

Appendix D

Formulas for the quantitative variables

D.1 DIRECTIONAL SELECTION

The main goal, from the technical side, is to have explicit formulas for the expectations of the macroscopic variables, in order to be able to make predictions of the course of evolution. That is, to put the statistical mechanical method ‘at work’. The formulas for polygenic traits are closely related to those of a single locus, which I will give in the following pages. The polygenic versions will be given in the following sub-section.

Remarks about the notation. The ‘per locus’ formulas will be always denoted with the subscript ℓ . The formulas can be represented by either regularized confluent hypergeometrics ${}_0F_1(;\cdot)$, or modified Bessel functions of fractional order $\mathcal{I}_\nu(\cdot)$. Although entirely equivalent, for some of the formulas I will provide both expressions. It is just a matter of taste which one to use. In general I am using variables scaled by population size, so mutation rate and selective values will be expressed as $N\mu$ and $N\beta$. Although simplifications with respect to N is often possible, I will leave all expressions in terms of the scaled variables. The reason is that the scaling *always* appears, and population size N rarely appears on its own.

The formulas here defined, as well as the evolutionary dynamics are implemented in Mathematica 6.0 packages, that are available upon request.

D.1.1 Statistics for traits with a single locus

Distribution of allele frequencies and the partition function

- The maxentropic distribution is

$$\psi = \frac{\phi}{Z} \exp[2N\beta\bar{z} + 2N\mu U] \quad (\text{D.1})$$

where the base density is

$$\phi = 1/p(1-p) \quad (\text{D.2})$$

- The partition function is

$$\begin{aligned} \mathbb{Z}_{\ell(N\mu, N\beta)} &= \mathcal{I}_{4N\mu + \frac{1}{2}}(2N\beta) \\ &= 2^{1-8N\mu} \Gamma(4N\mu) {}_0F_1\left(4N\mu + \frac{1}{2}; (N\beta)^2\right) \end{aligned} \quad (\text{D.3})$$

which is also the generating function for the macroscopics defined below.

- *Low mutation rates limit* ($4N\mu < 1$). The distribution has only two peaks at $\psi(0)$ and $\psi(1)$, and the partition function is

$$\mathbb{Z}_{\ell(N\beta)} = \cosh(2N\beta) . \quad (\text{D.4})$$

Genetic mutation variability

- Definition

$$U = 2 \log[p(1-p)] \quad (\text{D.5})$$

- Expectancy

$$\begin{aligned} \langle U \rangle_{\ell(N\mu, N\beta)} &= \frac{\partial \log(\mathbb{Z}_{\ell(N\mu, N\beta)})}{2N\partial\mu} \\ &= 2\Psi(4N\mu) - \log(16) + 2 \frac{{}_0F_1^{(1,0)}(4N\mu + \frac{1}{2}; (N\beta)^2)}{{}_0F_1(4N\mu + \frac{1}{2}; (N\beta)^2)} \end{aligned} \quad (\text{D.6})$$

where Ψ is the digamma function. The equation is to be computed numerically, or approximated at small β , for which it simplifies as

$$\langle U \rangle \simeq \Psi(8N\mu) - \log(16) + \left(\frac{\beta}{4N\mu + 1/2} \right)^2 .$$

- *Low mutation rates limit* ($4N\mu < 1$). This macroscopic does not need to be defined for low mutation rates to couple the distribution of the micro and macroscopic variables.

- Variance

$$\text{var}(U)_{\ell(N\mu, N\beta)} = \frac{\partial^2 \log(\mathbb{Z}_{\ell(N\mu, N\beta)})}{(2N)^2 \partial \mu^2} = \frac{\partial \langle U \rangle}{2N \partial \mu} \quad (\text{D.7})$$

$$\begin{aligned} &= 4\Psi'(4N\mu) - 4 \frac{{}_0F_1^{(2,0)}(4N\mu + 1/2; (N\beta)^2)}{{}_0F_1(4N\mu + 1/2; (N\beta)^2)} \\ &\quad + 4 \left[\frac{{}_0F_1^{(1,0)}(N\mu + 1/2; (N\beta)^2)}{{}_0F_1(4N\mu + 1/2; (N\beta)^2)} \right]^2 \end{aligned} \quad (\text{D.8})$$

‘Genetic variance’ of genetic variability This quantity is defined by the rate of change of U (Eq. 3.22), in analogy to the rate of change of the mean trait, that is proportional to genetic variance:

- Definition

$$H = 2(p(1-p))^{-1} - 4 \quad (\text{D.9})$$

- Expectancy

$$\langle H \rangle_{\ell(N\mu, N\beta)} = -8 + 2 \frac{\mathbb{Z}_{\ell(N\mu-1/4, N\beta)}}{\mathbb{Z}_{\ell(N\mu, N\beta)}} \quad (\text{D.10})$$

$$\begin{aligned} &= -4 + \frac{1}{4N\mu - 1/4} \frac{{}_0F_1(4N\mu - 1/2; (N\beta)^2)}{{}_0F_1(4N\mu + 1/2; (N\beta)^2)} \\ &= 4 \frac{N\mu + 1/4}{N\mu - 1/4} + \frac{N\beta \langle \bar{z} \rangle_{\ell(N\mu, N\beta)}}{(N\mu - 1/2)(N\mu + 1/2)} \end{aligned} \quad (\text{D.11})$$

— *Low mutation rates limit* ($4N\mu < 1$). As $4N\mu \downarrow 1$, $\langle U \rangle \uparrow \infty$. This macroscopic however does not need to be defined for low mutation rates to couple the dynamics of the micro and macroscopic variables.

Mean Trait

- Definition

$$\bar{z} = 2(p-1) \quad (\text{D.12})$$

- Expectancy

$$\begin{aligned}
 \langle \bar{z} \rangle_{\ell(N\mu, N\beta)} &= \frac{\partial \log(\mathbb{Z}_{\ell(N\mu, N\beta)})}{2N\partial\beta} & (D.13) \\
 &= \frac{\mathcal{I}_{4N\mu + \frac{1}{2}}(2N\beta)}{\mathcal{I}_{4N\mu - \frac{1}{2}}(2N\beta)} \\
 &= N\beta \frac{{}_0F_1(4N\mu + \frac{3}{2}; (N\beta)^2)}{{}_0F_1(4N\mu + \frac{1}{2}; (N\beta)^2)}
 \end{aligned}$$

— *Low mutation rates limit* ($4N\mu < 1$).

$$\langle \bar{z} \rangle_{\ell(N\beta)} = \tanh(2N\beta) \quad (D.14)$$

- Variance

$$\begin{aligned}
 \text{var}(\bar{z})_{\ell(N\mu, N\beta)} &= \frac{\partial^2 \log(\mathbb{Z}_{\ell(N\mu, N\beta)})}{(2N)^2 \partial\beta^2} = \frac{\partial \langle \bar{z} \rangle}{2N\partial\beta} & (D.15) \\
 &= 1 - \frac{\mathcal{I}_{4N\mu + 1/2}(2N\beta)}{\mathcal{I}_{4N\mu - 1/2}(2N\beta)} \left(\frac{4N\mu}{2N\beta} + \frac{\mathcal{I}_{4N\mu + 1/2}(2N\beta)}{\mathcal{I}_{4N\mu - 1/2}(2N\beta)} \right) \\
 &= 1 - \langle \bar{z} \rangle \left(\frac{4N\mu}{2N\beta} + \langle \bar{z} \rangle \right) & (D.16)
 \end{aligned}$$

— *Low mutation rates limit* ($4N\mu < 1$).

$$\text{var}(\bar{z})_{\ell(N\beta)} = \text{sech}^2(2N\beta) \quad (D.17)$$

Genetic variance

- Definition

$$\nu = 2p(1 - p) \quad (D.18)$$

- Expectancy

$$\langle \nu \rangle_{\ell(N\mu, N\beta)} = 2 \frac{\mathbb{Z}_{\ell(N\mu + 1/4, N\beta)}}{\mathbb{Z}_{\ell(N\mu, N\beta)}} \quad (D.19)$$

$$\begin{aligned}
 &= 2N\mu \frac{{}_0F_1(4N\mu + \frac{3}{2}; (N\beta)^2)}{{}_0F_1(4N\mu + \frac{1}{2}; (N\beta)^2)} \\
 &= \frac{2N\mu}{N\beta} \langle \bar{z} \rangle_{\ell(N\mu, N\beta)} & (D.20)
 \end{aligned}$$

— Low mutation rates limit ($4N\mu < 1$).

$$\langle \nu \rangle_{\ell(N\mu, N\beta)} = \frac{2N\mu}{N\beta} \tanh(2N\beta) \quad (\text{D.21})$$

Covariance between meant trait and genetic variability

$$\begin{aligned} \text{cov}(\bar{z}, U)_{\ell(N\mu, N\beta)} &= \frac{\partial^2 \log(\mathcal{Z}_{\ell(N\mu, N\beta)})}{(2N)^2 \partial\beta \partial\mu} \\ &= \frac{\partial \langle \bar{z} \rangle}{2N \partial\mu} = \frac{\partial \langle U \rangle}{2N \partial\beta} = \text{cov}(U, \bar{z}) \\ &= 2 \left[\frac{\mathcal{I}_{4N\mu+1/2}^{(1,0)}(2N\beta)}{\mathcal{I}_{4N\mu-1/2}(2N\beta)} - \frac{\mathcal{I}_{4N\mu+1/2}(2N\beta) \mathcal{I}_{4N\mu-1/2}^{(1,0)}(2N\beta)}{(\mathcal{I}_{4N\mu-1/2}(2N\beta))^2} \right] \end{aligned} \quad (\text{D.22})$$

D.1.2 Statistics for multivariate traits with unequal (and pleiotropic) effects

The statistics for the moments of a vector of mean traits $\langle \bar{z} \rangle$ results as an extension of the per-locus functions. I will give only the multivariate expressions, since the uni-variate traits are a special case. For the latter, some properties (similar as in the one-locus case) hold, which I will highlight.

Remarks about the notation. The ‘per locus’ sub-index will be used here also as an iterator (index for the summations and products). Hence, whenever a quantity has a subindex, it refers to the ‘per locus’ quantity evaluated at the effects of a given locus. These effects of each locus ℓ over every trait k are summarized in a matrix Υ ; each column of this matrix, $\vec{\gamma}_\ell$ contains the effects of one locus ℓ over each of the m traits; the effect of a locus ℓ over a trait k is then $\gamma_{k\ell}$, which for the univariate case will simply be written as γ_ℓ .

$$\Upsilon = \left(\begin{array}{ccc|ccc} \vdash \text{loci} \longrightarrow & & & \vec{\gamma}_\ell & & \\ \gamma_{11} & \gamma_{12} & \cdots & \begin{bmatrix} \gamma_{1\ell} \\ \gamma_{2\ell} \\ \vdots \\ \gamma_{m\ell} \end{bmatrix} & \cdots & \begin{bmatrix} \gamma_{1n} \\ \gamma_{2n} \\ \vdots \\ \gamma_{mn} \end{bmatrix} \\ \gamma_{21} & \gamma_{22} & \cdots & \vdots & \ddots & \vdots \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ \gamma_{m1} & \gamma_{m2} & \cdots & \vdots & \cdots & \vdots \end{array} \right) \begin{array}{l} \Upsilon \\ \text{traits} \\ \downarrow \end{array}$$

Similarly, each row of Υ represent the vector of effects of all loci over each of the traits.

The symbol \otimes represents the Kronecker (tensor, dyadic, or external) product, and will appear when using matrix notation.

Partition function

- Partition function

$$\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)} = \prod_{\ell=1}^n \mathbb{Z}_{\ell(N\mu, N\vec{\gamma}_\ell \cdot \vec{\beta})} \quad (\text{D.23})$$

— *Low mutation rates limit* ($4N\mu < 1$).

$$\mathbb{Z}_{(N\vec{\beta}|\Upsilon)} = \prod_{\ell=1}^n \cosh[2N\vec{\gamma}_\ell \cdot \vec{\beta}] \quad (\text{D.24})$$

Genetic mutation variability

- Definition

$$U = 2 \sum_{\ell=1}^n \log[p_\ell(1 - p_\ell)] \quad (\text{D.25})$$

- Expectancy

$$\begin{aligned} \langle U \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} &= \frac{\partial \log(\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)})}{2N\partial\mu} \quad (\text{D.26}) \\ &= 2 \sum_{\ell=1}^n \langle U \rangle_{\ell(N\mu, N\vec{\gamma}_\ell \cdot \vec{\beta})} \end{aligned}$$

- Variance

$$\text{var}(U)_{(N\mu, N\vec{\beta}|\Upsilon)} = \frac{\partial^2 \log(\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)})}{(2N)^2 \partial\mu^2} \quad (\text{D.27})$$

$$\begin{aligned} &= \frac{\partial \langle U \rangle}{2N\partial\mu} \\ &= \sum_{\ell=1}^n \text{var}(U)_{\ell(N\mu, N\vec{\gamma}_\ell \cdot \vec{\beta})} \quad (\text{D.28}) \end{aligned}$$

'Genetic variance' of genetic variability

- Definition

$$H = \sum_{\ell=1}^n 2[p_\ell(1-p_\ell)]^{-1} - 4 \quad (\text{D.29})$$

- Expectancy

$$\begin{aligned} \langle H \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} &= 2 \frac{\mathbb{Z}_{(N\mu-1/4, N\vec{\beta}|\Upsilon)}}{\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)}} - 4n \quad (\text{D.30}) \\ &= -4n + 2(N\mu - 1/4)^{-1} \sum_{\ell=1}^n \frac{{}_0F_1\left(4N\mu - 1/2; (N\vec{\gamma}_\ell \cdot \vec{\beta})^2\right)}{{}_0F_1\left(4N\mu + 1/2; (N\vec{\gamma}_\ell \cdot \vec{\beta})^2\right)} \\ &= 4n \frac{N\mu + 1/4}{N\mu - 1/4} + \frac{N\vec{\beta} \cdot \langle \vec{z} \rangle_{(N\mu, N\vec{\beta}|\Upsilon)}}{(N\mu - 1/2)(N\mu + 1/2)} \quad (\text{D.31}) \end{aligned}$$

Mean traits

- Definition

$$\vec{z} = \sum_{\ell=1}^n \vec{\gamma}_\ell (2p_\ell - 1) \quad (\text{D.32})$$

- Expectancies

$$\langle \vec{z} \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} = \frac{\partial \log(\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)})}{2N \partial \vec{\beta}} \quad (\text{D.33})$$

$$\begin{aligned} &= \sum_{\ell=1}^n \vec{\gamma}_\ell \frac{\mathcal{I}_{4N\mu+1/2}\left(2N\vec{\gamma}_\ell \cdot \vec{\beta}\right)}{\mathcal{I}_{4N\mu-1/2}\left(2N\vec{\gamma}_\ell \cdot \vec{\beta}\right)} \\ &= \sum_{\ell=1}^n \vec{\gamma}_\ell \langle \vec{z} \rangle_{\ell(N\mu, N\vec{\gamma}_\ell \cdot \vec{\beta})} \quad (\text{D.34}) \end{aligned}$$

— *Low mutation rates limit* ($4N\mu < 1$).

$$\langle \vec{z} \rangle_{(N\vec{\beta}|\Upsilon)} = \sum_{\ell=1}^n \vec{\gamma}_\ell \tanh[2N\vec{\gamma}_\ell \cdot \vec{\beta}] \quad (\text{D.35})$$

- Covariances of the mean traits.

$$\text{covar}(\bar{z}_j, \bar{z}_k)_{(N\mu, N\bar{\beta}|\Upsilon)} = \frac{\partial \log(\mathbb{Z}_{(N\mu, N\bar{\beta}|\Upsilon)})}{(2N)^2 \partial \beta_j \partial \beta_k} \quad (\text{D.36})$$

$$\begin{aligned} &= \frac{\partial \langle \bar{z}_j \rangle}{2N \partial \beta_k} = \frac{\partial \langle \bar{z}_k \rangle}{2N \partial \beta_j} \\ &= 2(\nu_{jk}^{\max} - \langle \nu_{jk} \rangle) - \sum_{\ell=1}^n \gamma_{j\ell} \gamma_{k\ell} \langle \bar{z} \rangle_{\ell(N\mu, N\bar{\gamma}_\ell \cdot \bar{\beta})}^2 \end{aligned} \quad (\text{D.37})$$

where

$$\nu_{jk}^{\max} = \frac{1}{2} \sum_{\ell=1}^n \gamma_{j\ell} \gamma_{k\ell} \quad (\text{D.38})$$

are the maximal genetic variances.

- Variances of the mean traits. The variance of a trait follows directly for $j = k$ in Eq. D.36. For univariate traits of equal effects

$$\text{var}(\bar{z}) = \nu^{\max} - \frac{2N\mu}{N\bar{\beta}} \langle \bar{z} \rangle - \langle \bar{z} \rangle^2. \quad (\text{D.39})$$

We can express the covariances in matrix form, as it is needed for the dynamics; $\mathcal{C} = \{\text{covar}(\bar{z}_j, \bar{z}_k)\}_{j,k=1}^m$ which results in:

$$\mathcal{C} = 2(\mathcal{G}^{\max} - \mathcal{G}) - \sum_{\ell=1}^n \bar{\gamma}_\ell \otimes \bar{\gamma}_\ell \langle \bar{z} \rangle_{\ell(N\mu, N\bar{\gamma}_\ell \cdot \bar{\beta})}^2, \quad (\text{D.40})$$

where the relation between the \mathcal{G} -matrix and the variance across phenotypes is revealed.

— *Low mutation rates limit* ($4N\mu < 1$).

$$\mathcal{C}_{(N\bar{\beta}|\Upsilon)} = \sum_{\ell=1}^n \bar{\gamma}_\ell \otimes \bar{\gamma}_\ell \text{sech}^2[2N\bar{\gamma}_\ell \cdot \bar{\beta}] \quad (\text{D.41})$$

Genetic variances, covariances, and the \mathcal{G} -matrix

- Definition

$$\nu_{jk} = 2 \sum_{\ell=1}^n \gamma_{j\ell} \gamma_{k\ell} p_\ell (1 - p_\ell) \quad (\text{D.42})$$

- Expectancies of the covariances

$$\langle \nu_{jk} \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} = 2 \frac{\mathbb{Z}_{(N\mu+1/4, N\vec{\beta}|\Upsilon)}}{\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)}} \quad (\text{D.43})$$

$$= 2N\mu \sum_{\ell=1}^n \frac{\gamma_{j\ell} \gamma_{k\ell}}{2N\vec{\gamma}_{\ell} \cdot \vec{\beta}} \langle \bar{z} \rangle_{\ell(N\mu, N\vec{\gamma}_{\ell} \cdot \vec{\beta})} \quad (\text{D.44})$$

- Expectancies of the genetic variances. These are defined by

$$\langle \nu_k \rangle \equiv \langle \nu_{kk} \rangle. \quad (\text{D.45})$$

In the case of univariate traits, setting ($m = 1$), comparing Eqns. D.32 and D.42 it holds true that

$$\langle \nu \rangle = \frac{2N\mu}{N\beta} \langle \bar{z} \rangle, \quad (\text{D.46})$$

for arbitrary number of loci and effects.

- Definition of the \mathcal{G} -matrix. Expressed in matrix form, the covariances are

$$\mathcal{G} = \{\nu_{jk}\}_{j,k=1}^m = \begin{pmatrix} \nu_{11} & \nu_{12} & \cdots & \nu_{1m} \\ \nu_{21} & \nu_{22} & \cdots & \nu_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ \nu_{m1} & \nu_{m2} & \cdots & \nu_{mm} \end{pmatrix} \quad (\text{D.47})$$

- Expectancies

$$\langle \mathcal{G} \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} = \left\langle \begin{pmatrix} \nu_{11} & \nu_{12} & \cdots & \nu_{1m} \\ \nu_{21} & \nu_{22} & \cdots & \nu_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ \nu_{m1} & \nu_{m2} & \cdots & \nu_{mm} \end{pmatrix} \right\rangle \quad (\text{D.48})$$

$$= 2N\mu \sum_{\ell=1}^n \vec{\gamma}_{\ell} \otimes \vec{\gamma}_{\ell} \frac{\langle \bar{z} \rangle_{\ell(N\mu, N\vec{\gamma}_{\ell} \cdot \vec{\beta})}}{2N\vec{\gamma}_{\ell} \cdot \vec{\beta}} \quad (\text{D.49})$$

— *Low mutation rates limit* ($4N\mu < 1$).

$$\langle \mathcal{G} \rangle_{(N\mu, N\vec{\beta}|\Upsilon)} = 2N\mu \sum_{\ell=1}^n \frac{\vec{\gamma}_{\ell} \otimes \vec{\gamma}_{\ell}}{2N\vec{\gamma}_{\ell} \cdot \vec{\beta}} \tanh[2N\vec{\gamma}_{\ell} \cdot \vec{\beta}] \quad (\text{D.50})$$

- Variance of the genetic co-variances

$$\text{var}(\nu_{jk}) = 4 \sum_{\ell=1}^n \tilde{\gamma}_{\ell}^2 \otimes \tilde{\gamma}_{\ell}^2 \frac{\mathbb{Z}_{(N\mu+1/2, 2N\tilde{\gamma}_{\ell}\cdot\vec{\beta})}}{\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)}} \quad (\text{D.51})$$

Covariance between meant trait and genetic variability

$$\text{covar}(\vec{z}, U)_{(N\mu, N\vec{\beta}|\Upsilon)} = \frac{\partial^2 \log(\mathbb{Z}_{(N\mu, N\vec{\beta}|\Upsilon)})}{(2N)^2 \partial \vec{\beta} \partial \mu} \quad (\text{D.52})$$

$$= \frac{\partial \langle U \rangle}{2N \partial \vec{\beta}} = \frac{\partial \langle \vec{z} \rangle}{2N \partial \mu} \quad (\text{D.53})$$

$$= \sum_{\ell=1}^n \tilde{\gamma}_{\ell} \text{covar}(\vec{z}, U)_{\ell(N\mu, N\tilde{\gamma}_{\ell}\cdot\vec{\beta})} \cdot \quad (\text{D.54})$$

Notice that this is a vector of the covariances between each mean trait and U .

D.2 STABILIZING SELECTION

Similar to the case of directional selection, in linkage equilibrium the statistics for polygenic characters depend on those of single loci, so I will first review these, and in the following subsection, the polygenic formulas.

Remarks about the notation. For clarity in reading the formulas I will use the following convention. The single locus formula will always be denoted by the symbol $\langle \dots \rangle_\ell$; the subscript ℓ is used to indicate single locus statistic. In the polygenic formulas this subscript will also be used as an iterator across the loci. Furthermore, the statistics for single locus are function of three parameters, that is the vector $(N\mu, N\beta, N\sigma)$. Also for notational simplicity this vector will be omitted, bearing in mind that single locus statistics require these three variables. The statistics for polygenic systems will not have any subscript. These statistics depend on the vector $(N\mu, N\beta, N\sigma, N\alpha)$ which will also be left implicit. However, some formulas (one and multiple loci) sometimes require evaluation of the parameters at different values. In those cases I will express this dependence explicitly. For example if I were to evaluate a given statistic X at a mutation rate $N\mu + 1$ (as it will be necessary to point out some properties and simplifications on the implementations) and at a selective gradient of $\beta\gamma$ I'd write $\langle X \rangle_{(N\mu=N\mu+1, N\beta=N\beta\gamma)}$, where the rest of the parameters are left untouched (in this case, $N\sigma$ and $N\alpha$).

D.2.1 Statistics for traits with a single locus

The distribution of allele frequencies and the partition function

- Distribution of allele frequencies

$$\begin{aligned} \psi_{\ell(p; N\mu, N\beta, N\sigma)} &:= \psi_\ell & \text{(D.55)} \\ &= \frac{\phi}{\mathcal{Z}_\ell} \exp [2N\beta(2p - 1) + 4N\sigma p(1 - p) + 4N\mu \log(p(1 - p))] . \end{aligned}$$

- Partition function. The partition function for the statistics of single locus characters under SSMD, unfortunately cannot be analytically integrated to give a closed solution. Yet properties and

relations exist that simplify calculations and give understanding of the dynamics.

$$\begin{aligned} \mathbb{Z}_\ell(N\mu, N\beta, N\sigma) &:= \mathbb{Z}_\ell & (D.56) \\ &= \int_0^1 dp [p(1-p)]^{-1} \times \\ &\times \exp [2N\beta(2p-1) + 4N\sigma p(1-p) + 4N\mu \log[p(1-p)]] . \end{aligned}$$

— *Approximation in series.* For practical purposes, it is sometimes useful to represent the partition function as a series, expanding over σ , which yields the following expression:

$$\begin{aligned} \mathbb{Z}_\ell &\simeq \sqrt{\pi} 2^{1-8N\mu} \times & (D.57) \\ &\times \sum_{i=0}^{\infty} \Gamma(4N\mu + i) {}_0F_1 \left(4N\mu + \frac{1}{2} + i; (N\beta)^2 \right) \frac{(16N\sigma)^i}{i!} \end{aligned}$$

The series is convergent, and numerically can be computed using Aitken’s method (Abramowitz and Stegun, 1972, Sect. 3.9.5, p. 18), since the Hypergeometric function decreases exponentially fast with the expansion index i . However, for weak $N\beta$ between 8 and 10 terms would be enough for a precision of $\sim 10^{-5}$. For strong $N\beta$ between 15 and 20 terms would give that precision. The calculations using the series are usually faster than the numerical or Monte Carlo integration.

Genetic mutation variability

- Definition. As in Eq. D.5.
- Expectancy

$$\begin{aligned} \langle U \rangle_\ell &= \frac{\partial \log(\mathbb{Z}_\ell)}{2N\partial\mu} & (D.58) \\ &= \int_0^1 U \psi_\ell dp \end{aligned}$$

- Variance.
- Variance. Calculated from the definition (see Eq. D.60 below)

$$\text{var}(U) = \langle U^2 \rangle - \langle U \rangle^2 . \quad (D.59)$$

Square genetic mutation variability

- Expectancy

$$\langle U^2 \rangle_\ell = \int_0^1 U^2 \psi_\ell dp \quad (\text{D.60})$$

'Genetic variance' of mutational variability

- Definition. As in Eq. D.9.
- Expectancy

$$\langle H \rangle_\ell = -4 + 2 \frac{\mathbb{Z}_\ell(N\mu=N\mu-1/4)}{\mathbb{Z}_\ell} \quad (\text{D.61})$$

Mean trait

- Definition. As in Eq. D.12
- Expectancy

$$\begin{aligned} \langle \bar{z} \rangle_\ell &= \frac{\partial \log(\mathbb{Z}_\ell)}{2N\partial\beta} \\ &= \int_0^1 \bar{z} \psi_\ell dp \end{aligned} \quad (\text{D.62})$$

- Variance. Calculated from the definition (see Eq. D.65 below)

$$\text{var}(\bar{z}) = \langle \bar{z}^2 \rangle - \langle \bar{z} \rangle^2 . \quad (\text{D.63})$$

Squared mean trait

- Definition

$$\begin{aligned} \bar{z}^2 &= (2p - 1)^2 \\ &= 1 - 2\nu \end{aligned} \quad (\text{D.64})$$

- Expectancy

$$\langle \bar{z}^2 \rangle_\ell = 1 - 2\langle \nu \rangle_\ell \quad (\text{D.65})$$

Genetic variance

- Definition. As in Eq. D.18.
- Expectancy

$$\langle \nu \rangle_\ell = 2 \frac{\mathbb{Z}_{\ell(N\mu=N\mu+1/4)}}{\mathbb{Z}_\ell} \quad (\text{D.66})$$

Third moment of allele frequencies

- Definition

$$m_{3z} \equiv \bar{z}\nu 2(2p-1)(1-p)p \quad (\text{D.67})$$

- Expectancy

$$\begin{aligned} \langle m_{3z} \rangle &\equiv \langle \bar{z}\nu \rangle_\ell = \langle \bar{z} \rangle_{\ell(N\mu=N\mu+1/4)} \langle \nu \rangle_\ell \\ &= \frac{N\beta}{N\sigma} \langle \nu \rangle_\ell - \frac{2N\mu}{N\sigma} \langle \bar{z} \rangle_\ell \end{aligned} \quad (\text{D.68})$$

Fourth moment of allele frequencies

- Definition

$$m_{4z} \equiv \bar{z}^2\nu = 2(2p-1)^2(1-p)p \quad (\text{D.69})$$

- Expectancy

$$\langle m_{4z} \rangle \equiv \langle \bar{z}^2\nu \rangle_\ell = \langle \bar{z}^2 \rangle_{\ell(N\mu=N\mu+1/4)} \langle \nu \rangle_\ell \quad (\text{D.70})$$

$$= \left(\frac{(N\beta)^2}{N\sigma} + 4N\mu \right) \langle \nu \rangle_\ell - \frac{2N\mu N\beta}{N\sigma} \langle \bar{z} \rangle_\ell - 2N\mu \quad (\text{D.71})$$

D.2.2 Statistics for polygenic traits with unequal effects

The computation of multi-locus statistics requires some tricks. There are several options. The first, is to compute the multidimensional integrals using Monte Carlo sampling. This is the least desirable, specially when the distribution of allele frequencies has most of the density near the borders (e.g. under disruptive selection, when we select for genetic variance, and/or at low mutation rates).

However, a neat approach is to transform the integrals from the variables $p \rightarrow r = p(1 - p)$. Then they are much better behaved to deal numerically (the peaks near the borders are not so steep, and the density is spread across the interval $r \in (0, 1/4)$). Then this integral can be partitioned to sum around the borders $p = \{0, 1\}$, and adding the results of the 2^N corners.

Another option, the one taken for now to achieve some level of analytic results, is to integrate the space of n variables ($\vec{p} = \{p_\ell\}_{\ell=1}^n$) constraining that they conform to a given value of the mean trait, and then integrate in the space of traits. In Section 7.2 I already showed how this method goes. I will focus now in the ways to compute the expectancies out of it.

Remarks about the notation. In this section I will use the following notation. Quantities $\langle A \rangle_{\gamma_\ell}$ are per-locus statistics, as above, but evaluated with scaled the scaled arguments $N\beta \rightarrow \gamma_\ell N\beta$ and $N\sigma \rightarrow \gamma_\ell^2 N\sigma$. That is

$$\langle A \rangle_{\gamma_\ell} = \langle A \rangle_{\ell(N\mu, \gamma_\ell N\beta, \gamma_\ell^2 N\sigma)} .$$

Partition function

$$\mathbb{Z} = \sqrt{\frac{\pi}{|2N\alpha|}} \int_{-\infty}^{\infty} \exp \left[-\frac{(2N\beta - i\omega)^2}{8N\alpha} \right] \prod_{\ell=1}^n \mathbb{Z}_\ell (N\beta = -\frac{i\omega}{2N} \gamma_\ell) d\omega \quad (\text{D.72})$$

(This is the same as Eq. 7.10). If we call

$$\mathbb{Z}_{\text{Ep}} = \sqrt{\frac{\pi}{|2N\alpha|}} \exp \left[-\frac{(2N\beta)^2}{8N\alpha} \right] \quad (\text{D.73})$$

$$\mathbb{Z}_{\text{Ad}} = \prod_{\ell=1}^n \mathbb{Z}_\ell \quad (\text{D.74})$$

we notice that:

1. \mathbb{Z}_{Ep} is a Gaussian function only of α, β and $i\omega$,
2. \mathbb{Z}_{Ad} is a function only of σ, μ and $i\omega$,
3. \mathbb{Z} is the convolution (in the variable $2N\beta$) of the ‘extensive’ single loci partition functions (without epistasis) (\mathbb{Z}_{Ad}), and the Gaussian distribution which induces the epistatic coupling (\mathbb{Z}_{Ep}).

Partitioning into the two terms, and expressing \mathbb{Z} as a convolution simplifies the calculations and the notation. The convolution is defined as:

$$\llbracket F_{1(x)} * F_{2(x)} \rrbracket_{(x)} := \int_{-\infty}^{\infty} F_{1(\omega)} F_{2(x-\omega)} d\omega .$$

Thus we can write the partition function as

$$\mathbb{Z} = \llbracket \mathbb{Z}_{\text{Ad}} * \mathbb{Z}_{\text{Ep}} \rrbracket_{(2N\beta)} , \quad (\text{D.75})$$

form equivalent to Eq. D.72, but in convolution notation. The convolution brackets are ‘permeable’ to the derivatives with respect to any of the parameters. Thus the statistical mechanical methods of calculating the observables from the partition function apply.

Genetic mutational variability

- Definition

$$U = 2 \sum_{\ell=1}^n \log[p_{\ell}(1 - p_{\ell})] \quad (\text{D.76})$$

- Expectancy

$$\langle U \rangle_{\ell} = \frac{\partial \log(\mathbb{Z})}{2N \partial \mu} \quad (\text{D.77})$$

$$= \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \langle U \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right] \right]_{(2N\beta)} \quad (\text{D.78})$$

$$(\text{D.79})$$

Squared mutational genetic variability

$$\langle U^2 \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \langle U^2 \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right] \right]_{(2N\beta)} \quad (\text{D.80})$$

‘Genetic variance’ of mutational variability

- Definition

$$H = 2 \sum_{\ell=1}^n ([p_{\ell}(1 - p_{\ell})]^{-1} - 2) \quad (\text{D.81})$$

- Expectancy

$$\langle H \rangle = -4n + 2 \frac{\mathbb{Z}_{(N\mu=N\mu-1/4)}}{\mathbb{Z}} \quad (\text{D.82})$$

$$= \mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \langle H \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} \quad (\text{D.83})$$

Mean trait

- Definition

$$\bar{z} = \sum_{\ell=1}^n \gamma_{\ell} (2p_{\ell} - 1) \quad (\text{D.84})$$

- Expectancy

$$\langle z \rangle = \frac{\partial \log(\mathbb{Z})}{2N\partial\beta} \quad (\text{D.85})$$

$$= \mathbb{Z}^{-1} \left[\mathbb{Z}_{\text{Ad}} * \left(\frac{-2N\beta}{4N\alpha} \mathbb{Z}_{\text{Ep}} \right) \right]_{(2N\beta)}$$

Squared mean trait

- Expectancy

$$\langle \bar{z}^2 \rangle = \frac{\partial \log(\mathbb{Z})}{2N\partial\alpha} \quad (\text{D.86})$$

$$= \mathbb{Z}^{-1} \left[\mathbb{Z}_{\text{Ad}} * \left(\mathbb{Z}_{\text{Ep}} \frac{2N\beta - 16N\alpha}{(8N\alpha)^2} \right) \right]_{(2N\beta)} \quad (\text{D.87})$$

Cubic mean trait

- Expectancy

$$\langle \bar{z}^3 \rangle = \mathbb{Z}^{-1} \left[\mathbb{Z}_{\text{Ad}} * \left(\frac{8N\alpha + 2N\beta(16N\alpha - 8N\beta)}{(8N\alpha)^3} \mathbb{Z}_{\text{Ep}} \right) \right]_{(2N\beta)} \quad (\text{D.88})$$

Quartic mean trait

- Expectancy

$$\langle \bar{z}^4 \rangle = \mathbb{Z}^{-1} \left[\mathbb{Z}_{\text{Ad}} * \left(\frac{(2N\beta - 16N\alpha)^2 + 2(16N\alpha)^2 - 128N\alpha N\beta}{(8N\alpha)^4} \mathbb{Z}_{\text{Ep}} \right) \right]_{(2N\beta)} \quad (\text{D.89})$$

Genetic variance

- Definition

$$\nu_z = 2 \sum_{\ell=1}^n \gamma_{\ell} p_{\ell} (1 - p_{\ell}) \quad (\text{D.90})$$

- Expectancy

$$\langle \nu_z \rangle = 2 \frac{\mathbb{Z}_{(N\mu=N\mu+1/4)}}{\mathbb{Z}} \quad (\text{D.91})$$

$$= \mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^2 \langle \nu_z \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} \quad (\text{D.92})$$

Squared genetic variance

- Expectancy

$$\langle \nu_z^2 \rangle = \mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^4 \langle \nu_z^2 \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} \quad (\text{D.93})$$

Third moment of allele frequencies

- Definition

$$m_{3z} = \sum_{\ell=1}^n \gamma_{\ell}^3 2(1 - 2p_{\ell})(1 - p_{\ell})p_{\ell} \quad (\text{D.94})$$

- Expectancy

$$m_{3z} = -\mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^3 \langle \bar{z} \nu \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} \quad (\text{D.95})$$

Fourth moment of allele frequencies

- Definition

$$m_{4z} = 2 \sum_{\ell=1}^n \gamma_{\ell}^4 (2p_{\ell} - 1)^2 (1 - p_{\ell}) p_{\ell} \quad (\text{D.96})$$

- Expectancy

$$\langle \bar{z}^2 \nu_z \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^4 \langle \bar{z}^2 \nu \rangle_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right] \right]_{(2N\beta)} \quad (\text{D.97})$$

Crossed moment: mean trait and mutational genetic variability

$$\langle \bar{z} U \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n U_{\gamma_{\ell}} \right) * \left(\frac{-2N\beta}{4N\alpha} \mathbb{Z}_{\text{Ep}} \right) \right] \right]_{(2N\beta)} \quad (\text{D.98})$$

Crossed moment: squared mean trait and mutational genetic variability

$$\langle \bar{z}^2 U \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \langle U \rangle_{\gamma_{\ell}} \right) * \left(\frac{2N\beta - 16N\alpha}{(8N\alpha)^2} \mathbb{Z}_{\text{Ep}} \right) \right] \right]_{(2N\beta)} \quad (\text{D.99})$$

Crossed moment: mean trait and genetic variance

$$\langle \bar{z} \nu_z \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^2 \langle \nu_z \rangle_{\gamma_{\ell}} \right) * \left(\frac{-2N\beta}{4N\alpha} \mathbb{Z}_{\text{Ep}} \right) \right] \right]_{(2N\beta)} \quad (\text{D.100})$$

Crossed moment: squared mean trait and genetic variance

$$\langle \bar{z}^2 \nu_z \rangle = \mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^2 \langle \nu_z \rangle_{\gamma_{\ell}} \right) * \left(\frac{2N\beta - 16N\alpha}{(8N\alpha)^2} \mathbb{Z}_{\text{Ep}} \right) \right] \right]_{(2N\beta)} \quad (\text{D.101})$$

Crossed moment: mean trait and third moment of allele frequencies

$$\langle \bar{z} m_{3z} \rangle = -\mathbb{Z}^{-1} \left[\left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^3 \langle \bar{z} \nu \rangle_{\gamma_{\ell}} \right) * \left(\frac{-2N\beta}{4N\alpha} \mathbb{Z}_{\text{Ep}} \right) \right] \right]_{(2N\beta)} \quad (\text{D.102})$$

Covariances of A_j A_k (not including the traits)

$$\text{cov}(A_j, A_k) = \mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^2 \langle A_j \rangle_{\gamma_{\ell}} \langle A_k \rangle_{\gamma_{\ell}} + \text{cov}(A_j, A_k)_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} - \langle A_j \rangle \langle A_k \rangle \quad (\text{D.103})$$

Variances of A_j (not including powers of the traits)

From the previous identity, it follows that

$$\text{var}(A_j) = \mathbb{Z}^{-1} \left[\left(\mathbb{Z}_{\text{Ad}} \sum_{\ell}^n \gamma_{\ell}^2 \langle A_j \rangle_{\gamma_{\ell}}^2 + \text{var}(A_j)_{\gamma_{\ell}} \right) * \mathbb{Z}_{\text{Ep}} \right]_{(2N\beta)} - \langle A_j \rangle^2. \quad (\text{D.104})$$