_i),$$

(3)

to leading order in $\delta t$, where $\delta t \equiv N^{-1}$ defines an increment of time. The diffusion limit is obtained as $\delta t \to 0$. The covariance between allele frequencies at different loci is $O(s^2 \delta t)$ and is therefore negligible in this limit, so we are justified in treating each locus independently as long as recombination is sufficient to maintain linkage equilibrium. In the diffusion framework the Kolmogorov forward equation (also known as the Fokker-Planck equation) describes the evolution of the allele frequency distribution over time,

$$\frac{\partial \phi(p_i, t)}{\partial t} = \frac{1}{2} \frac{\partial^2}{\partial p_i^2} [b(p_i) \phi(p_i, t)] - \frac{\partial}{\partial p_i} [a(p_i) \phi(p_i, t)],$$

(4)

where $\phi(p_i, t)$ is the probability density of $p_i$ at time $t$. This PDE is difficult to solve analytically and to our knowledge no analytical solution has been determined for the general case of selection, mutation and drift. In this case numerical methods have to be used to study the dynamics of the allele frequency distribution. The solution at equilibrium is easier to obtain and was given by [Kimura (1955)] confirming the result originally found by [Wright (1937)] using a different approach. For a good discussion of diffusion theory in the context of population genetics see, for example, [Crow and Kimura (1970)].

We have assumed that selection acts independently at each locus. This assumption can break down if $L$ is sufficiently large, because interference between loci results in a reduced effective population size and the introduction of significant linkage disequilibrium. This effect can be quantified if the population is at linkage equilibrium before selection by calculating the fitness variance in a finite population. The effective population size can then be determined using the arguments developed by [Robertson (1961)]. However, such interference will also generate strong linkage disequilibrium after selection which remains significant even under free recombination. We will therefore assume that $L$ is sufficiently small to make such effects negligible. A necessary condition for this to be the case is for $s^2 = o(L^{-1})$ while sufficient conditions depend on the rate of recombination.
C. Cumulants at linkage equilibrium

Under multiplicative selection we can consider the number of advantageous alleles per population member $Z_n \equiv \sum_{i=1}^{L} x_i^n$ to be a trait undergoing exponential selection. The first two cumulants are the mean and variance of the trait distribution while higher cumulants describe deviations from a Gaussian distribution. Let $K_m$ be the $m$th cumulant of the population. Each cumulant can be generated by differentiating the appropriate generating function (Stuart and Ord, 1987),

$$K_m = \lim_{\gamma \to 0} \frac{\partial^m}{\partial \gamma^m} G(\gamma) \quad \text{where} \quad G(\gamma) = \log \sum_{n=1}^{N} e^{\gamma Z_n}.$$  (5)

If we assume a sufficiently large population at linkage equilibrium then Eq. (5) can be written in terms of allele frequencies by replacing the sum in Eq. (5) by an average over the allele distribution defined in Eq. (1),

$$G(\gamma) = \log \sum_{\mathbf{x}} \phi(\mathbf{x}) e^{\gamma \sum_i x_i}$$

$$= \sum_{i=1}^{L} \log \left( p_i (e^{\gamma} - 1) + 1 \right).$$  (6)

In terms of allele frequencies the first few cumulants are,

$$K_1 = \sum_{i=1}^{L} p_i,$$

$$K_2 = \sum_{i=1}^{L} p_i (1 - p_i),$$

$$K_3 = \sum_{i=1}^{L} p_i (1 - p_i)(1 - 2p_i).$$  (7)

The first cumulant is the number of advantageous alleles within the population and the second cumulant measures the heterozygosity. From these equations we see that the expectation value of the trait cumulants is linearly related to the allele frequency moments.

Notice that each cumulant can be written as a sum over contributions from each locus. This is not generally true for other combinations of the trait distribution’s moments, such as the central moments. Because each locus is effectively subject to an independent diffusion process the central limit theorem ensures that fluctuations in each cumulant over an ensemble of populations undergoing an independent diffusion process will decrease with increased $L$. In the large $L$ limit the cumulants will evolve deterministically and will be described by the deterministic equations of motion derived below (recall, however, that we require $s^2 = o(L^{-1})$ for our approximation to
be valid, which limits the size of $L$). For finite $L$ our equations of motion will only give the mean
dynamical trajectory over an ensemble of populations. Figure 1 shows how fluctuations in the
cumulant dynamics are reduced as $L$ is increased. In section II.D we will show how the scale of
these fluctuations can be estimated from the expectation value of the cumulants.

D. Cumulant equations of motion

To calculate how the generating function for the cumulants changes over time we follow the
discussion given by Ewens (1979, p 136). First we write,

$$G(\gamma) = \sum_{i=1}^{L} g_\gamma(p_i) \quad \text{where} \quad g_\gamma(p_i) = \log \left( p_i (e^\gamma - 1) + 1 \right).$$  

(8)

Taylor expanding in orders of $\Delta p_i$ and taking the expectation it is straightforward to show that,

$$E_{t+\delta t}[g_\gamma(p_i)] \simeq E_t[g_\gamma(p_i)] + E_t[a(p_i)g'_\gamma(p_i) + \frac{1}{2} b(p_i)g''_\gamma(p_i)] \delta t,$$

(9)

where $a(p_i)$ and $b(p_i)$ are defined in Eq. (3). In the limit $\delta t \to 0$ we therefore obtain the rate of
change of the generating function for the expectation value of the cumulants,

$$\frac{d}{dt}E_t[G(\gamma)] = E_t \left[ \sum_{i=1}^{L} a(p_i)g'_\gamma(p_i) + \frac{1}{2} b(p_i)g''_\gamma(p_i) \right].$$  

(10)

The rate of change in the expectation value for each cumulant is given by differentiating Eq. (5),

$$\frac{d}{dt}E_t[K_n] = \lim_{\gamma \to 0} \frac{\partial^n}{\partial \gamma^n}E_t \left[ \sum_{i=1}^{L} a(p_i)g'_\gamma(p_i) + \frac{1}{2} b(p_i)g''_\gamma(p_i) \right].$$  

(11)

In order to get equations of motion for the cumulants we first calculate the right hand side of
Eq. (11) in terms of allele frequencies. We then use the relationship between the allele frequencies
and cumulants in Eq. (6) to obtain equations involving only cumulants. We automated this pro-
cess using the symbolic programming language Mathematica (Wolfram, 1999). However, since
submitting this article Prügel-Bennett has obtained a closed form expression for the dynamical
equations which is given in the authored appendix D.

We obtain a linear first order ODE for the expected cumulants $k_n(t) \equiv E_t[L^{-1}K_n]$ (we scale
the cumulants by a factor of $L^{-1}$ for convenience),

$$\frac{dk}{dt} = -Mk + d,$$

(12)
where \( \mathbf{d} = (\beta, \beta, \beta, \ldots)^T \) and,

\[
\mathbf{M} = \begin{pmatrix}
2\beta & -\alpha & 0 & 0 & \cdots \\
0 & 1 + 4\beta & -\alpha & 0 & \cdots \\
2\beta & 0 & 3(1 + 2\beta) & -\alpha & \cdots \\
0 & (1 + 8\beta) & 0 & 2(3 + 4\beta) & \cdots \\
\vdots & \vdots & \vdots & \vdots & \ddots \\
\end{pmatrix}.
\]

Unfortunately, the equation for each cumulant involves a cumulant of higher order, so that the system is intrinsically infinite dimensional. In the next section we describe some approximate solutions to this system of equations.

The cumulant equations derived above can easily be related to a set of equations describing the moments of the allele frequency distribution, since the cumulants are linearly related to these moments by Eq. (7). However, the results described in the next section will often rely on special features displayed by the cumulants which are not shared by the allele frequency moments. In particular, the truncated system obtained by setting moments above some order to zero is very poorly behaved in contrast to the truncated cumulant system used in sections III.A and III.C below.

### III. SOLVING THE DYNAMICS

The solution to Eq. (12) can be written in terms of a diagonal matrix of eigenvalues \( \mathbf{D} = [\lambda_i \delta_{ij}] \) and the associated matrix \( \mathbf{V} \) whose columns are eigenvectors of \( \mathbf{M} \) (defined by \( \mathbf{D} = \mathbf{V}^{-1}\mathbf{M}\mathbf{V} \)),

\[
\mathbf{k}(t) = \mathbf{k}^* + \mathbf{V} e^{-\mathbf{D}t} \mathbf{V}^{-1}(\mathbf{k}(0) - \mathbf{k}^*).
\]

Here, \( \mathbf{k}^* \equiv \mathbf{M}^{-1}\mathbf{d} \) is the fixed point. Properties of the fixed point are described in appendix A.

We have not been able to find a general result for the eigenvalues and eigenvectors of the full infinite dimensional system. In practice we find that a truncated system describes the dynamics well for a large range of parameters, as we will show in section III.A. In section III.B we use a perturbation expansion to solve the infinite dimensional system for small \( \alpha \). This expansion agrees with the zero mutation rate result due to (Kimura, 1955) but only provides a good approximation for \( \alpha \simeq 3 \) or less. In section III.C we give an approximation valid for low mutation rates which describes the system accurately for larger values of \( \alpha \). This approximation is based on the observation that there is a separation of time-scales between the slowest mode and the rest as the mutation rate is reduced. This slow mode is strongly coupled to the first cumulant and determines
its expected rate of change. The higher cumulants quickly relax to a quasi-equilibrium which can be determined analytically for a truncated system. The second cumulant (trait variance) of this quasi-equilibrium distribution determines the rate of change in the first cumulant, and hence the eigenvalue of the slow mode. The separation of time-scales persists for relatively large selection intensities and comparisons with simulations suggest that the resulting approximation works well up to at least $\alpha \simeq 10$.

A. Truncated system

A finite system of equations can be obtained by truncating the infinite system in Eq. (12). We create an $n$-dimensional truncated system by only considering cumulants of order $n$ and less. Setting $K_{n+1}$ to zero decouples the equations from higher cumulants. The solution is given by Eq. (14) with the infinite-dimensional matrix $M$ replaced by the $n$-dimensional square submatrix starting in its top left-hand corner. The resulting finite system provides a very good approximation for the dynamics of the lower order cumulants as long as $\alpha$ is not too large. An increased order of truncation is required to achieve accurate results as $\alpha$ is increased. This is demonstrated in Fig. (2) where we compare the fixed point of the cumulant equations for the truncated system to the known exact result derived from Wright’s distribution (see appendix A). As the truncation order increases the approximation rapidly converges toward the correct result. However, for larger $\alpha$ the speed of convergence is slower. It is interesting to note that the results do not seem to depend strongly on the mutation rate. This suggests that the truncated system will work well for a large range of mutation rates but may break down for large $\alpha$. In particular, we have limited our simulations to $\alpha \leq 10$ although a higher order truncation might allow accurate results for stronger selection.

In Fig. (3) we compare the solution of the eighth order truncated system to averaged simulation results. The symbols show the first two cumulants for $\alpha = 1, 5$ and $10$ and solid lines show the theory. We observe excellent agreement between the theory and simulations. A similar truncated system describing the dynamics of the allele frequency moments does not reproduce the dynamics or fixed point well unless selection is very weak ($\alpha \ll 1$) or mutation rates are high.
B. Perturbation theory

Perturbation theory allows the solution to an intractable linear system by expansion around a solvable limiting case (see, for example, Bender and Orszag, 1978). For $\alpha = 0$ the Jacobian matrix $M$ is lower triangular and the eigenvalues and eigenvectors can be determined exactly even for the full infinite dimensional system. Indeed, the diffusion theory for $\alpha = 0$ has an exact closed form solution (Kimura, 1964) and one can verify that the known eigenvalues agree with our zeroth order result. We expand around the zeroth order result to obtain a perturbation expansion of arbitrary order, as described in appendix B.

The 4th order expansion is given for two eigenvalues by Eqs. (B12) and (B13). For small $\beta$ these are the smallest eigenvalues and we observe that $\lambda_1 \propto \beta$ for all orders of expansion. For $\beta = 0$ the first eigenvalue is therefore zero and $\lambda_2$ determines the rate of decay under selection and drift. The expansion for $\lambda_2$ in this limiting case agrees with the expansion found by Kimura (1955) from an eigenvalue expansion of the diffusion equation. To our knowledge no similar result has previously been obtained for the case of mutation, selection and drift studied here.

In Fig. 4 we compare the 2nd and 6th order perturbation expansion result to eigenvalues of a truncated system. The truncation order was increased well beyond the point where the eigenvalues were observed to converge onto a limiting value. These figures suggest that the perturbation theory provides a good approximation up until about $\alpha = 3$, which agrees with Kimura’s observation in the zero mutation case (Kimura, 1955).

C. Separation of time-scales and adiabatic elimination

We will often be interested in the limiting case where the mutation rate is small. In this limit we find there is a separation of time-scales between the slowest mode, which is $O(\beta)$, and the rest, which are $O(1)$. This picture was confirmed for small $\alpha$ by the perturbation theory described in section III.B and appendix B. Figure 4 suggests that this behaviour also holds for larger selection intensities. In practice the dynamics will quickly relax to the slow mode, which will determine most of the system’s long term dynamics. Figure 5 shows the averaged velocity of a population as it approaches the fixed point. The simulation results approach an asymptotic value (derived below) as $\beta$ is decreased. Notice that the velocity is proportional to $\beta$ and that the slow mode becomes increasingly dominant as $\beta$ is reduced. Similar simulations were used by Prügel-Bennett (1999).
in order to compare the dynamics of populations with and without crossover, although the scaling relationship with the mutation rate was not considered explicitly in that study.

Once the population reaches the steady state it moves as a travelling wave, as has previously been observed by Bürger (1993), in marked contrast to the infinite population dynamics. Bürger argues that the velocity of the population is proportional to the population’s variance, which can be determined under the assumption of a balance between neutral mutation and drift. In the present case mutation is not neutral, and does change the population mean, so that Bürger’s approximation is not strictly applicable. Also, we find that the population’s variance depends on the selection intensity and cannot be calculated under a neutral model. However, the picture of a travelling wave is still applicable and for our model we can derive an analytical expression for the population’s velocity in the steady state in a similar spirit to Bürger’s approximation.

The asymptotic result shown in Fig. 5 is obtained by assuming an adiabatic elimination of fast variables for small $\beta$ (for a discussion on adiabatic elimination see, for example, Gardiner, 1985). We make the assumption that most of the first cumulant dynamics is determined by the slow mode. This is borne out by examination of the eigenvectors derived from perturbation theory, which show that the fast modes only couple to the first cumulant through terms which are $O(\beta)$ (this is demonstrated in appendix C). The higher cumulants have significant contributions from the fast modes. We can therefore think of the higher cumulants as fast variables which will rapidly converge to a quasi-equilibrium value which then changes slowly according to the slow mode. The coupling of the higher cumulants to the slow mode is through the first cumulant, so the quasi-equilibrium value is determined by solving the fixed point equations for the second and higher order cumulants for a particular value of the first cumulant. To calculate this fixed point we have to truncate the dynamical equations, as described in section III.A, and the quasi-equilibrium cumulants are found by solving a linear equation,

$$\sum_{j=2}^{n} M_{ij} k_j^e = \beta - M_{i1} k_1$$

for $2 \leq i \leq n$, \hspace{1cm} (15)

where $n$ is the truncation order. We then use the quasi-equilibrium variance $k_2^e$ to determine the rate of change of the first cumulant according to Eq. (12),

$$\frac{dk_1}{dt} = \alpha k_2^e + \beta (1 - 2k_1).$$

(16)

For an eighth-order cumulant truncation we find the following expression for the quasi-equilibrium
variance to first order in $\beta$,

$$k_2^e \simeq \beta \left( 1 + \frac{126 \alpha (2k_1 - 1)(4200 + 220\alpha^2 + \alpha^4)}{1587600 + 189000\alpha^2 + 2898\alpha^4 + \alpha^6} \right). \quad (17)$$

Higher order truncations result in similar rational expressions with higher order polynomials in $\alpha$ appearing in the numerator and denominator. The above expression was used to plot the theoretical lines in Fig. (5). The adiabatic elimination result is self-consistent since Eq. (16) demonstrates that only the $O(\beta)$ leading eigenvalue contributes to the decay of the first cumulant, as we initially assumed.

For weak selection, perturbation theory confirms the adiabatic elimination result. The term proportional to $k_1$ on the right hand side of Eq. (16) gives the leading eigenvalue and we can expand in $\alpha$,

$$\lambda_1 \simeq 2\beta \left( 1 + \frac{\alpha^2}{3} - \frac{\alpha^4}{45} + \cdots \right). \quad (18)$$

Comparison with Eq. (B12) to first order in $\beta$ shows that the results agree. However, the simulations in Fig. 5 indicate that the adiabatic elimination result provides a good approximation for much larger selection intensities than covered by the perturbation theory.

**D. Fluctuations**

We have mainly considered the averaged cumulant dynamics. However, the theory described here can also be used to estimate fluctuations from expected behaviour if we assume the same initial conditions at all loci. In this case there is an identical and independent diffusion process at all loci and we can consider the expected cumulants to be ensemble averages over loci and/or populations. For example, the variance of the mean is then given by,

$$\text{Var}(L^{-1}K_1) = \mathbb{E}_t \left[ \left( \frac{1}{L} \sum_{i=1}^{L} p_i \right)^2 \right] - \mathbb{E}_t \left[ \frac{1}{L} \sum_{i=1}^{L} p_i \right]^2 = L^{-1}[k_1(1-k_1) - k_2]. \quad (19)$$

where $k_n \equiv \mathbb{E}_t[L^{-1}K_n]$. This shows how the fluctuations fall off with increasing $L$, as previously observed in Fig. 1. We can similarly calculate the ensemble variance for the higher cumulants. It should be noted that the cumulants here describe an infinite population from which our finite population can be considered a sample. This sampling procedure will also introduce fluctuations in the measured cumulants, as quantified by Prügel-Bennett (1997).
IV. CONCLUSION

We studied the cumulant dynamics for a classical population genetics model, a finite population with two alleles at each locus evolving under multiplicative selection and reversible mutation. We identified the number of advantageous alleles as a trait undergoing exponential selection and the cumulants of the trait distribution were shown to be linearly related to moments of the allele frequency distribution. The dynamical equations were derived and formed a coupled infinite-dimensional linear system. A truncated system was shown to provide an excellent approximation to the full infinite-dimensional system for a broad range of parameters. For weak selection we developed an analytical approximation to the eigensystem of the full infinite-dimensional case using a perturbation expansion around the solvable limit of zero selection. To all orders in perturbation theory a single eigenvalue was shown to be proportional to the mutation rate, resulting in a separation of time-scales between different modes for low mutation rates. This separation of time-scales was observed to persist for stronger selection and allowed us to develop an analytical approximation to the leading eigenvalue in the limit of weak mutation. This approximation was shown to provide good results for larger selection intensities than covered by the perturbation expansion.

Cumulants have been shown to be useful for modelling a variety of polygenic systems (see, for example, Bürger, 2000) and here we have shown their potential for describing a finite population where genetic drift is non-negligible. Cumulants have a number of features which make them useful for modelling finite populations close to linkage equilibrium. Firstly, it was noted that each cumulant at linkage equilibrium can be written as a sum over contributions from each locus. This is not generally the case for other combinations of the trait moments, such as the central moments, and suggests that populations may be better described using cumulants rather than central moments since fluctuations will be reduced according to the central limit theorem. For the multiplicative selection case considered here the equations of motion were also linear, in which case fluctuations do not lead to strong systematic effects. This picture should be contrasted with cumulant equations describing finite asexual populations under multiplicative selection which are intrinsically far from linkage equilibrium, in which case fluctuations do contribute systematic effects and must be modelled explicitly (Prügel-Bennett, 1997). Secondly, although the trait cumulants are linearly related to the allele frequency moments, the latter do not share certain advantageous features displayed by the former. This is because the truncated equations of motion for the allele frequency moments do not describe the infinite-dimensional system well except under weak selection or high mutation
Whether cumulant dynamics will prove generally useful for describing finite populations with significant linkage disequilibrium is an open question. Infinite populations with linkage disequilibrium have recently been modelled using factorial cumulants (Dawson, 1999) but as we mentioned above, drift will introduce systematic effects which are typically difficult to model. Although approximations have been introduced which attempt to capture these fluctuations (Prügel-Bennett, 1997), the complexity and non-linearity of the resulting dynamical system make it difficult to draw general conclusions.

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**APPENDIX A: Fixed Point**

The fixed point of the allele frequency distribution for the model considered here was first determined by [Wright (1937)](https://www.jstor.org/stable/689386). [Kimura (1955)](https://www.jstor.org/stable/2505866) later showed this to also be the solution of the related diffusion equation with density given by,

$$\phi(\{p_1, p_2, \ldots, p_L\}) = C^{-L} \prod_{i=1}^{L} e^{2\alpha p_i} [p_i(1-p_i)]^{2\beta-1}, \quad (A1)$$

where,

$$C = \frac{\Gamma(2\beta)^2 F(2\beta, 4\beta, 2\alpha)}{\Gamma(4\beta)},$$

and $F(\cdot; \cdot; \cdot; \cdot)$ is the Kummer confluent Hypergeometric function. The moments of this distribution can be shown to be related through the following recursion formula,

$$2\alpha E(p_i^n) = (2 - n + 2\alpha - 4\beta)E(p_i^{n-1}) - (2 - n - 2\beta)E(p_i^{n-2}). \quad (A2)$$
We can use this to determine relationships between the expected population cumulants using the definition in Eq. (9). For the first few we find,

\[ \alpha_k^2 = \beta (2k_1 - 1), \]
\[ \alpha_k^3 = (1 + \alpha + 4\beta)k_2 - 2\beta k_1, \]
\[ \alpha_k^4 = 3(1 - \alpha + 2\beta)k_3 + (3 + 4\alpha + 12\beta)k_2 - 6\beta k_1. \]

As a check one can easily verify that these relationships satisfy Eq. (12) with \( \frac{dk}{dt} = 0 \). In an authored appendix to this paper, Prügel-Bennett shows that the expressions are exactly equivalent (appendix D).

APPENDIX B: Perturbation theory

Consider the linear system in Eq. (12). To determine the properties of the dynamics, we should study the eigenvalues and eigenvectors of \( M \). This we do below by expanding around the solution for \( \alpha = 0 \).

1. Notation

Denote the \( i \)th eigenvalue of \( M \) as \( \lambda(i) \); its associated eigenvector is \( e(i) \). Denote the associated eigenvector of the transpose of \( M \) as \( w(i) \). In Eq. (12), \( V \) is a matrix whose \( i \)th column is \( e(i) \) and \( V^{-1} \) is a matrix whose \( i \)th row is \( w(i) \).

We will expand in powers of \( \alpha \) and use superscripts to denote the order. So, \( M \) is written as

\[ M = M^0 - \alpha \Delta, \quad (B1) \]

where \( \Delta_{ij} = \delta_{ij+1} \). We likewise expand the eigenvalues and eigenvectors,

\[ e(i) = e^0(i) + \alpha e^1(i) + \alpha^2 e^2(i) + \ldots, \quad (B2) \]
\[ \lambda(i) = \lambda^0(i) + \alpha \lambda^1(i) + \alpha^2 \lambda^2(i) + \ldots, \quad (B3) \]
\[ V = E^0 + \alpha E^1 + \alpha^2 E^2 + \ldots, \quad (B4) \]
\[ V^{-1} = W^0 + \alpha W^1 + \alpha^2 W^2 + \ldots, \quad (B5) \]
\[ D = D^0 + \alpha D^1 + \alpha^2 D^2 + \ldots. \quad (B6) \]

The expansion is simple due to two properties of \( M^0 \),
1. $M^0$ is lower triangular, and

2. $M^0$ alternates with 0’s, i.e. $M_{ij}^0 \neq 0 \Rightarrow M_{i+1,j}^0 = M_{i,j+1}^0 = 0$.

2. Zeroth Order

Since $M^0$ is lower triangular, the eigenvalues are simply the diagonal elements,

$$\lambda^0(k) = M_{kk} = \frac{k(k-1)}{2} + 2k\beta.$$  \hspace{1cm} (B7)

The eigenvectors can be found recursively via back-substitution,

$$e^{0}(k)_j = \begin{cases} 
0; & \text{if } j < k \\
1; & \text{if } j = k \\
\sum_{m=k}^{j-1} M_{km} e^{0}(k)_m / \lambda^{0}(k) - \lambda^{0}(j); & \text{otherwise}
\end{cases}.$$  \hspace{1cm} (B8)

The eigenvectors of the transposed system can also be found. The result is

$$w^{0}(k)_j = \begin{cases} 
\sum_{m=j+1}^{k} M_{jm} w^{0}(k)_m / \lambda^{0}(k) - \lambda^{0}(j); & \text{if } j < k \\
1; & \text{if } j = k \\
0; & \text{if } j > k
\end{cases}.$$  \hspace{1cm} (B9)

The latter can be found either by truncating the transposed system at some order $n$, computing the first $n$ eigenvectors by back-substitution starting from the lower right, and then taking $n \rightarrow \infty$, or by ansatz. We will argue momentarily that these are the only eigenvectors of the infinite system.

It is clear that the right eigenvectors form a complete set and are defined without requiring any finite truncation\(^1\). The left eigenvectors can be found only by truncating the system to some order or by assuming that $w^{0}(k)_j = 0$ for all $j > k$. Thus, one might worry that there are other possible left eigenvalues. However, since all of the eigenvalues are distinct, the right and left eigenvectors must form a mutually orthogonal set. Those given in Eqs. (B8) and (B9) do, and so the left eigenvectors must form a complete set as well.

The result is that $E^0$ and $W^0$ have the same structure as $M^0$; lower triangular with alternating zero elements.

---

\(^1\) They are not, however, normalizable in infinite dimensions
3. Arbitrary Order

The $n$th order approximation to the eigenvalues and eigenvectors can be found in terms of the lower order approximations. The recursion is

$$M^0 E^n - E^n D^0 - D^n E^0 = \Delta E^{n-1} + \sum_{j=2}^{n-1} E^{n-j} D^j.$$  \hspace{1cm} (B10)

This must be solved for the $n$th order contribution to the eigenvectors, $E^n$, and to the eigenvalues, $D^n$. This is solvable because $E^0$ is lower triangular, so the upper triangular part of $E^n$ can be computed without knowledge of $D^n$. Then, since $M^0 - D^0$ is lower triangular with zeros on the diagonal, $D^n$ depends only on the upper triangular part of $E^n$. Once this is computed, the lower triangular part of $E^n$ can be found.

This equation does not determine the diagonal part of $E^n$. This is arbitrarily taken to be zero. In other words, $V_{ii} = 1$ to all orders which is like a choice of normalization for these non-normalizable vectors.

To find the left eigenvectors, we ensure that $W$ is the inverse of $E$ to $n$th order in $\alpha$. This requires that

$$W^n = - \left( \sum_{j=0}^{n-1} W^j E^{n-j} \right) W^0.$$ \hspace{1cm} (B11)

We find that each order introduces one higher upper diagonal element to $E$ and $W$. Thus, to compute $\lambda(k)$ to order $n$, one needs to truncate the system at an order higher than $k + n$.

4. Results

The expansion for the first two eigenvalues is given below,

$$\lambda(1) = 2\beta + \alpha^2 \frac{2\beta}{3 + 10\beta + 8\beta^2} - \alpha^4 \frac{2\beta(3 - 6\beta - 4\beta^2 + 16\beta^3)}{(1 + 2\beta)^3(3 + 4\beta)^3(5 + 4\beta)} + O(\alpha^6),$$ \hspace{1cm} (B12)

$$\lambda(2) = 1 + 4\beta + \alpha^2 \frac{1 + 8\beta^2}{2(1 + \beta)(1 + 2\beta)(5 + 4\beta)} - \alpha^4 \frac{1 - 278\beta + 492\beta^2 + 1392\beta^3 - 96\beta^4 - 2112\beta^5 - 640\beta^6 + 512\beta^7}{8(1 + \beta)^3(1 + 2\beta)^3(5 + 4\beta)(7 + 4\beta)} + O(\alpha^6).$$ \hspace{1cm} (B13)

As seen in Fig. 4, the series expansion to 6th order in $\alpha$ is accurate for $\alpha$ up to about 3.
APPENDIX C: Adiabatic elimination

The dynamical equation can be written as
\[ V^{-1} \frac{dK}{dt} = -DV^{-1}k + V^{-1}d. \] (C1)

To all orders in perturbation theory and to leading order in \( \beta \), this equation takes the following form,
\[
\begin{align*}
\dot{k}_1 + \alpha f_{12} k_2 + \alpha^2 f_{13} k_3 + \ldots &= e^{-\lambda(1)t} \left( k_1 + \alpha f_{12} k_2 + \alpha^2 f_{13} k_3 + \ldots \right) + \text{constant}, \\
\beta \alpha f_{21} \dot{k}_1 + \dot{k}_2 + \alpha f_{23} \dot{k}_3 + \ldots &= e^{-\lambda(2)t} \left( \beta \alpha f_{21} k_1 + k_2 + \alpha f_{23} k_3 + \ldots \right) + \text{constant}, \\
\beta f_{31} \dot{k}_1 + \alpha f_{32} \dot{k}_2 + \dot{k}_3 + \ldots &= e^{-\lambda(3)t} \left( \beta f_{31} k_1 + \alpha f_{32} k_2 + \alpha k_3 + \ldots \right) + \text{constant}, \\
\vdots & \vdots 
\end{align*}
\] (C2)

where \( \dot{k}_n \) is the time-derivative of \( k_n \) and the \( f_{ij} \)'s are trivially related to the eigenvectors but have the leading order in \( \beta \) pulled out. The structure of the eigenvectors and eigenvalues reveals three points,

- For all equations beyond the first one, coupling to \( k_1 \) and \( \dot{k}_1 \) is through terms which are \( O(\beta) \).
- The first eigenvalue is \( O(\beta) \); the remaining ones are \( O(1) \).
- Truncating the equations to have \( m \) components results in an error of \( O(\alpha^{m-i+1}) \) to the \( i \)th equation.

This shows why adiabatic elimination works. For \( \beta = 0 \), \((k_2, k_3, \ldots)\) satisfies a closed set of equations completely decoupled from \( k_1 \). Once the higher cumulants have decayed, \( k_1 \) becomes frozen. For \( \beta \) small, the coupling is present but weak and the higher cumulants will behave as a quasi-closed set decaying at a rate of \( O(1) \). The first cumulant will decay very slowly after the higher ones have decayed and will depend on them through their quasi-equilibrium values. As long as the selection intensity is not too large, truncating the system will result in small errors.

APPENDIX D: Explicit Form of the Cumulant Evolution Equations

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In this appendix we give an explicit form for the evolution equation (12). We also obtain an analogous equation for the moments. We can rederive the diffusion equation for the allele frequency distribution (equation (4)) directly from the matrix equation for the moments. This illustrates clearly the connection between a matrix equation formulation and a diffusion equation formulation.

This work was completed after receiving a preprint of the above paper by Rattray and Shapiro. It seems appropriate to publish these results at the same time as the paper.

1. Explicit Evolution Equation

Equation (12) can be written explicitly in terms of binomial coefficients

\[ \frac{dk_n}{dt} = \beta + \alpha k_{n+1} - \sum_{m=2}^{n} \left( 2\beta \binom{n}{m-1} + \binom{n}{m-2} \right) I[n + m \text{ is even}] k_m \]  

(D1)

where we denote the indicator function by

\[ I[predicate] = \begin{cases} 
1 & \text{if } predicate \text{ is true} \\
0 & \text{if } predicate \text{ is false} 
\end{cases} \]

We can write an equivalent set of equations for the allele frequency moments \( \mu_n = E_0 [p^n] \).

\[ \frac{d\mu_{k+1}}{dt} = - (k + 1) \left( \alpha \mu_{k+2} + \left( 2\beta - \alpha + \frac{k}{2} \right) \mu_{k+1} - \left( \beta + \frac{k}{2} \right) \mu_k \right) \]  

(D2)

This equation still holds for \( k = 0 \) provided we interpret \( \mu_0 = 1 \). We can obtain the diffusion equation (4) directly from this equation.

Sketch of Proof

The proof of equation (D1) follows from two observation. Unfortunately, it involves rather laboured algebraic manipulations. We therefore give only an outline of the proof below.

The first observation (already discussed in section II) is that the cumulant equations all decouple over the loci. We can therefore consider the cumulants for a single locus. We can write an analogous equation to equation (11) for the single-locus cumulants (we drop the loci subscript \( i \) as it plays no part in what follows)

\[ \frac{dk_n}{dt} = E_i \left[ a(p) \frac{\partial K_n^{sl}(p)}{\partial p} + \frac{b(p)}{2} \frac{\partial^2 K_n^{sl}(p)}{\partial p^2} \right] \]  

(D3)
with \( a(p) = \alpha p (1 - p) + \beta(1 - 2p) \), \( b(p) = p (1 - p) \),

\[
K^\text{sl}_{n}(p) = \frac{\partial^n g_{\gamma}(p)}{\partial \gamma^n}, \quad g_{\gamma}(p) = \log(p(e^\gamma - 1) + 1)
\]  

(D4)

and where we have used

\[
k_n = \mathbb{E}_t[K^\text{sl}_{n}(p)].
\]  

(D5)

The \( k_n \) used here refers to a single-locus cumulant; it differs from \( k_n \) used in the main paper, which is the single-locus cumulant averaged over all loci. Only when the initial conditions at all loci are the same will these quantities coincide.

The second observation is a consequence of equations (D4) and (D5), namely that the cumulants \( k_n \) are linearly related to the allele frequency moments \( \mu_n = \mathbb{E}_t[p^n] \). We can write the cumulants as

\[
k_n = \mathbb{E}_t[K^\text{sl}_{n}(p)] = \sum_{l>0} \left[ \begin{array}{c} n \\ l \end{array} \right] \mathbb{E}_t[p^l] = \sum_{l} \left[ \begin{array}{c} n \\ l \end{array} \right] \mu_l
\]  

(D6)

where \( \left[ \begin{array}{c} n \\ l \end{array} \right] \) are the coefficients of the Taylor expansion of \( \mathbb{E}_t[K^\text{sl}_{n}(p)] = g_{\gamma}(p) \). They are zero for \( l > n \). We can write the moments in terms of cumulants

\[
\mu_l = \sum_{n>0} \left\{ \begin{array}{c} l \\ n \end{array} \right\} k_n.
\]  

(D7)

The rest of the calculation involves expanding \( K^\text{sl}_{n}(p) \) as a polynomial in \( p \) and performing the average to obtain equations in terms of the moments. We then expand the moments in terms of the cumulants \( k_n \). This gives us equations in terms of the coefficients \( \left[ \begin{array}{c} n \\ l \end{array} \right] \) and \( \left\{ \begin{array}{c} l \\ n \end{array} \right\} \). We can then use a series of identities for the coefficient to write the solution in the form of equation (D1).

**Identities for Coefficients**

There are six identities among the coefficients that we use extensively. The first two identities are recursion relations that can be derived from the generating function given in equation (D4)

\[
\left[ \begin{array}{c} n \\ l \end{array} \right] = l \left[ \begin{array}{c} n-1 \\ l \end{array} \right] - (l-1) \left[ \begin{array}{c} n-1 \\ l-1 \end{array} \right],
\]  

(D8)

\[
\left\{ \begin{array}{c} l \\ n \end{array} \right\} = \left\{ \begin{array}{c} l-1 \\ n \end{array} \right\} - \frac{1}{(l-1)} \left\{ \begin{array}{c} l-1 \\ n-1 \end{array} \right\}.
\]  

(D9)

Using the boundary conditions \( \left[ \begin{array}{c} n \\ 0 \end{array} \right] = \left\{ \begin{array}{c} k \\ 0 \end{array} \right\} = 0 \) and \( \left[ \begin{array}{c} 1 \\ 1 \end{array} \right] = \left\{ \begin{array}{c} 1 \\ 1 \end{array} \right\} = 1 \) we can generate all the coefficients. The next two identities express the fact that the two sets of coefficients allow us to
go from cumulants to moments and back to cumulants or from moments to cumulants and back to moments

\[ \sum_{l>0} \binom{n}{l} \binom{l}{m} = I[n = m], \]  
(D10)

\[ \sum_{n>0} \binom{k}{n} \binom{n}{l} = I[k = l]. \]  
(D11)

The final identities relate the coefficients \( \binom{l}{m} \) and \( \binom{n}{l} \) to binomial coefficients

\[ \sum_{l>0} \binom{n}{l+1} \binom{l}{m} = -\binom{n-1}{m-1} + I[n = m], \]  
(D12)

\[ \sum_{l>0} l \binom{n}{l} \binom{l}{m} = (-1)^{n+m} \binom{n}{m-1} + I[n = m-1]. \]  
(D13)

These two identities can be proved by induction using the recursion relations (D8) and (D9) together with the well known recursion relation for binomial coefficients. The coefficients used here are analogous to Stirling numbers in that they obey a second order recursion relation, although the recursion relations are different. Similar identities hold for Stirling numbers; these are developed in the book Concrete Mathematics (Graham, Knuth and Patashnik, 2nd Ed. 1995).

**Derivation of Equation (D1)**

We show explicitly how to obtain the terms in equation (D1) proportional to \( \alpha \) and \( \beta \), the remaining (diffusion) term follows similarly, although it requires a few more lines a algebraic manipulation. We start from equation (D3). The term proportional to \( \alpha \) is given by

\[ E_t \left[ \alpha p (1-p) \frac{\partial K_n(p)}{\partial p} \right] = E_t \left[ \alpha p (1-p) \sum_{l>0} \binom{n}{l} lp^{l-1} \right] \]

\[ = \alpha \sum_{l>0} \binom{n}{l} l (\mu_l - \mu_{l+1}) \]

\[ = \alpha \sum_{m>0} \sum_{l>0} \binom{n}{l} l \left( \binom{l}{m} - \binom{l+1}{m} \right) k_m \]

\[ = \alpha \sum_{m>0} \sum_{l>0} \left( l \binom{n}{l} + (l-1) \binom{n}{l-1} \right) \binom{l}{m} k_m \]
\[
\sum_{m>0} \sum_{l>0} \binom{n+1}{l} \binom{l}{m} k_m = \alpha k_{n+1}
\]

where we used equations (D6), (D7), (D8) and (D10) respectively in the derivation. The term proportional to \( \beta \) is give by

\[
\mathbb{E}_t \left[ \beta (1 - 2p) \frac{\partial K_n(p)}{\partial p} \right] = \mathbb{E}_t \left[ \beta \sum_{l>0} \binom{n}{l} l (p^{l-1} - 2p^l) \right]
\]

\[
= \beta \binom{n}{1} + \beta \sum_{l>0} \left( (l+1) \binom{n}{l+1} - 2l \binom{n}{l} \right) \mathbb{E}_t [p^l]
\]

\[
= \beta + \beta \sum_{l>0} \left( (l+1) \binom{n}{l+1} - l \binom{n}{l} - l \binom{n}{l} \right) \mu_l
\]

\[
= \beta + \beta \sum_{m>0} \sum_{l>0} \left( (l+1) \binom{n+1}{l+1} - l \binom{n}{l} \right) \binom{l}{m} k_m
\]

\[
= \beta + \beta \sum_{m>0} \left( - \binom{n}{m-1} - (-1)^{n+m} \binom{n}{m-1} \right) k_m
\]

\[
= \beta - 2\beta \sum_{m>0} \binom{n}{m-1} \left\lfloor n + m, \text{ even} \right\rfloor k_m
\]

where we used equations (D4), (D8), (D7), (D12) and (D13) respectively. The last term follows similarly. Putting these together we obtain equation (D11).

2. Dynamics of the Moments

Having developed the machinery to go from cumulants to moments we can now easily obtain a recursion relation for the moments. Although cumulant expansions typically have much better convergence properties than moment expansions (and are therefore more useful in obtaining approximate solutions), for this problem the dynamics for the moments turns out to have a simpler form than that for the cumulants. This allows us to rederive the diffusion equation for the allele frequencies.

Using equation (D6) we can write equation (D3) in terms of moments

\[
\sum_{l>0} \binom{n}{l} \frac{d\mu_l}{dt} = \sum_{l>0} \binom{n}{l} l \left( \alpha (\mu_l - \mu_{l+1}) + \beta (\mu_{l-1} - 2\mu_l) + \frac{(l-1)}{2} (\mu_{l-1} - \mu_l) \right).
\]
We can obtain a differential equation for the moments by multiplying both sides of equation (D14) by \( \binom{k+1}{n} \) and summing over \( n \). Using the identity (D11) we find

\[
\frac{d\mu_{k+1}}{dt} = (k + 1) \left( \alpha (\mu_{k+1} - \mu_{k+2}) + \beta (\mu_{k} - 2\mu_{k+1}) + \frac{k}{2} (\mu_{k} - \mu_{k+1}) \right). \tag{D15}
\]

Rearranging gives equation (D2).

Equation (D2) is a linear transformation of the differential equation (D1) for the cumulants. To see this more directly we can consider the coefficients \( U_{l,n} = \binom{l}{n} \) as elements of a lower-triangular matrix \( U \). The coefficients \( \binom{n}{l} \) are the elements of the matrix \( U^{-1} \). We can write equation (D2) as a matrix equation analogous to equation (12)

\[
\frac{d\mu}{dt} = U \frac{dk}{dt} = -\bar{M} \mu + \bar{d} \tag{D16}
\]

where \( \bar{M} = UMU^{-1} \) and \( \bar{d} = Ud \) with \( d_k = \beta I[k = 1] \). The matrix \( \bar{M} \) is tridiagonal.

**Obtaining the Diffusion Equation**

Using equation (D2), we can obtain the diffusion equation for allele frequencies. We first obtain a partial differential equation for the characteristic function

\[
\tilde{\phi}(z, t) = 1 + \sum_{k>0} \frac{\mu_k (iz)^k}{k!} = \int e^{izp} \phi(p, t) \, dp. \tag{D17}
\]

To do this, we multiplying equation (D2) by \((iz)^{k+1}/k!\) and sum over \( k \), giving

\[
\frac{\partial \tilde{\phi}}{\partial t} = -iz \left( -\left( \alpha + \frac{iz}{2} \right) \frac{\partial^2 \tilde{\phi}}{\partial z^2} + i \left( 2\beta - \alpha - \frac{iz}{2} \right) \frac{\partial \tilde{\phi}}{\partial z} - \beta \tilde{\phi} \right). \tag{D18}
\]

Taking the inverse Fourier transform we obtain the diffusion equation for the single-locus allele frequencies

\[
\frac{\partial \phi}{\partial t} = \frac{\partial}{\partial p} \left( \frac{p (1-p) \partial \phi}{2} - \left( \alpha p (1-p) + \left( \beta - \frac{1}{2} \right) (1-2p) \right) \phi \right). \tag{D19}
\]

This can be re-written in the form of equation (4). Setting the right-hand side of this equation to zero we easily obtain the fixed point solution \( \phi(p, \infty) \), which was first found by Wright (1937).

Since the diffusion equation was derived directly from the moment equations (D2), the fixed points will have the same moments, and as equations (D2) are just a linear transformation of cumulant equations (D1), the fixed point will have the same cumulants.
We can obtain eigenvalue equations from the diffusion equation by looking for solutions of the form \( \phi(p, t) = \phi(p, \infty) + \rho(t) \psi(p) \). This reduces the problem to solving a eigenvalue differential equation, subject to boundary conditions. However, these equations are, in general, difficult to solve as they require solving a boundary value problem, often with complicated boundary conditions.

The similarity between diffusion equation problem and quantum mechanics has often been observed. Here we note another connection. Moving between a matrix equation and diffusion equation parallels the connection between Heisenberg’s matrix formulation of quantum mechanics and Schrödinger’s differential equation.
FIG. 1 The first two cumulants are shown from a single realisation of the evolutionary dynamics for populations with differing numbers of loci: $L = 32$ (left) and $L = 3200$ (right). Both populations evolve under multiplicative selection, reversible mutation and free recombination, with $N = 500$, $\alpha = 5$ and $\beta = 0.01$ ($\alpha \equiv Ns$ and $\beta \equiv Nu$).

FIG. 2 Fixed point cumulant results from the truncated cumulant equations ($k_n^*$) are compared to cumulants derived from Wright’s distribution ($\tilde{k}_n$) as the truncation order is increased. The top figures show the difference between the first and second cumulant results for $\beta = 1$, using a logarithmic scale. The bottom figures show the first cumulant results for lower mutation rates, $\beta = 0.1$ and $\beta = 10^{-3}$. The symbols denote different selection intensities, with $\alpha = 1(\circ)$, $2(\triangle)$, $5(\circ)$ and $10(\times)$.

FIG. 3 The averaged dynamics are shown for the first two cumulants with $\alpha = 1(\circ)$, $5(\triangle)$ and $10(\times)$. The eight cumulant theory is shown by the solid lines. The results were averaged over 500 iterations of the evolutionary dynamics with free recombination, $N = 200$ and $\beta = 0.01$. In each case the population was initialised with all alleles set to zero.
FIG. 4 Approximate results for the two lowest eigenvalues given by the perturbation theory are compared to results from the 16 cumulant truncated system (solid lines). The 2nd order (dot-dashed) and 6th order (dashed) perturbation theory results are shown for various $\alpha$, for $\beta = 0.1$ (left) and $\beta = 0.01$ (right).

FIG. 5 The average rate of change in the mean is shown as a function of the mean for $\alpha = 1$ (left) and $\alpha = 10$ (right). The symbols show results averaged over up to 1000 iterations of the evolutionary dynamics, with $\beta = 1(o)$, $0.1(\times)$ and $0.01(\triangle)$. The solid line shows the eight cumulant adiabatic elimination result for small $\beta$ (see Eqs. 16 and 17). Populations were either initialised with alleles all set to zero, giving a positive rate of change, or were initialised with alleles all set to one, giving a negative rate of change. The populations were then given enough time to converge close to the fixed point. For $\alpha = 1$ we chose $L = 960$ and $N = 100$ and for $\alpha = 10$ we chose $L = 96$ and $N = 200$. In each case the populations were subject to free recombination.
Fig. 1
\[ \beta = 1 \]

\[ |k_1^* - \tilde{k}_1| \]

No. of cumulants

\[ \beta = 0.1 \]

\[ |k_1^* - \tilde{k}_1| \]

No. of cumulants

\[ \beta = 10^{-3} \]

\[ |k_1^* - \tilde{k}_1| \]

No. of cumulants

Fig. 2
Fig. 3
\[ \beta = 0.1 \]

\[ \lambda_1 \]

\[ \alpha \]

\[ \lambda_2 \]

\[ \alpha \]

\[ \beta = 0.01 \]

\[ \lambda_1 \]

\[ \alpha \]

\[ \lambda_2 \]

\[ \alpha \]

Fig. 4
\[ \frac{1}{\beta} \frac{d k_1}{d t} \]

\[ \alpha = 1 \]

\[ \alpha = 10 \]

Fig. 5